**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)}

SLFEQLGGQAAVQAVTAQFYANIQADATVATFFNGIDMPNQTNKTAAFLCAALGGPNAWTGRNLKEVHANMGVSNAQFTTVIGHLRSALTGAGVAAALVEQTVAVAETVRGDVVTV

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

SLFAKLGGREAVEAAVDKFYNKIVADPTVSTYFSNTDMKVQRSKQFAFLAYALGGASEWKGKDMRTAHKDLVPHLSDVHFQAVARHLSDTLTELGVPPEDITDAMAVVASTRTEVLNMPQQ

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

GLLSRLRKREPISIYDKIGGHEAIEVVVEDFYVRVLADDQLSAFFSGTNMSRLKGKQVEFFAAALGGPEPYTGAPMKQVHQGRGITMHHFSLVAGHLADALTAAGVPSETITEILGVIAPLAVDVTS

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

KVAELANAVVSNADQKDLLRMSWGVLSVDMEGTGLMLMANLFKTSPSAKGKFARLGDVSAGKDNSKLRGHSITLMYALQNFVDALDDVERLKCVVEKFAVNHINRQISADEFGEIVGPLRQTLKARMGNYFDEDTVAAWASLVAVVQASL

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

SLSAAQKDNVKSSWAKASAAWGTAGPEFFMALFDAHDDVFAKFSGLFSGAAKGTVKNTPEMAAQAQSFKGLVSNWVDNLDNAGALEGQCKTFAANHKARGISAGQLEAAFKVLAGFMKSYGGDEGAWTAVAGALMGMIRPDM

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

TLTKHEQDILLKELGPHVDTPAHIVETGLGAYHALFTAHPQYISHFSRLEGHTIENVMQSEGIKHYARTLTEAIVHMLKEISNDAEVKKIAAQYGKDHTSRKVTKDEFMSGEPIFTKYFQNLVKDAEGKAAVEKFLKHVFPMMAAEI

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

GLSAAQRQVVASTWKDIAGSDNGAGVGKECFTKFLSAHHDMAAVFGFSGASDPGVADLGAKVLAQIGVAVSHLGDEGKMVAEMKAVGVRHKGYGNKHIKAEYFEPLGASLLSAMEHRIGGKMNAAAKDAWAAAYADISGALISGLQS

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

SLSAAEADLAGKSWAPVFANKNANGLDFLVALFEKFPDSANFFADFKGKSVADIKASPKLRDVSSRIFTRLNEFVNNAANAGKMSAMLSQFAKEHVGFGVGSAQFENVRSMFPGFVASVAAPPAGADAAWTKLFGLIIDALKAAGA

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

GLSDGEWHLVLNVWGKVETDLAGHGQEVLIRLFKSHPETLEKFDKFKHLKSEDDMRRSEDLRKHGNTVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSKHPAEFGADAQAAMKKALELFRNDIAAKYKELGFHG

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

LSADQISTVQASFDKVKGDPVGILYAVFKADPSIMAKFTQFAGKDLESIKGTAPFETHANRIVGFFSKIIGELPNIEADVNTFVASHKPRGVTHDQLNNFRAGFVSYMKAHTDFAGAEAAWGATLDTFFGMIFSKM

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

ALVEDNNAVAVSFSEEQEALVLKSWAILKKDSANIALRFFLKIFEVAPSASQMFSFLRNSDVPLEKNPKLKTHAMSVFVMTCEAAAQLRKAGKVTVRDTTLKRLGATHLKYGVGDAHFEVVKFALLDTIKEEVPADMWSPAMKSAWSEAYDHLVAAIKQEMKPAE

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

VLSSQNKKAIEELGNLIKANAEAWGADALARLFELHPQTKTYFSKFSGFEACNEQVKKHGKRVMNALADATHHLDNLHLHLEDLARKHGENLLVDPHNFHLFADCIVVTLAVNLQAFTPVTHCAVDKFLELVAYELSSCYR

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

SLSATDKARVKALWDKIEGKSAELGAEALGRMLVSFPQTKIYFSEWGQDLGPQTPQVRNHGAVIMAAVGKAVKSIDNLVGGLSQLSELHAFKLRVDPANFKILAHNIILVISMYFPGDFTPEVHLSVDKFLACLALALSEKYR

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

VKLSEDQEHYIKGVWKDVDHKQITAKALERVFVVYPWTTRLFSKLQGLFSANDIGVQQHADKVQRALGEAIDDLKKVEINFQNLSGKHQEIGVDTQNFKLLGQTFMVELALHYKKTFRPKEHAAAYKFFRLVAEALSSNYH

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

VDWTDAERAAIKALWGKIDVGEIGPQALSRLLIVYPWTQRHFKGFGNISTNAAILGNAKVAEHGKTVMGGLDRAVQNMDNIKNVYKQLSIKHSEKIHVDPDNFRLLGEIITMCVGAKFGPSAFTPEIHEAWQKFLAVVVSALGRQYH

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

VHWTQEERDEISKTFQGTDMKTVVTQALDRMFKVYPWTNRYFQKRTDFRSSIHAGIVVGALQDAVKHMDDVKTLFKDLSKKHADDLHVDPGSFHLLTDCIIVELAYLRKDCFTPHIQGIWDKFFEVVIDAISKQYH

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

PIVDTGSVAPLSAAEKTKIRSAWAPVYSTYETSGVDILVKFFTSTPAAQEFFPKFKGLTTADELKKSADVRWHAERIINAVDDAVASMDDTEKMSMKLRNLSGKHAKSFQVDPEYFKVLAAVIADTVAAGDAGFEKLMSMICILLRSAY

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

ANKTRELCMKSLEHAKVDTSNEARQDGIDLYKHMFENYPPLRKYFKSREEYTAEDVQNDPFFAKQGQKILLACHVLCATYDDRETFNAYTRELLDRHARDHVHMPPEVWTDFWKLFEEYLGKKTTLDEPTKQAWHEIGREFAKEINK

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

GLTAAQIKAIQDHWFLNIKGCLQAAADSIFFKYLTAYPGDLAFFHKFSSVPLYGLRSNPAYKAQTLTVINYLDKVVDALGGNAGALMKAKVPSHDAMGITPKHFGQLLKLVGGVFQEEFSADPTTVAAWGDAAGVLVAAMK

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

GATQSFQSVGDLTPAEKDLIRSTWDQLMTHRTGFVADVFIRIFHNDPTAQRKFPQMAGLSPAELRTSRQMHAHAIRVSALMTTYIDEMDTEVLPELLATLTRTHDKNHVGKKNYDLFGKVLMEAIKAELGVGFTKQVHDAWAKTFAIVQGVLITKHAS

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

MLTQKTKDIVKATAPVLAEHGYDIIKCFYQRMFEAHPELKNVFNMAHQEQGQQQQALARAVYAYAENIEDPNSLMAVLKNIANKHASLGVKPEQYPIVGEHLLAAIKEVLGNAATDDIISAWAQAYGNLADVLMGMESELYERSAEQPGG

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

GFKQDIATIRGDLRTYAQDIFLAFLNKYPDERRYFKNYVGKSDQELKSMAKFGDHTEKVFNLMMEVADRATDCVPLASDANTLVQMKQHSSLTTGNFEKLFVALVEYMRASGQSFDSQSWDRFGKNLVSALSSAGMK

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

MKTPLTEAIAAADSQGRFLSNTELQVVNGRYNRATSSLEAAKALTANADRLISGAANAVYSKFPYTTQMPGPNYSSTAIGKAKCARDIGYYLRMVTYCLVVGGTGPMDDYLVAGLEEINRTFELSPSWYIEALKYIKNNHGLSGDVANEANTYIDYAINTLS

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

SIVTKSIVNADAEARYLSPGELDRIKSFVTSGERRVRIAETMTGARERIIKQAGDQLFGKRPDVVSPGGNAYGADMTATCLRDLDYYLRLITYGIVAGDVTPIEEIGVVGVREMYKSLGTPIEAIAEGVRAMKSVATSLLSGADAAEAGSYFDYLIGAMS

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

MQDAITAVINSSDVQGKYLDTAALEKLKSYFSTGELRVRAATTIAANAAAIVKEAVAKSLLYSDITRPGGNMYTTRRYAACIRDLDYYLRYATYAMLAGDPSILDERVLNGLKETYNSLGVPISATVQAIQAMKEVTASLVGPDAGKEMGVYFDYICSGLS

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

MKSVITTTISAADAAGRYPSTSDLQSVQGNIQRAAARLEAAEKLGSNHEAVVKEAGDACFSKYGYNKNPGEAGENQEKINKCYRDIDHYMRLINYTLVVGGTGPLDEWGIAGAREVYRTLNLPSAAYIAAFVFTRDRLCIPRDMSAQAGVEFCTALDYLINSLS

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

MLDAFSRVVVNSDSKAAYVSGSDLQALKTFINDGNKRLDAVNYIVSNSSCIVSDAISGMICENPGLITPGGNCYTNRRMAACLRDGEIILRYVSYALLAGDASVLEDRCLNGLKETYIALGVPTNSTVRAVSIMKAAAVCFISNTASQRKVEVIEGDCSALASEVASYCDRVVAAVS

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

MTHFIESLEAIKPYIIGNSRTADQGTNIQTPAQMAKYHQFSGCINCGLCYAACPQFGLNPEFIGPAAITLAHRYNEDSRDHGKKERMAQLNSQNGVWSCTFVGYCSEVCPKHVDPAAAIQQGKVESSKDFLIATLKPR

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

TGNWFNGMSQRVESWIHAQKEHDISKLEERIEPEVAQEVFELDRCIECGCCIAACGTKIMREDFVGAAGLNRVVRFMIDPHDERTDEDYYELIGDDDGVFGCMTLLACHDVCPKNLPLQSKIAYLRRKMVSVN

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

MDYFTLFGLPARYQLDTQALSLRFQDLQRQYHPDKFASGSQAEQLAAVQQSATINQAWQTLRHPLMRAEYLLSLHG

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

MGKDYYQTLGLARGASDEEIKRAYRRQALRYHPDKNKEPGAEEKFKEIAEAYDVLSDPRKREIFDRYGEEGLKGSGC

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

MDRVLSRADKERLLELLKLPRQLWGDFGRMQQAYKQQSLLLHPDKGGSHALMQELNSLWGTFKTEVYNLRMNLGGTGFQ

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

SHMREESLQLMDLLGLERSAWGNIPLMRKAYLKKCKEFHPDKGGDEEKMKKMNTLYKKMEDGVKYAHQPDFGGFWDATEIPTYGTDEWEQWWNAFNEENLFCSEEMPSSDDEAT

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

AALAEIVAQLNIYQSQVELIQQQMEAVRATISELEILEKTLSDIQGKDGSETLVPVGAGSFIKAELKDTSEVIMSVGAGVAIKKNFEDAMESIKSQKNELESTLQKMGENLRAITDIMMKLSPQAEELLAAVA

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

QNVQHQLAQFQQLQQQAQAISVQKQTVEMQINETQKALEELSRAADDAEVYKSSGNILIRVAKDELTEELQEKLETLQLREKTIERQEERVMKKLQEMQVNIQEAMK

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

QDLDEARAMEAKRKAEEHISSSHGDVDYAQASAELAKAIAQLRVIELTKK

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

DMLDLGAAKANLEKAQSELLGAADEATRAEIQIRIEANEALVKAL

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

VHKLEPKDHLKPQNLEGISNEQIEPHFEAHYKGYVAKYNEIQEKLADQNFADRSKANQNYSEYRELKVEETFNYMGVVLHELYFGMLTP

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

VIQLKRYEFPQLPYKVDALEPYISKDIIDVHYNGHHKGYVNGANSLLDRLEKLIKGDLPQGQYDLQGILRGLTFNINGHKLHAIYWNNMA

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

PYPFKLPDLGYPYEALEPHIDAKTMEIHHQKHHGAYVTNLNAALEKYPYLHGVEVEVLLRHLAALPQDIQTAVRNNGGGHLNHSLFWRLLTP

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

MTHELISLPYAVDALAPVISKETVEFHHGKHLKTYVDNLNKLIIGTEFENADLNTIVQKSEGGIFNNAGQTLNHNLYFTQFRPG

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

PEFLEDPSVLTKDKLKSELVANNVTLPAGEQRKDVYVQLYLQHLTARNRPPLPAGT

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

RQEDKDDLDVTELTNEDLLDQLVKYGVNPGPIVGTTRKLYEKKLLKLREQGTESRSS

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

VDAEAVVQQKCISCHGGDLTGASAPAIDKAGANYSEEEILDIILNGQGGMPGGIAKGAEAEAVAAWLAEKK

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

EADLALGKAVFDGNCAACHAGGGNNVIPDHTLQKAAIEQFLDGGFNIEAIVYQIENGKGAMPAWDGRLDEDEIAGVAAYVYDQAAGNKW

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

ADGAALYKSCVGCHGADGSKQAMGVGHAVKGQKADELFKKLKGYADGSYGGEKKAVMTNLVKRYSDEEMKAMADYMSKL

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

QADGAKIYAQCAGCHQQNGQGIPGAFPPLAGHVAEILAKEGGREYLILVLLYGLQGQIEVKGMKYNGVMSSFAQLKDEEIAAVLNHIATAWGDAKKVKGFKPFTAEEVKKLRAKKLTPQQVLAERKKLGLK

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

VELTESTRTIPLDEAGGTTTLTARQFTNGQKIFVDTCTQCHLQGKTKTNNNVSLGLADLAGAEPRRDNVLALVEFLKNPKSYDGEDDYSELHPNISRPDIYPEMRNYTEDDIFDVAGYTLIAPKLDERWGGTIYF

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

AKESTGFKPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTDAIINKNVKWDEDSMSEYLTNPKKYIPGTKMAFAGLKKEKDRNDLITYMTKAAK

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

EDAKAGEAVFKQCMTCHRADKNMVGPALAGVVGRKAGTAAGFTYSPLNHNSGEAGLVWTADNIVPYLADPNAFLKKFLTEKGKADQAVGVTKMTFKLANEQQRKDVVAYLATLK

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

NEGDAAKGEKEFNKCKACHMIQAPDGTDIKGGKTGPNLYGVVGRKIASEEGFKYGEGILEVAEKNPDLTWTEANLIEYVTDPKPLVKKMTDDKGAKTKMTFKMGKNQADVVAFLAQDDPDAXXXXXXXXXXXXX

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

GGGARSGDDVVAKYCNACHGTGLLNAPKVGDSAAWKTRADAKGGLDGLLAQSLSGLNAMPPKGTCADCSDDELKAAIGKMSGL

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

QDGEALFKSKPCAACHSVDTKMVGPALKEVAAKNAGVEGAADTLALHIKNGSQGVWGPIPMPPNPVTEEEAKILAEWVLSLK

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

APQFFNIIDGSPLNFDDAMEEGRDTEAVKHFLETGENVYNEDPEILPEAEELYAGMCSGCHGHYAEGKIGPGLNDAYWTYPGNETDVGLFSTLYGGATGQMGPMWGSLTLDEMLRTMAWVRHLYTGDPKDASWLTDEQKAGFTPFQP

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

DGESIYINGTAPTCSSCHDRGVAGAPELNAPEDWADRPSSVDELVESTLAGKGAMPAYDGRADREDLVKAIEYMLSTL

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

YDAAAGKATYDASCAMCHKTGMMGAPKVGDKAAWAPHIAKGMNVMVANSIKGYKGTKGMMPAKGGNPKLTDAQVGNAVAYMVGQSK

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

GDTSPAQLIAGYEAAAGAPADAERGRALFLSTQTGGKPDTPSCTTCHGADVTRAGQTRTGKEIAPLAPSATPDRFTDSARVEKWLGRNCNSVIGRDCTPGEKADLLAWLAAQ

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

DVTNAEKLVYKYTNIAHSANPMYEAPSITDGKIFFNRKFKTPSGKEAACASCHTNNPANVGKNIVTGKEIPPLAPRVNTKRFTDIDKVEDEFTKHCNDILGADCSPSEKANFIAYLLTETKPTK

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

SQWGSGKNLYDKVCGHCHKPEVGVGPVLEGRGLPEAYIKDIVRNGFRAMPAFPASYVDDESLTQVAEYLSSLPA

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

AGDAEAGQGKVAVCGACHGVDGNSPAPNFPKLAGQGERYLLKQLQDIKAGSTPGAPEGVGRKVLEMTGMLDPLSDQDLEDIAAYFSSQKGSV

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

GYADPALAKQGEKLFRGGKLDQGMPACTGCHAPNGVGNDLAGFPKLGGQHAAYTAKQLTDFREGNRTNDGDTMIMRGVAAKLSNKDIEALSSYIQGLH

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

EPTAEMLTNNCAGCHGTHGNSVGPASPSIAQMDPMVFVEVMEGFKSGEIASTIMGRIAKGYSTADFEKMAGYFKQQTYQP

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

AKQSFDTALADTGAKLHDKYCEKCHVEGGKPLADEEDYHILAGQWTPYLQYAMSDFREERRPMEKKMASKLRELLKAEGDAGLDALFAFYASQQ

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

DALHDQASALFKPIPEQVTELRGQPISEQQRELGKKLFFDPRLSRSHVLSCNTCHNVGTGGADNVPTSVGHGWQKGPRNSPTVFNAVFNAAQFWDGRAKDLGEQAKGPIQNSVEMHSTPQLVEQTLGSIPEYVDAFRKAFPKAGKPVSFDNMALAIEAYEATLV

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

TPDSPFDLYLKGDDKALDAQQKKGLKAFMDSGCSACHNGINLGGQAYFPFGLVKKPDASVLPSGDKGRFAVTKTQSDEYVFRAAPLRNVALTAPYFHSGQVWELKDAVAIMGNAQLGKQLAPDDVENIVAFLHSLSGKQPRVEYPLLPASTETTPRPAE

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

VTGEEVLQNACAACHVQHEDGRWERIDAARKTPEGWDMTVTRMMRNHGVALEPEERAAIVRHLSDTRGLSLAETEERRYILEREP

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

VAWDEGPDTSMTQTCGRCHSYARVALQRRTPEDWKHLVNFHLGQFPTLEYQALARDRDWWGIAQAEIIPFLARTYPLGEA

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

EQGPSLLQNKCMGCHIPEGNDTYSRISHQRKTPEGWLMSIARMQVMHGLQISDDDRRTLVKYLADKQGLAPSETDGVRYAMERR

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

TKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKTITIAPELADLLSGEPL

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

MARIDPTKKGRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEVRVYNWFANRRKEEAFRHKLAMDTYKLN

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

METLVQARKRKRTSIENRVRWSLETMFLKCPKPSLQQITHIANQLGLEKDVVRVWFCNRRQKGKRSS

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

ARTFDWMKVKRNPPKTAKVSEPGLGSPSGLRTNFTTRQLTELEKEFHFNKYLSRARRVEIAATLELNETQVKIWFQNRRMKQKKRERE

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

RKRRNFNKQATEILNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKNIGKFQEEANIYAA

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

MKTTRVRTVLNEKQLHTLRTCYAANPRPDALMKEQLVEMTGLSPRVIRVWFQNKRCKDKKRSIMMK

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

ASDGLPNKKRKRRVLFTKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKTKRAQNEKGYEGHP

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

KQRRSRTTFSASQLDELERAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRKQHTSVS

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

GRPRAINKHEQEQISRLLEKGHPRQQLAIIFGIGVSTLYRYFPASSIKKRMN

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

GRKRKIDRDAVLNMWQQGLGASHISKTMNIARSTVYKVINESN

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

PRGSALSDTERAQLDVMKLLNVSLHEMSRKISRSRHCIRVYLKDPVSYGTS

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

MIARPTLEAHDYDREALWSKWDNASDSQRRLAEKWLPAVQAADEMLNQGISTKTAFATVAGHYQVSASTLRDKYYQVQKFAKPDWAAALVDGRGASRRN

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

MNVHKSEFDEDAWQFLIADYLRPEKPAFRKCYERLELAAREHGWSIPSRATAFRRIQQLDEAMVVACREGEHALM

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

EVKKSSWTEEEDRIIFEAHKVLGNRWAEIAKLLPGRTDNAVKNHWNSTIKRKVDT

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

NPELNKGPWTKEEDQRVIEHVQKYGPKRWSDIAKHLKGRIGKQCRERWHNHLNPEVK

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

GRIAFTDADDVAILTYVKENARSPSSVTGNALWKAMEKSSLTQHSWQSLKDRYLKHLRG

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

KASFTDEEDEFILDVVRKNPTRRTTHTLYDEISHYVPNHTGNSIRHRFRVYLSKRLEYVYEVDKFGKLVRDDDGNLIKTKVLPPSI

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

KRKFSADEDYTLAIAVKKQFYRDLFQIDPDTGRSLITDEDTPTAIARRNMTMDPNHVPGSEPNFAAYRTQSRRGPIAREFFKHFAEEHAAHTENAWRDRFRKFLLAYGIDDYISYYEAEKAQNREPEPMKNLTNRPKRPGVPTPGNYNS

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

MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCR

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

KTNKLSPYDKLEGLLIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASNGWLDRFRRRRS

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

DAITIHSILDWIEDNLESPLSLEKVSERSGYSKWHLQRMFKKETGHSLGQYIRS

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

RKMTEIAQKLKESNEPILYLAERYGFESQQTLTRTFKNYFDVPPHKYRMTNMQGESRFLHPL

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

RRLSKSAVALRLTARPILDIALQYRFDSQQTFTRAFKKQFAQTPALYRRSPEWSAFGIRPPLRLG

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

SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAVEILARHHDYS

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

NLKDKILGVAKELFIKNGYNATTTGEIVKLSESSKGNLYYHFKTKENLFLEILNIEESKWQEQWKKEQIKA

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

MRSSAKQEELVKAFKALLKEEKFSSQGEIVAALQEQGFDNINQSKVSRMLTKFGAVRTRNAKMEMVYCLPAELGVPTT

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

KGQRHIKIREIITSNEIETQDELVDMLKQDGYKVTQATVSRDIKELHLVKVPTNNGSYKYSLPADQRFNPLSKLKR

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

DVTGRIAQTLLNLAKQPDAMTHPDGMQIKITRQEIGQIVGCSRETVGRILKMLEDQNLISAHGKTIVVYGT

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

DIKQRIAGFFIDHANTTGRQTQGGVIVSVDFTVEEIANLIGSSRQTTSTALNSLIKEGYISRQGRGHYTIPNLVRLKAAA

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

LFNEIIPLGRLIHMVNQKKDRLLNEYLSPLDITAAQFKVLCSIRCAACITPVELKKVLSVDLGALTRMLDRLVCKGWVERLPNPNDKRGVLVKLTTGGAAICEQCHQLVGQDLHQELTKNLTADEVATLEYLLKKVLP

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

MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN

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

AITKINDCFELLSMVTYADKLKSLIKKEFSISFEEFAVLTYISENKEKEYYLKDIINHLNYKQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRIT

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

SPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHDGICEIHVAKYAEIFGLTSAEASKDIRQALKSFAGKEVVFYRPEEDAGDEKGYESFPWFIKPAHSPSRGLYSVHINPYLIPFFIGLQ

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

NRFTQFRLSETKEITNPYAMRLYESLCQYRKPDGSGIVSLKIDWIIERYQLPQSYQRMPDFRRRFLQVCVNEINSRTPMRLSYIEKKKGRQTTHIVFSFRDIT

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

LGLEKRDREILEVLILRFGGGPVGLATLATALSEDPGTLEEVHEPYLIRQGLLKRTPRGRVPTELAYRHLGYPPPV

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

ISEEVLIGLPLHEKLFLLAIVRSLKISHTPYITFGDAEESYKIVCEEYGERPRVHSQLWSYLNDLREKGIVETRQNKRGEGVRGRTTLISIGTEPLDTLEAVITKLIKEELR

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

VPKRVYWEMLATNLTDKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGFDEVIETIENDIKGLINTGIFIEIKGRFYQLKDHILQFVIPNRGVTKQLV

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

IRTFGWVQNPGKFENLKRVVQVFDRNSKVHNEVKNIKIPTLVKESKIQKELVAIMNQHDLIYTYKELVGTGTSIRSEAPCDAIIQATIADQGNKKGYIDNWSSDGFLRWAHALGFIEYINKSDSFVITDVGLAYSKSAD

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

GSAIEKEILIEAISSYPPAIRILTLLEDGQHLTKFDLGKNLGFSGESGFTSLPEGILLDTLANAMPKDKGEIRNNWEGSSDKYARMIGGWLDKLGLVKQGKKEFIIPTLGKPDNKEFISHAFKITGEGLKVLRRAKGSTKFTR

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

QTEDSACLSAMVLTTNLVYPAVLNAAIDLNLFEIIAKATPPGAFMSPSEIASKLPASTQHSDLPNRLDRMLRLLASYSVLTSTTRTIEDGGAERVYGLSMVGKYLVPDES

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

RKPSEIFKAQALLYKHIYAFIDSMSLKWAVEMNIPNIIQNHGKPISLSNLVSILQVPSSKIGNVRRLMRYLAHNGFFEIITKEEESYALTVASELLVRGSD

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

SRRNAWGNQSYAELISQAIESAPEKRLTLAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKVHNEATGKSSWWMLNPEGG

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

VKPPYSYIALITMAILQSPQKKLTLSGICEFISNRFPYYREKFPAWQNSIRHNLSLNDCFVKIPREPGNPGKGNYWTLDPQSEDMFDNGSFLRRRKR

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

SRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWK

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

GKGLRHFSMKVCEKVQRKGTTSYNEVADELVSEFTNSNNHLAADSAYDQKNIRRRVYDALNVLMAMNIISKEKKEIKWIGLP

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

LSSHFQELSIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLQKEAGTPPLWKIAVSD

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

NLEQKILQVLSDDGGPVKIGQLVKKCQVPKKTLNQVLYRLKKEDRVSSPEPATWSIG

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

GQVIEVPPTLIYMYVRDVPVRVAQARFLLAKIKREYGTLPFAYRWLQNDMPEGQLKLALKTLEKAGAIYGYPVLKEI

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

HDDMECSHYMKNFDVGHVPIRLPRTKHLLNVINENFGTLAFCRRWLDRLGESKYLMALKNLCDLGIVDPYPPLC

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

VIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLARGREYSAMERSIDVQISRLRRMVEEDPAHPRYIQTVWGLGYVFVPD

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

SKSTKLVCGDLILDTATKKAYRGSKEIDLTKKEYQILEYLVMNKNRVVTKEELQEHLWSFDDEVFSDVLRSHIKNLRKKVDKGFKKKIIHTVRGIGYVARDE

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

MAVEEVIEMQGLSLDPTSHRVMAGEEPLEMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYVEDRTVDVHIRRLRKALEPGGHDRMVQTVRGTGYRFSTRF

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

SKPLLTKREREVFELLVQDKTTKEIASELFISEKTVRNHISNAMQKLGVKGRSQAVVELLRMGELEL

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

ERDVNQLTPRERDILKLIAQGLPNKMIARRLDITESTVKVHVKHMLKKMKLKSRVEAAVWVHQERIF

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

MRVPFSWLKAYVPELESPEVLEERLAGLGFETDRIERVXEEVVLDLEVTPNRPDALGLLGLARDLHALGYALVEPEAA

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

PPEAIPFRPEYANRLLGTSYPEAEQIAILKRLGCRVEGEGPTYRVTPPSHRLDLRLEEDLVEEVARIQGYETIPL

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

ESYYSIGEVSKLANVSIKALRYYDKIDLFKPAYVDPDTSYRYYTDSQLIHLDLIKSLKYIGTPLEEMKKAQDLEMEELFAFYTEQERQIREKLDFLSALEQTISLVKKRMKRQMEYPA

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

KYQVKQVAEISGVSIRTLHHYDNIELLNPSALTDAGYRLYSDADLERLQQILFFKEIGFRLDEIKEMLDHPNFDRKAALQSQKEILMKKKQRMDEMIQTIDRTLLS

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

QNLDLQLYMRDCELAESWMSAREAFLNADDDANAGGNVEALIKKHEDFDKAINGHEQKIAALQTVADQLIAQNHYASNLVDEKRKQVLERWRHLKEGLIEKRSRLGD

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

MVHQFFRDMDDEESWIKEKKLLVSSEDYGRDLTGVQNLRKKHKRLEAELAAHEPAIQSVLDTGKKLSDDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQRLEESLEYQ

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

QFVANVEEEEAWINEKMTLVASEDYGDTLAAIQGLLKKHEAFETDFTVHKDRVNDVCANGEDLIKKNNHHVENITAKMKGLKGKVSDLEKAAAQRKAKLDENSA

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

SSAVNQENERLMEEYERLASELLEWIRRTIPWLENRTPEKTMQAMQKKLEDFRDYRRKHKPPKVQEKCQLEINFNTLQTKLRISNRPAFMPSEGKMVSDIAGAWQRLEQAEKGYEEWLLNEIRRL

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

HANERLRRQFAAQANAIGPWIQNKMEEIARSSIQITGALEDQMNQLKQYEHNIINYKNNIDKLEGDHQLIQEALVFDNKHTNYTMEHIRVGWELLLTTIARTINEVETQILTRD

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

GSSNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILLQKDYESASLTEVRALLRKHEAFESDLAAHQDRVEQIAAIAQELNELDYHDAVNVNDRCQKICDQWDRLGTLTQKRREALERMEKLL

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

ETIDQLHLEFAKRAAPFNNWMEGAMEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIMAIQNEVEKVIQSYNIRISSSNPYSTVTMDELRTKWDKVKQLVPIRDQSLQEELARQHAN

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

DESRVENPDERVVIQHNWHELRLFMWDYVGIVRTTKRLERALRRITMLQQEIDEYYAHFRVSNNLLELRNLVQVAELIVRCAMMRKESRGLHFTLDYPELLTHSGPSILSP

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

DGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKLAELQERFKRVRITDTSSVFNTDLLYTIELGHGLNVAECMAHSAMARKESRGAHQRLDEGCTERDDVNFLKHTLAFRDADGTTRLEYSDVKITTLPP

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

KGTEDVFKIKNRMKDVMDDNVGIFRDGPHLEKSVKELEELYKKSKNVGIKNKRLHANPELEEAYRVPMMLKVALCVAKGALDRTESRGAHNREDYPKRDDINWLNRTLASWPNPEQTLPTLEYEALDVNEMEIAPRYRGYGAKGNYIENPLSVKRQEEIDKIQSELEAAGKDRHAIQEALMPYELPAKYKARNERLGD

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

TADDVNPEYILPWQGLVRLQKIMDEYAAGIATIYKTNEKMLQRALELLAFLKEDLEKLAARDLHELMRAWELVHRVWTAEAHVRHMLFRKETRWPGYYYRTDYPELNDEEWKCFVCSKYDAEKDEWTFEKVPYVQVIEWSF

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

DACEQAAIQCVESACESLCTEGEDRTGCYMYIYSNCPPYV

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

DECANAAAQCSITLCNLYCGPLIEICELTVMQNCEPPFS

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

SQAEFDKAAEEVKHLKTKPADEEMLFIYSHYKQATVGDINTERPGMLDFKGKAKWDAWNELKGTSKEDAMKAYIDKVEELKKKYGI

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

HMAQQVFEEECVSFINGLPRTINNLPNELKLDLYKYYKQSTIGNCNIKEPSAHKYIDRKKYEEAWKSVENLNREDAQKKRYVDIVSEIFPYWQD

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

DVSEELIQDITQRLFFLQVKEGILNDDIYCPPETAVLLASYAVQSKYGDFNKEVHKSGYLAGDKLLPQRVLEQHKLNKDQWEERIQVWHEEHRGMLREDAVLEYLKIAQDL

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

PDPAQLTEDITRYYLCLQLRQDIVAGRLPCSFATLALLGSYTIQSELGDYDPELHGVDYVSDFKLAPNQTKELEEKVMELHKSYRSMTPAQADLEFLENAKKLSMY

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

HYVEPKFLNKAFEVALKVQIIAGFDRGLVKWLRVHGRTLSTVQKKALYFVNRRYMQTHWANYMLWINKKIDALGRTPVVGDYTRLGAEIGRRIDMAYFYDFLKDKNMIPKYLPYMEEINRMRPADVPVKYM

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

FDDVVVSRQEQSYVQRGMVNFLDEEMHKLVKRFRDMRWNLGPGFVFLLKKVNRERMMRYCMDYARYSKKILQLKHLPVNKKTLTKMGRFVGYRNYGVIRELYADVFRDVQGFRGPKMTAAMRKYSSKDPGTFPCKNE

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

GKGDPKKPRGKMSSYAFFVQTSREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGE

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

SDKPKRPLSAYMLWLNSARESIKRENPGIKVTEVAKRGGELWRAMKDKSEWEAKAAKAKDDYDRAVKEFEANG

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

MVTPREPKKRTTRKKKDPNAPKRALSAYMFFANENRDIVRSENPDITFGQVGKKLGEKWKALTPEEKQPYEAKAQADKKRYESEKELYNATLA

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

MQDRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMHREKYPNYKYRPRRKAKMLPK

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

MHIKKPLNAFMLYMKEMRANVVAESTLKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYGKKKKRKREK

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

MKKLKKHPDFPKKPLTPYFRFFMEKRAKYAKLHPEMSNLDLTKILSKKYKELPEKKKMKYIQDFQREKQEFERNLARFREDHPDLIQNAKK

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

SGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTDSHKA

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

VTKTQKKGDKKRKKSRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK

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

PRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

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

KGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVTYTEHAKRKTVTAMDVVYALKRQGRTLYGFGG

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

MELPIAPIGRIIKDAGAERVSDDARITLAKILEEMGRDIASEAIKLARHAGRKTIKAEDIELAVRRFK

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

ELPKAAIERIFRQGIGERRLSQDAKDTIYDFVPTMAEYVANAAKSVLDASGKKTLMEEHLKALADVLMVEGVEDYDGELFGRATVRRILKRAGIERASSDAVDLYNKLICRATEELGEKAAEYADEDGRKTVQGEDVEKAITYSMPKGGEL

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

PKDAQVIMSILKELNVQEYEPRVVNQLLEFTFRYVTSILDDAKVYANHARKKTIDLDDVRLATEVTLD

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

MLYGSSISAESMKVIAESIGVGSLSDDAAKELAEDVSIKLKRIVQDAAKFMNHAKRQKLSVRDIDMSLKV

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

LFSKELRCMMYGFGDDQNPYTESVDILEDLVIEFITEMTHKAMSI

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

FSEEQLNRYEMYRRSAFPKAAIKRLIQSITGTSVSQNVVIAMSGISKVFVGEVVEEALDVCEKWGEMPPLQPKHMREAVRRLKSKGQIP

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

ARFPPARIKKIMQTDEEIGKVAAAVPVIISRALELFLESLLKKACQVTQSRNAKTMTTSHLKQCIE

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

DDLTIPRAAINKMIKETLPNVRVANDARELVVNCCTEFIHLISSEANEICNKSEKKTISPEHVIQALESLGFGSYISEVKEVLQECKTVALKRRKASSRLENLGIPEEELLRQQQELFAKARQQQAELAQQEWLQ

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

QSKPEDLLKLRQGLMQTLKSQWVPIAGFAAGKADLPADAAQRAENMAMVAKLAPIGWAKGTEALPNGETKPEAFGSKSAEFLEGWKALATESTKLAAAAKAGPDALKAQAAATGKVCKACHEEFKQD

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

AGLSPEEQIETRQAGYEFMGWNMGKIKANLEGEYNAAQVEAAANVIAAIANSGMGALYGPGTDKNVGDVKTRVKPEFFQNMEDVGKIAREFVGAANTLAEVAATGEAEAVKTAFGDVGAACKSCHEKYRAK

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

QFQKPGDAIEYRQSAFTLIANHFGRVAAMAQGKAPFDAKVAAENIALVSTLSKLPLTAFGPGTDKGHGTEAKPAVWSDAAGFKAAADKFAAAVDKLDAAGKTGDFAQIKAAVGETGGACKGCHDKFKE

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

ADTKEVLEAREAYFKSLGGSMKAMTGVAKAFDAEAAKVEAAKLEKILATDVAPLFPAGTSSTDLPGQTEAKAAIWANMDDFGAKGKAMHEAGGAVIAAANAGDGAAFGAALQKLGGTCKACHDDYREED

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

QTDVIAQRKAILKQMGEATKPIAAMLKGEAKFDQAVVQKSLAAIADDSKKLPALFPADSKTGGDTAALPKIWEDKAKFDDLFAKLAAAATAAQGTIKDEASLKANIGGVLGNCKSCHDDFRAKKS

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

SYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWKPSPQVTVRFPDSDFKVYRYNAVLDPLVTALLGAFDTRNRIIEVENQANPTTAETLDATRRVDDATVAIRSAINNLIVELIRGTGSYNRSSFESSSGLVWTSGPAT

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

AYNPITPSKLIAFSASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSALPSSVVDINSRFPDAGFYAFLNGPVLRPIFVSLLSSTDTRNRVIEVVDPSNPTTAESLNAVKRTDDASTAARAEIDNLIESISKGFDVYDRASFEAAFSVVWSEATTSKA

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

KAHVLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKRGNMVRAARALLSAVTRLLILADMADVYKLLVQLKVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMAAKRQQELKDVGNRDQMAAARGILQKNVPILYTASQACLQHPDVAAYKANRDLIYKQLQQAVTGISNAAQA

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

DLRRQLRKAVMDHVSDSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACSISNNEEGVKLVRMSASQLEALCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDITS

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

IDDFLAVSENHILEDVNKCVIALQEKDVDGLDRTAGAIRGRAARVIHVVTSEMDNYEPGVYTEKVLEATKLLSNTVMPRFTEQVEAAVEALSSDPAQPMDENEFIDASRLVYDGIRDIRKAVLM

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

KDEEFPEQKAGEAINQPMMMAARQLHDEARKWSSKGNDIIAAAKRMALLMAEMSRLVRGGSGNKRALIQCAKDIAKASDEVTRLAKEVAKQCTDKRIRTNLLQVCERIPTISTQLKILSTVKATMLGRTNISDEESEQATEMLVHNAQNLMQSVKETVREAEAASIKIRTDAGFTLRWVRK

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

ASSAVVFKQMVLQQALPMTLKGLDKASELATLTPEGLAREHSRLASGDGALRSLSTALAGIRAGSQVEESRIQAGRLLERSIGGIALQQWGTTGGAASQLVLDASPELRREITDQLHQVMSEVALLRQAVESEVS

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

SKQPLLDIALKGLKRTLPQLEQMDGNSLRENFQEMASGNGPLRSLMTNLQNLNKIPEAKQLNDYVTTLTNIQVGVARFSQWGTCGGEVERWVDKASTHELTQAVKKIHVIAKELKNVTAELEKIEAGAPM

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

TSFSDSIKQLAAETLPKYMQQLNSLDAEMLQKNHDQFATGSGPLRGSITQCQGLMQFCGGELQAEASAILNTPVCGIPFSQWGTIGGAASAYVASGVDLTQAANEIKGLAQQMQKLLSLM

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

MFQQLSARLQEAIGRLRGRGRITEEDLKATLREIRRALMDADVNLEVARDFVERVREEALGKQVLESLTPAEVILATVYEALKEALGG

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

LLDNLRDTVRKFLTGSSSYDKAVEDFIKELQKSLISADVNVKLVFSLTNKIKERLKNEKPPTYIERREWFIKIVYDELSNLFGG

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

RSLLKTKENLGSGFISLFRGKKIDDDLFEELEEQLLIADVGVETTRKIITNLTEGASRKQLRDAEALYGLLKEEMGEILAKVDE

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

GAMEKFKTLLYDIPIECMEVSEEIISYAKLQLGKKLNDSIYVSLTDHINFAIQRNQKGLDIKNALLWETKRLYKDEFAIGKEALVMVKNKTGVSLPEDEAGFIALHIVNAELNEE

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

MPNIINITKVMEEILSIVKYHFKIEFNEESLHYYRFVTDLKFFAQRLFNGTHMESEDDFLLDTVKEKYHRAYECTKKIQTYIEREYEHKLTSDELLYLTIDIERVVK

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

MKSLKGSRTEKNILTAFAGESQARNRYNYFGGQAKKDGFVQISDIFAETADQEREHAKRLFKFLEGGDLEIVAAFPAGIIADTHANLIASAAGEHHEYTEMYPSFARIAREEGYEEIARVFASIAVAEEFHEKRFLDFARNIKEGRV

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

MKGDAKVIEFLNAALRSELTAISQYWVHFRLQEDWGLAKMAKKSREESIEEMGHADKIIARILFLEGHPNLQKLDPLRIGEGPRETLECDLAGEHDALKLYREARDYCAEVGDIVSKNIFESLITDEEGHVDFLETQISLYDRLGPQGFALLNAAPMDAA

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

MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLDGAGAFLFAHASEESDHAKKLITYLNETDSHVELQEVKQPEQNFKSLLDVFEKTYEHEQFITKSINTLVEHMLTHKDYSTFNFLQWYVSEQHEEEALFRGIVDKIKLIGEHGNGLYLADQYIKNIALSR

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

SKATNLLYTRNDVSDSEKKATVELLNRQVIQFIDLSLITKQAHWNMRGANFIAVHEMLDGFRTALIDHLDTMAERAVQLGGVALGTTQVINSKTPLKSYPLDIHNVQDHLKELADRYAIVANDVRKAIGEAKDDDTADILTAASRDLDKFLWFIECNIE

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

VDTKEFLNHQVANLNVFTVKIHQIHWYMRGHNFFTLHEKMDDLYSEFGEQMDEVAERLLAIGGSPFSTLKEFLENASVEEAPYTKPKTMDQLMEDLVGTLELLRDEYKQGIELTDKEGDDVTNDMLIAFKASIDKHIWMFKAFLGKAPLE

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

TSQIRQNYSTEVEAAVNRLVNLHLRASYTYLSLGFFFDRDDVALEGVGHFFRELAEEKREGAERLLEFQNDRGGRALFQDVQKPSQDEWGKTQEAMEAALAMEKNLNQALLDLHALGSARADPHLCDFLESHYLDKEVKLIKKMGNHLTNLRRVAGPQPAQTGAPQGSLGEYLFERLTLK

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

ERRRGLTDPEMAAVILKALPEAPLDGNNKMGYFVTPRWKRLTEYEALTVYAQPNADWIAGGLDWGDWTQKFHGGRPSWGNETTELRTVDWFKHRDPLRRWHAPYVKDKAEEWRYTDRFLQGYSADGQIRAMNPTWRDEFINRYWGAFLFNEYGLFNAHSQGAREALSDVTRVSLAFWGFDKIDIAQMIQLERGFLAKIVPGFDESTAVPKAEWTNGEVYKSARLAVEGLWQEVFDWNESAFSVHAVYDALFGQFVRREFFQRLAPRFGDNLTPFFINQAQTYFQIAKQGVQDLYYNCLGDDPEFSDYNRTVMRNWTGKWLEPTIAALRDFMGLFAKLPAGTTDKEEITASLYRVVDDWIEDYASRIDFKADRDQIVKAVLAGLK

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

AANRAPTSVNAQEVHRWLQSFNWDFKNNRTKYATKYKMANETKEQFKLIAKEYARMEAVKDERQFGSLQVALTRLNAGVRVHPKWNETMKVVSNFLEVGEYNAIAATGMLWDSAQAAEQKNGYLAQVLDEIRHTHQCAYVNYYFAKNGQDPAGHNDARRTRTIGPLWKGMKRVFSDGFISGDAVECSLNLQLVGEACFTNPLIVAVTEWAAANGDEITPTVFLSIETDELRHMANGYQTVVSIANDPASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYGSKFKVEPWVKTWDRWVYEDWGGIWIGRLGKYGVESPRSLKDAKQDAYWAHHDLYLLAYALWPTGFFRLALPDQEEMEWFEANYPGWYDHYGKIYEEWRARGCEDPSSGFIPLMWFIENNHPIYIDRVSQVPFCPSLAKGASTLRVHEYNGEMHTFSDQWGERMWLAEPERYECQNIFEQYEGRELSEVIAELHGLRSDGKTLIAQPHVRGDKLWTLDDIKRLNCVFKNPVKAF

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

AYTTFSQTKNDQLKEPMFFGQPVNVARYDQQKYDIFEKLIEKQLSFFWRPEEVDVSRDRIDYQALPEHEKHIFISNLKYQTLLDSIQGRSPNVALLPLISIPELETWVETWAFSETIHSRSYTHIIRNIVNDPSVVFDDIVTNEQIQKRAEGISSYYDELIEMTSYWHLLGEGTHTVNGKTVTVSLRELKKKLYLCLMSVNALEAIRFYVSFACSFAFAERELMEGNAKIIRLIARDEALHLTGTQHMLNLLRSGADDPEMAEIAEECKQECYDLFVQAAQQEKDWADYLFRDGSMIGLNKDILCQYVEYITNIRMQAVGLDLPFQTRSNPIPWINTWLV

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

SNEYDEYIANHTDPVKAINWNVIPDEKDLEVWDRLTGNFWLPEKIPVSNDIQSWNKMTPQEQLATMRVFTGLTLLDTIQGTVGAISLLPDAETMHEEAVYTNIAFMESVHAKSYSNIFMTLASTPQINEAFRWSEENENLQRKAKIIMSYYNGDDPLKKKVASTLLESFLFYSGFYLPMYLSSRAKLTNTADIIRLIIRDESVHGYYIGYKYQQGVKKLSEAEQEEYKAYTFDLMYDLYENEIEYTEDIYDDLGWTEDVKRFLRYNANKALNNLGYEGLFPTDETKVSPAILSSLS

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

LNKELETLREENRVKSDMLKEKLSKDAENHKAYLKSHQVHRHKLKEMEKEEPLLNEDKERTVLFPIKYHEIWQAYKRAEASFWTAEEIDLSKDIHDWNNRMNENERFFISRVLAFFAASDGIVNENLVENFSTEVQIPEAKSFYGFQIMIENIHSETYSLLIDTYIKDPKESEFLFNAIHTIPEIGEKAEWALRWIQDADALFGERLVAFASIEGVFFSGSFASIFWLKKRGMMPGLTFSNELICRDEGLHTDFACLLFAHLKNKPDPAIVEKIVTEAVEIEQRYFLDALPVALLGMNADLMNQYVEFVADRLLVAFGNKKYYKVENPFDFMEN

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

MPPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVRELRERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDHFSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLSAEGQKAQDYVCRLPPRIRRLEERAQGRAKEAPTMPFSWIFDRQVKL

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

PLPQSFLLKCLEQMRKVQADGTALQETLCATHQLCHPEELVLLGHALGIPQPPLSSCSSQALQLMGCLRQLHSGLFLYQGLLQALAGISPELAPTLDTLQLDTTDFAINIWQQMEDLGMAPAVPPTQGTMPAFTSAFQRRAGGVLVASNLQSFLELAYRALRHFAK

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

LTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRALRQM

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

EFEKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLDSIP

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

SPLPITPVNATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPFPNNLDKLCGPNVTDFPPFHANGTEKAKLVELYRMVAYLSASLTNITRDQKVLNPSAVSLHSKLNATIDVMRGLLSNVLCRLCNKYRVGHVDVPPVPDHSDKEVFQKKKLGCQLLGTYKQVISVVVQAF

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

TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLTDGSPRTGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRRDMTYVATYLRIVQCRSVEGSCGF

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

AQHPPYCRNQPGKCQIPLQSLFDRATTVANYNSKLAGEMVNRFDEQYGQGINSESKVINCHTSSITTPNSKAEAINTEDKILFKLVISLLHSWDEPLHHAVTELANSKGTSPALLTKAQEIKEKAKVLVDGVEVIQKRIHPGEKNEPYPVWSEQSSLTSQDENVRRVAFYRLFHCLHRDSSKIYTYLRILKCRLTSC

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

PHRRDLCSRSIWLARKIRSDLTALTESYVKHQGLNKNINLDSADGMPVASTDQWSELTEAERLQENLQAYRTFHVLLARLLEDQQVHFTPTEGDFHQAIHTLLLQVAAFAYQIEELMILLEYKIPRNEADGMPINVGDGGLFEKKLWGLKVLQELSQWTVRSIHDLRFISSHQTGIP

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

IQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPEASGLETLDSLGGVLEASGYSTEVVALSRLQGSLQDMLWQLDLSPGC

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

GSCSKEYRVLLGQLQKQTDLMQDTSRLLDPYIRIQGLDVPKLREHCRERPGAFPSEETLRGLGRRGFLQTLNATLGCVLHRLADLEQRLPKAQDLERSGLNIEDLEKLQMARPNILGLRNNIYCMAQLLDNSDTAEPTKAGRGASQPPTPTPASDAFQRKLEGCRFLHGYHRFMHSVGRVFSKW

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

QNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS

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

APPRLICDSRVLERYLLEAKEAEKITTGCAEHCSLNEKITVPDTKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVKSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAISNSDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR

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

RSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFDCWEP

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

HKCDITLQAIIKTLNSLTEQKTLCTELTVTDIFAASKNTTEKETFCRAATVLRQFYSHHEKDTRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTIMREKYSKCSS

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

IPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEWI

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

SEYCSHMIGSGHLQSLQRLIDSQMETSCQITFEFVDQEQLKDPVCYLKKAFLLVQDIMEDTMRFRDNTPNAIAIVQLQELSLRLKSCFTKDYEEHDKACVRTFYETPLQLLEKVKNVFNETKNLLDKDWNIFSKNCNNSFAECSSQGH

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

TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDDELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP

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

NVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVS

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

STKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

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

ANCSIMIDEIIHHLKRPPNPLLDPNNLNSEDMDILMERNLRTPNLLAFVRAVKHLENASAIESILKNLLPCLPLATAAPTRHPIHIKDGDWNEFRRKLTFYLKTLENAQAQQ

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

GGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFN

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

TQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRN

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

MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN

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

CYLSRKLMLDARENLKLLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEMLQQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPIVTVKKYFQGIYDYLQEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTK

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

MQDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIDELIQVMAELGANV

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

LADDLGNLVQRTRAMLFRFAEGRIPEPVAGEELAEGTGLAGRLRPLVRELKFHVALEEAMAYVKALNRYINEKKPWELFKKEPEEARAVLYRVVEGLRIASILLTPAMPDKMAELRRALGLKEEVRLEEAERWGLAEPRPIPEEAPVLFPKK

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

VVNLASRNAGFINKRFDGVLASELADPQLYKTFTDAAEVIGEAWESREFGKAVREIMALADLANRYVDEQAPWVVAKQEGRDADLQAICSMGINLFRVLMTYLKPVLPKLTERAEAFLNTELTWDGIQQPLLGHKVNPFKALYNRIDMRQVEALVEASKE

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

YFLTLWNVYSFFVTYANLDRPDLKNPPPPEKRPEMDRWLLARMQDLIQRVTEALEAYDPTTSARALRDFVVEDLSQWYVRRNRRRFWKNEDALDREAAYATLYEALVLVATLAAPFTPFLAEVLWQNLVRSVRLEAKESVHLADWPEADPALADEALVAQMRAVLKVVDLARAARAKSGV

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

YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNIYQEVQNFINVELSNFYLDYGKDILYIEQRDSHIRRSMQTVLYQILVDMTKLLAPILVHTAEEVWSHTPHVKEESVHLADMPKVVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNASEFLTSFDALHQLFIVSQVKVVDKLDDQATAYEHGDIVIEHADGEKCERCWNYSEDLGAVDELTHLCPRCQQVVKSLV

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

ANKLYNAARFVLLSREGFQAKEDTPTLADRFMRSRLSRGVEEITALYEALDLAQAAREVYELVWSEFCDWYLEAAKPALKAGNAHTLRTLEEVLAVLLKLLHPMMPFLTSELYQALTGKEELALEAWPEPGGRDEEAERAFEALKQAVTAVRALKAEAGLPPAQEVRVYLEGETAPVEENLEVFRFLSRADLLPERPAKALVKAMPRVTARMPLEGLLDVEEWRRRQEKRLKELLALAERSQRKLASPGFREKAPKEVVEAEEARLKENLEQAERIREALSQIG

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

DTGPYLQYAHSRLRSVERNASGITQEKWINADFSLLKEPAAKLLIRLLGQYPDVLRNAIKTHEPTTVVTYLFKLTHQVSSCYDVLWVAGQTEELATARLALYGAARQVLYNGMRLLGLTPVERM

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

GDTGPYVQYAHARAHSILRKAGEWGAPDLSQATPYERALALDLLDFEEAVLEAAEERTPHVLAQYLLDLAASWNAYYNARENGQPATPVLTAPEGLRELRLSLVQSLQRTLATGLDLLGIPAPEVM

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

STIEERVKKIIGEQLGVKQEEVTNNASFVEDLGADSLDTVELVMALEEEFDTEIPDEEAEKITTVQAAIDYINGHQA

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

MATLLTTDDLRRALVECAGETDGTDLSGDFLDLRFEDIGYDSLALMETAARLESRYGVSIPDDVAGRVDTPRELLDLINGALAEAA

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

PKAQNIRQGAKEPYPEFVDRLLSQIKSEGHPQEISKFLTDTLTIQNANEECRNAMRHLRPEDTLEEKMYACRDIG

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

PSWASILQGLEEPYHAFVERLNIALDNGLPEGTPKDPILRSLAYSNANKECQKLLQARGHTNSPLGDMLRACQTWTPKDKTKVL

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

GPWADITQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRAAPSTLTTPGEIIKYVLDRQKIAP

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

GSHMSKEPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRSPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNAPESEYYKCANILEKFFFSKIKEAGLIDK

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

GTTVHCDYLNRPHKSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINP

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

VRLTPTMMLYSGRSQDGSHLLKSGRYLQQELPVRIAHRIKGFRSLPFIIGCNPTILHVHELYIRAFQKLTDFPPIKDQADEAQYCQLVRQLLDDHKDVVTLLAEGLRESRKHIEDEKLVRYFLDKTLTSRLGIRMLATHHLALHEDKP

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

ASLAGAPKYIEHFSKFSPSPLSMKQFLDFGSSNACEKTSFTFLRQELPVRLANIMKEINLLPDRVLSTPSVQLVQSWYVQSLLDIMEFLDKDPEDHRTLSQFTDALVTIRNRHNDVVPTMAQGVLEYKDTYGDDPVSNQNIQYFLDRFYLSRISIRMLINQHTLIFD

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

GAGFKVAMGAFDKERPVVAAGAVGLAQRALDEATKYALERKTFGKLLVEHQAISFMLAEMAMKVELARMSYQRAAWEVDSGRRNTYYASIAKAFAGDIANQLATDAVQILGGNGFNTEYPVEKLMRDAKIYQIYGGTSQIQRLIVAREHIDKYKN

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

KGVYVLMSGLDLERLVLAGGPLGLMQAVLDHTIPYLHVREAFGQKIGHFQLMQGKMADMYTRLMACRQYVYNVAKACDEGHCTAKDCAGVILYSAECATQVALDGIQCFGGNGYINDFPMGRFLRDAKLYEIGAGTSEVRRLVIGRAFNAD

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

MAAGVKQLADDRTLLMAGVSHDLRTPLTRIRLATEMMSEQDGYLAESINKDIEECNAIIEQFIDYLR

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

SQTVRVDIEKLDNLMDLMGELVIARSRILETLKKYNIKELDESLSHLSRITLDLQNVVMKIR

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

STKKKPLTQEQLEDARRLKAIYEKKKNELGLSQESLADKLGMGQSGIGALFNGINALNAYNAALLAKILKVSVEEFSPSIAREIYEMYEAVS

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

MQTLSERLKKRRIALKMTQTELATKAGVKQQSIQLIEAGVTKRPRFLFEIAMALNCDPVWLQYGT

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

MNTQLMGERIRARRKKLKIRQAALGKMVGVSNVAISQWERSETEPNGENLLALSKALQCSPDYLLKGDLSQTNVAY

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

MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEEVKPFPSNKKTTA

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

CSNEKARDWHRADVIAGLKKRKLSLSALSRQFGYAPTTLANALERHWPKGEQIIANALETKPEVIWPSRYQAGE

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

GFDLNDFLEQLRQMKNMGGMASLMGKLPGMGQIPDNVKSQMDDKVLVRMEAIINSMTMKERAKPEIIKGSRKRRIAAGSGMQVQDVNRLLKQFDDMQRMMKKMK

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

QFTLRDMYEQFQNIMKMGPFSQILGMIPGFGTDFMSKGNEQESMARLKKLMTIMDSMNDQELDSTDGAKVFSKQPGRIQRVARGSGVSTRDVQELLTQYTKFAQMVK

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

ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQVRALEKARS

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

MELKRKTTNADRRKAATMRERRRLSKVNEAFETLKRSTSSNPNQRLPKVEILRNAIRYIEGLQALLRD

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

MDEKRRAQHNEVERRRRDKINNWIVQLSKIIPDSSMESTKSGQSKGGILSKASDYIQELRQSNHR

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

MKRESHKHAEQARRNRLAVALHELASLIPAEWKQQNVSAAPSKATTVEAACRYIRHLQQNGST

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

QSRGEKRTAHNAIEKRYRSSINDKIIELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLSLRTAVHKSKSLK

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

GSELETAMETLINVFHAHSGKEGDKYKLSKKELKDLLQTELSSFLDVQKDADAVDKIMKELDENGDGEVDFQEFVVLVAALTVACNNFFWENS

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

SNTQAERSIIGMIDMFHKYTRRDDKIDKPSLLTMMKENFPNFLSACDKKGTNYLADVFEKKDKNEDKKIDFSEFLSLLGDIATDYHKQSHGAAPCSGGSQ

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

PTETERCIESLIAIFQKHAGRDGNNTKISKTEFLIFMNTELAAFTQNQKDPGVLDRMMKKLDLDSDGQLDFQEFLNLIGGLAIACHDSFIKSTQK

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

TCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIEHIMEDLDTNADKQLSFEEFIMLMARL

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

ASMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMKEDAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVTEEDIEDLMKDSDKNNDGRIDFDEFLKMMEGVQ

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

SDLWVQKMKTYFNRIDFDKDGAITRMDFESMAERFAKESEMKAEHAKVLMDSLTGVWDNFLTAVAGGKGIDETTFINSMKEMVKNPEAKSVVEGPLPLFFRAVDTNEDNNISRDEYGIFFGMLGLDKTMAPASFDAIDTNNDGLLSLEEFVIAGSDFFMNDGDSTNKVFWGPLV

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

GLNDFQKQKIKFTFDFFLDMNHDGSIQDNDFEDMMTRYKEVNKGSLSDADYKSMQASLEDEWRDLKGRADINKDDVVSWEEYLAMWEKTIATCKSVADLPAWCQNRIPFLFKGMDVSGDGIVDLEEFQNYCKNFQLQCADVPAVYNVITDGGKVTFDLNRYKELYYRLLTSPAADAGNTLMGQKP

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

EEEILRAFKVFDANGDGVIDFDEFKFIMQKVGEEPLTDAEVEEAMKEADEDGNGVIDIPEFMDLIKKS

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

AAPKARALGPEEKDECMKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGDKKNIGPEEWLTLCSKWVRQDD

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

SSKYAVKLKTDFDNPRWIKRHKHMFDFLDINGNGKITLDEIVSKASDDICAKLEATPEQTKRHQVCVEAFFRGCGMEYGKEIAFPQFLDGWKQLATSELKKWARNEPTLIREWGDAVFDIFDKDGSGTITLDEWKAYGKISGISPSQEDCEATFRHCDLDNSGDLDVDEMTRQHLGFWYTLDPEADGLYGNGVP

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

MAEALFKEIDVNGDGAVSYEEVKAFVSKKRAIKNEQLLQLIFKSIDADGNGEIDQNEFAKFYGSIQGQDLSDDKIGLKVLYKLMDVDGDGKLTKEEVTSFFKKHGIEKVAEQVMKADANGDGYITLEEFLEFSL

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

STDDSPYKQAFSLFDRHGTGRIPKTSIGDLLRACGQNPTLAEITEIESTLPAEVDMEQFLQVLNRPNGFDMPGDPEEFVKGFQVFDKDATGMIGVGELRYVLTSLGEKLSNEEMDELLKGVPVKDGMVNYHDFVQMILAN

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

LPQKQIQEMKEAFSMIDVDRDGFVSKEDIKAISEQLGRAPDDKELTAMLKEAPGPLNFTMFLSIFSDKLSGTDSEETIRNAFAMFDEQETKKLNIEYIKDLLENMGDNFNKDEMRMTFKEAPVEGGKFDYVKFTAMIKGSGE

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

FDETEIEDFKEAFTVIDQNADGIIDKDDLRETFAAMGRLNVKNEELDAMIKEASGPINFTVFLTMFGEKLKGADPEDVIMGAFKVLDPDGKGSIKKSFLEELLTTGGGRFTPEEIKNMWAAFPPDVAGNVDYKNICYVITHGEDA

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

LSQDEIDDLKDVFELFDFWDGRDGAVDAFKLGDVCRCLGINPRNEDVFAVGGTHKMGEKSLPFEEFLPAYEGLMDCEQGTFADYMEAFKTFDREGQGFISGAELRHVLTALGERLSDEDVDEIIKLTDLQEDLEGNVKYEDFVKKVMAGPYP

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

SYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDIFDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRFAFRIYDMDKDGYISNGELFQVLKMMVGNNLKDTQLQQIVDKTIINADKDGDGRISFEEFCAVVGGLDIHKKMVVDV

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

LSKEILEELQLNTKFTEEELSSWYQSFLKECPSGRITRQEFQTIYSKFFPEADPKAYAQHVFRSFDANSDGTLDFKEYVIALHMTSAGKTNQKLEWAFSLYDVDGNGTISKNEVLEIVTAIFKMISPEDTKHLPEDENTPEKRAEKIWGFFGKKDDDKLTEKEFIEGTLANKEILRLIQFEPQKVKEKLK

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

MGAKTSKLSKDDLTCLKQSTYFDRREIQQWHKGFLRDCPSGQLAREDFVKIYKQFFPFGSPEDFANHLFTVFDKDNNGFIHFEEFITVLSTTSRGTLEEKLSWAFELYDLNHDGYITFDEMLTIVASVYKMMGSMVTLNEDEATPEMRVKKIFKLMDKNEDGYITLDEFREGSKVDPSIIGALNLYDGLI

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

GQQFSWEEAEENGAVGAADAAQLQEWYKKFLEECPSGTLFMHEFKRFFKVPDNEEATQYVEAMFRAFDTNGDNTIDFLEYVAALNLVLRGTLEHKLKWTFKIYDKDRNGCIDRQELLDIVESIYKLKKACSVEVEAEQQGKLLTPEEVVDRIFLLVDENGDGQLSLNEFVEGARRDKWVMKMLQMDLNP

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

SKELLAEYQDLTFLTKQEILLAHRRFCELLPQEQRSVESSLRAQVPFEQILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFDDDGTLNREDLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASSFKIVL

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

LSLTQLSSGNPVYEKYYRQVEAGNTGRVLALDAAAFLKKSGLPDLILGKIWDLADTDGKGVLSKQEFFVALRLVACAQNGLEVSLSSLSLAVPPPRFHD

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

TWVVSPAEKAKYDEIFLKTDKDMDGFVSGLEVREIFLKTGLPSTLLAHIWSLCDTKDCGKLSKDQFALAFHLISQKLIKGIDPPHVLTPEMIPPS

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

GSLQDNSSYPDEPWRITEEQREYYVNQFRSLQPDPSSFISGSVAKNFFTKSKLSIPELSYIWELSDADCDGALTLPEFCAAFHLIVARKNGYPLPEGLPPTLQPEFIVTD

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

PGPGGGPGPAAGAALPDQSFLWNVFQRVDKDRSGVISDNELQQALSNGTWTPFNPVTVRSIISMFDRENKAGVNFSEFTGVWKYITDWQNVFRTYDRDNSGMIDKNELKQALSGFGYRLSDQFHDILIRKFDRQGRGQIAFDDFIQGCIVLQRLTDIFRRYDTDQDGWIQVSYEQYLSMVF

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

FPGQTQDPLYGYFAAVAGQDGQIDADELQRCLTQSGIAGGYKPFNLETCRLMVSMLDRDMSGTMGFNEFKELWAVLNGWRQHFISFDTDRSGTVDPQELQKALTTMGFRLSPQAVNSIAKRYSTNGKITFDDYIACCVKLRALTDSFRRRDTAQQGVVNFPYDDFIQCVMSV

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

NKMNFKELKDFLKELNIQVDDGYARKIFRECDHSQTDSLEDEEIETFYKMLTQRAEIDRAFEEAAGSAETLSVERLVTFLQHQQREEEAGPALALSLIERYEPSETAKAQRQMTKDGFLMYLLSADGNAFSLAHRRVYQDM

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

EIEANLEEFDISEDDIDDGVRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKSDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIELDLISWLCFSVL

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

HPKMTELYQSLADLNNVRFSAYRTAMKLRRLQKALCLDLLSLSAACDALDQHNLKQNDQPMDILQIINCLTTIYDRLEQEHNNLVNVPLCVDMCLNWLLNVYDTGRTGRIRVLSFKTGIISLCKA

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

HLEDKYRYLFKQVASSTGFCDQRRLGLLLHDSIQIPRQLGEVASFGGSNIEPSVRSCFQFANNKPEIEAALFLDWMRLEPQSMVWLPVLHRVAAAET

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

TFRITKADAAEFWRKAFGEKTIVPWKSFRQALHEVHPISSGLEAMALKSTIDLTCNDYISVFEFDIFTRLFQPWSSLLRNWNSLAV

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

MADTDTAEQVIASFRILASDKPYILAEELRRELPPDQAQYCIKRMPAYSGPGSVPGALDYAAFSSALYGESDL

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

ETPREKLKQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAFCILKRAGFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFFKCVHDNRS

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

SQEVMKNLSLNFGKALDECKKEMTLTDAINEDFYNFWKEGYEIKNRETGCAIMCLSTKLNMLDPEGNLHHGNAMEFAKKHGADETMAQQLIDIVHGCEKSTPANDDKCIWTLGVATCFKAEIHKLNWAPSMDVAVGE

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

EEPGSGIGYPYDNNTLPYVAPGPTDSRAPCPALNALANHGYIPHDGRAISRETLQNAFLNHMGIANSVIELALTNAFVVCEYVTGSDCGDSLVNLTLLAEPHAFEHDHSFSRKDYKQGVA

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

NSNDFIDNRNFDAETFQTSLDVVAGKTHFDYADMNEIRLQRESLSNELDFPGWFTESKPIQNVESGFIFALVSDFNLPDNDENPLVRIDWWKYWFTNESFPYHLGWHPPSPAREIEFVTSASSAVLAASVTSTPSSLPSGAIGPGAEAVPLSFASTMTPFLLATNAPYYAQDPTLGPND

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

MPQTERQLRVWIEGATGRRIGDNFMDGLKDGVILCELINKLQPGSVQKVNDPVQNWHKLENIGNFLRAIKHYGVKPHDIFEANDLFENTNHTQVQSTLIALASQAKTK

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

YSEEEKYAFVNWINKALENDPDCRHVIPMNPNTDDLFKAVGDGIVLCKMINLSVPDTIDERAINKKKLTPFIIQENLNLALNSASAIGCHVVNIGAEDLRAGKPHLVLGLLWQIIKIGLFADIELSRNEAL

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

TLEELMKLSPEELLLRWANFHLENSGWQKINNFSADIKDSKAYFHLLNQIAPKGQKEGEPRIDINMSGFNETDDLKRAESMLQQADKLGCRQFVTPADVVSGNPKLNLAFVANLFN

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

DVQKKTFTKWINARFSKSGKPPINDMFTDLKDGRKLLDLLEGLTGTSLPKERGSTRVHALNNVNRVLQVLHQNNVELVNIGGTDIVDGNHKLTLGLLWSIILHWQVKDVMKDVMSDLQQTN

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

VKNVMKNIMAGLQQTNSEKILLSWVRQSTRNYPQVNVINFTTSWSDGLALNALIHSHRPDLFDWNSVVSQQSATQRLEHAFNIARYQLGIEKLLDPEDVDTTYPDKKSILMYITSLFQVLPQQVSIE

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

MKGMSKMPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGRIGA

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

ARDDPHFNFRMPMEVREKLKFRAEANGRSMNSELLQIVQDALSKPSPVTGYRNDAERLADEQSELV

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

MKKRLTITLSESVLENLEKMAREMGLSKSAMISVALENYKKGQ

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

AEWSGEYISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFLHAFTGQPLPDDADLRKERSDEIPEAAKEIMREMGINPETWEY

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

GGDLGKDLTQAWAVAMALGVEDKVTVPLFEGVQKTQTIRSASDIRDVFINAGIKGEEYDAAWNS

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

GNMGQAMSKAYATMIALEVEDKMVPVMFNRIHTLRKPPKDEQELRQIFLDEGIDAAKFDAAYNG

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

GLYGKDQQEAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETLLSQNQGGKTFIVGDQISFADYNLLDLLLIHEVLAPGCLDAFPLLSAYVGRLSARPKLKAFLASPEYVNLPINGNGKQ

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

RKHNMCGETEEEKIRVDIIENQVMDFRTQLIRLCYSSDHEKLKPQYLEELPGQLKQFSMFLGKFSWFAGEKLTFVDFLTYDILDQNRIFDPKCLDEFPNLKAFMCRFEALEKIAAYLQSDQFCKMPINNKMAQWGNKPVC

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

DLYGKDMKERALIDMYSEGILDLTEMIMQLVICPPDQKEAKTALAKDRTKNRYLPAFEKVLKSHGQDYLVGNKLTRVDIHLLELLLYVEEFDASLLTSFPLLKAFKSRISSLPNVKKFLQPGSQRKLPMDAKQIEEARKIYKF

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

TPDHWYPSDLQARARVHEYLGWHADCIRGTFGIPLWVQVLGPLIGVQVPEEKVERNRTAMDQALQWLEDKFLGDRPFLAGQQVTLADLMALEELMQPVALGYELFEGRPRLAAWRGRVEAFLGAELCQEAHSIILSILEQAAKKTLPTPSPEAYQAMLLRIARIP

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

DLAGKTELEQCQVDAVVDTLDDFMSLFPWAEENQDLKERTFNDLLTRQAPHLLKDLDTYLGDKEWFIGNYVTWADFYWDICSTTLLVLKPDLLGIYPRLVSLRNKVQAIPAISAWILKRPQTKL

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

LDGKTSLEKYRVDEITETLQDIFNDVVKIKFAPEAAKEAVQQNYEKSCKRLAPFLEGLLVSNGGGDGFFVGNSMTLADLHCYVALEVPLKHTPELLKDCPKIVALRKRVAECPKIAAYLKKRPVRDF

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

LPDDPYEKACQKMILELFSKVPSLVGSFIRSQNKEDYAGLKEEFRKEFTKLEEVLTNKKTTFFGGNSISMIDYLIWPWFERLEAMKLNECVDHTPKLKLWMAAMKEDPTVSALLTSEKDWQGFLELYLQNSPEACDYGL

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

GTDLLPATASAAKLEVWLEVESHHFYPNASPLVFQLLVRPLLGGAPDAAVVDKHAEQLAKVLDVYEAHLARNKYLAGDEFTLADANHASYLLYLSKTPKAGLVAARPHVKAWWEAIVARPAFQKTVAAIPLPPPP

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

PLLPRDLHKRAVNYQAMSIVLSGIQPHQNLAVIRYIEEKINVEEKTAWVNNAITKGFTALEKLLVNCAGKHATGDEIYLADLFLAPQIHGAINRFQINMEPYPTLAKCYESYNELPAFQNALPEKQPDAPSST

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

QLLAPVNSISRYKTIEWLNYIATELHKGFTPLFRPDTPEEYKPTVRAQLEKKLQYVNEALKDEHWICGQRFTIADAYLFTVLRWAYAVKLNLEGLEHIAAFMQRMAERPEVQDALSAEGLK

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

LGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSRRASVGSRMHYPGAFTYSPTPVTSGIGIGMSAMGS

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

GLAPAEGSLDRYRLLSRLSFLGSEFHKAFVPLFAPATSDEAKAAAAESVKNHLAALDKELAGRDHYAGNAFSVADIYLYVMLGWPAYVGIDMAAYPALGAYAGKIAQRPAVGAALKAEGLA

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

PLLTGKRSPAIEEWLRKVNGYANKLLLPRFAKSAFDEFSTPAARKYFVDKKEASAGNFADLLAHSDGLIKNISDDLRALDKLIVKPNAVNGELSEDDIQLFPLLRNLTLVAGINWPSRVADYRDNMAKQTQINLLSSMAI

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

LWSDDLADQSQINAWLFFQTSGHAPMIGQALHFRYFHSQKIASAVERYTDEVRRVYGVVEMALAERREALVMELDTENAAAYSAGTTPMSQSRFFDYPVWLVGDKLTIADLAFVPWNNVVDRIGINIKIEFPEVYKWTKHMMRRPAVIKAL

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

RYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLPEGVDETSAEDEGVSQRKFLDGNELTLADCNLLPKLHIVQVVCKKYRGFTIPEAFRGVHRYLSNAYAREEFASTCPDDEEIELAYEQVAKAL

>d1dn1b\_ a.47.2.1 (B:) Syntaxin 1A N-terminal domain {Rat (Rattus norvegicus)}

DRFMDEFFEQVEEIRGFIDKIAENVEEVKRKHSAILASPNPDEKTKEELEELMSDIKKTANKVRSKLKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFVEVMSEYNATQSDYRERCKGRIQRQLEITGRTTTSEELEDMLESGNPAIFASGIIMDSSISKQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAV

>d1fioa\_ a.47.2.1 (A:) Sso1 {Baker's yeast (Saccharomyces cerevisiae)}

MHDFVGFMNKISQINRDLDKYDHTINQVDSLHKRLLTEVNEEQASHLRHSLDNFVAQATDLQFKLKNEIKSAQRDGIHDTNKQAQAENSRQRFLKLIQDYRIVDSNYKEENKEQAKRQYMIIQPEATEDEVEAAISDVGGQQIFSQALLNANRRGEAKTALAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQ

>d1hs7a\_ a.47.2.1 (A:) Vam3p N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TNQKTKELSNLIETFAEQSRVLEKECTKIGSKRDSKELRYKIETELIPNCTSVRDKIESNILIHQNGKLSADFKNLKTKYQSLQQSYNQRKSLFPLK

>d1cfaa\_ a.50.1.1 (A:) C5a anaphylotoxin {Human (Homo sapiens)}

MLQKKIEEIAAKYKHSVVKKCCYDGASVNNDETCEQRAARISLGPRCIKAFTECCVVASQLRANISHKDMC

>d0c3a\_\_ a.50.1.1 (-) C3a anaphylotoxin {Human (Homo sapiens)}

SVQLTEKRMNKVGKYPKELRKCCEDGMRQNPMRFSCQRRTRFISLGEACKKVFLDCCNYITELRRQHARASHLGLAR

>d1hyp\_\_ a.52.1.1 (-) Soybean hydrophobic protein {Soybean (Glycine max)}

PSCPDLSICLNILGGSLGTVDDCCALIGGLGDIEAIVCLCIQLRALGILNLNRNLQLILNSCGRSYPSNATCPRT

>d1fk5a\_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Maize (Zea mays)}

AISCGQVASAIAPCISYARGQGSGPSAGCCSGVRSLNNAARTTADRRAACNCLKNAAAGVSGLNAGNAASIPSKCGVSIPYTISTSTDCSRVN

>d1hssa\_ a.52.1.2 (A:) 0.19 alpha-amylase inhibitor {Wheat (Triticum aestivum)}

MCYPGQAFQVPALPACRPLLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSMLDSMYKEHGAQEGQAGTGAFPRCRREVVKLTAASITAVCRLPIVVDASGDGAYVCKDVAAYPDA

>d1tmqb\_ a.52.1.2 (B:) Trypsin/alpha-amylase inhibitor RBI {Ragi (Elucine coracana gaertneri), seeds}

SVGTSCIPGMAIPHNPLDSCRWYVSTRTCGVGPRLATQEMKARCCRQLEAIPAYCRCEAVRILMDGVVTSSGQHEGRLLQDLPGCPRQVQRAFAPKLVTEVECNLATIHGGPFCLSL

>d1ihfa\_ a.55.1.1 (A:) Integration host factor (IHF) {Escherichia coli}

ALTKAEMSEYLFDKLGLSKRDAKELVELFFEEIRRALENGEQVKLSGFGNFDLRDKNQRPGRNPKTGEDIPITARRVVTFRPGQKLKSRVENASPK

>d1ihfb\_ a.55.1.1 (B:) Integration host factor (IHF) {Escherichia coli}

MTKSELIERLATQQSHIPAKTVEDAVKEMLEHMASTLAQGERIEIRGFGSFSLHYRAPRTGRNPKTGDKVELEGKYVPHFKPGKELRDRANIYG

>d1hns\_\_ a.55.1.1 (-) DNA-binding domain of H1 protein, (H-NS) {Escherichia coli}

AQRPAKYSYVDENGETKTWTGQGRTPAVIKKAMDEQGKSLDDFLIKQ

>d1b8za\_ a.55.1.1 (A:) HU protein {Thermotoga maritima}

MNKKELIDRVAKKAGAKKKDVKLILDTILETITEALAKGEKVQIVGFGSFEVRKAAARKGVNPQTRKPITIPERKVPKFKPGKALKEKVK

>d1exea\_ a.55.1.1 (A:) Transcription factor 1, TF1 {Bacteriophage SPO1 (Bacillus subtilis)}

MNKTELIKAIAQDTGLTQVSVSKMLASFEKIITETVAKGDKVQLTGFLNIKPVARQARKGFNPQTQEALEIAPSVGVSVKPGESLKKAAEGLKYEDFAK

>d1hlra1 a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio gigas}

QPENLHPLQKAWVLHGGAQCGFCSPGFIVSAKGLLDTNADPSREDVRDWFQKHRNACRCTGYKPLVDAVMDAAAVINGKKPETDLEFKMPADGRIWGSKYPRPTAVAKVTGTL

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

NKGVLHAVQEGFYKEHGLQCGFCTPGMLMRAYRFLQENPNPTEAEIRMGMTGNLCRCTGYQNIVKAVQYAARKLQE

>d1b4fa\_ a.60.1.2 (A:) EphB2 receptor {Human (Homo sapiens)}

PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMMEDILRVGVTLAGHQKKILNSIQVMRAQMNQIQS

>d1coka\_ a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}

YHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDLKQGHDY

>d1cuk\_2 a.60.2.1 (65-142) DNA helicase RuvA subunit, middle domain {Escherichia coli}

NKQERTLFKELIKTNGVGPKLALAILSGMSAQQFVNAVEREEVGALVKLPGIGKKTAERLIVEMKDRFKGLHGDLFTP

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

DAENRDLFLALLSVSGVGPRLAMATLAVHDAAALRQALADSDVASLTRVPGIGRRGAERIVLELADKVGPV

>d1coo\_\_ a.60.3.1 (-) C-terminal domain of RNA polymerase alpha subunit {Escherichia coli}

FDPILLRPVDDLELTVRSANCLKAEAIHYIGDLVQRTEVELLKTPNLGKKSLTEIKDVLASRGLSLGMRLENWPPASIADE

>d1doqa\_ a.60.3.1 (A:) C-terminal domain of RNA polymerase alpha subunit {Thermus thermophilus}

EQEEELDLPLEELGLSTRVLHSLKEEGIESVRALLALNLKDLKNIPGIGERSLEEIKEALEKKGFTLKE

>d1dk2a\_ a.60.6.1 (A:) DNA polymerase beta, N-terminal (8 kD)-domain {Rat (Rattus norvegicus)}

SKRKAPQETLNGGITDMLVELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPGVGTKIAEKIDEFLATGKLRKLEK

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

KKISQYACQRRTTLNNYNQLFTDALDILAENDELRENEGSCLAFMRASSVLKSLPFPITSMKDTEGIPCLGDKVKSIIEGIIEDGESSEAKAVLN

>d1tfr\_1 a.60.7.1 (183-305) T4 RNase H {Bacteriophage T4}

GSAEIDCMTKILKGDKKDNVASVKVRSDFWFTRVEGERTPSMKTSIVEAIANDREQAKVLLTESEYNRYKENLVLIDFDYIPDNIASNIVNYYNSYKLPPRGKIYSYFVKAGLSKLTNSINEF

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

LRPDQWADYRALTGDESDNLPGVKGIGEKTARKLLEEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREPDRERLRAFLERLEFGSLLHEFGLLE

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

VDDVEQFISLKAIMGDLGDNIRGVEGIGAKRGYNIIREFGNVLDIIDQLPLPGKQKYIQNLNASEELLFRNLILVDLPTYCVDAIAAVGQDVLDKFTKDILEIAE

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

LTREKLIELAILVGTDYNPGGIKGIGLKKALEIVRHSKDPLAKFQKQSDVDLYAIKEFFLNPPVTDNYNLVWRDPDEEGILKFLCDEHDFSEERVKNGLERLKKAIKSGKQSTLESWFKR

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

SDEVRKNLMDMFRDRQAFSEHTWKMLLSVCRSWAAWCKLNNRKWFPAEPEDVRDYLLYLQARGLAVKTIQQHLGQLNMLHRRSGLPRPSDSNAVSLVMRRIRKENVDAGE

>d1a0p\_1 a.60.9.1 (3-100) Recombinase XerD {Escherichia coli}

QDLARIEQFLDALWLEKNLAENTLNAYRRDLSMMVEWLHHRGLTLATAQSDDLQALLAERLEGGYKATSSARLLSAVRRLFQYLYREKFREDDPSAHL

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

PQFDILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWMITHNGTAIKRATFMSYNTIISNSLSFDIVNKSLQFKYKTQKATILEASLKKLIPAWEFTIIPYYGQKHQSDITDIVSSLQLQFES

>d1aep\_\_ a.63.1.1 (-) Apolipophorin-III {African locust (Locusta migratoria)}

NIAEAVQQLNHTIVNAAHELHETLGLPTPDEALNLLTEQANAFKTKIAEVTTSLKQEAEKHQGSVAEQLNAFARNLNNSIHDAATSLNLQDQLNSLQSALTNVGHQWQDIATKTQASAQEAWAPVQSALQEAAEKTKEAAANLQNSIQSAVQK

>d1eq1a\_ a.63.1.1 (A:) Apolipophorin-III {Manduca sexta}

DAPAGGNAFEEMEKHAKEFQKTFSEQFNSLVNSKNTQDFNKALKDGSDSVLQQLSAFSSSLQGAISDANGKAKEALEQARQNVEKTAEELRKAHPDVEKEANAFKDKLQAAVQTTVQESQKLAKEVASNMEETNKKLAPKIKQAYDDFVKHAEEVQKKLHEAATKQ

>d1hm6a\_ a.65.1.1 (A:) Annexin I {Pig (Sus scrofa)}

AMVSEFLKQAWFIDNEEQEYIKTVKGSKGGPGSAVSPYPTFNPSSDVEALHKAITVKGVDEATIIEILTKRTNAQRQQIKAAYLQEKGKPLDEALKKALTGHLEEVALALLKTPAQFDADELRAAMKGLGTDEDTLNEILASRTNREIREINRVYKEELKRDLAKDITSDTSGDYQKALLSLAKGDRSEDLAINDDLADTDARALYEAGERRKGTDLNVFITILTTRSYPHLRRVFQKYSKYSKHDMNKVLDLELKGDIENCLTVVVKCATSKPMFFAEKLHQAMKGIGTRHKTLIRIMVSRSEIDMNDIKACYQKLYGISLCQAILDETKGDYEKILVALCG

>d1dk5a\_ a.65.1.1 (A:) Annexin 24(ca32) {Bell pepper (Capsicum annuum)}

HHHHMASLTVPAHVPSAAEDCEQLRSAFKGWGTNEKLIISILAHRTAAQRKLIRQTYAETFGEDLLKELDRELTHDFEKLVLVWTLDPSERDAHLAKEATKRWTKSNFVLVELACTRSPKELVLAREAYHARYKKSLEEDVAYHTTGDHRKLLVPLVSSYRYGGEEVDLRLAKAESKILHEKISDKAYSDDEVIRILATRSKAQLNATLNHYKDEHGEDILKQLEDGDEFVALLRATIKGLVYPEHYFVEVLRDAINRRGTEEDHLTRVIATRAEVDLKIIADEYQKRDSIPLGRAIAKDTRGDYESMLLALLGQE

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

GEKATKVQDIKNNLKEAIETIVAAMSNLVPPVELANPENQFRVDYILSVMNVPDFDFPPEFYEHAKALWEDEGVRACYERSNEYQLIDCAQYFLDKIDVIKQDDYVPSDQDLLRCR

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

YSLEECLEFIAIIYGNTLQSILAIVRAMTTLNIQYGDSARQDDARKLMHMADTIEEGTMPKEMSDIIQRLWKDSGIQACFDRASEYQLNDSAGYYLSDLERLVTPGYVPTEQDVLRSRVKT

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

TRAMKQVAGTMKLELAQYREVAAFAQFGSDLDAATQQLLSRGVRLTELLKQGQYSPMAIEEQVAVIYAGVRGYLDKLEPSKITKFENAFLSHVISQHQALLGKIRTDGKISEESDAKLKEIVTNFLAGFEA

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

MDPNIVGSEHYDVARGVQKILQDYKSLQDIIAILGMDELSEEDKLTVSRARKIQRFLSQPFQVAEVFTGHLGKLVPLKETIKGFQQILAGEYDHLPEQAFYMVGPIEEAVAKADKLAE

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

NSIIQRISKFDNILKDKTIINQQDLRQISWNGIPKIHRPVVWKLLIGYLPVNTKRQEGFLQRKRKEYRDSLKHTFSDQHSRDIPTWHQIEIDIPRTNPHIPLYQFKSVQNSLQRILYLWAIRHPASGYVQGINDLVTPFFETFLTEYLPPSQIDDVEIKDPSTYMVDEQITDLEADTFWCLTKLLEQITDNYIH

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

GQPGILRQVKNLSQLVKRIDADLYNHFQNEHVEFIQFAFRWMNCLLMREFQMGTVIRMWDTYLSETSQEVTSSYSMSSNDIKPPVTPTEPRVASFVTPTKDFQSPTTALSNMTPNNAVEDSGKMRQSSLNEFHVFVCAAFLIKWSDQLMEMDFQETITFLQNPPTKDWTETDIEMLLSEAFIWQSLYK

>d1ak4c\_ a.73.1.1 (C:) HIV-1 capsid protein {Human immunodeficiency virus type 1}

PIVQNLQGQMVHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRLHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTHNPPIPVGEIYKRWIILGLNKIVRMY

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

PRGYTTWVNTIQTNGLLNEASQNLFGILSVDCTSEEMNAFLDVVPGQAGQKQILLDAIDKIADDWDNRHPLPNAPLVAPPQGPIPMTARFIRGLGVPRERQMEPAFDQFRQTYRQWIIEAMSEGIKVMIGK

>d1g03a\_ a.73.1.1 (A:) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

PVMHPHGAPPNHRPWQMKDLQAIKQEVSQAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCSSLVASLHHQQLDSLISEAETRGITSYNPLAGPLRVQANNPQQQGLRREYQQLWLAAFAALPGSAKDPSWA

>d1em9a\_ a.73.1.1 (A:) RSV capsid protein {Rous sarcoma virus}

PVVIKTEGPAWTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVILGPAPYALWMDAWGVQLQTVIAAATRDPRHPANGQGRGERTNLNRLKGLADGMVGNPQGQAALLRPGELVAITASALQAFREVARLA

>d1vin\_1 a.74.1.1 (181-308) Cyclin A {Cow (Bos taurus)}

DIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYIDRFLSSMSVLRGKLQLVGTAAMLLASKFEEIYPPEVAEFVYITDDTYTKKQVLRMEHLVLKVLAFDLAA

>d1vin\_2 a.74.1.1 (309-432) Cyclin A {Cow (Bos taurus)}

PTINQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAAAAFHLALYTVTGQSWPESLVQKTGYTLETLKPCLLDLHQTYLRAPQHAQQSIREKYKNSKYHGVSLLNPPETLNL

>d1jkw\_1 a.74.1.1 (11-161) Cyclin H (mcs2) {Human (Homo sapiens)}

WTFSSEEQLARLRADANRKFRCKAVANGKVLPNDPVFLEPHEEMTLCKYYEKRLLEFCSVFKPAMPRSVVGTACMYFKRFYLNNSVMEYHPRIIMLTCAFLACKVDEFNVSSPQFVGNLRESPLGQEKALEQILEYELLLIQQLNFHLIVH

>d1jkw\_2 a.74.1.1 (162-287) Cyclin H (mcs2) {Human (Homo sapiens)}

NPYRPFEGFLIDLKTRYPILENPEILRKTADDFLNRIALTDAYLLYTPSQIALTAILSSASRAGITMESYLSESLMLKENRTCLSQLLDIMKSMRNLVKKYEPPRSEEVAVLKQKLDRCHSAELAL

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

RVLNNLKLRELLLPKFTSLWEIQTEVTVDNRTILLTWMHLLCESFELDKSVFPLSVSILDRYLCKKQGTKKTLQKIGAACVLIGSKIRTVKPMTVSKLTYLSCDCFTNLELINQEKDILEALKWDTE

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

AVLATDFLIPLCNALKIPEDLWPQLYEAASTTICKALIQPNIALLSPGLICAGGLLTTIETDNTNCRPWTCYLEDLSSILNFSTNTVRTVKDQVSEAFSLYD

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

FQGFLDSSLLNEEDCRQMIYRSEREHDARMVGVNVDQHFTSQYRKVLTTWMFCVCKDLRQDNNVFPLAVALLDELFLSTRIDRENYQSTAAVALHIAGKVRAYMPIKATQLAYLCGGATTADKLLTLEVKSLDTLSWVADR

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

CLSTDLICYILHIMHAPREDYLNIYNLCRPKIFCALCDGRSAMKRPVLITLACMHLTMNQKYDYYENRIDGVCKSLYITKEELHQCCDLVDIAIVSFDENYFKINA

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

LCEDRIFYNILEIEPRFLTSDSVFGTFQQSLTSHMRKLLGTWMFSVCQEYNLEPNVVALALNLLDRLLLIKQVSKEHFQKTGSACLLVASKLRSLTPISTSSLCYAAADSFSRQELIDQEKELLEKLAWRTE

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

AVLATDVTSFLLLKLVGGSQHLDFWHHEVNTLITKALVDPLTGSLPASIISAAGCALLVPANVIPQDTHSGGVVPQLASILGCDVSVLQAAVEQILTSVSDFDLRI

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

AMMNAFKEITTMADRINLPRNKVDRTNNLFRQAYEQKSLKGRANDAIASACLYIACRQEGVPRTFKEICAVSRISKKEIGRCFKLILKALETSVD

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

LITTGDFMSRFCSNLCLPKQVQMAATHIARKAVELDLVPGRSPISVAAAAIYMASQASAEKRTQKEIGDIAGVADVTIRQSYRLIYPRAPDLFPTDFKFDTPVDKLPQL

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

NLAFALSELDRITAQLKLPRHVEEEAARLYREAVRKGLIRGRSIESVMAACVYAACRLLKVPRTLDEIADIARVDKKEIGRSYRFIARNLNLTPKKLF

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

VKPTDYVNKFADELGLSEKVRRRAIEILDEAYKRGLTSGKSPAGLVAAALYIASLLEGEKRTQREVAEVARVTEVTVRNRYKELVEKLKIKVPIA

>d1guxa\_ a.74.1.3 (A:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}

NTIQQLMMILNSASDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGVRLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSGTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSDSPLFDLIKQSK

>d1guxb\_ a.74.1.3 (B:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}

TSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHI

>d1rss\_\_ a.75.1.1 (-) Ribosomal protein S7 {Thermus thermophilus}

LQPDLVYGDVLVTAFINKIMRDGKKNLAARIFYDACKIIQEKTGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSPRRQQSLALRWLVQAANQRPERRAAVRIAHELMDAAEGKGGAVKKKEDVERMAEANRAYAHYRW

>d1iqva\_ a.75.1.1 (A:) Ribosomal protein S7 {Archaeon Pyrococcus horikoshii}

IKVMGRWSTEDVEVKDPSLKPYINLEPRLLPHTHGRHAKKHFGKANVHIVERLINKVMRSGGSHYKVAGHFMRREHRSLNSKKVRAYEVVKEAFKIIEKRTGKNPIQVLVWAIENAAPREDTTSVMFGGIRYHVAVDISPLRRLDVALRNIALGASAKCYRTKMSFAEALAEEIILAANKDPKSYAYSKKLEIERIAESSR

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

TLDDDQALSLVEAMVEANGERVMALINEAAARGIEWEALLVEMLGLLHRIAMVQLSPAALGNDMAAIELRMRELARTIPPTDIQLYYQTLLIGRKELPYAPDRRMGVEMTLLRALAFHPRMPLPEP

>d1a5t\_1 a.80.1.1 (208-330) delta prime subunit {Escherichia coli}

DNWQARETLCQALAYSVPSGDWYSLLAALNHEQAPARLHWLATLLMDALKRHHGAAQVTNVDVPGLVAELANHLSPSRLQAILGDVCHIREQLMSVTGINRELLITDLLLRIEHYLQPGVVLP

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

FTPFHWVDALLMGKSKRALHILQQLRLEGSEPVILLRTLQRELLLLVNLKRQSAHTPLRALFDKHRVWQNRRGMMGEALNRLSQTQLRQAVQLLTRTELTLKQDYGQSVWAELEGLSLLLCHKPLAD

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

RARPEDIREMMLLALKGNFLKAREKLREILLKQGLSGEDVLVQMHKEVFNLPIEEPKKVLLADKIGEYNFRLVEGANEIIQLEALLAQFTLIGKK

>d1ngr\_\_ a.77.1.1 (-) p75 low affinity neurotrophin receptor {Rat (Rattus norvegicus)}

GNLYSSLPLTKREEVEKLLNGDTWRHLAGELGYQPEHIDSFTHEACPVRALLASWGAQDSATLDALLAALRRIQRADIVESLCSE

>d1ddf\_\_ a.77.1.1 (-) Fas {Human (Homo sapiens)}

METVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLVLEHHHHHH

>d1a1w\_\_ a.77.1.1 (-) FADD (Mort1) {Human (Homo sapiens)}

MDPFLVLLHSVSSSLSSSELTELKYLCLGRVGKRKLERVQSGLDLFSMLLEQNDLEPGHTELLRELLASLRRHDLLRRVDDFE

>d1e41a\_ a.77.1.1 (A:) FADD (Mort1) {Human (Homo sapiens)}

GSHMGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGA

>d3crd\_\_ a.77.1.1 (-) Raidd CARD domain {Human (Homo sapiens)}

MEARDKQVLRSLRLELGAEVLVEGLVLQYLYQEGILTENHIQEINAQTTGLRKTMLLLDILPSRGPKAFDTFLDSLQEFPWVREKLKKAREEAMTDLPAG

>d1cy5a\_ a.77.1.1 (A:) Apoptotic protease activating factor 1, APAF-1 {Human (Homo sapiens)}

MDAKARNCLLQHREALEKDIKTSYIMDHMISDGFLTISEEEKVRNEPTQQQRAAMLIKMILKKDNDSYVSFYNALLHEGYKDLAALLHDGIPV

>d3ygsp\_ a.77.1.1 (P:) Procaspase 9 prodomain {Human (Homo sapiens)}

SMDEADRRLLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRRDQARQLIIDLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAG

>d1dgna\_ a.77.1.1 (A:) Iceberg {Human (Homo sapiens)}

ADQLLRKKRRIFIHSVGAGTINALLDCLLEDEVISQEDMNKVRDENDTVMDKARVLIDLVTGKGPKSCCKFIKHLCEEDPQLASKMGLH

>d1d2za\_ a.77.1.1 (A:) Pelle death domain {Drosophila melanogaster}

LDNTMAIRLLPLPVRAQLCAHLDALDVWQQLATAVKLYPDQVEQISSQKQRGRSASNEFLNIWGGQYNHTVQTLFALFKKLKLHNAMRLIKDYVSEDLHKYI

>d1d2zb\_ a.77.1.1 (B:) Tube death domain {Drosophila melanogaster}

LSSKYSRNTELRRVEDNDIYRLAKILDENSCWRKLMSIIPKGMDVQACSGAGCLNFPAEIKKGFKYTAQDVFQIDEAANRLPPDQSKSQMMIDEWKTSGKLNERPTVGVLLQLLVQAELFSAADFVALDFLNESTPARPVDGPGALISLE

>d1eyva\_ a.79.1.1 (A:) Antitermination factor NusB {Mycobacterium tuberculosis}

GRHQARKRAVALLFEAEVRGISAAEVVDTRAALAEAKPDIARLHPYTAAVARGVSEHAAHIDDLITAHLRGWTLDRLPAVDRAILRVSVWELLHAADVPEPVVVDEAVQLAKELSTDDSPGFVNGVLGQVM

>d1ey1a\_ a.79.1.1 (A:) Antitermination factor NusB {Escherichia coli}

MKPAARRRARECAVQALYSWQLSQNDIADVEYQFLAEQDVKDVDVLYFRELLAGVATNTAYLDGLMKPYLSRLLEELGQVEKAVLRIALYELSKRSDVPYKVAINEAIELAKSFGAEDSHKFVNGVLDKAAPVIRPNKK

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

AASERRRLYPPSAEYPDLRKHNNCMASHLTPAVYARLCDKTTPTGWTLDQCIQTGVDNPGHPFIKTVGMVAGDEETYEVFADLFDPVIQERHNGYDPRTMKH

>d1bg0\_1 a.83.1.1 (2-95) Arginine kinase {Horseshoe crab (Limulus polyphemus)}

VDQATLDKLEAGFKKLQEASDCKSLLKKHLTKDVFDSIKNKKTGMGATLLDVIQSGVENLDSGVGIYAPDAESYRTFGPLFDPIIDDYHGGFKL

>d1lla\_1 a.85.1.1 (2-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus polyphemus)}

LHDKQIRICHLFEQLSSATVIGDGDKHKHSDRLKNVGKLQPGAIFSCFHPDHLEEARHLYEVFWEAGDFNDFIEIAKEARTFVNEGLFAFAAEVAVLHRDDCKGLYVP

>d1hc2\_1 a.85.1.1 (5-135) Hemocyanin, N-terminal domain {Spiny lobster (Panulirus interruptus)}

TGNAQKQQDINHLLDKIYEPTKYPDLKDIAENFNPLGDTSIYNDHGAAVETLMKELNDHRLLEQRHWYSLFNTRQRKEALMLFAVLNQCKEWYCFRSNAAYFRERMNEGEFVYALYVSVIHSKLGDGIVLP

>d1lla\_2 a.86.1.1 (110-379) Hemocyanin {Horseshoe crab (Limulus polyphemus)}

PVQEIFPDKFIPSAAINEAFKKAHVRPEFDESPILVDVQDTGNILDPEYRLAYYREDVGINAHHWHWHLVYPSTWNPKYFGKKKDRKGELFYYMHQQMCARYDCERLSNGMHRMLPFNNFDEPLAGYAPHLTHVASGKYYSPRPDGLKLRDLGDIEISEMVRMRERILDSIHLGYVISEDGSHKTLDELHGTDILGALVESSYESVNHEYYGNLHNWGHVTMARIHDPDGRFHEEPGVMSDTSTSLRDPIFYNWHRFIDNIFHEYKNTLK

>d1hc2\_2 a.86.1.1 (136-398) Hemocyanin {Spiny lobster (Panulirus interruptus)}

PLYQITPHMFTNSEVIDKAYSAKMTQKPGTFNVSFTGTKKNREQRVAYFGEDIGMNIHHVTWHMDFPFWWEDSYGYHLDRKGELFFWVHHQLTARFDFERLSNWLDPVDELHWDRIIREGFAPLTSYKYGGEFPVRPDNIHFEDVDGVAHVHDLEITESRIHEAIDHGYITDSDGHTIDIRQPKGIELLGDIIESSKYSSNVQYYGSLHNTAHVMLGRQGDPHGKFNLPPGVMEHFETATRDPSFFRLHKYMDNIFKKHTDSF

>d1js8a1 a.86.1.1 (A:2503-2791) Functional unit from octopus hemocyanin {Giant octopus (Octopus dofleini)}

AIIRKNVNSLTPSDIKELRDAMAKVQADTSDNGYQKIASYHGIPLSCHYENGTAYACCQHGMVTFPNWHRLLTKQMEDALVAKGSHVGIPYWDWTTTFANLPVLVTEEKDNSFHHAHIDVANTDTTRSPRAQLFDDPDKGDKSFFYRQIALALEQTDFCDFEIQFEIGHNAIHSWVGGSSPYGMSTLHYTSYDPLFYLHHSNTDRIWSVWQALQKYRGLPYNTANCEINKLVKPLKPFNLDTNPNAVTKAHSTGATSFDYHKLGYDYDNLNFHGMTIPELEEHLKEIQH

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

EQTYYDLVKAFMAEIRQYIRELNLIIKVFREPFVSNSKLFSANDVENIFSRIVDIHELSVKLLGHIEDTVEMTDEGSPHPLVGSCFEDLAEELAFDPYESYARDILRPGFHDRFLSQLSKPGAALYLQSIGEGFKEAVQYVLPRLLLAPVYHCLHYFELLKQLEEKSEDQEDKECLKQAITALLNVQSGMEKICSKSLAKRRLSESA

>d1by1a\_ a.87.1.1 (A:) beta-pix {Human (Homo sapiens)}

MKGFDTTAINKSYYNVVLQNILETENEYSKELQTVLSTYLRPLQTSEKLSSANISYLMGNLEEICSFQQMLVQSLEECTKLPEAQQRVGGCFLNLMPQMKTLYLTYCANHPSAVNVLTEHSEELGEFMETKGASSPGILVLTTGLSKPFMRLDKYPTLLKELERHMEDYHTDRQDIQKSMAAFKNLSAQCQEVRKRKELELQILTEAIR

>d1f5xa\_ a.87.1.1 (A:) RhoGEF Vav {Mouse (Mus musculus)}

MKGDEIYEDLMRLESVPTPPKMTEYDKRCCCLREIQQTEEKYTDTLGSIQQHFMKPLQRFLKPQDMETIFVNIEELFSVHTHFLKELKDALAGPGATTLYQVFIKYKERFLVYGRYCSQVESASKHLDQVATAREDVQMKLEECSQRANNGRFTLRDLLMVPMQRVLKYHLLLQELVKHTQDATEKENLRLALDAMRDLAQCVNEVKR

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

QLSDADKLRKVICELLETERTYVKDLNCLMERYLKPLQKETFLTQDELDVLFGNLTEMVEFQVEFLKTLEDGVRLVPDLEKLEKVDQFKKVLFSLGGSFLYYADRFKLYSAFCASHTKVPKVLVKAKTDTAFKAFLDAQNPRQQHSSTLESYLIKPIQRVLKYPLLLRELFALTDAESEEHYHLDVAIKTMNKVASHINEMQKIHE

>d1e6ya1 a.89.1.1 (A:1284-1569) Alpha chain {Archaeon Methanosarcina barkeri}

RRARGPNEPGGLSFGHLSDIVQTSRVSEDPAKIALEVVGAGCMLYDQIWLGSYMSGGVGFTQYATAAYTDDILDNNTYYDVDYINDKYNGAATVGKDNKVKASLEVVKDIATESTLYGIETYEKFPTALEDHFGGSQRATVLAAAAGVACSLATGNANAGLSGWYLSMYLHKEAWGRLGFFGFDLQDQCGATNVLSYQGDEGLPDELRGPNYPNYAMNVGHQGGYAGIAQAAHSGRGDAFTVNPLLKVCFADDLLPFNFAEPRREFGRGAIREFVPAGERSLVIPA

>d1hbnb1 a.89.1.1 (B:189-443) Beta chain {Archaeon Methanobacterium thermoautotrophicum}

GYALRNIMVNHVVAATLKNTLQAAALSTILEQTAMFEMGDAVGAFERMHLLGLAYQGMNADNLVFDLVKANGKEGTVGSVIADLVERALEDGVIKVEKELTDYKVYGTDDLAMWNAYAAAGLMAATMVNQGAARAAQGVSSTLLYYNDLIEFETGLPSVDFGKVEGTAVGFSFFSHSIYGGGGPGIFNGNHIVTRHSKGFAIPCVAAAMALDAGTQMFSPEATSGLIKEVFSQVDEFREPLKYVVEAAAEIKNEI

>d1agre\_ a.91.1.1 (E:) Regulator of G-protein signalling 4, RGS4 {Rat (Rattus norvegicus)}

VSQEEVKKWAESLENLINHECGLAAFKAFLKSEYSEENIDFWISCEEYKKIKSPSKLSPKAKKIYNEFISVQATKEVNLDSCTREETSRNMLEPTITCFDEAQKKIFNLMEKDSYRRFLKSRFYLDLT

>d1fqia\_ a.91.1.1 (A:) RGS9, RGS domain {Cow (Bos taurus)}

KLVDIPTKMRVERWAFNFSELIRDPKGRQSFQHFLRKEFSGENLGFWEACEDLKYGDQSKVKEKAEEIYKLFLAPGARRWINIDGKTMDITVKGLKHPHRYVLDAAQTHIYMLMKKDSYARYLKSPIYKEMLAKAIEP

>d1dk8a\_ a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}

GSASPTPPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYTRTGSESPKV

>d1iapa\_ a.91.1.1 (A:) p115RhoGEF {Human (Homo sapiens)}

SQFQSLEQVKRRPAHLMALLQHVALQFEPGPLLCCLHADMLGSLGPKEAKKAFLDFYHSFLEKTAVLRVPVPPNVAFELDRTRADLISEDVQRRFVQEVVQSQQVAVGRQLEDFRSKRLMGMTPWEQELAQLEAWVGRDRASYEARERHVAERLLMHLEEMQHTISTDEEKSAAVVNAIGLYMRHLGVRT

>d1htjf\_ a.91.1.1 (F:) Pdz-RhoGEF RGS-like domain {Human (Homo sapiens)}

ESDIIFQDLEKLKSRPAHLGVFLRYIFSQADPSPLLFYLCAEVYQQASPKDSRSLGKDIWNIFLEKNAPLRVKIPEMLQAEIDSRLRNSEDARGVLCEAQEAAMPEIQEQIHDYRTKRTLGLGSLYGENDLLDLDGDPLRERQVAEKQLAALGDILSAYAADRSAPMDFALNTYMSHAGIRL

>d1jdra\_ a.93.1.1 (A:) Cytochrome c peroxidase, CCP {Baker's yeast (Saccharomyces cerevisiae)}

TTPLVHVASVEKGRSYEDFQKVYNAIALKLREDDEYDNYIGYGPVLVRLAWHTSGTWDKHDNTGGSYGGTYRFKKEFNDPSNAGLQNGFKFLEPIHKEFPWISSGDLFSLGGVTAVQEMQGPKIPWRCGRVDTPEDTTPDNGRLPDADKDADYVRTFFQRLNMNDREVVALMGAHTLGKTHLKNSGYEGPWTANNNVFDNSFYLNLLNEDWKLEKNDANNEQWDSKSGYMMLPTDYSLIQDPKYLSIVKEYANDQDKFFKDFSKAFEKLLENGITFPKDAPSPFIFKTLEEQGL

>d1mn2\_\_ a.93.1.1 (-) Manganese peroxidase {Basidomycetos fungus (Phanerochaete chrysosporium)}

AVCPDGTRVSHAACCAFIPLAQDLQETIFQNECGQDAHEVIRLTFHDAIAISRSQGPKAGGGADGSMLLFPTVEPNFSANNGIDDSVNNLIPFMQKHNTISAADLVQFAGAVALSNCPGAPRLEFLAGRPNKTIAAVDGLIPEPQDSVTKILQRFEDAGGFTPFEVVSLLASHSVARANKVDQTIDAAPFDSTPFTFDTQVFLEVLLKGVGFPGSANNTGEVASPLPLGSGSDTGEMRLQSDFALAHDPRTACIWQGFVNEQAFMAASFRAAMSKLAVLGHNRNSLIDCSDVVPVPKPATGQPAMFPASTGPQDLELSCPSERFPTLTTQPGASQSLIAHCPDGSMSCPGVQFNGPA

>d1apxa\_ a.93.1.1 (A:) Ascorbate peroxidase {Pea (Pisum sativum)}

GKSYPTVSPDYQKAIEKAKRKLRGFIAEKKCAPLILRLAWHSAGTFDSKTKTGGPFGTIKHQAELAHGANNGLDIAVRLLEPIKEQFPIVSYADFYQLAGVVAVEITGGPEVPFHPGREDKPEPPPEGRLPDATKGSDHLRDVFGKAMGLSDQDIVALSGGHTIGAAHKERSGFEGPWTSNPLIFDNSYFTELLTGEKDGLLQLPSDKALLTDSVFRPLVEKYAADEDVFFADYAEAHLKLSELGFAEA

>d1bgp\_\_ a.93.1.1 (-) Plant peroxidase {Barley (Hordeum vulgare), peroxidase 1}

AEPPVAPGLSFDFYWQTCPRAESIVREFVQEAVRKDIGLAAGLLRLHFHDCFVQGCDASVLLDGSATGPGEQQAPPNLTLRPSAFKAVNDIRDRLERECRGAVVSCSDILALAARDSVVVSGGPDYRVPLGRRDSRSFASTQDVLSDLPGPSSNVQSLLALLGRLGLDATDLVTISGGHTIGLAHCSSFEDRLFPRPDPTISPTFLSRLKRTCPAKGTDRRTVLDVRTPNVFDNKYYIDLVNREGLFVSDQDLFTNAITRPIVERFAQSQQDFFEQFGVSIGKMGQMRVRTSDQGEVRRNCSVRNPGPG

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

CPEQDKYRTITGMCNNRRSPTLGASNRAFVRWLPAEYEDGFSLPYGWTPGVKRNGFPVALARAVSNEIVRFPTDQLTPDQERSLMFMQWGQLLDHDLDFTPEPAXVNCETSCVQQPPCFPLKIPPNDPRIKNQADCIPFFRSCPACPGSNITIRNQINALTSFVDASMVYGSEEPLARNLRNMSNQLGLLAVNQRFQDNGRALLPFDNLHDDPCLLTNRSARIPCFLAGDTRSSEMPELTSMHTLLLREHNRLATELKSLNPRWDGERLYQEARKIVGAMVQIITYRDYLPLVLGPTAMRKYLPTYRSYNDSVDPRIANVFTNAFRYGHTLIQPFMFRLDNRYQPMEPNPRVPLSRVFFASWRVVLEGGIDPILRGLMATPAKLNRQNQIAVDEIRERLFEQVMRIGLDLPALNMQRSRDHGLPGYNAWRRFCGLPQPETVGQLGTVLRNLKLARKLMEQYGTPNNIDIWMGGVSEPLKRKGRVGPLLACIIGTQFRKLRDGDRFWWENEGVFSMQQRQALAQISLPRIICDNTGITTVSKNNIFMSNSYPRDFVNCSTLPALNLASWREA

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

FLTRIKLLLKPTPNTVHYILTHFKGVWNIVNNIPFLRSLIMKYVLTSRSYLIDSPPTYNVHYGYKSWEAFSNLSYYTRALPPVADDCPTPMGVKGNKELPDSKEVLEKVLLRREFIPDPQGSNMMFAFFAQHFTAQFFKTDHKRGPGFTRGLGHGVDLNHIYGETLDRQHKLRLFKDGKLKYQVIGGEVYPPTVKDTQVEMIYPPHIPENLQFAVGQEVFGLVPGLMMYATIWLREHQRVCDILKQEHPEWGDEQLFQTSKLILIGETIKIVIEDYVQHLSGYHFKLKFDPELLFNQQFQYQNRIASEFNTLYHWHPLLPDTFNIEDQEYSFKQFLYNNSILLEHGLTQFVESFTRQIAGRVAGGRNVPIAVQAVAKASIDQSREMKYQSLNEYRKRFSLKPYTSFEELTGEKEMAAELKALYSDIDVMELYPALLVEKPRPDAIFGETMVELGAPFSLKGLMGNPICSPQYWKPSTFGGEVGFKIINTASIQSLICNNVKGCPFTSFNVQ

>d1mun\_\_ a.96.1.2 (-) Catalytic domain of MutY {Escherichia coli}

MQASQFSAQVLDWYDKYGRKTLPWQIDKTPYKVWLSEVMLQQTQVATVIPYFERFMARFPTVTDLANAPLDEVLHLWTGLGYYARARNLHKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLSLGKHFPILNGNVKRVLARCYAVSGWPGKKEVENKLWSLSEQVTPAVGVERFNQAMMDLGAMICTRSKPKCSLCPLQNGCIAAANNSWALYPGKKPK

>d1keaa\_ a.96.1.2 (A:) Thymine-DNA glycosylase {Archaeon Methanobacterium thermoformicicum}

DATNKKRKVFVSTILTFWNTDRRDFPWRHTRDPYVILITEILLRRTTAGHVKKIYDKFFVKYKCFEDILKTPKSEIAKDIKEIGLSNQRAEQLKELARVVINDYGGRVPRNRKAILDLPGVGKYTCAAVMCLAFGKKAAMVDANFVRVINRYFGGSYENLNYNHKALWELAETLVPGGKCRDFNLGLMDFSAIICAPRKPKCEKCGMSKLCSYYEKC

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

AARPGLRLPGCVDAFEQGVRAILGQLVSVAMAAKLTARVAQLYGERLDDFPEYICFPTPQRLAAADPQALKALGMPLKRAEALIHLANAALEGTLPMTIPGDVEQAMKTLQTFPGIGRWTANYFALRGWQAKDVFLPDDYLIKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDEA

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

DPIECLFSFICSSNNNIARITGMVERLCQAFGPRLIQLDDVTYHGFPSLQALAGPEVEAHLRKLGLGYRARYVSASARAILEEQGGLAWLQQLRESSYEEAHKALCILPGVGTKVADCICLMALDKPQAVPVDVHMWHIAQRDYSWHPTTSQAKGPSPQTNKELGNFFRSLWGPYAGWAQAVLFSADL

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

LPLPEPGEEAALAGLRAFLEAKLPRYAEERDRLDGEGGSRLSPYFALGVLSPRLAAWEAERRGGEGARKWVAELLWRDFSYHLLYHFPWMAERPLDPRFQAFPWQEDEALFQAWYEGKTGVPLVDAAMRELHATGFLSNRARMNAAQFAVKHLLLPWKRCEEAFRHLLLDGDRAVNLQGWQWAGGLGVDAAPYFRVFNPVLQGERHDPEGRWLKRWAPEYPSYAPKDPVVDLEEARRRYLRLARD

>d1qnf\_1 a.99.1.1 (205-475) FAD-binding (C-terminal) domain of DNA photolyase {Anacystis nidulans}

PVEPGETAAIARLQEFCDRAIADYDPQRNFPAEAGTSGLSPALKFGAIGIRQAWQAASAAHALSRSDEARNSIRVWQQELAWREFYQHALYHFPSLADGPYRSLWQQFPWENREALFTAWTQAQTGYPIVDAAMRQLTETGWMHNRCRMIVASFLTKDLIIDWRRGEQFFMQHLVDGDLAANNGGWQWSASSGMDPKPLRIFNPASQAKKFDATATYIKRWLPELRHVHPKDLISGEITPIERRGYPAPIVNHNLRQKQFKALYNQLKAAI

>d2pgd\_1 a.100.1.1 (177-473) 6-phosphogluconate dehydrogenase (6PGD) {Sheep (Ovis orientalis aries)}

GAGHFVKMVHNGIEYGDMQLICEAYHLMKDVLGLGHKEMAKAFEEWNKTELDSFLIEITASILKFQDADGKHLLPKIRDSAGQKGTGKWTAISALEYGVPVTLIGEAVFARCLSSLKDERIQASKKLKGPQNIPFEGDKKSFLEDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGGCIIRSVFLGKIKDAFDRNPGLQNLLLDDFFKSAVENCQDSWRRAISTGVQAGIPMPCFTTALSFYDGYRHAMLPANLIQAQRDYFGAHTYELLAKPGQFIHTNWTGHGG

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

GAGSCVKMYHNSGEYAILQIWGEVFDILRAMGLNNDEVAAVLEDWKSKNFLKSYMLDISIAAARAKDKDGSYLTEHVMDRIGSKGTGLWSAQEALEIGVPAPSLNMAVVSRQFTMYKTERQANASNAPGITQSPGYTLKNKSPSGPEIKQLYDSVCIAIISCYAQMFQCLREMDKVHNFGLNLPATIATFRAGCILQGYLLKPMTEAFEKNPNISNLMCAFQTEIRAGLQNYRDMVALITSKLEVSIPVLSASLNYVTAMFTPTLKYGQLVSLQRDVFGRHGYERVDKDGRESFQWPELQ

>d1gai\_\_ a.102.1.1 (-) Glucoamylase {Aspergillus awamori, variant x100}

ATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIVVASPSTDNPDYFYTWTRDSGLVIKTLVDLFRNGDTDLLSTIEHYISSQAIIQGVSNPSGDLSSGGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSAATEIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCSWCDSQAPQILCYLQSFWTGSYILANFDSSRSGKDTNTLLGSIHTFDPEAGCDDSTFQPCSPRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDSYYNGNPWFLCTLAAAEQLYDALYQWDKQGSLEITDVSLDFFKALYSGAATGTYSSSSSTYSSIVSAVKTFADGFVSIVETHAASNGSLSEQFDKSDGDELSARDLTWSYAALLTANNRRNSVVPPSWGETSASSVPGTCAATSASGTYSSVTVTSWPSIVATG

>d1ayx\_\_ a.102.1.1 (-) Glucoamylase {Baker's yeast (Saccharomycopsis fibuligera)}

AYPSFEAYSNYKVDRTDLETFLDKQKEVSLYYLLQNIAYPEGQFNNGVPGTVIASPSTSNPDYYYQWTRDSAITFLTVLSELEDNNFNTTLAKAVEYYINTSYNLQRTSNPSGSFDDENHKGLGEPKFNTDGSAYTGAWGRPQNDGPALRAYAISRYLNDVNSLNEGKLVLTDSGDINFSSTEDIYKNIIKPDLEYVIGYWDSTGFDLWEENQGRHFFTSLVQQKALAYAVDIAKSFDDGDFANTLSSTASTLESYLSGSDGGFVNTDVNHIVENPDLLQQNSRQGLDSATYIGPLLTHDIGESSSTPFDVDNEYVLQSYYLLLEDNKDRYSVNSAYSAGAAIGRYPEDVYNGDGSSEGNPWFLATAYAAQVPYKLAYDAKSASNDITINKINYDFFNKYIVDLSTINSAYQSSDSVTIKSGSDEFNTVADNLVTFGDSFLQVILDHINDDGSLNEQLNRYTGYSTGAYSLTWSSGALLEAIRLRNKVKALA

>d1cem\_\_ a.102.1.2 (-) CelA cellulase {Clostridium thermocellum}

AGVPFNTKYPYGPTSIADNQSEVTAMLKAEWEDWKSKRITSNGAGGYKRVQRDASTNYDTVSEGMGYGLLLAVCFNEQALFDDLYRYVKSHFNGNGLMHWHIDANNNVTSHDGGDGAATDADEDIALALIFADKQWGSSGAINYGQEARTLINNLYNHCVEHGSYVLKPGDRWGGSSVTNPSYFAPAWYKVYAQYTGDTRWNQVADKCYQIVEEVKKYNNGTGLVPDWCTASGTPASGQSYDYKYDATRYGWRTAVDYSWFGDQRAKANCDMLTKFFARDGAKGIVDGYTIQGSKISNNHNASFIGPVAAASMTGYDLNFAKELYRETVAVKDSEYYGYYGNSLRLLTLLYITGNFPNPLSDL

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

EPAFNYAEALQKSMFFYEAQRSGKLPENNRVSWRGDSGLNDGADVGLDLTGGWYDAGDHVKFGFPMAFTATMLAWGAIESPEGYIRSGQMPYLKDNLRWVNDYFIKAHPSPNVLYVQVGDGDADHKWWGPAEVMPMERPSFKVDPSCPGSDVAAETAAAMAASSIVFADDDPAYAATLVQHAKQLYTFADTYRGVYSDCVPAGAFYNSWSGYQDELVWGAYWLYKATGDDSYLAKAEYEYDFLSTEQQTDLRSYRWTIAWDDKSYGTYVLLAKETGKQKYIDDANRWLDYWTVGVNGQRVPYSPGGMAVLDTWGALRYAANTAFVALVYAKVIDDPVRKQRYHDFAVRQINYALGDNPRNSSYVVGFGNNPPRNPHHRTAHGSWTDSIASPAENRHVLYGALVGGPGSPNDAYTDDRQDYVANEVATDYNAGFSSALAMLVEEYGGTPLADFPPTEEPDG

>d1clc\_1 a.102.1.2 (135-575) CelD cellulase {Clostridium thermocellum}

AMNVYEDAFKTAMLGMYLLRCGTSVSATYNGIHYSHGPCHTNDAYLDYINGQHTKKDSTKGWHDAGDYNKYVVNAGITVGSMFLAWEHFKDQLEPVALEIPEKNNSIPDFLDELKYEIDWILTMQYPDGSGRVAHKVSTRNFGGFIMPENEHDERFFVPWSSAATADFVAMTAMAARIFRPYDPQYAEKCINAAKVSYEFLKNNPANVFANQSGFSTGEYATVSDADDRLWAAAEMWETLGDEEYLRDFENRAAQFSKKIEADFDWDNVANLGMFTYLLSERPGKNPALVQSIKDSLLSTADSIVRTSQNHGYGRTLGTTYYWGCNGTVVRQTMILQVANKISPNNDYVNAALDAISHVFGRNYYNRSYVTGLGINPPMNPHDRRSGADGIWEPWPGYLVGGGWPGPKDWVDIQDSYQTNEIAINWNAALIYALAGFVNYN

>d1faea\_ a.102.1.2 (A:) Processive endocellulase CelF (Cel48F) {Clostridium cellulolyticum}

ASSPANKVYQDRFESMYSKIKDPANGYFSEQGIPYHSIETLMVEAPDYGHVTTSEAMSYYMWLEAMHGRFSGDFTGFDKSWSVTEQYLIPTEKDQPNTSMSRYDANKPATYAPEFQDPSKYPSPLDTSQPVGRDPINSQLTSAYGTSMLYGMHWILDVDNWYGFGARADGTSKPSYINTFQRGEQESTWETIPQPCWDEHKFGGQYGFLDLFTKDTGTPAKQFKYTNAPDADARAVQATYWADQWAKEQGKSVSTSVGKATKMGDYLRYSFFDKYFRKIGQPSQAGTGYDAAHYLLSWYYAWGGGIDSTWSWIIGSSHNHFGYQNPFAAWVLSTDANFKPKSSNGASDWAKSLDRQLEFYQWLQSAEGAIAGGATNSWNGRYEAVPSGTSTFYGMGYVENPVYADPGSNTWFGMQVWSMQRVAELYYKTGDARAKKLLDKWAKWINGEIKFNADGTFQIPSTIDWEGQPDTWNPTQGYTGNANLHVKVVNYGTDLGCASSLANTLTYYAAKSGDETSRQNAQKLLDAMWNNYSDSKGISTVEQRGDYHRFLDQEVFVPAGWTGKMPNGDVIKSGVKFIDIRSKYKQDPEWQTMVAALQAGQVPTQRLHRFWAQSEFAVANGVYAILFPD

>d1dl2a\_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

GAGEMRDRIESMFLESWRDYSKHGWGYDVYGPIEHTSHNMPRGNQPLGWIIVDSVDTLMLMYNSSTLYKSEFEAEIQRSEHWINDVLDFDIDAEVNVFETTIRMLGGLLSAYHLSDVLEVGNKTVYLNKAIDLGDRLALAFLSTQTGIPYSSINLHSGQAVKNHADGGASSTAEFTTLQMEFKYLAYLTGNRTYWELVERVYEPLYKNNDLLNTYDGLVPIYTFPDTGKFGASTIRFGSRGDSFYEYLLKQYLLTHETLYYDLYRKSMEGMKKHLLAQSKPSSLWYIGEREQGLHGQLSPKMDHLVCFMGGLLASGSTEGLSIHEARRRPFFSKSDWDLAKGITDTCYQMYKQSSSGLAPEIVVFNDGNIKQDGWWRSSVGDFFVKPLDRHNLQRPETVESIMFMYHLSHDHKYREWGAEIATSFFENTCVDCNDPKLRRFTSLSDCITLPTKKSNNMESFWLAETLKYLYILFLDEFDLTKVVFNTEAHPFPVLDEEILKSQSLTTGWSL

>d1hcua\_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Trichoderma reesei}

KRGSPNPTRAAAVKAAFQTSWNAYHHFAFPHDDLHPVSNSFDDERNGWGSSAIDGLDTAILMGDADIVNTILQYVPQINFTTTAVANQGSSVFETNIRYLGGLLSAYDLLRGPFSSLATNQTLVNSLLRQAQTLANGLKVAFTTPSGVPDPTVFFNPTVRRSGASSNNVAEIGSLVLEWTRLSDLTGNPQYAQLAQKGESYLLNPKGSPEAWPGLIGTFVSTSNGTFQDSSGSWSGLMDSFYEYLIKMYLYDPVAFAHYKDRWVLGADSTIGHLGSHPSTRKDLTFLSSYNGQSTSPNSGHLASFGGGNFILGGILLNEQKYIDFGIKLASSYFGTYTQTASGIGPEGFAWVDSVTGAGGSPPSSQSGFYSSAGFWVTAPYYILRPETLESLYYAYRVTGDSKWQDLAWEALSAIEDACRAGSAYSSINDVTQANGGGASDDMESFWFAEALKYAYLIFAEESDVQVQATGGNKFVFNTEAHPFSIRS

>d1fo3a\_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Human (Homo sapiens)}

QGPVHLNYRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEARKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGKKDGLVPMFINTHSGLFTHLGVFTLGARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRTHLLRHSEPSKLTFVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQMNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLLRPETVESLFYLYRVTGDRKYQDWGWEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLDAYVFNTEAHPLPIWT

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

GTAELIMKRVMLDLKKPLRNMDKVAEKNLNTLQPDGSWKDVPYKDDAMTNWLPNNHLLQLETIIQAYIEKDSHYYGDDKVFDQISKAFKYWYDSDPKSRNWWHNEIATPQALGEMLILMRYGKKPLDEALVHKLTERMKRGEPEKKTGANKTDIALHYFYRALLTSDEALLSFAVKELFYPVQFVHYEEGLQYDYSYLQHGPQLQISSYGAVFITGVLKLANYVRDTPYALSTEKLAIFSKYYRDSYLKAIRGSYMDFNVEGRGVSRPDILNKKAEKKRLLVAKMIDLKHTEEWADAIARTDSTVAAGYK

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

EDNFTKLLDKWNDVTIGNYVYDTNDSNMQKLNQKLDETNAKNIEAIKLDSNRTFLWKDLDNLNNSAQLTATYRRLEDLAKQITNPHSTIYKNEKAIRTVKESLAWLHQNFYNVNKDIEGSANWWDFEIGVPRSITGTLSLMNNYFTDAEIKTYTDPIEHFVPDAEYFRKTLVNPFKALGGNLVDMGRVKIIEGLLRKDNTIIEKTSHSLKNLFTTATKAEGFYADGSYIDHTNVAYTGAYGNVLIDGLTQLLPIIQETDYKISNQELDMVYKWINQSFLPLIVKGELMDMSRGRSISREAASSHAAAVEVLRGFLRLANMSNEERNLDLKSTIKTIITSNKFYNVFNNLKSYSDIANMNKLLNDSTVATKP

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

APAYARTLDRAVEYLLSCQKDEGYWWGPLXISPVWDTGLAVLALRAAGLPADHDRLVKAGEWLLDRQITVPGDWAVKRPNLKPGGFAFQFDNVYYPDVCDTAVVVWALNTLRLPDERRRRDAMTKGFRWIVGMQSSNGGWGAYDVDNTSDLPNHIPFSDFGEVTDPPSEDVTAHVLECFGSFGYDDAWKVIRRAVEYLKREQKPDGSWFGRWGVNYLYGTGAVVSALKAVGIDTREPYIQKALDWVEQHQNPDGGWGEDCRSYEDPAYAGKGASTPSQTAWALMALIAGGRAESEAARRGVQYLVETQRPDGGWDEPYYTGTGFPGDFYLGYTMYRHVFPTLALGRYKQAIER

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

LSNVTMEAEYVLLCHILDRVDRDRMEKIRRYLLHEQREDGTWALYPGGPPDLDTTIEAYVALKYIGMSRDEEPMQKALRFIQSQGGIESSRVFTRMWLALVGEYPWEKVPMVPPEIMFLGKRMPLNIYEFGSWARATVVALSIVMSRQPVFPLPERARVPELYETDVPPRRRGAKGGGGWIFDALDRALHGYQKLSVHPFRRAAEIRALDWLLERQAGDGSWGGIQPPWFYALIALKILDMTQHPAFIKGWEGLELYGVELDYGGWMFQAS

>d1d8db\_ a.102.4.3 (B:) Protein farnesyltransferase, beta-subunit {Rat (Rattus norvegicus)}

PVWSEPLYSLRPEHARERLQDDSVETVTSIEQAKVEEKIQEVFSSYKFNHLVPRLVLQREKHFHYLKRGLRQLTDAYECLDASRPWLCYWILHSLELLDEPIPQIVATDVCQFLELCQSPDGGFGGGPGQYPHLAPTYAAVNALCIIGTEEAYNVINREKLLQYLYSLKQPDGSFLMHVGGEVDVRSAYCAASVASLTNIITPDLFEGTAEWIARCQNWEGGIGGVPGMEAHGGYTFCGLAALVILKKERSLNLKSLLQWVTSRQMRFEGGFQGRCNKLVDGCYSFWQAGLLPLLHRALHAQGDPALSMSHWMFHQQALQEYILMCCQCPAGGLLDKPGKSRDFYHTCYCLSGLSIAQHFGSGAMLHDVVMGVPENVLQPTHPVYNIGPDKVIQATTHFLQKPVPGF

>d1dceb\_ a.102.4.3 (B:) Rab geranylgeranyltransferase, beta subunit {Rat (Rattus norvegicus)}

TQQKDVTIKSDAPDTLLLEKHADYIASYGSKKDDYEYCMSEYLRMSGVYWGLTVMDLMGQLHRMNKEEILVFIKSCQHECGGVSASIGHDPHLLYTLSAVQILTLYDSIHVINVDKVVAYVQSLQKEDGSFAGDIWGEIDTRFSFCAVATLALLGKLDAINVEKAIEFVLSCMNFDGGFGCRPGSESHAGQIYCCTGFLAITSQLHQVNSDLLGWWLCERQLPSGGLNGRPEKLPDVCYSWWVLASLKIIGRLHWIDREKLRSFILACQDEETGGFADRPGDMVDPFHTLFGIAGLSLLGEEQIKPVSPVFCMPEEVLQRVNVQPELVS

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

ASSTNLKDILADLIPKEQARIKTFRQQHGNTAVGQITVDMMYGGMRGMKGLVYETSVLDPDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLIAKLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEKLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNVLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIKLVDSK

>d1aj8a\_ a.103.1.1 (A:) Citrate synthase {Archaeon Pyrococcus furiosus}

LAKGLEDVYIDQTNICYIDGKEGKLYYRGYSVEELAELSTFEEVVYLLWWGKLPSLSELENFKKELAKSRGLPKEVIEIMEALPKNTHPMGALRTIISYLGNIDDSGDIPVTPEEVYRIGISVTAKIPTIVANWYRIKNGLEYVPPKEKLSHAANFLYMLHGEEPPKEWEKAMDVALILYAEHEINASTLAVMTVGSTLSDYYSAILAGIGALKGPIHGGAVEEAIKQFMEIGSPEKVEEWFFKALQQKRKIMGAGHRVYKTYDPRARIFKKYASKLGDKKLFEIAERLERLVEEYLSKKGISINVDYWSGLVFYGMKIPIELYTTIFAMGRIAGWTAHLAEYVSHNRIIRPRLQYVGEIGKKYLPIELRR

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

EPTIHKGLAGVTADVTAISKVNSDTNSLLYRGYPVQELAAKCSFEQVAYLLWNSELPNDSELKAFVNFERSHRKLDENVKGAIDLLSTACHPMDVARTAVSVLGANHARAQDSSPEANLEKAMSLLATFPSVVAYDQRRRRGEELIEPREDLDYSANFLWMTFGEEAAPEVVEAFNVSMILYAEHSFNASTFTARVITSTLADLHSAVTGAIGALKGPLHGGANEAVMHTFEEIGIRKDESLDEAATRSKAWMVDALAQKKKVMGFGHRVYKNGDSRVPTMKSALDAMIKHYDRPEMLGLYNGLEAAMEEAKQIKPNLDYPAGPTYNLMGFDTEMFTPLFIAARITGWTAHIMEQVADNALIRPLSEYNGPEQRQVP

>d1dz4a\_ a.104.1.1 (A:) Cytochrome P450-CAM {Pseudomonas putida}

LAPLPPHVPEHLVFDFDMYNPSNLSAGVQEAWAVLQESNVPDLVWTRCNGGHWIATRGQLIREAYEDYRHFSSECPFIPREAGEAYDFIPTSMDPPEQRQFRALANQVVGMPVVDKLENRIQELACSLIESLRPQGQCNFTEDYAEPFPIRIFMLLAGLPEEDIPHLKYLTDQMTRPDGSMTFAEAKEALYDYLIPIIEQRRQKPGTDAISIVANGQVNGRPITSDEAKRMCGLLLVGGLDTVVNFLSFSMEFLAKSPEHRQELIQRPERIPAACEELLRRFSLVADGRILTSDYEFHGVQLKKGDQILLPQMLSGLDERENACPMHVDFSRQKVSHTTFGHGSHLCLGQHLARREIIVTLKEWLTRIPDFSIAPGAQIQHKSGIVSGVQALPLVWDPATTKAV

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

TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVDIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGI

>d1jfba\_ a.104.1.1 (A:) Cytochrome P450-NOR, nitric reductase {Fungus (Fusarium oxysporum)}

APSFPFSRASGPEPPAEFAKLRATNPVSQVKLFDGSLAWLVTKHKDVCFVATSEKLSKVRTRQGFPELSASGKQAAKAKPTFVDMDPPEHMHQRSMVEPTFTPEAVKNLQPYIQRTVDDLLEQMKQKGCANGPVDLVKEFALPVPSYIIYTLLGVPFNDLEYLTQQNAIRTNGSSTAREASAANQELLDYLAILVEQRLVEPKDDIISKLCTEQVKPGNIDKSDAVQIAFLLLVAGNATMVNMIALGVATLAQHPDQLAQLKANPSLAPQFVEELCRYHTASALAIKRTAKEDVMIGDKLVRANEGIIASNQSANRDEEVFENPDEFNMNRKWPPQDPLGFGFGDHRCIAEHLAKAELTTVFSTLYQKFPDLKVAVPLGKINYTPLNRDVGIVDLPVIF

>d1jipa\_ a.104.1.1 (A:) Cytochrome P450-ERYF {Saccaropolyspora erythraea}

TTVPDLESDSFHVDWYRTYAELRETAPVTPVRFLGQDAWLVTGYDEAKAALSDLRLSSDPKKKYPGVEVEFPAYLGFPEDVRNYFATNMGTSDPPTHTRLRKLVSQEFTVRRVEAMRPRVEQITAELLDEVGDSGVVDIVDRFAHPLPIKVICELLGVDEKYRGEFGRWSSEILVMDPERAEQRGQAAREVVNFILDLVERRRTEPGDDLLSALIRVQDDDDGRLSADELTSIALVLLLAGFESSVSLIGIGTYLLLTHPDQLALVRRDPSALPNAVEEILRYIAPPETTTRFAAEEVEIGGVAIPQYSTVLVANGAANRDPKQFPDPHRFDVTRDTRGHLSFGQGIHFCMGRPLAKLEGEVALRALFGRFPALSLGIDADDVVWRRSLLLRGIDHLPVRLDG

>d1cpt\_\_ a.104.1.1 (-) Cytochrome P450-TERP {Pseudomonas sp.}

MDARATIPEHIARTVILPQGYADDEVIYPAFKWLRDEQPLAMAHIEGYDPMWIATKHADVMQIGKQPGLFSNAEGSEILYDQNNEAFMRSISGGCPHVIDSLTSMDPPTHTAYRGLTLNWFQPASIRKLEENIRRIAQASVQRLLDFDGECDFMTDCALYYPLHVVMTALGVPEDDEPLMLKLTQDFFGVEAARRFHETIATFYDYFNGFTVDRRSCPKDDVMSLLANSKLDGNYIDDKYINAYYVAIATAGHDTTSSSSGGAIIGLSRNPEQLALAKSDPALIPRLVDEAVRWTAPVKSFMRTALADTEVRGQNIKRGDRIMLSYPSANRDEEVFSNPDEFDITRFPNRHLGFGWGAHMCLGQHLAKLEMKIFFEELLPKLKSVELSGPPRLVATNFVGGPKNVPIRFTKA

>d1e9xa\_ a.104.1.1 (A:) Cytochrome p450 14 alpha-sterol demethylase (cyp51) {Mycobacterium tuberculosis}

MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQLAGKQVVLLSGSHANEFFFRAGDDDLDQAKAYPFMTPIFGEGVVFDASPERRKEMLHNAALRGEQMKGHAATIEDQVRRMIADWGEAGEIDLLDFFAELTIYTSSACLIGKKFRDQLDGRFAKLYHELERGTDPLAYVDPYLPIESFRRRDEARNGLVALVADIMNGRIANPPTDKSDRDMLDVLIAVKAETGTPRFSADEITGMFISMMFAGHHTSSGTASWTLIELMRHRDAYAAVIDELDELYGDGRSVSFHALRQIPQLENVLKETLRLHPPLIILMRVAKGEFEVQGHRIHEGDLVAASPAISNRIPEDFPDPHDFVPARYEQPRQEDLLNRWTWIPFGAGRHRCVGAAFAIMQIKAIFSVLLREYEFEMAQPPESYRNDHSKMVVQLAQPACVRYRRRT

>d1io7a\_ a.104.1.1 (A:) CYP119 {Archaeon Sulfolobus solfataricus}

MYDWFSEMRKKDPVYYDGNIWQVFSYRYTKEVLNNFSKFSSDLTGYHERLEDLRNGKIRFDIPTRYTMLTSDPPLHDELRSMSADIFSPQKLQTLETFIRETTRSLLDSIDPREDDIVKKLAVPLPIIVISKILGLPIEDKEKFKEWSDLVAFRLGKPGEIFELGKKYLELIGYVKDHLNSGTEVVSRVVNSNLSDIEKLGYIILLLIAGNETTTNLISNSVIDFTRFNLWQRIREENLYLKAIEEALRYSPPVMRTVRKTKERVKLGDQTIEEGEYVRVWIASANRDEEVFHDGEKFIPDRNPNPHLSFGSGIHLCLGAPLARLEARIAIEEFSKRFRHIEILDTEKVPNEVLNGYKRLVVRLKS

>d1dt6a\_ a.104.1.1 (A:) Mammalian cytochrome p450 2c5 {Rabbit (Oryctolagus cuniculus)}

PPGPTPFPIIGNILQIDAKDISKSLTKFSECYGPVFTVYLGMKPTVVLHGYEAVKEALVDLGEEFAGRGSVPILEKVSKGLGIAFSNAKTWKEMRRFSLMTLRNFGMGKRSIEDRIQEEARCLVEELRKTNASPCDPTFILGCAPCNVICSVIFHNRFDYKDEEFLKLMESLHENVELLGTPWLQVYNNFPALLDYFPGIHKTLLKNADYIKNFIMEKVKEHQKLLDVNNPRDFIDCFLIKMEQENNLEFTLESLVIAVSDLFGAGTETTSTTLRYSLLLLLKHPEVAARVQEEIERVIGRHRSPCMQDRSRMPYTDAVIHEIQRFIDLLPTNLPHAVTRDVRFRNYFIPKGTDIITSLTSVLHDEKAFPNPKVFDPGHFLDESGNFKKSDYFMPFSAGKRMCVGEGLARMELFLFLTSILQNFKLQSLVEPKDLDITAVVNGFVSVPPSYQLCFIPIHH

>d1etob\_ a.105.1.1 (B:) FIS protein {Escherichia coli}

MFEQRVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQPLLDMVMQYTLGNQTRAALMMGINRGTLRKKLKKYGMN

>d1ntca\_ a.105.1.1 (A:) DNA-binding domain of NTRC {Salmonella typhimurium}

MDLPGELFEASTPDSPSHLPPDSWATLLAQWADRALRSGHQNLLSEAQPELERTLLTTALRHTQGHKQEAARLLGWGAATLTAKLKELGME

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

IADKQKFMLVVREKVNKLRNDPVAGGGLPKYGTAVLVNIINENGLYPVKNFQTGVYPYAYEQSGEAMAAKYLVRNKPCYACPIGCGRVNRLPTVGETEGPEYESVWALGANLGINDLASIIEANHMCDELGLDTISTGGTLATAMELYEKGHIKDEELGDAPPFRWGNTEVLHYYIEKIAKREGFGDKLAEGSYRLAESYGHPELSMTVKKLELPAYDPRGAEGHGLGYATNNRGGCHIKNYMISPEILGYPYKMDPHDVSDDKIKMLILFQDLTALIDSAGLCLFTTFGLGADDYRDLLNAALGWDFTTEDYLKIGERIWNAERLFNLKAGLDPARDDTLPKRFLEEPMPEGPNKGHTVRLKEMLPRYYKLRGWTEDGKIPKEKLEELGIAEFY

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

DKEELKKLSQEAYNEILNSPGYPFWKRQGTMAAVEWCNTNYALPTRNFSDGYFEFARSIDGYTMEGMKVQQRGCPYCNMPCGNVVLDAEGQESELDYENVALLGSNLGIGKLNEVSVLNRIADEMGMDTISLGVSIAHVMEAVERGILKEGPTFGDFKGAKQLALDIAYRKGELGNLAAEGVKAMAEKLGTHDFAMHVKGLEVSGYNCYIYPAMALAYGTSAIGAHHKEAWVIAWEIGTAPIEGEKAEKVEYKISYDPIKAQKVVELQRLRGGLFEMLTACRLPWVEVGLSLDYYPKLLKAITGVTYTWDDLYKAADRVYSLIRAYWVREFNGKWDRKMDYPPKRWFTEGLKSGPHKGEHLDEKKYDELLSEYYRIRGWDERGIPKKETLKELDLDFVIPELEKVTNLE

>d1qi9a\_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Ascophyllum nodosum}

TCSTSDDADDPTPPNERDDEAFASRVAAAKRELEGTGTVCQINNGETDLAAKFHKSLPHDDLGQVDADAFAALEDCILNGDLSICEDVPVGNSEGDPVGRLVNPTAAFAIDISGPAFSATTIPPVPTLPSPELAAQLAEVYWMALARDVPFMQYGTDDITVTAAANLAGMEGFPNLDAVSIGSDGTVDPLSQLFRATFVGVETGPFISQLLVNSFTIDSITVEPKQETFAPDVNYMVDFDEWLNIQNGGPPAGPELLDDELRFVRNARDLARVTFTDNINTEAYRGALILLGLDAFNRAGVNGPFIDIDRQAGFVNFGISHYFRLIGAAELAQRSSWYQKWQVHRFARPEALGGTLHLTIKGELNADFDLSLLENAELLKRVAAINAAQNPNNEVTYLLPQAIQEGSPTHPSYPSGHATQNGAFATVLKALIGLDRGGDCYPDPVYPDDDGLKLIDFRGSCLTFEGEINKLAVNVAFGRQMLGIHYRFDGIQGLLLGETITVRTLHQELMTFAEESTFEFRLFTGEVIKLFQDGTFTIDGFKCPGLVYTGVENCV

>d1qhba\_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Red algae (Corallina officinalis)}

GIPADNLQSRAKASFDTRVAAAELALARGAVPSFANGEELLYRNSETGDPSFIGSFTKGLPHDDNGAIIDPDDFLAFVRAINSGDEKEIAALTLGPARDPETGLPIWRSDLANSLDLEVRGWENSSAGLTFDLEGPDAQSVAMPPAPVLTSPELIAEMAELYLMALGRDIEFSEFDSPKNAAFIRSAIERLNGLEWFNTPAKLGDPPAEIRRRRGEVTVGNLFRGILPGSEVGPYLSQFIIVGSKQIGSATVGNKTLVSPNAADEFDGEIAYGSITISQRVRIATPGRDFMTDLKVFLDVQDAADFRGFESYEPGARLIRTIRDLATWVHFDSLYEAYLNACLILLANGVPFDPNLPFQQEDKLDNQDVFVNFGSAHVLSLVTEVATRALKAVRYQKFNIHRRLRPEATGGLISVNKNAFLKSESVFPEVDVLVEELSSILDDSASSNEKQNIADGDVSPGKSFLLPMAFAEGSPFHPSYGSGHAVVAGACVTILKAFFDANFQIDQVFEVDTDEDKLVKSSFPGPLTVAGELNKLADNVAIGRNMAGVHYFSDQFESLLLGEQIAIGILEEQSLTYGENFFFNLPKFDGTTIQI

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

RGQDTLFSVLDETRTAPGRRLLQSWLRHPLLDRGPLEARLDRVEGFVREGALREGVRRLLYRLADLERLATRLELGRASPKDLGALRRSLQILPELRALLGEEVGLPDLSPLKEELEAALVEDPPLKVSEGGLIREGYDPDLDALRAAHREGVAYFLELEERERERTGIPTLKVGYNAVFGYYLEVTRPYYERVPKEYRPVQTLKDRQRYTLPEMKEKEREVYRLEALIRRREEEVFLEVRERAKRQAEALREAARILAELDVYAALAEVAVRYG

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

DAATRRNLEITQNLAGGAENTLASVLDCTVTPMGSRMLKRWLHMPVRDTRVLLERQQTIGALQDFTAGLQPVLRQVGDLERILARLALRTARPRDLARMRHAFQQLPELRAQLETVDSAPVQALREKMGEFAELRDLLERAIIDTPPVLVRDGGVIASGYNEELDEWRALADGATDYLERLEVRERERTGLDTLKVGFNAVHGYYIQISRGQSHLAPINYMRRQTLKNAERYIIPELKEYEDKVLTSKGKALALEKQLYEELFDLLLPHLEALQQSASALAELDVLVNLAERAYTLN

>d1tx4a\_ a.116.1.1 (A:) p50 RhoGAP domain {Human (Homo sapiens)}

PLPNQQFGVSLQHLQEKNPEQEPIPIVLRETVAYLQAHALTTEGIFRRSANTQVVREVQQKYNMGLPVDFDQYNALHLPAVILKTFLRELPEPLLTFDLYPHVVGFLNIDESQRVPATLQVLQTLPEENYQVLRFLTAFLVQISAHSDQNKMTNTNLAVVFGPNLLWAKDAAITLKAINPINTFTKFLLDHQGELF

>d1pbwa\_ a.116.1.1 (A:) p85 alpha subunit RhoGAP domain {Human (Homo sapiens)}

LPDLAEQFAPPDIAPPLLIKLVEAIEKKGLECSTLYRTQSSSNLAELRQLLDCDTPSVDLEMIDVHVLADAFKRYLLDLPNPVIPAAVYSEMISLAPEVQSSEEYIQLLKKLIRSPSIPHQYWLTLQYLLKHFFKLSQTSSKNLLNARVLSEIFSPMLFRFSAASSDNTENLIKVIEILISTEW

>d1f7ca\_ a.116.1.1 (A:) Graf {Chicken (Gallus gallus)}

AQLDSIGFSIIKKCIHAVETRGINEQGLYRIVGVNSRVQKLLSILMDPKTATETETEICAEWEIKTITSALKTYLRMLPGPLMMYQFQRSFIKAAKLENQESRVSEIHSLVHRLPEKNRQMLHLLMNHLAKVADNHKQNLMTVANLGVVFGPTLLRPQEETVAAIMDIKFQNIVIEILIENHEKIFNTVPE

>d1wer\_\_ a.116.1.2 (-) p120GAP domain {Human (Homo sapiens)}

MPEEEYSEFKELILQKELHVVYALSHVCGQDRTLLASILLRIFLHEKLESLLLCTLNDREISMEDEATTLFRATTLASTLMEQYMKATATQFVHHALKDSILKIMESKQSCELSPSKLEKNEDVNTNLTHLLNILSELVEKIFMASEILPPTLRYIYGCLQKSVQHKWPTNTTMRTRVVSGFVFLRLICPAILNPRMFNIISDSPSPIAARTLILVAKSVQNLANLVEFGAKEPYMEGVNPFIKSNKHRMIMFLDELGNVPELPDTTEHSRTDLSRDLAALHEICVAHSDELRTLSNERGAQQHVLKKLLAITELLQQKQNQYT

>d1nf1a\_ a.116.1.2 (A:) GAP related domain of neurofibromin {Human (Homo sapiens)}

ERLVELVTMMGDQGELPIAMALANVVPCSQWDELARVLVTLFDSRHLLYQLLWNMFSKEVELADSMQTLFRGNSLASKIMTFCFKVYGATYLQKLLDPLLRIVITSSDWQHVSFEVDPTRLEPSESLEENQRNLLQMTEKFFHAIISSSSEFPPQLRSVCHCLYQVVSQRFPQNSIGAVGSAMFLRFINPAIVSPYEAGILDKKPPPIIERGLKLMSKILQSIANHVLFTKEEHMRPFNDFVKSNFDAARRFFLDIASDCPTSDAVNHSLSFISDGNVLALHRLLWNNQEKIGQYLSSNRDHKAVGRRPFDKMATLLAYLGPPE

>d1h6oa\_ a.146.1.1 (A:) TRF1 {Human (Homo sapiens)}

EDAGLVAEAEAVAAGWMLDFLCLSLCRAFRDGRSEDFRRTRNSAEAIIHGLSSLTACQLRTIYICQFLTRIAAGKTLDAQFENDERITPLESALMIWGSIEKEHDKLHEEIQNLIKIQAIAVCMENGNFKEAEEVFERIFGDPNSHMPFKSKLLMIISQKDTFHSFFQHFSYNHMMEKIKSYVNYVLSEKSSTFLMKAAAKVVE

>d1h6pa\_ a.146.1.1 (A:) TRF2 {Human (Homo sapiens)}

AGEARLEEAVNRWVLKFYFHEALRAFRGSRYGDFRQIRDIMQALLVRPLGKEHTVSRLLRVMQCLSRIEEGENLDCSFDMEAELTPLESAINVLEMIKTEFTLTEAVVESSRKLVKEAAVIICIKNKEFEKASKILKKHMSKDPTTQKLRNDLLNIIREKNLAHPVIQNFSYETFQQKMLRFLESHLDDAEPYLLTMAKKALK

>d1jdha\_ a.118.1.1 (A:) beta-Catenin {Human (Homo sapiens)}

AVVNLINYQDDAELATRAIPELTKLLNDEDQVVVNKAAVMVHQLSKKEASRHAIMRSPQMVSAIVRTMQNTNDVETARCTAGTLHNLSHHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLLHQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSVCSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTSRHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIVIRGLNTIPLFVQLLYSPIENIQRVAAGVLCELAQDKEAAEAIEAEGATAPLTELLHSRNEGVATYAAAVLFRMS

>d1iala\_ a.118.1.1 (A:) Importin alpha {Mouse (Mus musculus)}

DEQMLKRRNVSSFPDDATSPLQENRNNQGTVNWSVEDIVKGINSNNLESQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGKTDCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAHISEQAVWALGNIAGDGSAFRDLVIKHGAIDPLLALLAVPDLSTLACGYLRNLTWTLSNLCRNKNPAPPLDAVEQILPTLVRLLHHNDPEVLADSCWAISYLTDGPNERIEMVVKKGVVPQLVKLLGATELPIVTPALRAIGNIVTGTDEQTQKVIDAGALAVFPSLLTNPKTNIQKEATWTMSNITAGRQDQIQQVVNHGLVPFLVGVLSKADFKTQKEAAWAITNYTSGGTVEQIVYLVHCGIIEPLMNLLSAKDTKIIQVILDAISNIFQAAEKLGETEKLSIMIEECGGLDKIEALQRHENESVYKASLNLIEKYF

>d1qgra\_ a.118.1.1 (A:) Importin beta {Human (Homo sapiens)}

MELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSKDPDIKAQYQQRWLAIDANARREVKNYVLHTLGTETYRPSSASQCVAGIACAEIPVNQWPELIPQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIIQGMRKEEPSNNVKLAATNALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQNLVKIMSLYYQYMETYMGPALFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEAAEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDDDDWNPCKAAGVCLMLLATCCEDDIVPHVLPFIKEHIKNPDWRYRDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVYLAPLLQCLIEGLSAEPRVASNVCWAFSSLAEAAYEAADVADDQEEPATYCLSSSFELIVQKLLETTDRPDGHQNNLRSSAYESLMEIVKNSAKDCYPAVQKTTLVIMERLQQVLQMESHIQSTSDRIQFNDLQSLLCATLQNVLRKVQHQDALQISDVVMASLLRMFQSTAGSGGVQEDALMAVSTLVEVLGGEFLKYMEAFKPFLGIGLKNYAEYQVCLAAVGLVGDLCRALQSNIIPFCDEVMQLLLENLGNENVHRSVKPQILSVFGDIALAIGGEFKKYLEVVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDQENVHPDVMLVQPRVEFILSFIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEARPMIHELLTEGRRSKTNKAKTLARWATKELRKLKNQA

>d1qbkb\_ a.118.1.1 (B:) Karyopherin beta2 {Human (Homo sapiens)}

YEWKPDEQGLQQILQLLKESQSPDTTIQRTVQQKLEQLNQYPDFNNYLIFVLTKLKSEDEPTRSLSGLILKNNVKAHFQNFPNGVTDFIKSECLNNIGDSSPLIRATVGILITTIASKGELQNWPDLLPKLCSLLDSEDYNTCEGAFGALQKICEDSAEILDSDVLDRPLNIMIPKFLQFFKHSSPKIRSHAVACVNQFIISRTQALMLHIDSFTENLFALAGDEEPEVRKNVCRALVMLLEVRMDRLLPHMHNIVEYMLQRTQDQDENVALEACEFWLTLAEQPICKDVLVRHLPKLIPVLVNGMKYSDIDIILLKGDVEEDETIPDSEQDIRPRFHRSRTVAQQHDEDGIEEEDDDDDEIDDDDTISDWNLRKCSAAALDVLANVYRDELLPHILPLLKELLFHHEWVVKESGILVLGAIAEGCMQGMIPYLPELIPHLIQCLSDKKALVRSITCWTLSRYAHWVVSQPPDTYLKPLMTELLKRILDSNKRVQEAACSAFATLEEEACTELVPYLAYILDTLVFAFSKYQHKNLLILYDAIGTLADSVGHHLNKPEYIQMLMPPLIQKWNMLKDEDKDLFPLLECLSSVATALQSGFLPYCEPVYQRCVNLVQKTLAQAMLNNAQPDQYEAPDKDFMIVALDLLSGLAEGLGGNIEQLVARSNILTLMYQCMQDKMPEVRQSSFALLGDLTKACFQHVKPCIADFMPILGTNLNPEFISVCNNATWAIGEISIQMGIEMQPYIPMVLHQLVEIINRPNTPKTLLENTAITIGRLGYVCPQEVAPMLQQFIRPWCTSLRNIRDNEEKDSAFRGICTMISVNPSGVIQDFIFFCDAVASWINPKDDLRDMFCKILHGFKNQVGDENWRRFSDQFPLPLKERLAAFYGV

>d1b3ua\_ a.118.1.2 (A:) Constant regulatory domain of protein phosphatase 2a, pr65alpha {Human (Homo sapiens)}

AAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSTIALALGVERTRSELLPFLTDTIYDEDEVLLALAEQLGTFTTLVGGPEYVHCLLPPLESLATVEETVVRDKAVESLRAISHEHSPSDLEAHFVPLVKRLAGGDWFTSRTSACGLFSVCYPRVSSAVKAELRQYFRNLCSDDTPMVRRAAASKLGEFAKVLELDNVKSEIIPMFSNLASDEQDSVRLLAVEACVNIAQLLPQEDLEALVMPTLRQAAEDKSWRVRYMVADKFTELQKAVGPEITKTDLVPAFQNLMKDCEAEVRAAASHKVKEFCENLSADCRENVIMSQILPCIKELVSDANQHVKSALASVIMGLSPILGKDNTIEHLLPLFLAQLKDECPEVRLNIISNLDCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIIEYMPLLAGQLGVEFFDEKLNSLCMAWLVDHVYAIREAATSNLKKLVEKFGKEWAHATIIPKVLAMSGDPNYLHRMTTLFCINVLSEVCGQDITTKHMLPTVLRMAGDPVANVRFNVAKSLQKIGPILDNSTLQSEVKPILEKLTQDQDVDVKYFAQEALTVLSLA

>d1hu3a\_ a.118.1.2 (A:) Eukaryotic initiation factor eIF4G {Human (Homo sapiens)}

SDPENIKTQELFRKVRSILNKLTPQMFNQLMKQVSGLTVDTEERLKGVIDLVFEKAIDEPSFSVAYANMCRCLVTLKVPMADKPGNTVNFRKLLLNRCQKEFEKDKADDDVFEKKQKELEAASAPEERTRLHDELEEAKDKARRRSIGNIKFIGELFKLKMLTEAIMHDCVVKLLKNHDEESLECLCRLLTTIGKDLDFEKAKPRMDQYFNQMEKIVKERKTSSRIRFMLQDVIDLRLCNWVS

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

TEDHLESLICKVGEKSACSLESNLEGLAGVLEADLPNYKSKILRLLCTVARLLPEKLTIYTTLVGLLNARNYNFGGEFVEAMIRQLKESLKANNYNEAVYLVRFLSDLVNCHVIAAPSMVAMFENFVSVTQEEDVPQVRRDWYVYAFLSSLPWVGKELYEKKDAEMDRIFANTESYLKRRQKTHVPMLQVWTADKPHPQEEYLDCLWAQIQKLKKDRWQERHILRPYLAFDSILCEALQHNLPPFTPPPHTEDSVYPMPRVIFR

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

MFDYTDDPEGPVMPGSHSVERFVIEENLHCIIKSHWKERKTCAAQLVSYPGKNKIPLNYHIVEVIFAELFQLPAPPHIDVMYTTLLIELCKLQPGSLPQVLAQATEMLYMRLDTMNTTCVDRFINWFSHHLSNFQFRWSWEDWSDCLSQDPESPKPKFVREVLEKCMRLSYHQRILDIVPPTFSALCPSN

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

PTCIYKYGDESSNSLPGHSVALCLAVAFKSKATNDEIFSILKDVPNPNQDDDDDEGFSFNPLKIEVFVQTLLHLAAKSFSHSFSALAKFHEVFKTLAESDEGKLHVLRVMFEVWRNHPQMIAVLVDKMIRTQIVDCAAVANWIFSSELSRDFTRLFVWEILHSTIRKMNKHVLKIQKELEEAKEKLARQHDGVLEEQIERLQEKVESAQSEQKNLFLVIFQRFIMILTEHLVRCETDGTSVLTPWYKNCIERLQQIFLQHHQIIQQYMVTLENLLFTAELDPHILAVFQQFCALQA

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

PLALLLDSSLEGEFDLVQRIIYEVDDPSLPNDEGITALHNAVCAGHTEIVKFLVQFGVNVNAADSDGWTPLHCAASCNNVQVCKFLVESGAAVFAMTYSDMQTAADKCEEMEEGYTQCSQFLYGVQEKMG

>d1awcb\_ a.118.2.1 (B:) GA bindinig protein (GABP) beta 1 {Mouse (Mus musculus)}

DLGKKLLEAARAGQDDEVRILMANGAPFTTDWLGTSPLHLAAQYGHFSTTEVLLRAGVSRDARTKVDRTPLHMAASEGHANIVEVLLKHGADVNAKDMLKMTALHWATEHNHQEVVELLIKYGADVHTQSKFCKTAFDISIDNGNEDLAEILQ

>d1blxb\_ a.118.2.1 (B:) Cell cycle inhibitor p19ink4D {Mouse (Mus musculus)}

VCVGDRLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNVQDASGTSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFLAPESDLHHRDASGLTPLELARQRGAQNLMDILQGHMMIP

>d1iknd\_ a.118.2.1 (D:) I-kappa-B-alpha {Human (Homo sapiens)}

DGDSFLHLAIIHEEKALTMEVIRQVKGDLAFLNFQNNLQQTPLHLAVITNQPEIAEALLGAGCDPELRDFRGNTPLHLACEQGCLASVGVLTQSCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVELLVSLGADVNAQEPCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQGYSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTES

>d1k1aa\_ a.118.2.1 (A:) bcl-3 {Human (Homo sapiens)}

EDGDTPLHIAVVQGNLPAVHRLVNLFQQGGRELDIYNNLRQTPLHLAVITTLPSVVRLLVTAGASPMALDRHGQTAAHLACEHRSPTCLRALLDSAAPGTLDLEARNYDGLTALHVAVNTECQETVQLLLERGADIDAVDIKSGRSPLIHAVENNSLSMVQLLLQHGANVNAQMYSGSSALHSASGRGLLPLVRTLVRSGADSSLKNCHNDTPLMVARSRRVIDILRG

>d1myo\_\_ a.118.2.1 (-) Myotrophin {Rat (Rattus norvegicus)}

MCDKEFMWALKNGDLDEVKDYVAKGEDVNRTLEGGRKPLHYAADCGQLEILEFLLLKGADINAPDKHHITPLLSAVYEGHVSCVKLLLSKGADKTVKGPDGLTALEATDNQAIKALLQ

>d1sw6a\_ a.118.2.1 (A:) Swi6 ankyrin-repeat fragment {Baker's yeast (Saccharomyces cerevisiae)}

GPIITFTHDLTSDFLSSPLKIMKALPSPVVNDNEQKMKLEAFLQRLLFPEIQEMPTSLNNDSSNRNSEGGSSNQQQQHVSFDSLLQEVNDAFPNTQLNLNIPVDEHGNTPLHWLTSIANLELVKHLVKHGSNRLYGDNMGESCLVKAVKSVNNYDSGTFEALLDYLYPCLILEDSMNRTILHHIIITSGMTGCSAAAKYYLDILMGWIVKKQNRPIQSGTNEKESKPNDKNGERKDSILENLDLKWIIANMLNAQDSNGDTCLNIAARLGNISIVDALLDYGADPFIANKSGLRPVDFGAG

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

ADTAAKLHSLCEAVKTRDIFGLLQAYADGVDLTEKIPLANGHEPDETALHLAVRSVDRTSLHIVDFLVQNSGNLDKQTGKGSTALHYCCLTDNAECLKLLLRGKASIEIANESGETPLDIAKRLKHEHCEELLTQALSGRFNSHVHVEYEWRLL

>d1d8da\_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Rat (Rattus norvegicus)}

FLSLDSPTYVLYRDRAEWADIDPVPQNDGPSPVVQIIYSEKFRDVYDYFRAVLQRDERSERAFKLTRDAIELNAANYTVWHFRRVLLRSLQKDLQEEMNYIIAIIEEQPKNYQVWHHRRVLVEWLKDPSQELEFIADILNQDAKNYHAWQHRQWVIQEFRLWDNELQYVDQLLKEDVRNNSVWNQRHFVISNTTGYSDRAVLEREVQYTLEMIKLVPHNESAWNYLKGILQDRGLSRYPNLLNQLLDLQPSHSSPYLIAFLVDIYEDMLENQCDNKEDILNKALELCEILAKEKDTIRKEYWRYIGRSLQSKHSRESDIPASV

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

MHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQAGELDESVLELTSQILGANPDFATLWNCRREVLQHLETEKSPEESAALVKAELGFLESCLRVNPKSYGTWHHRCWLLSRLPEPNWARELELCARFLEADERNFHCWDYRRFVAAQAAVAPAEELAFTDSLITRNFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPENVLLKELELVQNAFFTDPNDQSAWFYHRWLLGRAEXLFRCELSVEKSTVLQSELESCKELQELEPENKWCLLTIILLMRALDPLLYEKETLQYFSTLKAVDPMRAAYLDDLRSKFLLENSVLKMEYADV

>d1a17\_\_ a.118.8.1 (-) Protein phosphatase 5 {Human (Homo sapiens)}

PPADGALKRAEELKTQANDYFKAKDYENAIKFYSQAIELNPSNAIYYGNRSLAYLRTECYGYALGDATRAIELDKKYIKGYYRRAASNMALGKFRAALRDYETVVKVKPHDKDAKMKYQECNKIVKQKAFERAIAGDEHKRSVVDSLDIESMTIEDEYS

>d1elra\_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}

GKQALKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYITNQAAVYFEKGDYNKCRELCEKAIEVGRENREDYRQIAKAYARIGNSYFKEEKYKDAIHFYNKSLAEHRTPDVLKKCQQAEKILKEQ

>d1elwa\_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}

EQVNELKEKGNKALSVGNIDDALQCYSEAIKLDPHNHVLYSNRSAAYAKKGDYQKAYEDGCKTVDLKPDWGKGYSRKAAALEFLNRFEEAKRTYEEGLKHEANNPQLKEGLQNMEAR

>d1qqea\_ a.118.8.1 (A:) Vesicular transport protein sec17 {Baker's yeast (Saccharomyces cerevisiae)}

ISDPVELLKRAEKKGVPSSGFMKLFSGSDSYKFEEAADLCVQAATIYRLRKELNLAGDSFLKAADYQKKAGNEDEAGNTYVEAYKCFKSGGNSVNAVDSLENAIQIFTHRGQFRRGANFKFELGEILENDLHDYAKAIDCYELAGEWYAQDQSVALSNKCFIKCADLKALDGQYIEASDIYSKLIKSSMGNRLSQWSLKDYFLKKGLCQLAATDAVAAARTLQEGQSEDPNFADSRESNFLKSLIDAVNEGDSEQLSEHCKEFDNFMRLDKWKITILNKIKESIQQQEDD

>d1hh8a\_ a.118.8.1 (A:) Neutrophil cytosolic factor 2 (NCF-2, p67-phox) {Human (Homo sapiens)}

SLVEAISLWNEGVLAADKKDWKGALDAFSAVQDPHSRICFNIGCMYTILKNMTEAEKAFTRSINRDKHLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQLIDYKILGLQFKLFACEVLYNIAFMYAKKEEWKKAEEQLALATSMKSEPRHSKIDKAMECVWKQKLYEPVVIPVGRLFRPNERQVAQL

>d1fcha\_ a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Human (Homo sapiens)}

SATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLELKPDNQTALMALAVSFTNESLQRQACEILRDWLRYTPAYAHLVTPAEEGAGGAGLGPSKRILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRALELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSDAYGAADARDLSTLLTMFGLPQ

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

GSGDSHPDFPEDADVDLKDVDKILLISEDLKNIGNTFFKSQNWEMAIKKYTKVLRYVEGSRAAAEDADGAKLQPVALSCVLNIGACKLKMSDWQGAVDSCLEALEIDPSNTKALYRRAQGWQGLKEYDQALADLKKAQEIAPEDKAIQAELLKVKQKIKAQKDKEKAAY

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

MFRSSFCKNLENATSHLRLEPDWPSILLICDEINQKDVTPKNAFAAIKKKMNSPNPHSSCYSLLVLESIVKNCGAPVHEEVFTKENCEMFSSFLESTPHENVRQKMLELVQTWAYAFRSSDKYQAIKDTMTILKAKGHTFPELRE

>d1elka\_ a.118.9.2 (A:) Tom1 protein {Human (Homo sapiens)}

SDFLLGNPFSSPVGQRIEKATDGSLQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLETCVKNCGHRFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRSSPDLTGVVTIYEDLRRKGLEFPM

>d1juqa\_ a.118.9.2 (A:) Gga3 {Human (Homo sapiens)}

ESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEGPQIAVRLLAHKIQSPQEWEALQALTVLEACMKNCGRRFHNEVGKFRFLNELIKVVSPKYLGDRVSEKVKTKVIELLYSWTMALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLI

>d2tct\_2 a.121.1.1 (68-208) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

LPAAGESWQSFLRNNAMSFRRALLRYRDGAKVHLGTRPDEKQYDTVETQLRFMTENGFSLRDGLYAISAVSHFTLGAVLEQQEHTAALTDRPAAPDENLPPLLREALQIMDSDDGEQAFLHGLESLIRGFEVQLTALLQIV

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

KTNREKFYLYNELSLTTEYYYPLQNAIIEFYTEYYKTNSINEKMNKLENKYIDAYHVIFKEGNLNGEWSINDVNAVSKIAANAVNGIVTFTHEQNINERIKLMNKFSQIFLNGLS

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

VSWDSLPDELLLGIFSCLCLPELLKVSGVCKRWYRLASD

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

IPVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFNIKNDFTEEEEAQVRKENQWC

>d1g5ya\_ a.123.1.1 (A:) Retinoid-X receptor (RXR-alpha) {Human (Homo sapiens)}

PVERILEAELAVEPKTETYVEANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSELPLDDQVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSAGVGAIFDRVLTELVSKMRDMQMDKTELGCLRAIVLFNPDSKGLSNPAEVEALREKVYASLEAYCKHKYPEQPGRFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAP

>d1fcya\_ a.123.1.1 (A:) Retinoic acid receptor gamma (RAR-gamma) {Human (Homo sapiens)}

ASPQLEELITKVSKAHQETFPSLCQLGKYTTNSSADHRVQLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFAGQLLPLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLQEPLLEALRLYARRRRPSQPYMFPRMLMKITDLRGISTKGAERAITLKMEIPGPMPPLIREMLE

>d1a28a\_ a.123.1.1 (A:) Progesterone receptor {Human (Homo sapiens)}

QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMKESSFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFPEMMSEVIAAQLPKILAGMVKPLLFHK

>d3erda\_ a.123.1.1 (A:) Estrogen receptor alpha {Human (Homo sapiens)}

SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRLH

>d2prga\_ a.123.1.1 (A:) Peroxisome proliferator activated receptor gamma, PPAR-gamma {Human (Homo sapiens)}

ESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY

>d1ilga\_ a.123.1.1 (A:) Pregnane x receptor, PXR {Human (Homo sapiens)}

GLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFGI

>d1ie9a\_ a.123.1.1 (A:) Vitamin D nuclear receptor {Human (Homo sapiens)}

DSLRPKLSEEQQRIIAILLDAHHKTYDPTYSDFCQFRPPVRVNDGGGSVTLELSQLSMLPHLADLVSYSIQKVIGFAKMIPGFRDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMSWTCGNQDYKYRVSDVTKAGHSLELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTLQTYIRCRHPPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKLTPLVLEVFG

>d1bsxa\_ a.123.1.1 (A:) Thyroid hormone receptor beta (TR-beta) {Human (Homo sapiens)}

KPEPTDEEWELIKTVTEAHVATNAQGSHWKQKRKFLPEDIGQAPIVNAPEGGKVDLEAFSHFTKIITPAITRVVDFAKKLPMFCELPCEDQIILLKGCCMEIMSLRAAVRYDPESETLTLNGEMAVTRGQLKNGGLGVVSDAIFDLGMSLSSFNLDDTEVALLQAVLLMSSDRPGLACVERIEKYQDSFLLAFEHYINYRKHHVTHFWPKLLMKVTDLRMIGACHASRFLHMKVECPTELFPPLFLEVFED

>d1hg4a\_ a.123.1.1 (A:) Ultraspiracle protein, usp {Drosophila melanogaster}

FSIERIIEAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVSALCQVVNKQLFQMVEYARMMPHFAQVPLDDQVILLKAAWIELLIANVAWCSIVSLDDGGAGGGGGGLGHDGSFERRSPGLQPQQLFLNQSFSYHRNSAIKAGVSAIFDRILSELSVKMKRLNLDRRELSCLKAIILYNPDIRGIKSRAEIEMCREKVYACLDEHCRLEHPGDDGRFAQLLLRLPALRSISLKCQDHLFLFRITSDRPLEELFLEQLEAPPPPG

>d1ah7\_\_ a.124.1.1 (-) Bacterial phosholipase C {Bacillus cereus}

WSAEDKHKEGVNSHLWIVNRAIDIMSRNTTLVKQDRVAQLNEWRTELENGIYAADYENPYYDNSTFASHFYDPDNGKTYIPFAKQAKETGAKYFKLAGESYKNKDMKQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPQGFHSKYENFVDTIKDNYKVTDGNGYWNWKGTNPEEWIHGAAVVAKQDYSGIVNDNTKDWFVKAAVSQEYADKWRAEVTPMTGKRLMDAQRVTAGYIQLWFDTYGDR

>d1ca1\_1 a.124.1.1 (1-249) Alpha-toxin, N-terminal domain {Clostridium perfringens}

WDGKIDGTGTHAMIVTQGVSILENDLSKNEPESVRKNLEILKENMHELQLGSTYPDYDKNAYDLYQDHFWDPDTDNNFSKDNSWYLAYSIPDTGESQIRKFSALARYEWQRGNYKQATFYLGEAMHYFGDIDTPYHPANVTAVDSAGHVKFETFAEERKEQYKINTVGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSHSWDDWDYAAKVTLANSQKGTAGYIYRFLHDVSEGNDP

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

HKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQ

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

RLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLI

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

KQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALG

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

CKEFSHLGKEDFTSLSLVLYSRKFPSGTFEQVSQLVKEVVSLTEACCAEGADPDCYDTRTSALSAKSCESNSPFPVHPGTAECCTKEGLERKLCMAALKHQPQEFPTYVEPTNDEICEAFRKDPKEYANQFMWEYSTNYGQAPLSLLVSYTKSYLSMVGSCCTSASPTVCFLKERLQLKHLSLLTT

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

LSNRVCSQYAAYGEKKSRLSNLIKLAQKVPTADLEDVLPLAEDITNILSKCCESASEDCMAKELPEHTVKLCDNLSTKNSKFEDCCQEKTAMDVFVCTYFMPAAQLPELPDVELPTNKDVCDPGNTKVMDKYTFELSRRTHLPEVFLSKVLEPTLKSLGECCDVEDSTTCFNAKGPLLKKELSSFIDK

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

GQELCADYSENTFTEYKKKLAERLKAKLPDATPTELAKLVNKRSDFASNCCSINSPPLYCDSEIDAELKNI

>d1jswa\_ a.127.1.1 (A:) L-aspartate ammonia lyase {Escherichia coli}

MSNNIRIEEDLLGTREVPADAYYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKKAAAMANKELQTIPKSVANAIIAACDEVLNNGKCMDQFPVDVYQGGAGTSVNMNTNEVLANIGLELMGHQKGEYQYLNPNDHVNKCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRTQLQDAVPMTLGQEFRAFSILLKEEVKNIQRTAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIEATSDCGAYVMVHGALKRLAVKMSKICNDLRLLSSGPRAGLNEINLPELQAGSSIMPAKVNPVVPEVVNQVCFKVIGNDTTVTMAAEAGQLQLNVMEPVIGQAMFESVHILTNACYNLLEKCINGITANKEVCEGYVYNSIGIVTYLNPFIGHHNGDIVGKICAETGKSVREVVLERGLLTEAELDDIFSV

>d1yfm\_\_ a.127.1.1 (-) Fumarase {Baker's yeast (Saccharomyces cerevisiae)}

SFRTETDAFGEIHVPADKYWGAQTQRSFQNFKIGGARERMPLPLVHAFGVLKKSAAIVNESLGGLDPKISKAIQQAADEVASGKLDDHFPLVVFQTGSGTQSNMNANEVISNRAIEILGGKIGSKQVHPNNHCNQSQSSNDTFPTVMHIAASLQIQNELIPELTNLKNALEAKSKEFDHIVKIGRTHLQDATPLTLGQEFSGYVQQVENGIQRVAHSLKTLSFLAQGGTAVGTGLNTKPGFDVKIAEQISKETGLKFQTAPNRFEALAAHDAIVECSGALNTLACSLFKIAQDIRYLGSGPRCGYHELMLPENEPGSSIMPGKVNPTQNEALTQVCVQVMGNNAAITFAGSQGQFELNVFKPVMIANLLNSIRLITDAAYSFRVHCVEGIKANEPRIHELLTKSLMLVTALNPKIGYDAASKVAKNAHKKGITLKESALELGVLTEKEFDEWVVPEHML

>d1i0aa\_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Turkey (Meleagris gallopavo), delta-crystallin}

GRFVGSVDPIMEILSSSISTEQRLTEVDIQASMAYAKALEKASILTKTELEKILSGLEKISEESSKGVLVMTQSDEDIQTAIERRLKELIGDIAGKLQTGRSRNEQVVTDLKLLLKSSISVISTHLLQLIKTLVERAAIEIDIIMPGYTHLQKALPIRWSQFLLSHAVALTRDSERLGEVKKRITVLPLGSGVLAGNPLEIDRELLRSELDMTSITLNSIDAISERDFVVELISVATLLMIHLSKLAEDLIIFSTTEFGFVTLSDAYSTGSSLLPQKKNPDSLELIRSKAGRVFGRLAAILMVLKGIPSTFSKDLQEDKEAVLDVVDTLTAVLQVATGVISTLQINKENMEKALTPELLSTDLALYLVRKGMPIRQAQTASGKAVHLAETKGITINNLTLEDLKSISPLFASDVSQVFSVVNSVEQYTAVGGTAKSSVTAQIEQLRELLKKQK

>d1c3ca\_ a.127.1.1 (A:) Adenylosuccinate lyase {Thermotoga maritima}

VERYSLSPMKDLWTEEAKYRRWLEVELAVTRAYEELGMIPKGVTERIRNNAKIDVELFKKIEEKTNHDVVAFVEGIGSMIGEDSRFFHYGLTSSDVLDTANSLALVEAGKILLESLKEFCDVLWEVANRYKHTPTIGRTHGVHAEPTSFGLKVLGWYSEMKRNVQRLERAIEEVSYGKISGAVGNYANVPPEVEEKALSYLGLKPEPVSTQVVPRDRHAFYLSTLAIVAAGIERIAVEIRHLQRTEVLEVEEPFRKGQRGSSAMPHKKNPITCERLTGLSRMMRAYVDPSLENIALWHERDISHSSVERYVFPDATQTLYYMIVTATNVVRNMKVNEERMKKNIDLTKGLVFSQRVLLKLIEKGLTRKEAYDIVQRNALKTWNSEKHFLEYLLEDEEVKKLVTKEELEELFDISYYLKHVDHIFERFEK

>d1dofa\_ a.127.1.1 (A:) Adenylosuccinate lyase {Archaeon Pyrobaculum aerophilum}

HVSPFDWRYGSEEIRRLFTNEAIINAYLEVERALVCALEELGVAERGCCEKVNKASVSADEVYRLERETGHDILSLVLLLEQKSGCRYVHYGATSNDIIDTAWALLIRRALAAVKEKARAVGDQLASMARKYKTLEMVGRTHGQWAEPITLGFKFANYYYELYIACRQLALAEEFIRAKIGGAVGTMASWGELGLEVRRRVAERLGLPHHVITTQVAPRESFAVLASALALMAAVFERLAVEIRELSRPEIGEVVEGGGGSSAMPHKANPTASERIVSLARYVRALTHVAFENVALWHERDLTNSANERVWIPEALLALDEILTSALRVLKNVYIDEERITENLQKALPYILTEFHMNRMIKEGASRAEAYKKAKEVKALTFEYQKWPVERLIEDALSLKLC

>d1di1a\_ a.128.1.4 (A:) Aristolochene synthase {Fungus (Penicillium roqueforti)}

TPPPTQWSYLCHPRVKEVQDEVDGYFLENWKFPSFKAVRTFLDAKFSEVTCLYFPLALDDRIHFACRLLTVLFLIDDVLEHMSFADGEAYNNRLIPISRGDVLPDRTKPEEFILYDLWESMRAHDAELANEVLEPTFVFMRAQTDRARLSIHELGHYLEYREKDVGKALLSALMRFSMGLRLSADELQDMKALEANCAKQLSVVNDIYSYDKEEEASRTGHKEGAFLCSAVKVLAEESKLGIPATKRVLWSMTREWETVHDEIVAEKIASPDGCSEAAKAYMKGLEYQMSGNEQWSKTTR

>d1ps1a\_ a.128.1.4 (A:) Pentalenene synthase {Streptomyces sp., UC5319}

QDVDFHIPLPGRQSPDHARAEAEQLAWPRSLGLIRSDAAAERHLRGGYADLASRFYPHATGADLDLGVDLMSWFFLFDDLFDGPRGENPEDTKQLTDQVAAALDGPLPDTAPPIAHGFADIWRRTCEGMTPAWCARSARHWRNYFDGYVDEAESRFWNAPCDSAAQYLAMRRHTIGVQPTVDLAERAGRFEVPHRVFDSAVMSAMLQIAVDVNLLLNDIASLEKEEARGEQNNMVMILRREHGWSKSRSVSHMQNEVRARLEQYLLLESCLPKVGEIYQLDTAEREALERYRTDAVRTVIRGSYDWHRSSG

>d1psj\_\_ a.133.1.2 (-) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}

SLIQFETLIMKVAKKSGMFWYSNYGCYCGWGGQGRPQDATDRCCFVHDCCYGKVTGCDPKMDVYSFSEENGDIVCGGDDPCKKEICECDRAAAICFRDNLTLYNDKKYWAFGAKNCPQEESEPC

>d1hn4a\_ a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}

GISSRALWQFRSMIKCAIPGSHPLMDFNNYGCYCGLGGSGTPVDELDRCCETHDNCYRDAKNLDSCKFLVDNPYTESYSYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHKNLDTKKYC

>d1kbhb\_ a.153.1.1 (B:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}

PNRSISPSALQDLLRTLKSPSSPQQQQQVLNILKSNPQLMAAFIKQRTAKYVANQPGMQ

>d1kbha\_ a.153.1.1 (A:) Nuclear receptor coactivator ACTR {Human (Homo sapiens)}

EGQSDERALLDQLHTLLSNTDATGLEEIDRALGIPELVNQGQALEPK

>d1gg2g\_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

SIAQARKLVEQLKMEANIDRIKVSKAAADLMAYCEAHAKEDPLLTPVPASENPF

>d1tbge\_ a.137.3.1 (E:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

APVINIEDLTEKDKLKMEVDQLKKEVTLERMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKELK

>d1aqe\_\_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

TFEIPESVTMSPKQFEGYTPKKGDVTFNHASHMDIACQQCHHTVPDTYTIESCMTEGCHDNIKERTEISSVERTFHTTKDSEKSCVGCHRELKRQGPSDAPLACNSCHVQ

>d2cy3\_\_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

ADAPGDDYVISAPEGMKAKPKGDKPGALQKTVPFPHTKHATVECVQCHHTLEADGGAVKKCTTSGCHDSLEFRDKANAKDIKLVENAFHTQCIDCHKALKKDKKPTGPTACGKCHTTN

>d1wad\_\_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio gigas}

VDVPADGAKIDFIAGGEKNLTVVFNHSTHKDVKCDDCHHDPGDKQYAGCTTDGCHNILDKADKSVNSWYKVVHDAKGGAKPTCISCHKDKAGDDKELKKKLTGCKGSACHP

>d3caoa\_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio africanus}

EDMTHVPTDAFGKLERPAAVFNHDEHNEKAGIESCNACHHVWVNGVLAEDEDSVGTPCSDCHALEQDGDTPGLQDAYHQQCWGCHEKQAKGPVMCGECHVKN

>d1hh5a\_ a.138.1.1 (A:) Cytochrome c7 (cytochrome c551.5) {Desulfuromonas acetoxidans}

ADVVTYENKKGNVTFDHKAHAEKLGCDACHEGTPAKIAIDKKSAHKDACKTCHKSNNGPTKCGGCHIK

>d19hca\_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

AALEPTDSGAPSAIVMFPVGEKPNPKGAAMKPVVFNHLIHEKKIADCETCHHTGDPVSCSTCHTVEGKAEGDYITLDRAMHATDIAARAKGNTPTSCVSCHQSETKERRECAGCHAITTPKDDEAWCATCHDITPSMTPSEMQKGIAGTLLPGDNEALAAETVLAEATVAPVSPMLAPYKVVIDALADKYEPSDFTHRRHLTSLMESIKDDKLAQAFHDKPEILCATCHHRSPLSLTPPKCGSCHTKEIDAADPGRPNLMAAYHLECMGCHKGMAVARPRDTDCTTCHKAAA

>d1fgja\_ a.138.1.3 (A:) Hydroxylamine oxidoreductase, HAO {Nitrosomonas europaea}

DISTVPDETYDALKLDRGKATPKETYEALVKRYKDPAHGAGKGTMGDYWEPIAISIYMDPNTFYKPPVSPKEVAERKDCVECHSDETPVWVRAWKRSTHANLDKIRNLKSDDPLYYKKGKLEEVENNLRSMGKLGEKETLKEVGCIDCHVDVNKKDKADHTKDIRMPTADTCGTCHLREFAERESERDTMVWPNGQWPAGRPSHALDYTANIETTVWATMPQREVAEGCTMCHTNQNKCDNCHTRHEFSAAESRKPEACATCHSGVDHNNWEAYTMSKHGKLAEMNRDKWNWEVRLKDAFSKGGQNAPTCAACHMEYEGEYTHNITRKTRWANYPFVPGIAENITSDWSEARLDSWVLTCTQCHSERFARSYLDLMDKGTLEGLAKYQEANAIVHKMYEDGTLTGQKTNRPNPPEPEKPGFGIFTQLFWSKGNNPASLELKVLEMGENNLAKMHVGLAHVNPGGWTYTEGWGPMNRAYVEIQDEYTKMQELSALQARVN

>d1ft5a\_ a.138.1.3 (A:) Cytochrome c554 {Nitrosomonas europaea}

ADAPFEGRKKCSSCHKAQAQSWKDTAHAKAMESLKPNVKKEAKQKAKLDPAKDYTQDKDCVGCHVDGFGQKGGYTIESPKPMLTGVGCESCHGPGRNFRGDHRKSGQAFEKSGKKTPRKDLAKKGQDFHFEERCSACHLNYEGSPWKGAKAPYTPFTPEVDAKYTFKFDEMVKEVKAMHEHYKLEGVFEGEPKFKFHDEFQASAKPAKKGK

>d1ddca\_ a.138.1.3 (A:) Dimeric di-heme split-soret cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

RFDQVGGAFGWKPHKLDPKECAQVAYDGYWYKGFGCGFGAFYSIVGLMGEKYGAPYNQFPFAMLEANKGGISDWGTIYGALYGAAATFSLFWGRKEVHPMVNELFRWYEVTKLPIFNPGDAAQGVKGDLPMSASDSVLCHISVSKWCYENKIEATSKQRSERAGRLTADAAFKAAEIINTKIDQGKDFKSTFPMQASVSSCGECHMTKGNDANWAKGIMDCTPCHSGTAATQNKFVNH

>d1qdba\_ a.138.1.3 (A:) Cytochrome c nitrite reductase {Sulfurospirillum deleyianum}

GIAGKEKSEEWAKYYPRQFDSWKKTKEYDSFTDMLAKDPALVIAWSGYAFSKDYNSPRGHYYALQDNVNSLRTGAPVDAKTGPLPTACWTCKSPDVPRLIEEDGELEYFTGKWAKYGSQIVNVIGCANCHDDKTAELKVRVPHLNRGLQAAGLKTFEESTHQDKRTLVCAQCHVEYYFKKTEWKDAKGADKTAMVVTLPWANGVGKDGNAGVEGMIKYYDEINFSDWTHNISKTPMLKAQHPGFEFWKSGIHGQKGVSCADCHMPYTQEGSVKYSDHQVKENPLDSMDQSCMNCHRESESKLRGIVHQKYERKEFLNKVAFDNIGKAHLETGKAIEAGASDEELKEVRKLIRHGQFKADMAIAAHGNYFHAPEETLRLLAAGSDDAQKARLLLVKILAKHGVMDYIAPDFDTKDKAQKLAKVDIAALAAEKMKFKQTLEQEWKKEAKAKGRANPELYKDVDTINDGKSSWNKK

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

ADNLAEFHVQNQECDSCHTPDGELSNDSLTYENTQCVSCHGTLAEVAETTKHEHYNAHASHFPGEVACTSCHSAHEKSMVYCDSCHSFDFNMPYAKKWLRDE

>d1neu\_\_ b.1.1.1 (-) Myelin membrane adhesion molecule P0 {Rat (Rattus norvegicus)}

IVVYTDREVYGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAKGQPYIDEVGTFKERIQWVGDPSWKDGSIVIHNLDYSDNGTFTCDVKNPPDIVGKTSQVTLYVFE

>d1eaja\_ b.1.1.1 (A:) Coxsackie virus and adenovirus receptor (Car), domain 1 {Human (Homo sapiens)}

FARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKKAPGVANKKIHLVVLV

>d1qfoa\_ b.1.1.1 (A:) N-terminal domain of sialoadhesin {Mouse (Mus musculus)}

TWGVSSPKNVQGLSGSCLLIPCIFSYPADVPVSNGITAIWYYDYSGKRQVVIHSGDPKLVDKRFRGRAELMGNMDHKVCNLLLKDLKPEDSGTYNFRFEISDSNRWLDVKGTTVTVTT

>d1bqhg\_ b.1.1.1 (G:) CD8 {Mouse (Mus musculus)}

KPQAPELRIFPKKMDAELGQKVDLVCEVLGSVSQGCSWLFQNSSSKLPQPTFVVYMASSHNKITWDEKLNSSKLFSAMRDTNNKYVLTLNKFSKENEGYYFCSVISNSVMYFSSVVPVLQKV

>d1cdy\_1 b.1.1.1 (1-97) N-terminal domain of CD4 {Human (Homo sapiens)}

KKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKSPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV

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

FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVV

>d1hnf\_1 b.1.1.1 (4-104) CD2, first domain {Human (Homo sapiens)}

TNALETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEKETFKEKDTYKLFKNGTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQE

>d1qa9b\_ b.1.1.1 (B:) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}

SSQQIYGVKYGNVTFHVPSNQPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTKSGSLTIYNLTSSDEDEYEMESPNITDSMKFFLYVGES

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

VIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVK

>d1i85a\_ b.1.1.1 (A:) CD86 (b7-2), N-terminal domain {Human (Homo sapiens)}

MLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLA

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

KGSVYTAQSDVQVPENESIKLTCTYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFSSVTRKDNGEYTCMVSEEGGQNYGEVSIHLTVL

>d1jmaa\_ b.1.1.1 (A:) HSV glycoprotein D {Herpes simplex virus type 1}

KYALADASLKMADPNRFRGKDLPVLDQLTDPPGVRRVYHIQAGLPDPFQPPSLPITVYYAVLERACRSVLLNAPSEAPQIVRGASEDVRKQPYNLTIAWFRMGGNCAIPITVMEYTECSYNKSLGACPIRTQPRWNYYDSFSAVSEDNLGFLMHAPAFETAGTYLRLVKINDWTEITQFILEHRAKGSCKYALPLRIPPSACLSPQAYQQGVTVDSIGMLPRFIPENQRTVAVYSLKIAGWHGPKAPYTSTLLPPELSE

>d1hzhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

QVQLVQSGAEVKKPGASVKVSCQASGYRFSNFVIHWVRQAPGQRFEWMGWINPYNGNKEFSAKFQDRVTFTADTSANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYYMDVWGKGTTVIVSS

>d1a3rl1 b.1.1.1 (L:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 8F5 (mouse), kappa L chain}

DIVMTQSPSSLTVTTGEKVTMTCKSSQSLLNSRTQKNYLTWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLSISGVQAEDLAVYYCQNNYNYPLTFGAGTKLELKRADAAPT

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

QVQLLESGPGLVRPSETLSLTCTVSGFSLTSFSVSWVRHPSGKGPEWMGRMWYDGYTAYNSALKSRLSISRDTSKNQVFLKMNSLQTDDTGTYYCTRDLYGGYPLGFWYFDFWGPG

>d1jtpa\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-lysozyme antibody}

DVQLQASGGGSVQAGGSLRLSCAASGYTIGPYCMGWFRQAPGKEREGVAAINMGGGITYYADSVKGRFTISQDNAKNTVYLLMNSLEPEDTAIYYCAADSTIYASYYECGHGLSTGGYGYDSWGQGTQVTVSSRR

>d1mcww1 b.1.1.1 (W:1-111) Immunoglobulin (variable domains of L and H chains) {Heterologous L chain dimer MCG-WEIR hybrid (human)}

ESALTQPASVSGSPGQSITVSCAGHTSDVADSNSISWFQQHPDKAPKLLIYAVTFRPSGIPLRFSGSKSGNTASLTISGLLPDDEADYFCMSYLSDASFVFGSGTKVTVLR

>d1b88a\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

MQQVRQSPQSLTVWEGETAILNCSYENSAFDYFPWYQQFPGEGPALLISILSVSNKKEDGRFTIFFNKREKKLSLHIADSQPGDSATYFCAASASFGDNSKLIWGLGTSLVVNP

>d1fo0a\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

KVTQTQTSISVMEKTTVTMDCVYETQDSSYFLFWYKQTASGEIVFLIRQDSYKKENATVGHYSLNFQKPKSSIGLIITATQIEDSAVYFCAMRGDYGGSGNKLIFGTGTLLSVKP

>d1i9ea\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

QSVTQPDARVTVSEGASLQLRCKYSYSATPYLFWYVQYPRQGLQLLLKYYSGDPVVQGVNGFEAEFSKSNSSFHLRKASVHWSDSAVYFCAVSGFASALTFGSGTKVIVLPYIQN

>d1bec\_1 b.1.1.1 (3-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

AVTQSPRNKVAVTGGKVTLSCQQTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIPDGYKASRPSQEQFSLILELATPSQTSVYFCASGGGRGSYAEQFFGPGTRLTVLE

>d1kb5b\_ b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRTLYCTCSAAPDWGASAETLYFGSGTRLTVL

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

DSGVVQSPRHIIKEKGGRSVLTCIPISGHSNVVWYQQTLGKELKFLIQHYEKVERDKGFLPSRFSVQQFDDYHSEMNMSALELEDSAMYFCASSLRWGDEQYFGPGTRLTVLE

>d1hxma1 b.1.1.1 (A:1-120) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}

AIELVPEHQTVPVSIGVPATLRCSMKGEAIGNYYINWYRKTQGNTMTFIYREKDIYGPGFKDNFQGDIDIAKNLAVLKILAPSERDEGSYYCACDTLGMGGEYTDKLIFGKGTRVTVEPR

>d1hxmb1 b.1.1.1 (B:1-123) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

AGHLEQPQISSTKTLSKTARLECVVSGITISATSVYWYRERPGEVIQFLVSISYDGTVRKESGIPSGKFEVDRIPETSTSTLTIHNVEKQDIATYYCALWEAQQELGKKIKVFGPGTKLIITD

>d1tvda\_ b.1.1.1 (A:) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

DKVTQSSPDQTVASGSEVVLLCTYDTVYSNPDLFWYRIRPDYSFQFVFYGDDSRSEGADFTQGRFSVKHILTQKAFHLVISPVRTEDSATYYCAFTLPPPTDKLIFGKGTRVTVEP

>d1ah1\_\_ b.1.1.1 (-) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}

AMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYYLGIGNGTQIYVIDPEPCPDSDQEPK

>d3frua1 b.1.1.2 (A:179-269) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}

KEPPSMRLKARPGNSGSSVLTCAAFSFYPPELKFRFLRNGLASGSGNCSTGPNGDGSFHAWSLLEVKRGDEHHYQCQVEHEGLAQPLTVDL

>d1i4fb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKWDRDM

>d1zaga1 b.1.1.2 (A:184-277) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}

QDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDVLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEA

>d1hyrc1 b.1.1.2 (C:181-274) MHC I homolog {Human (Homo sapiens), Mic-a}

TVPPMVNVTRSEASEGNITVTCRASGFYPWNITLSWRQDGVSLSHDTQQWGDVLPDGNGTYQTWVATRICQGEEQRFTCYMEHSGNHSTHPVPS

>d1c16a1 b.1.1.2 (A:181-276) MHC I homolog {Mouse (Mus musculus), t22}

RSDPPKAHVTRHPRPEGDVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFQKWAAVVVPLGKEQSYTCHVYHEGLPEPLILRWGG

>d1igtb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

PCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKG

>d1dn0b2 b.1.1.2 (B:121-225) Immunoglobulin (constant domains of L and H chains) {Fab Kau cold agglutinin (human) IgM, kappa L chain}

GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMAGTDEHVVCKVQHPNGNKEKNVPLPV

>d2ig2h2 b.1.1.2 (H:120-231) Immunoglobulin (constant domains of L and H chains) {Fab KOL (human), lambda L chain}

STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP

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

ESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMSNQLTLPAVECPEGESVKCSVQHDSNPVQELDVNCSG

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

QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVNAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPAECS

>d2hmic2 b.1.1.2 (C:108-214) Immunoglobulin (constant domains of L and H chains) {Fab 28 against HIV-1 RT (mouse), kappa L chain}

RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVAWAIDGSAAANGVLNSWTDQDSKDSTYSMSSTLTLTADEYEAANSYTCAATHKTSTSPIVKSFNANEC

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

VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG

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

PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSV

>d1pfc\_\_ b.1.1.2 (-) Immunoglobulin (constant domains of L and H chains) {Fc (guinea pig)}

RTISKAKGPPRIPEVYLLPPPRNELSKKKVSLTCMITGFYPADINVEWDSSEPSDYKNTPPVFDTDGSFFLYSRLKVDTDAWNNGESFTCSVMHEALPNHVIQKSISRSPG

>d1g84a\_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {C epsilon2 domain from IgE (human)}

SRDFTPPTVKILQSSSDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKSA

>d1tcra2 b.1.1.2 (A:118-213) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

IQNPEPAVYALKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDATVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPC

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

DLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRAD

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

SQPHTKPSVFVMKNGTNVACLVKEFYPKDIRINLVSSKKITEFDPAIVISPSGKYNAVKLGKYEDSNSVTCSVQHDNKTVHSTDFE

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

KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIKIHWEEKKSNTILGSQEGNTMKTNDTYMKFSWLTVPEKSLDKEHRCIVRHENNKNGVDQEIIFPPI

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

QEKPVAWLSSVPSSAHGHRQLVCHVSGFYPKPVWVMWMRGDQEQQGTHRGDFLPNADETWYLQATLDVEAGEEAGLACRVKHSSLGGQDIILYW

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

SRGFPIAEVFTLKPLEFGKPNTLVCFVSNLFPPMLTVNWHDHSVPVEGFGPTFVSAVDGLSFQAFSYLNFTPEPSDIFSCIVTHEPDRYTAIAYWVPRNALPS

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

TRPPSVQVAKTTPFNTREPVMLACYVWGFYPAEVTITWRKNGKLVMHSSAHKTAQPNGDWTYQTLSHLALTPSYGDTYTCVVEHIGAPEPILRDWTPG

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

RRVEPKVTVYPSKTQPLQHHNLLVCSVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA

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

TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEISSADLVPR

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

FPKDPEIHLSGPLEAGKPITVKCSVADVYPFDRLEIDLLKGDHLMKSQEFLEDADRKSLETKSLEVTFTPVIEDIGKVLVCRAKLHIDEMDSVPTVRQAVKELQVYISP

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

YWTPERVELAPLPSWQPVGKNLTLRCQVEGGAPRANLTVVLLRGEKELKREPAVGEPAEVTTTVLVRRDHHGANFSCRTELDLRPQGLELFENTSAPYQLQTFVLPAT

>d1zxq\_1 b.1.1.3 (87-192) Second domain of intercellular cell adhesion molecule-2 (ICAM-2) {Human (Homo sapiens)}

PPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRNFSCLAVLDLMSRGGNIFHKHSAPKMLEIY

>d1cdy\_2 b.1.1.3 (98-178) CD4 {Human (Homo sapiens)}

FGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA

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

MRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWVLNPEAGMWQCLLSDSGQVLLESNIKVLP

>d1hnf\_2 b.1.1.3 (105-182) CD2, second domain {Human (Homo sapiens)}

RVSKPKISWTCINTTLTCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKESSVEPVSCPEK

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

ADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTA

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

FKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPLNGKVTNEGTTSTLTMNPVSFGNEHSYLCTATCESRKLEKGIQVEIYS

>d1iam\_2 b.1.1.4 (1-82) N-terminal domain of intracellular adhesion molecule-1, ICAM-1 {Human (Homo sapiens)}

QTSVSPSKVILPRGGSVLVTCSTSCDQPKLLGIETPLPKKELLLPGNNRKVYELSNVQEDSQPMCYSNCPDGQSTAKTFLTV

>d1zxq\_2 b.1.1.4 (1-86) N-terminal domain of intracellular adhesion molecule-2, ICAM-2 {Human (Homo sapiens)}

KVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVGGLETSLNKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESMNSNVSVYQ

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

LQVDIVPSQGEISVGESKFFLCQVAGDAKDKDISWFSPNGEKLSPNQQRISVVWNDDDSSTLTIYNANIDDAGIYKCVVTAEDGTQSEATVNVKIFQ

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

KLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWKHKGRDVILKKDVRFIVLSNNYLQIRGIKKTDEGTYRCEGRILARGEINFKDIQVIV

>d1ie5a\_ b.1.1.4 (A:) Neural cell adhesion molecule (NCAM) {Chicken (Gallus gallus)}

GKDIQVIVNVPPSVRARQSTMNATANLSQSVTLACDADGFPEPTMTWTKDGEPIEQEDNEEKYSFNYDGSELIIKKVDKSDEAEYICIAENKAGEQDATIHLKVFAK

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

VKPLQVEPPEPVVAVALGASRQLTCRLACADRGASVQWRGLDTSLGAVQSDTGRSVLTVRNASLSAAGTRVCVGSCGGRTFQHTVQLLVY

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

AFPNQLTVSPAALVPGDPEVACTAHKVTPVDPNALSFSLLVGGQELEGAQALGPEVQEEEEEPQGDEDVLFRVTERWRLPPLGTPVPPALYCQATMRLPGLELSHRQAIPVLIEGR

>d1fhga\_ b.1.1.4 (A:) Telokin {Turkey (Meleagris gallopavo)}

AEEKPHVKPYFTKTILDMEVVEGSAARFDCKVEGYPDPEVMWFKDDNPVKESRHFQIDYDEEGNCSLTISEVCGDDDAKYTCKAVNSLGEATCTAELLVETM

>d1g1ca\_ b.1.1.4 (A:) Titin {Human (Homo sapiens), different modules}

SMEAPKIFERIQSQTVGQGSDAHFRVRVVGKPDPECEWYKNGVKIERSDRIYWYWPEDNVCELVIRDVTGEDSASIMVKAINIAGETSSHAFLLVQAK

>d1nct\_\_ b.1.1.4 (-) Titin {Human (Homo sapiens), different modules}

SKTTLAARILTKPRSMTVYEGESARFSCDTDGEPVPTVTWLRKGQVLSTSARHQVTTTKYKSTFEISSVQASDEGNYSVVVENSEGKQEAEFTLTIQK

>d1koa\_1 b.1.1.4 (6265-6361) Twitchin {Nematode (Caenorhabditis elegans)}

QPRFIVKPYGTEVGEGQSANFYCRVIASSPPVVTWHKDDRELKQSVKYMKRYNGNDYGLTINRVKGDDKGEYTVRAKNSYGTKEEIVFLNVTRHSEP

>d1wiu\_\_ b.1.1.4 (-) Twitchin {Nematode (Caenorhabditis elegans)}

LKPKILTASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGDSGAALAPELLVDAKSSTTSIFFPSAKRADSGNYKLKVKNELGEDEAIFEVIVQ

>d1tiu\_\_ b.1.1.4 (-) Twitchin {Human (Homo sapiens), Ig repeat 27}

LIEVEKPLYGVEVFVGETAHFEIELSEPDVHGQWKLKGQPLTASPDCEIIEDGKKHILILHNCQLGMTGEVSFQAANAKSAANLKVKEL

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

DKCKEREEKIILVSSANEIDVRPCPLNPNEHKGTITWYKDDSKTPVSTEQASRIHQHKEKLWFVPAKVEDSGHYYCVVRNSSYCLRIKISAKFVENEPNLC

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

YNAQAIFKQKLPVAGDGGLVCPYMEFFKNENNELPKLQWYKDCKPLLLDNIHFSGVKDRLIVMNVAEKHRGNYTCHASYTYLGKQYPITRVIEFITLEENKPT

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

RPVIVSPANETMEVDLGSQIQLICNVTGQLSDIAYWKWNGSVIDEDDPVLGEDYYSVENPANKRRSTLITVLNISEIESRFYKHPFTCFAKNTHGIDAAYIQLIYPV

>d1cvsc1 b.1.1.4 (C:149-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}

MPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPQPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVER

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

RSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDGLPYLKVLKAAGVNTTDKEIEVLYIRNVTFEDAGEYTCLAGNSIGISFHSAWLTVL

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

KYPVLKDQPAEVLFRENNPTVLECIIEGNDQGVKYSWKKDGKSYNWQEHNAALRKDEGSLVFLRPQASDEGHYQCFAETPAGVASSRVISFRKT

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

YLIASPAKTHEKTPIEGRPFQLDCVLPNAYPKPLITWKKRLSGADPNADVTDFDRRITAGPDGNLYFTIVTKEDVSDIYKYVCTAKNAAVDEEVVLVEYEIKGVTKDNSGY

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

KGEPVPQYVSKDMMAKAGDVTMIYCMYGSNPMGYPNYFKNGKDVNGNPEDRITRHNRTSGKRLLFKTTLPEDEGVYTCEVDNGVGKPQKHSLKLTVV

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

SAPKYEQKPEKVIVVKQGQDVTIPCKVTGLPAPNVVWSHNAKPLSGGRATVTDSGLVIKGVKNGDKGYYGCRATNEHGDKYFETLVQVN

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

RSYGPVFEEQPAHTLFPEGSAEEKVTLTCRARANPPATYRWKMNGTELKMGPDSRYRLVAGDLVISNPVKAKDAGSYQCVATNARGTVVSREASLRF

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

GFLQEFSAEERDPVKITEGWGVMFTCSPPPHYPALSYRWLLNEFPNFIPADGRRFVSQTTGNLYIAKTEASDLGNYSCFATSHIDFITKSVFSKFSQLSLAAEDA

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

RQYAPSIKAKFPADTYALTGQMVTLECFAFGNPVPQIKWRKLDGSQTSKWLSSEPLLHIQNVDFEDEGTYECEAENIKGRDTYQGRIIIHA

>d1cs6a4 b.1.1.4 (A:300-388) Axonin-1 {Ckicken (Gallus gallus)}

QPDWLDVITDTEADIGSDLRWSCVASGKPRPAVRWLRDGQPLASQNRIEVSGGELRFSKLVLEDSGMYQCVAENKHGTVYASAELTVQA

>d1gl4b\_ b.1.1.4 (B:) Perlecan Ig3 domain {Mouse (Mus musculus)}

PIMVTVEEQRSQSVRPGADVTFICTAKSKSPAYTLVWTRLHNGKLPSRAMDFNGILTIRNVQPSDAGTYVCTGSNMFAMDQGTATLHVQ

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

VPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGG

>d1fltx\_ b.1.1.4 (X:) Second domain of the Flt-1 receptor {Human (Homo sapiens)}

GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQT

>d1he7a\_ b.1.1.4 (A:) NGF binding domain of trkA receptor {Human (Homo sapiens)}

SHMPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRLNQPTHVNNGNYTLLAANPFGQASASIMAAFMDNPFEFNPE

>d1fcga1 b.1.1.4 (A:4-88) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIa}

APPKAVLKLEPPWINVLQEDSVTLTCQGARSPESDSIQWFHNGNLIPTHTQPSYRFKANNNDSGEYTCQTGQTSLSDPVHLTVLF

>d1fnla2 b.1.1.4 (A:87-175) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), III}

HIGWLLLQAPRWVFKEEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKATLKDSGSYFCRGLVGSKNVSSETVNITITQA

>d1nkr\_1 b.1.1.4 (6-101) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42 kir}

RKPSLLAHPGPLVKSEETVILQCWSDVMFEHFLLHREGMFNDTLRLIGEHHDGVSKANFSISRMTQDLAGTYRCYGSVTHSPYQVSAPSDPLDIVI

>d1g0xa1 b.1.1.4 (A:2-97) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}

HLPKPTLWAEPGSVITQGSPVTLRCQGGQETQEYRLYREKKTAPWITRIPQELVKKGQFPIPSITWEHAGRYRCYYGSDTAGRSESSDPLELVVTG

>d1g0xa2 b.1.1.4 (A:98-198) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}

AYIKPTLSAQPSPVVNSGGNVTLQCDSQVAFDGFILCKEGEDEHPQCLNSQPHARGSSRAIFSVGPVSPSRRWWYRCYAYDSNSPYEWSLPSDLLELLVLG

>d1f42a1 b.1.1.4 (A:1-87) The p40 domain of interleukin-12 (IL-12 beta chain), N-teminal domain {Human (Homo sapiens)}

IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKED

>d1jbja1 b.1.1.4 (A:101-186) CD3 gamma chain ectodomain fragment {Mouse (Mus musculus)}

KKDGSQTNKAKNLVQVDGSRGDGSVLLTCGLTDKTIKWLKDGSIISPLNATKNTWNLGNNAKDPRGTYQCQGAKETSNPLQVYYRM

>d1jbja2 b.1.1.4 (A:1-100) CD3 epsilon chain ectodomain fragment {Mouse (Mus musculus)}

DDAENIEYKVSISGTSVELTCPLDSDENLKWEKNGQELPQKHDKHLVLQDFSEVEDSGYYVCYTPASNKNTYLYLKARVGSADDAKKDAAKKDDAKKDDA

>d1k3ia1 b.1.1.5 (A:538-639) Galactose oxidase, C-terminal domain {Fungi (Fusarium spp)}

GNLATRPKITRTSTQSVKVGGRITISTDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGGNSYSFQVPSDSGVALPGYWMLFVMNSAGVPSVASTIRVTQ

>d1qba\_1 b.1.1.5 (781-885) Bacterial chitobiase, c-terminal domain {Serratia marcescens}

GETHFVDTQALEKDWLRFANILGQRELAKLDKGGVAYRLPVPGARVAGGKLEANIALPGLGIEYSTDGGKQWQRYDAKAKPAVSGEVQVRSVSPDGKRYSRAEKV

>d1svb\_1 b.1.1.5 (303-395) Envelope glycoprotein, domain III (C-terminal) {Tick-borne encephalitis virus}

TYTMCDKTKFTWKRAPTDSGHDTVVMEVTFSGTKPCRIPVRAVAHGSPDVNVAMLITPNPTIENNGGGFIEMQLPPGDNIIYVGELSHQWFQK

>d1kcla1 b.1.1.5 (A:496-581) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different strains}

TATPTIGHVGPMMAKPGVTITIDGRGFGSSKGTVYFGTTAVSGADITSWEDTQIKVKIPAVAGGNYNIKVANAAGTASNVYDNFEV

>d1smaa1 b.1.1.5 (A:1-123) Maltogenic amylase, N-terminal domain {Thermus sp.}

MRKEAIHHRSTDNFAYAYDSETLHLRLQTKKNDVDHVELLFGDPYEWHDGAWQFQTMPMRKTGSDGLFDYWLAEVKPPYRRLRYGFVLRAGGEKLVYTEKGFYHEAPSDDTAYYFCFPFLHRV

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

MLLEAIFHEAKGSYAYPISETQLRVRLRAKKGDVVRCEVLYADRYASPEEELAHALAGKAGSDERFDYFEALLECSTKRVKYVFLLTGPQGEAVYFGETGFSAERSKAGVFQYAYIHRSE

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

TFAYKIDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASEIPDPASRYQPEGVHGPSQIIQESKE

>d1bf2\_1 b.1.1.5 (1-162) Isoamylase, N-terminal domain {Pseudomonas amyloderamosa}

AINSMSLGASYDAQQANITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAVTVPVSSIKAAGITGAVYYGYRAWGPNWPYASNWGKGSQAGFVSDVDANGDRFNPNKLLLDPYAQEVSQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLV

>d1lla\_3 b.1.1.5 (380-628) Hemocyanin, C-terminal domain {Horseshoe crab (Limulus polyphemus)}

PYDHDVLNFPDIQVQDVTLHARVDNVVHTFMREQELELKHGINPGNARSIKARYYHLDHEPFSYAVNVQNNSASDKHATVRIFLAPKYDELGNEIKADELRRTAIELDKFKTDLHPGKNTVVRHSLDSSVTLSHQPTFEDLLHGVGLNEHKSEYCSCGWPSHLLVPKGNIKGMEYHLFVMLTDWDKDKVDGSESVACVDAVSYCGARDHKYPDKKPMGFPFDRPIHTEHISDFLTNNMFIKDIKIKFHE

>d1hc2\_3 b.1.1.5 (399-653) Hemocyanin, C-terminal domain {Spiny lobster (Panulirus interruptus)}

PPYTHDNLEFSGMVVNGVAIDGELITFFDEFQYSLINAVDSGENIEDVEINARVHRLNHNEFTYKITMSNNNDGERLATFRIFLCPIEDNNGITLTLDEARWFCIELDKFFQKVPSGPETIERSSKDSSVTVPDMPSFQSLKEQADNAVNGGHDLDLSAYERSCGIPDRMLLPKSKPEGMEFNLYVAVTDGDKDTEGHNGGHDYGGTHAQCGVHGEAYPDNRPLGYPLERRIPDERVIDGVSNIKHVVVKIVHHL

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

EDRVFAGFLLRTIGQSADVNFDVCTKDGECTFGGTFCILGGEHEMFWAFDRLFKYDITTSLKHLRLDAHDDFDIKVTIKGIDGHVLSNKYLSPPTVFLAPA

>d1clc\_2 b.1.1.5 (35-134) CelD cellulase, N-terminal domain {Clostridium thermocellum}

IETKVSAAKITENYQFDSRIRLNSIGFIPNHSKKATIAANCSTFYVVKEDGTIVYTGTATSMFDNDTKETVYIADFSSVNEEGTYYLAVPGVGKSVNFKI

>d1f1sa2 b.1.1.5 (A:171-248) Hyaluronate lyase precatalytic domain {Streptococcus agalactiae}

SEHPQPVTTQIEKSVNTALNKNYVFNKADYQYTLTNPSLGKIVGGILYPNATGSTTVKISDKSGKIIKEVPLSVTAST

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

AAPGKPTIAWGNTKFAIVEVDQAATAYNNLVKVKNAADVSVSWNLWNGDTGTTAKVLLNGKEAWSGPSTGSSGTANFKVNKGGRYQMQVALCNADGCTASDATEIVVAD

>d1f13a1 b.1.1.5 (A:5-190) Transglutaminase N-terminal domain {Human (Homo sapiens)}

RTAFGGRRAVPPNNSNAAEDDLPTVELQGVVPRGVNLQEFLNVTSVHLFKERWDTNKVDHHTDKYENNKLIVRRGQSFYVQIDFSRPYDPRRDLFRVEYVIGRYPQENKGTYIPVPIVSELQSGKWGAKIVMREDRSVRLSIQSSPKCIVGKFRMYVAVWTPYGVLRTSRNPETDTYILFNPWCED

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

GLIVDVNGRSHENNLAHRTREIDRERLIVRRGQPFSITLQCSDSLPPKHHLELVLHLGKRDEVVIKVQKEHGARDKWWFNQQGAQDEILLTLHSPANAVIGHYRLAVLVMSPDGHIVERADKISFHMLFNPWCRD

>d1eut\_1 b.1.1.5 (403-505) Sialidase, "linker" domain {Micromonospora viridifaciens}

GICAPFTIPDVALEPGQQVTVPVAVTNQSGIAVPKPSLQLDASPDWQVQGSVEPLMPGRQAKGQVTITVPAGTTPGRYRVGATLRTSAGNASTTFTVTVGLLD

>d1qfha1 b.1.1.5 (A:646-749) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}

KPAPSAEHSYAEGEGLVKVFDNAPAEFTIFAVDTKGVARTDGGDPFEVAINGPDGLVVDAKVTDNNDGTYGVVYDAPVEGNYNVNVTLRGNPIKNMPIDVKCIE

>d1qfha2 b.1.1.5 (A:750-857) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}

GANGEDSSFGSFTFTVAAKNKKGEVKTYGGDKFEVSITGPAEEITLDAIDNQDGTYTAAYSLVGNGRFSTGVKLNGKHIEGSPFKQVLGNPGKKNPEVKSFTTTRTAN

>d1doab\_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}

EPTAEQLAQIAAENEEDEHSVNYKPPAQKSIQEIQELDKDDESLRKYKEALLGRVAVSADPNVPNVVVTRLTLVCSTAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMVGSYGPRAEEYEFLTPMEEAPKGMLARGSYNIKSRFTDDDRTDHLSWEWNLTIKKEWKD

>d1cf1a1 b.1.1.5 (A:10-182) Arrestin {Cow (Bos taurus), visual arrestin}

HVIFKKISRDKSVTIYLGKRDYIDHVERVEPVDGVVLVDPELVKGKRVYVSLTCAFRYGQEDIDVMGLSFRRDLYFSQVQVFPPVGASGATTRLQESLIKKLGANTYPFLLTFPDYLPCSVMLQPAPQDVGKSCGVDFEIKAFATHSTDVEEDKIPKKSSVRLLIRKVQHAPR

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

ERPGPQPTAETTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLFNTAQYKCPVAMEEADDTVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASSTLLREGANREILGIIVSYKVKVKLVVSRGGLLGDLASSDVAVELPFTLMHPKPKEEPPHREVPEHETPVDTNLIELDTNDDDIVFEDFAR

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

LPMVERQDTDSCLVYGGQQMILTGQNFTSESKVVFTEKTTDGQQIWEMEATVDKDKSQPNMLFVEIPEYRNKHIRTPVKVNFYVINGKRKRSQPQHFTYHPV

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

VPEILKKSLHSCSVKGEEEVFLIGKNFLKGTKVIFQENVSDENSWKSEAEIDMELFHQNHLIVKVPPYHDQHITLPVSVGIYVVTNAGRSHDVQPFTYTPD

>d1nfia1 b.1.1.5 (A:190-314) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Human (Homo sapiens)}

NTAELKICRVNRNSGSCLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRIEEKRKRTYETFKSIMK

>d1ahm\_\_ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides farinae), Der f 2}

DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKIEIKASLDGLEIDVPGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKLIGDNGVLACAIATHGKIRD

>d1soxa1 b.1.1.5 (A:344-466) Sulfite oxidase, C-terminal domain {Chicken (Gallus gallus)}

ELPVQSAVTQPRPGAAVPPGELTVKGYAWSGGGREVVRVDVSLDGGRTWKVARLMGDKAPPGRAWAWALWELTVPVEAGTELEIVCKAVDSSYNVQPDSVAPIWNLRGVLSTAWHRVRVSVQD

>d1cvra1 b.1.1.5 (A:351-432) Gingipain R (RgpB), C-terminal domain {Porphyromonas gingivalis}

PTEMQVTAPANISASAQTFEVACDYNGAIATLSDDGDMVGTAIVKDGKAIIKLNESIADETNLTLTVVGYNKVTVIKDVKVE

>d1h6ta1 b.1.1.6 (A:241-321) Internalin B {Listeria monocytogenes}

ECLNKPINHQSNLVVPNTVKNTDGSLVTPEIISDDGDYEKPNVKWHLPEFTNEVSFIFYQPVTIGKAKARFHGRVTQPLKE

>d1ehxa\_ b.1.1.6 (A:) Cellulosomal scaffoldin protein CipC, module x2.1 {Clostridium cellulolyticum}

MQDPTINPTSISAKAGSFADTKITLTPNGNTFNGISELQSSQYTKGTNEVTLLASYLNTLPENTTKTLTFDFGVGTKNPKLTITVLPKDIPGLE

>d1im3d\_ b.1.1.6 (D:) Cytomegalovirus protein US2 {Human cytomegalovirus}

PWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPEL

>d1jjua3 b.1.1.6 (A:274-351) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}

AAPQVLAVAPARLKIGEETQLRVAGTGLGSDLTLPEGVAGSVESAGNGVTVLKLTATGTPGPVSLELGGQKVDLVAYD

>d1jjua4 b.1.1.6 (A:352-489) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}

RPDRISIVPDLTIARIGGNGGPIPKVPAQFEAMGWLNGPDGQPGTGDDIALGAFPASWATDNFDEEAEKMQDAKYAGSIDDTGLFTPAEAGPNPERPMQTNNAGNLKVIATVDAEGEPLSAEAHLYATVQRFVDAPIR

>d1jmxa3 b.1.1.6 (A:282-363) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Pseudomonas putida}

GKARLLAVQPAFIKAGGESEITLVGSGLAGKPDLGAGVEVTEVLEQTPTLVRLKARAAADAKPGQREVAVGTLKGVNLAVYD

>d2hft\_1 b.1.2.1 (1-106) Extracellular region of human tissue factor {Human (Homo sapiens)}

SGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLET

>d2hft\_2 b.1.2.1 (107-211) Extracellular region of human tissue factor {Human (Homo sapiens)}

NLGQPTIQSFEQVGTKVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSQEKGEFRSGKKTAKTNTNEFLIDVDKGENYCFSVQAVIPSRTVNRKSTDSPVECMG

>d1fnf\_1 b.1.2.1 (1142-1235) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

PLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDDKESVPISDTIIPA

>d1fnf\_2 b.1.2.1 (1236-1326) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

VPPPTDLRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVAELSISPSDNAVVLTNLLPGTEYVVSVSSVYEQHESTPLRGRQKTG

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

PAPTDLKFTQVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSSSVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLE

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

NVSPPRRARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKPDVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTA

>d1j8ka\_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

NIDRPKGLAFTDVDVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTAELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPA

>d2fnba\_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

MRGSEVPQLTDLSFVDITDSSIGLRWTPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYYTVTGLEPGIDYDISVITLINGGESAPTTLTQQT

>d2mfn\_1 b.1.2.1 (1-92) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}

GLDSPTGFDSSDITANSFTVHWVAPRAPITGYIIRHHAEHSVGRPRQDRVPPSRNSITLTNLNPGTEYVVSIIAVNGREESPPLIGQQATVS

>d2mfn\_2 b.1.2.1 (93-184) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}

DIPRDLEVIASTPTSLLISWEPPAVSVRYYRITYGETGGNSPVQEFTVPGSKSTATINNIKPGADYTITLYAVTGRGDSPASSKPVSINYKT

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

DNPKDLEVSDPTETTLSLRWRRPVAKFDRYRLTYVSPSGKKNEMEIPVDSTSFILRGLDAGTEYTISLVAEKGRHKSKPTTIKGSTV

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

VGSPKGISFSDITENSATVSWTPPRSRVDSYRVSYVPITGGTPNVVTVDGSKTRTKLVKLVPGVDYNVNIISVKGFEESEPISGILKT

>d1ten\_\_ b.1.2.1 (-) Tenascin {Human (Homo sapiens)}

RLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKDVPGDRTTIDLTEDENQYSIGNLKPDTEYEVSLISRRGDMSSNPAKETFTT

>d1cfb\_1 b.1.2.1 (610-709) Neuroglian, two amino proximal Fn3 repeats {Drosophila melanogaster}

IVQDVPNAPKLTGITCQADKAEIHWEQQGDNRSPILHYTIQFNTSFTPASWDAAYEKVPNTDSSFVVQMSPWANYTFRVIAFNKIGASPPSAHSDSCTTQ

>d1cfb\_2 b.1.2.1 (710-814) Neuroglian, two amino proximal Fn3 repeats {Drosophila melanogaster}

PDVPFKNPDNVVGQGTEPNNLVISWTPMPEIEHNAPNFHYYVSWKRDIPAAAWENNNIFDWRQNNIVIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDR

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

DLGAPQNPNAKAAGSRKIHFNWLPPSGKPMGYRVKYWIQGDSESEAHLLDSKVPSVELTNLYPYCDYEMKVCAYGAQGEGPYSSLVSCRTHQ

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

EVPSEPGRLAFNVVSSTVTQLSWAEPAETNGEITAYEVCYGLVNDDNRPIGPMKKVLVDNPKNRMLLIENLRESQPYRYTVKARNGAGWGPEREAIINLATQP

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

EPKFTKCRSPERETFSCHWTDEVHHGTKNEGPIQLFYTRRNTQEWTQEWKECPDYVSAGENSCYFNSSFTSIAIPYCIKLTSNGGTVDEKCFSVDEIVQ

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

PDPPIALNWTLLNVSLTGIHADIQVRWEAPRNADIQKGWMVLEYELQYKEVNETKWKMMDPILTTSVPVYSLKVDKEYEVRVRSKQRNSGNYGEFSEVLYVTLPQM

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

DPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGQYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHIN

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

EVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGQGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSEWSEPVSLLT

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

LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYI

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

VQPDPPLELAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWEIHFAGQQTEFKILSLHPGQKYLVQVRCKPDHGYWSAWSPATFIQIPS

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

FKVLQEPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPSEHV

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

KPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVNIWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQAYNTTWSEWSPSTKWH

>d1egja\_ b.1.2.1 (A:) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

IQMAPPSLNVTKDGDSYSLRWETMKMRYEHIDHTFEIQYRKDTATWKDSKTETLQNAHSMALPALEPSTRYWARVRVRTSRTGYNGIWSEWSEARSWDTES

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

EETIPLQTLRCYNDYTSHITCRWADTQDAQRLVNVTLIRRVNEDLLEPVSCDLSDDMPWSACPHPRCVPRRCVIPCQSFVVTDVDYFSFQPDRPLGTRLTVTL

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

TQHVQPPEPRDLQISTDQDHFLLTWSVALGSPQSHWLSPGDLEFEVVYKRLQDSWEDAAILLSNTSQATLGPEHLMPSSTYVARVRTRLAPGSRLSGRPSKWSPEVCWDSQPGD

>d1gh7a3 b.1.2.1 (A:218-316) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

EAQPQNLECFFDGAAVLSCSWEVRKEVASSVSFGLFYKPSPDAGSAVLLREEECSPVLREGLGSLHTRHHCQIPVPDPATHGQYIVSVQPRRAEKHIKS

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

AGYPPASPSNLSCLMHLTTNSLVCQWEPGPETHLPTSFILKSFRSRADCQYQGDTIPDCVAKKRQNNCSIPRKNLLLYQYMAIWVQAENMLGSSESPKLCLDPMDVV

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

KLEPPMLQALDIGPDVVSHQPGCLWLSWKPWKPSEYMEQECELRYQPQLKGANWTLVFHLPSSKDQFELCGLHQAPVYTLQMRCIRSSLPGFWSPWSPGLQLRPTM

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

VPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGK

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

IGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCITIFN

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

GLPPEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVDYSTVYFVNIEVWVEAENALGKVTSDHINFDPV

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

YKVKPNPPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRPSKEPSF

>d1i1ra1 b.1.2.1 (A:2-101) Cytokyne receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

LLDPCGYISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIASLNIQLTCNILTFGQLEQNVYGITIISG

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

GTELPSPPSVWFEAEFFHHILHWTPIPQQSESTCYEVALLRYGIESWNSISQCSQTLSYDLTAVTLDLYHSNGYRARVRAVDGSRHSQWTVTNTRFSVD

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

EVTLTVGSVNLEIHNGFILGKIQLPRPKMAPAQDTYESIFSHFREYEIAIRKVPGQFTFTHKKVKHEQFSLLTSGEVGEFCVQVKPSVASRSNKGMWSKEECISLT

>d1bpv\_\_ b.1.2.1 (-) Type I titin module {Human (Homo sapiens)}

SPIDPPGKPVPLNITRHTVTLKWAKPEYTGGFKITSYIVEKRDLPNGRWLKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPPSEPSDAITCRDDVEA

>d1f42a2 b.1.2.1 (A:88-211) The p40 domain of interleukin-12 (IL-12 beta chain), domains 2 and 3 {Human (Homo sapiens)}

GIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDII

>d1f42a3 b.1.2.1 (A:212-306) The p40 domain of interleukin-12 (IL-12 beta chain), domains 2 and 3 {Human (Homo sapiens)}

KPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS

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

TQISDFHVATRFNDDFSRAVLEAEVQMCGELRDYLRVTVSLWQGETQVASGTAPFGGEIIDERGGYADRVTLRLNVENPKLWSAEIPNLYRAVVELHTADGTLIEAEACDVGFR

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

FFQFRLSGQTIEVTSEYLFRHSDNELLHWMVALDGKPLASGEVPLDVAPQGKQLIELPELPQPESAGQLWLTVRVVQPNATAWSEAGHISAWQQWRLAENLSVTL

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

TYIDDITVTTSVEQDSGLVNYQISVKGSNLFKLEVRLLDAENKVVANGTGTQGQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTSLGPVSDFYTLPVGIRT

>d1f13a2 b.1.5.1 (A:516-627) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}

SNVDMDFEVENAVLGKDFKLSITFRNNSHNRYTITAYLSANITFYTGVPKAEFKKETFDVTLEPLSFKKEAVLIQAGEYMGQLLEQASLHFFVTARINETRDVLAKQKSTVL

>d1f13a3 b.1.5.1 (A:628-728) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}

TIPEIIIKVRGTQVVGSDMTVTVEFTNPLKETLRNVWVHLDGPGVTRPMKKMFREIRPNSTVQWEEVCRPWVSGHRKLIASMSSDSLRHVYGELDVQIQRR

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

RLQLSIKHAQPVFGTDFDVIVEVKNEGGRDAHAQLTMLAMAVTYNSLRRGECQRKTISVTVPAHKAHKEVMRLHYDDYVRCVSEHHLIRVKALLDAPGENGPIMTVANIPLS

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

TPELLVQVPGKAVVWEPLTAYVSFTNPLPVPLKGGVFTLEGAGLLSATQIHVNGAVAPSGKVSVKLSFSPMRTGVRKLLVDFDSDRLKDVKGVTTVVVHKK

>d1ncia\_ b.1.6.1 (A:) N-cadherin (neural) {Mouse (Mus musculus)}

GSDWVIPPINLPENSRGPFPQELVRIRSGRDKNLSLRYSVTGPGADQPPTGIFIINPISGQLSVTKPLDRELIARFHLRAHAVDINGNQVENPIDIVINVID

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

NDNRPEFLHQVWNGSVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRIVSQAPSTPSPNMFTINNETGDIITVAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTD

>d1noa\_\_ b.1.7.1 (-) Neocarzinostatin {Streptomyces carzinostaticus}

AAPTATVTPSSGLSDGTVVKVAGAGLQAGTAYDVGQCAWVDTGVLACNPADFSSVTADANGSASTSLTVRRSFEGFLFDGTRWGTVDCTTAACQVGLSDAAGNGPEGVAISFN

>d1akp\_\_ b.1.7.1 (-) Kedarcidin (apo form) {Actimomycete, strain L585-6}

ASAAVSVSPATGLADGATVTVSASGFATSTSATALQCAILADGRGACNVAEFHDFSLSGGEGTTSVVVRRSFTGYVMPDGPEVGAVDCDTAPGGCEIVVGGNTGEYGNAAISFG

>d1srda\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Spinach (Spinacia oleracea)}

ATKKAVAVLKGTSNVEGVVTLTQEDDGPTTVNVRISGLAPGKHGFHLHEFGDTTNGCMSTGPHFNPDKKTHGAPEDEVRHAGDLGNIVANTDGVAEATIVDNQIPLTGPNSVVGRALVVHELEDDLGKGGHELSPTTGNAGGRLACGVVGLTPV

>d1eqwa\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Salmonella typhimurium}

NTLTVKMNDALSSGTGENIGEITVSETPYGLLFTPHLNGLTPGIHGFHVHTNPSCMPGMKDGKEVPALMAGGHLDPEKTGKHLGPYNDKGHLGDLPGLVVNADGTATYPLLAPRLKSLSELKGHSLMIHKGGDNYSDKPAPLGGGGARFACGVIE

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

GKPNSSAVAILETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIHEKGDVSKGVESTGKVWHKFDEPIECFNESDLGKNLYSGKTFLSAPLPTWQLIGRSFVISKSLNHPENEPSSVKDYSFLGVIARSAGVWENNKQVCACTGKTVWEERKDALA

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

GSPGIRLGSSEDNFARFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFLNFTPTLICADDLQTNLNLQTKPVDPTVDGGAQVQQVVNIECISDFTEAPVLNIQFRYGGTFQNVSVKLPITLNK

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

GGYVAPKAVWLPAVKAKGLEISGTFTHRQGHIYMEMNFTNKALQHMTDFAIQFNKNSFGVIPSTPLAIHTPLMPNQSIDVSLPLNTLGPVMKMEPLNNLQVAVKNNIDVFYFSCLIPLNV

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

PVITVNAGLEVYPSILNQDNKTCSLPGTALKVSCFNVRFCLKADGKGVLPRKLNFQVELLLDKLKQKGAIRRALFLYSRSPSHSKNMTISRGGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAADTTGLQPILNQFTPANISRQAHILLDCGE

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

DNVCKPKLEVSVDSDQKKIYIGDDNPLTLIVKAQNQGEGAYEAELIVSIPLQADFIGVVRNNEALARLSCAFKTENQTRQVVCDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLQIQSSNLFDKVSPVVSHKVDLA

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

VLAAVEIRGVSSPDHVFLPIPNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQWPYKYNNNTLLYILHYDIDGPMNCTSDMEINPLRIKISSLQTTEKNDTVAGQGERDHLITKRDLALSEGDIHTLGCGVAQCLKIVCQVGRLDRGKSAILYVKSLLWTETFMNKENQNHSYSLKSSASFNVIEFPYKNLPIEDITNSTLVTTNVTWGIQ

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

EFPVSEARVLEDRPLSDKGSGDSSQVTQVSPQRIALRLRPDDSKNFSIQVRQXVELEVRDLPEELSLSFNATCLNNEVIPGLKSCMGLKIGDTVSFSIEAKVRGCPQEKEKSFTIKPVGFKDSLIVQVTFDCD

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

AVSLDRTRAVFDGSEKSMTLDISNDNKQLPYLAQAWIENENQEKIITGPVIATPPVQRLDPGAKSMVRLSTTPDISKLPQDRESLFYFNLREIPPRSEKANVVQIALCTKIKLFYRPAAIKTRP

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

GVALGATRVIYPAGQKQVQLAVTNNDENSTYLIQSWVENADGVKDGRFIVTPPLFAMKGKKENTLRILDATNNQLPQDRESLFWMNVKAIPSMDKSKLTENTLQLAIISRIKLYYRPAKLA

>d1dqia\_ b.1.13.1 (A:) Superoxide reductase (SOR) {Archaeon Pyrococcus furiosus}

MISETIRSGDWKGEKHVPVIEYEREGELVKVKVQVGKEIPHPNTTEHHIRYIELYFLPEGENFVYQVGRVEFTAHGESVNGPNTSDVYTEPIAYFVLKTKKKGKLYALSYCNIHGLWENEVTLE

>d1dfx\_1 b.1.13.1 (37-125) Desulfoferrodoxin C-terminal domain {Desulfovibrio desulfuricans}

VEGSTDGAMEKHVPVIEKVDGGYLIKVGSVPHPMEEKHWIEWIELLADGRSYTKFLKPGDAPEAFFAIDASKVTAREYCNLHGHWKAEN

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

ASITEIKADKTTAVANGQDAITYTVKVMKGDKPVSNQEVTFTTTLGKLSNSTEKTDTNGYAKVTLTSTTPGKSLVSARVSDVAVDVKAPEVEFFT

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

TLTIDDGNIEIVGTGVKGKLPTVWLQYGQVNLKASGGNGKYTWRSANPAIASVDASSGQVTLKEKGTTTISVISSDNQTATYTIATPNS

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

TIAADKSTLAAVPTSIIADGLMASTITLELKDTYGDPQAGANVAFDTTLGNMGVITDHNDGTYSAPLTSTTLGVATVTVKVDGAAFSVPSVTVNFT

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

ADPIPDAGRSSFTVSTPDILADGTMSSTLSFVPVDKNGHFISGMQGLSFTQNGVPVSISPITEQPDSYTATVVGNSVGDVTITPQVDTLILSTLQKKISLFPV

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

PTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSSFTPNVSVNDQGQVTITYQTYSEVAVTAKSKKFPSYSVSYRFYP

>d1exh\_\_ b.2.2.1 (-) Exo-1,4-beta-D-glycanase (cellulase, xylanase), cellulose-binding domain, CBD {Cellulomonas fimi}

ASSGPAGCQVLWGVNQWNTGFTANVTVKNTSSAPVDGWTLTFSFPSGQQVTQAWSSTVTQSGSAVTVRNAPWNGSIPAGGTAQFGFNGSHTGTNAAPTAFSLNGTPCTVG

>d1hejc\_ b.2.2.1 (C:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}

TGSCSVSAVRGEEWADRFNVTYSVSGSSSWVVTLGLNGGQSVQSSWNAALTGSSGTVTARPNGSGNSFGVTFYKNGSSATPGATCATG

>d1g43a\_ b.2.2.2 (A:) Cellusomal scaffolding protein A, scafoldin {Clostridium cellulolyticum}

AGTGVVSVQFNNGSSPASSNSIYARFKVTNTSGSPINLADLKLRYYYTQDADKPLTFWCDHAGYMSGSNYIDATSKVTGSFKAVSPAVTNADHYLEVALNSDAGSLPAGGSIEIQTRFARNDWSNFDQSNDWSYTAAGSYMDWQKISAFVGGTLAYGSTP

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

PEIFVEAQINTPGTTFTEIKAMIRNQSGWPARMLDKGTFRYWFTLDEGVDPADITVSSAYNQCATPEDVHHVSGDLYYVEIDCTGEKIFPGGQSEHRREVQFRIAGGPGWDPSNDWSFQGIGNELAPAPYIVLYDDGVPVWGTAP

>d1aoha\_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

AVRIKVDTVNAKPGDTVRIPVRFSGIPSKGIANCDFVYSYDPNVLEIIEIEPGELIVDPNPTKSFDTAVYPDRKMIVFLFAEDSGTGAYAITEDGVFATIVAKVKSGAPNGLSVIKFVEVGGFANNDLVEQKTQFFDGGVNVG

>d1g1ka\_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

ASLKVTVGTANGKPGDTVTVPVTFADVAKMKNVGTCNFYLGYDASLLEVVSVDAGPIVKNAAVNFSSSASNGTISFLFLDNTITDELITADGVFANIKFKLKSVTAKTTTPVTFKDGGAFGDGTMSKIASVTKTNGSVTIDPG

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

FACKTANGTAIPIGGGSANVYVNLAPVVNVGQNLVVDLSTQIFCHNDYPETITDYVTLQRGSAYGGVLSNFSGTVKYSGSSYPFPTTSETPRVVYNSRTDKPWPVALYLTPVSSAGGVAIKAGSLIAVLILRQTNNYNSDDFQFVWNIYANNDVVVPT

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

GGCDVSARDVTVTLPDYPGSVPIPLTVYCAKSQNLGYYLSGTTADAGNSIFTNTASFSPAQGVGVQLTRNGTIIPANNTVSLGAVGTSAVSLGLTANYARTGGQVTAGNVQSIIGVTFVYQ

>d1pdkb\_ b.2.3.2 (B:) PapK pilus subunit {Escherichia coli}

LLDRPCHVSGDSLNKHVVFKTRASRDFWYPPGRSPTESFVIRLENCHATAVGKIVTLTFKGTEEAALPGHLKVTGVNAGRLGIALLDTDGSSLLKPGTSHNKGQGEKVTGNSLELPFGAYVVATPEALRTKSVVPGDYEATATFELTYR

>d1ycsa\_ b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Human (Homo sapiens)}

VPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEE

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

KKSPMLCGQYPVKSEGKELKIVVQPETQHRARYLTEGSRGSVKDRTQQGFPTVKLEGHNEPVVLQVFVGNDSGRVKPHGFYQACRVTGRNTTPCKEVDIEGTTVIEVGLDPSNNMTLAVDCVGILKLRNADVEARIGIAGSKKKSTRARLVFRVNIMRKDGSTLTLQTPSSPILCTQPAG

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

GPYLQILEQPKQRGFRFRYVCEGPSHGGLPGASSEKNKKSYPQVKICNYVGPAKVIVQLVTNGKNIHLHAHSLVGKHCEDGVCTVTAGPKDMVVGFANLGILHVTKKKVFETLEARMTEACIRGYNPGLLVHSDLAYLQAEGGGDRQLTDREKEIIRQAAVQQTKEMDLSVVRLMFTAFLPDSTGSFTRRLEPVVSDAIYDSKAPNASNLKI

>d1bvoa\_ b.2.5.1 (A:) Dorsal homologue Gambif1 {African malaria mosquito (Anopheles gambiae)}

PYVEITEQPHPKALRFRYECEGRSAGSIPGVNTTAEQKTFPSIQVHGYRGRAVVVVSCVTKEGPEHKPHPHNLVGKEGCKKGVCTVEINSTTMSYTFNNLGIQCVKKKDVEEALRLRQEIRVDPFRTGFGHAKEPGSIDLNAVRLCFQVFLEGQQRGRFTEPLTPVVSDIIYDKK

>d1xbra\_ b.2.5.1 (A:) T domain from Brachyury transcription factor {African clawed frog (Xenopus laevis)}

ELKVSLEERDLWTRFKELTNEMIVTKNGRRMFPVLKVSMSGLDPNAMYTVLLDFVAADNHRWKYVNGEWVPGGKPEPQAPSCVYIHPDSPNFGAHWMKDPVSFSKVKLTNKMNGGGQIMLNSLHKYEPRIHIVRVGGTQRMITSHSFPETQFIAVTAYQNEEITALKIKHNPFAKAFLDAKERN

>d1bg1a2 b.2.5.1 (A:322-575) STAT3b {Mouse (Mus musculus)}

VVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKY

>d1h9da\_ b.2.5.1 (A:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

VLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATAAMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRR

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

LSGTQTSVVFTVKSAPPTNLGDKIYLTGNIPELGNWSTDTSGAVNNAQGPLLAPNYPDWFYVFSVPAGKTIQFKFFIKRADGTIQWENGSNHVATTPTGATGNITVTWQN

>d1acz\_\_ b.3.1.1 (-) Glucoamilase, granular starch-binding domain {Aspergillus niger}

CTTPTAVAVTFDLTATTTYGENIYLVGSISQLGDWETSDGIALSADKYTSSDPLWYVTVTLPAGESFEYKFIRIESDDSVEWESDPNREYTVPQACGTSTATVTDTWR

>d1cqya\_ b.3.1.1 (A:) beta-amylase {Bacillus cereus}

TPVMQTIVVKNVPTTIGDTVYITGNRAELGSWDTKQYPIQLYYDSHSNDWRGNVVLPAERNIEFKAFIKSKDGTVKSWQTIQQSWNPVPLKTTSHTSSW

>d1dmha\_ b.3.6.1 (A:) Catechol 1,2-dioxygenase {Acinetobacter calcoaceticus}

VKIFNTQDVQDFLRVASGLEQEGGNPRVKQIIHRVLSDLYKAIEDLNITSDEYWAGVAYLNQLGANQEAGLLSPGLGFDHYLDMRMDAEDAALGIENATPRTIEGPLYVAGAPESVGYARMDDGSDPNGHTLILHGTIFDADGKPLPNAKVEIWHANTKGFYSHFDPTGEQQAFNMRRSIITDENGQYRVRTILPAGYGCPPEGPTQQLLNQLGRHGNRPAHIHYFVSADGHRKLTTQINVAGDPYTYDDFAYATREGLVVDAVEHTDPEAIKANDVEGPFAEMVFDLKLTRLVDGVDNQVVDRPRLAV

>d1eo9a\_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Acinetobacter calcoaceticus, adp1}

ELKETPSQTGGPYVHIGLLPKQANIEVFEHNLDNNLVQDNTQGQRIRLEGQVFDGLSLPLRDVLIEIWQADTNGVYPSQADTQGKQVDPNFLGWGRTGADFGTGFWSFNTIKPGAVPGRKGSTQAPHISLIIFARGINIGLHTRVYFDDEAEANAKDPVLNSIEWATRRQTLVAKREERDGEVVYRFDIRIQGENETVFFDI

>d1eo9b\_ b.3.6.1 (B:) Protocatechuate-3,4-dioxygenase, beta chain {Acinetobacter calcoaceticus, adp1}

IIWGAYAQRNTEDHPPAYAPGYKTSVLRSPKNALISIAETLSEVTAPHFSADKFGPKDNDLILNYAKDGLPIGERVIVHGYVRDQFGRPVKNALVEVWQANASGRYRHPNDQYIGAMDPNFGGCGRMLTDDNGYYVFRTIKPGPYPWRNRINEWRPAHIHFSLIADGWAQRLISQFYFEGDTLIDSCPILKTIPSEQQRRALIALEDKSNFIEADSRCYRFDITLRGRRATYFENDLT

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

ETVQVNLPVSLEDLFVGKKKSFKIGRKGPHGASEKTQIDIQLKPGWKAGTKITYKNQGDYNPQTGRRKTLQFVIQEKSHP

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

NFKRDGDDLIYTLPLSFKESLLGFSKTIQTIDGRTLPLSRVQPVQPSQTSTYPGQGMPTPKNPSQRGNLIVKYKVDYPISLNDAQKRAID

>d1id2a\_ b.6.1.1 (A:) Amicyanin {Paracoccus versutus (Thiobacillus versutus)}

QDKITVTSEKPVAAADVPADAVVVGIEKMKYLTPEVTIKAGETVYWVNGEVMPHNVAFKKGIVGEDAFRGEMMTKDQAYAITFNEAGSYDYFCTPHPFMRGKVIVE

>d1kdj\_\_ b.6.1.1 (-) Plastocyanin {Fern (Adiantum capillus-veneris)}

AKVEVGDEVGNFKFYPDSITVSAGEAVEFTLVGETGHNIVFDIPAGAPGTVASELKAASMDENDLLSEDEPSFKAKVSTPGTYTFYCTPHKSANMKGTLTVK

>d1nin\_\_ b.6.1.1 (-) Plastocyanin {Anabaena variabilis}

ETYTVKLGSDKGLLVFEPAKLTIKPGDTVEFLNNKVPPHNVVFDAALNPAKSADLAKSLSHKQLLMSPGQSTSTTFPADAPAGEYTFYCEPHRGAGMVGKITVAG

>d1bqk\_\_ b.6.1.1 (-) Pseudoazurin {Achromobacter cycloclastes}

ADFEVHMLNKGKDGAMVFEPASLKVAPGDTVTFIPTDKGHNVETIKGMIPDGAEAFKSKINENYKVTFTAPGVYGVKCTPHYGMGMVGVVQVGDAPANLEAVKGAKNPKKAQERLDAALAALGN

>d2cbp\_\_ b.6.1.1 (-) Plantacyanin {Cucumber (Cucumis sativus)}

AVYVVGGSGGWTFNTESWPKGKRFRAGDILLFNYNPSMHNVVVVNQGGFSTCNTPAGAKVYTSGRDQIKLPKGQSYFICNFPGHCQSGMKIAVNAL

>d1cc3a\_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}

AECSVDIQGNDQMQFNTNAITVDKSCKQFTVNLSHPGNLPKNVMGHNWVLSTAADMQGVVTDGMASGLDKDYLKPDDSRVIAHTKLIGSGEKDSVTFDVSKLKEGEQYMFFCSELCGINHALMKGTLTLK

>d1qhqa\_ b.6.1.1 (A:) Auracyanin {Chloroflexus aurantiacus}

ANAPGGSNVVNETPAQTVEVRAAPDALAFAQTSLSLPANTVVRLDFVNQNNLGVQHNWVLVNGGDDVAAAVNTAAQNNADALFVPPPDTPNALAWTAMLNAGESGSVTFRTPAPGTYLYICTFPGHYLAGMKGTLTVTP

>d1e30a\_ b.6.1.1 (A:) Rusticyanin {Thiobacillus ferrooxidans}

LDTTWKEATLPQVKAMLEKDTGKVSGDTVTYSGKTVHVVAAAVLPGFPFPSFEVHDKKNPTLEIPAGATVDVTFINTNKGFGHSFDITKKGPPYAVMPVIDPIVAGTGFSPVPKDGKFGYTNFTWHPTAGTYYYVCQIPGHAATGQFGKIVVK

>d1jer\_\_ b.6.1.1 (-) Stellacyanin {Cucumber (Cucumis sativus)}

MQSTVHIVGDNTGWSVPSSPNFYSQWAAGKTFRVGDSLQFNFPANAHNVHEMETKQSFDACNFVNSDNDVERTSPVIERLDELGMHYFVCTVGTHCSNGQKLSINVVAAN

>d1ibya\_ b.6.1.4 (A:) Red copper protein nitrosocyanin {Nitrosomonas europaea}

EHNFNVVINAYDTTIPELNVEGVTVKNIRAFNVLNEPETLVVKKGDAVKVVVENKSPISEGFSIDAFGVQEVIKAGETKTISFTADKAGAFTIWCQLHPKNIHLPGTLNVVE

>d1fwxa1 b.6.1.4 (A:452-581) Nitrous oxide reductase, C-terminal domain {Paracoccus denitrificans}

SVWDRNDPMWAETRAQAEADGVDIDNWTEEVIRDGNKVRVYMSSVAPSFSIESFTVKEGDEVTVIVTNLDEIDDLTHGFTMGNYGVAMEIGPQMTSSVTFVAANPGVYWYYCQWFCHALHMEMRGRMLVEPK

>d1fftb1 b.6.1.2 (B:118-283) Quinol oxidase (CyoA) {Escherichia coli}

KPLAHDEKPITIEVVSMDWKWFFIYPEQGIATVNEIAFPANTPVYFKVTSNSVMNSFFIPRLGSQIYAMAGMQTRLHLIANEPGTYDGISASYSGPGFSGMKFKAIATPDRAAFDQWVAKAKQSPNTMSDMAAFEKLAAPSEYNQVEYFSNVKPDLFADVINKFMA

>d1ar1b1 b.6.1.2 (B:108-252) Cytochrome c oxidase {Paracoccus denitrificans}

NDPDLVIKAIGHQWYWSYEYPNDGVAFDALMLEKEALADAGYSEDEYLLATDNPVVVPVGKKVLVQVTATDVIHAWTIPAFAVKQDAVPGRIAQLWFSVDQEGVYFGQCSELCGINHAYMPIVVKAVSQEKYEAWLAGAKEEFAA

>d2cuab\_ b.6.1.2 (B:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYTLATHTAGVIPAGKLERVDPTTVRQEGPWADPAQAVVQTGPNQYTVYVLAFAFGYQPNPIEVPQGAEIVFKITSPDVIHGFHVEGTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE

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

ATAAEIAALPRQKVELVDPPFVHAHSQVAEGGPKVVEFTMVIEEKKIVIDDAGTEVHAMAFNGTVPGPLMVVHQDDYLELTLINPETNTLMHNINFHAATGALGGGGLTEINPGEKTILRFKATKPGVFVYHCAPPGMVPWHVVSGMNGAIMVLPREGLHDGK

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

QGKPLHYDRAYTIGEFDLYIPKGPDGKYKDYATLAESYGDTVQVMRTLTPSHIVFNGKVGALTGANALTAKVGETVLLIHSQANRDTRPHLIGGFGDWVWETGKFANPPQRDLETWFIRGGSAGAALYTFKQPGVYAYLNHNLIEAFELGAAGHIKVEGKWNDDLMKQIKAPAPIPR

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

ELPVIDAVTTHAPEVPPAIDRDYPAKVRVKMETVEKTMKMDDGVEYRYWTFDGDVPGRMIRVREGDTVEVEFSNNPSSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPGLYIYHCAVAPVGMHIANGMYGLILVEPKEGLPKV

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

DKEFYIVQGDFYTKGKKGAQGLQPFDMDKAVAEQPEYVVFNGHVGALTGDNALKAKAGETVRMYVGNGGPNLVSSFHVIGEIFDKVYVEGGKLINENVQSTIVPAGGSAIVEFKVDIPGNYTLVDHSIFRAFNKGALGQLKVEGAENPEIM

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

RPTLPIPDLLTTDARNRIQLTIGAGQSTFGGKTATTWGYNGNLLGPAVKLQRGKAVTVDIYNQLTEETTLHWHGLEVPGEVDGGPQGIIPPGGKRSVTLNVDQPAATCWFHPHQHGKTGRQVAMGLAGLVVIEDDEILKL

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

MLPKQWGIDDVPVIVQDKKFSADGQIDYQLDVMTAAVGWFGDTLLTNGAIYPQHAAPRGWLRLRLLNGCNARSLNFATSDNRPLYVIASDGGLLPEPVKVSELPVLMGERFEVLVEVNDNKPFDLVTLPVSQMGMAIAPFDKPHPVMRIQPIAISASGALPDTLS

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

SLPALPSLEGLTVRKLQLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQMMGHMGHGNMNHMNHGGKFDFHHANKINGQAFDMNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILSENGKPPAAHRAGWKDTVKVEGNVSEVLVKFNHDAPKEHAYMAHCHLLEHEDTGMMLGFTV

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

SQIRHYKWEVEYMFWAPNCNENIVMGINGQFPGPTIRANAGDSVVVELTNKLHTEGVVIHWHGILQRGTPWADGTASISQCAINPGETFFYNFTVDNPGTFFYHGHLGMQRSAGLYGSLIVDPPQGKKE

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

PFHYDGEINLLLSDWWHQSIHKQEVGLSSKPIRWIGEPQTILLNGRGQFDCSIAAKYDSNLEPCKLKGSESCAPYIFHVSPKKTYRIRIASTTALAALNFAIGNHQLLVVEADGNYVQPFYTSDIDIYSGESYSVLITTDQNPSENYWVSVGTRARHPNTPPGLTLLNYLPNSVSKLPTSPPPQTPAWDDFDRSKNFTYRITAAMGSPK

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

PPVKFNRRIFLLNTQNVINGYVKWAINDVSLALPPTPYLGAMKYNLLHAFDQNPPPEVFPEDYDIDTPPTNEKTRIGNGVYQFKIGEVVDVILQNANMMKENLSETHPWHLHGHDFWVLGYGDGKFSAEEESSLNLKNPPLRNTVVIFPYGWTAIRFVADNPGVWAFHCHIEPHLHMGMGVVFAEGVEKVGRIPTKALACGGTAKSLINNPKNP

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

AIVNSVDTMTLTNANVSPDGFTRAGILVNGVHGPLIRGGKNDNFELNVVNDLDNPTMLRPTSIHWHGLFQRGTNWADGADGVNQCPISPGHAFLYKFTPAGHAGTFWYHSHFGTQYCDGLRGPMVIYDDND

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

PHAALYDEDDENTIITLADWYHIPAPSIQGAAQPDATLINGKGRYVGGPAAELSIVNVEQGKKYRMRLISLSCDPNWQFSIDGHELTIIEVDGELTEPHTVDRLQIFTGQRYSFVLDANQPVDNYWIRAQPNKGRNGLAGTFANGVNSAILRYAGAANADPTTSANPNPAQL

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

NEADLHALIDPAAPGIPTPGAADVNLRFQLGFSGGRFTINGTAYESPSVPTLLQIMSGAQSANDLLPAGSVYELPRNQVVELVVPAGVLGGPHPFHLHGHAFSVVRSAGSSTYNFVNPVKRDVVSLGVTGDEVTIRFVTDNPGPWFFHCHIEFHLMNGLAIVFAEDMANTVDANNPPVEWAQLCEIYDDLPPEATSIQTV

>d1kcw\_1 b.6.1.3 (1-192) Ceruloplasmin {Human (Homo sapiens)}

KEKHYYIGIIETTWDYASDHGEKKLISVDTEHSNIYLQNGPDRIGRLYKKALYLQYTDETFRTTIEKPVWLGFLGPIIKAETGDKVYVHLKNLASRPYTFHSHGITYYKEHEGAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCVTRIYHSHIDAPKDIASGLIGPLIICKKDSLDKEKEK

>d1kcw\_3 b.6.1.3 (347-553) Ceruloplasmin {Human (Homo sapiens)}

IRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTRIGGSYKKLVYREYTDASFTNRKERGPEEEHLGILGPVIWAEVGDTIRVTFHNKGAYPLSIEPIGVRFNKNNEGTYYSPNYNPQSRSVPPSASHVAPTETFTYEWTVPKEVGPTNADPVCLAKMYYSAVDPTKDIFTGLIGPMKICKKGSLHANGRQK

>d1kcw\_4 b.6.1.3 (554-705) Ceruloplasmin {Human (Homo sapiens)}

DVDKEFYLFPTVFDENESLLLEDNIRMFTTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGLTMCKGDSVVWYLFSAGNEADVHGIYFSGNTYLWRGERRDTANLFPQTSLTLHMWPDTEGTFNVECLTTDHYTGGMKQKYTVNQCRRQSED

>d1qasa2 b.7.1.1 (A:626-756) PI-specific phospholipase C isozyme D1 (PLC-D1), C-terminal domain {Rat (Rattus norvegicus)}

WRPERLRVRIISGQQLPKVNKNKNSIVDPKVIVEIHGVGRDTGSRQTAVITNNGFNPRWDMEFEFEVTVPDLALVRFMVEDYDSSSKNDFIGQSTIPWNSLKQGYRHVHLLSKNGDQHPSATLFVKISIQD

>d1rlw\_\_ b.7.1.1 (-) Domain from cytosolic phospholipase A2 {Human (Homo sapiens)}

SSHKFTVVVLRATKVTKGAFGDMLDTPDPYVELFISTTPDSRKRTRHFNNDINPVWNETFEFILDPNQENVLEITLMDANYVMDETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMSLEVASS

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

YRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTRREDKFMYFEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFWVNTFFIPGPEEVDNDKEYLVLTLTKNDLDKANKDKANRYFSPNFKVKLYFTKTV

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

CDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDN

>d1bdya\_ b.7.1.1 (A:) Domain from protein kinase C delta {Rat (Rattus norvegicus)}

MAPFLRISFNSYELGSLQAEDDASQPFCAVKMKEALTTDRGKTLVQKKPTMYPEWKSTFDAHIYEGRVIQIVLMRAAEDPMSEVTVGVSVLAERCKKNNGKAEFWLDLQPQAKVLMCVQYFLE

>d1gmia\_ b.7.1.1 (A:) Domain from protein kinase C epsilon {Rat (Rattus rattus)}

MVVFNGLLKIKICEAVSLKPTAWSLRDAVGPRPQTFLLDPYIALNVDDSRIGQTATKQKTNSPAWHDEFVTDVCNGRKIELAVFHDAPIGYDDFVANCTIQFEELLQNGSRHFEDWIDLEPEGKVYVIIDLSGSSG

>d1k5wa\_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}

KLGDICFSLRYVPTAGKLTVVILEAKNLKKMDVGGLSDPYVKIHLMQNGKRLKKKKTTIKKNTLNPYYNESFSFEVPFEQIQKVQVVVTVLDYDKIGKNDAIGKVFVGYNSTGAELRHWSDMLANPRRPIAQWHTLQVEEEVDAMLAV

>d1rsy\_\_ b.7.1.2 (-) Synaptogamin I {Rat (Rattus norvegicus)}

GGGILDSMVEKEEPKEEEKLGKLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLLPDKKKKFETKVHRKTLNPVFNEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNTVDFGHVTEEWRDLQSA

>d1dsya\_ b.7.1.2 (A:) C2 domain from protein kinase c (alpha) {Rat (Rattus norvegicus)}

TEKRGRIYLKAEVTDEKLHVTVRDAKNLIPMDPNGLSDPYVKLKLIPDPKNESKQKTKTIRSTLNPQWNESFTFKLKPSDKDRRLSVEIWDWDRTTRNDFMGSLSFGVSELMKMPASGWYKLLNQEEGEYYNVPIPE

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

NEVWQDQLILNKVSGGYRIENPTPYYVTVIGLGGSEKQAEEGEFETVMLSPRSEQTVKSANYNTPYLSYINDYGGRPVLSFICNGSRCSVK

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

LPPDQAAEKLRFRRSANSLTLINPTPYYLTVTELNAGTRVLENALVPPMGESAVKLPSDAGSNITYRTINDYGALTPKMTGVME

>d1kvp\_\_ b.10.1.1 (-) Bacteriophage capsid proteins {Bacteriophage phi-X174}

SNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPLRRGLAIDSTVDIFTFYVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIPKHLFQGYLNIYNNYFKAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTGMAPVTTKFRDVPNLSGTPLIFRDNKGRTIKTGQLGIGPVDAGFLVAQNTAQAANGERAIPSNLWADLSNATSIDIMGLQAAYANLHTDQERDYFMQRYRDVISSFGGKTSYDADNRPLLVMRSNLWASGYDVDGTDQTSLGQFSGRVQQTYKHSVPRFFVPEHGTMFTLALVRFPPTATKEIQYLNAKGALTYTDIAGDPVLYGNLPPREISMKDVFRSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLEGFPFIQEPPSGDLQERVLIRHHDYDQCFQSVQLLQWNSQVKFNVTVYRNLPTTRDSIMTS

>d1gff2\_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage G4}

MFQKFISKHNAPINSTQLAATKTPAVAAPVLSVPNLSRSTILINATTTAVTTHSGLCHVVRIDETNPTNHHALSIAGSLSNVPADMIAFAIRFEVADGVVPTAVPALYDVYPIETFNNGKAISFKDAVTIDSHPRTVGNDVYAGIMLWSNAWTASTISGVLSVNQVNREATVLQPLK

>d1stma\_ b.10.1.2 (A:) SPMV coat protein {Satellite panicum mosaic virus}

AAATSLVYDTCYVTLTERATTSFQRQSFPTLKGMGDRAFQVVAFTIQGVSAAPLMYNARLYNPGDTDSVHATGVQLMGTVPRTVRLTPRVGQNNWFFGNTEEAETILAIDGLVSTKGANAPSNTVIVTGCFRLAPSELQSS

>d1a34a\_ b.10.1.2 (A:) STMV coat protein {Satellite tobacco mosaic virus}

TGDNSNVVTMIRAGSYPKVNPTPTWVRAIPFEVSVQSGIAFKVPVGSLFSANFRTDSFTSVTVMSVRAWTQLTPPVNEYSFVRLKPLFKTGDSTEEFEGRASNINTRASVGYRIPTNLRQNTVAADNVCEVRSNCRQVALVISCCFN

>d2stv\_\_ b.10.1.2 (-) STNV coat protein {Satellite tobacco necrosis virus}

TMRAVKRMINTHLEHKRFALINSGNTNATAGTVQNLSNGIIQGDDINQRSGDQVRIVSHKLHVRGTAITVSQTFRFIWFRDNMNRGTTPTVLEVLNTANFMSQYNPITLQQKRFTILKDVTLNCSLTGESIKDRIINLPGQLVNYNGATAVAASNGPGAIFMLQIGDSLVGLWDSSYEAVYTDA

>d1smvc\_ b.10.1.2 (C:) SMV coat potein {Sesbania mosaic virus}

QAGISMAPSAQGAMVRIRNPAVSSSRGAITVLHCELTAEIGVTDSIVVSSELVMPYTVGTWLRGVADNWSKYSWLSVRYTYIPSCPSSTAGSIHMGFQYDMADTVPVSVNKLSNLRGYVSGQVWSGSAGLCFINNSRCSDTSTAISTTLDVSELGKKWYPYKTSADYATAVGVDVNIATDLVPARLVIALLDGSSSTAVAAGRIYDTYTIQMIEPTASALNL

>d1f2nc\_ b.10.1.2 (C:) RYMV capsid protein {Rice yellow mottle virus}

AEPQLQRAPVAQASRISGTVPGPLSSNTWPLHSVEFLADFKRSSTSADATTYDCVPFNLPRVWSLARCYSMWKPTRWDVVYLPEVSATVAGSIEMCFLYDYADTIPRYTGKMSRTAGFVTSSVWYGAEGCHLLSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVVNTILPARLAVRSSIKPTVSDTPGKLYVIASMVLRDPVDPTLNT

>d1bmv1\_ b.10.1.2 (1:) BPMV coat protein {Bean pod mottle virus}

SISQQTVWNQMATVRTPLNFDSSKQSFCQFSVDLLGGGISVDKTGDWITLVQNSPISNLLRVAAWKKGCLMVKVVMSGNAAVKRSDWASLVQVFLTNSNSTEHFDACRWTKSEPHSWELIFPIEVCGPNNGFEMWSSEWANQTSWHLSFLVDNPKQSTTFDVLLGISQNFEIAGNTLMPAFSVPQ

>d1bmv2\_ b.10.1.2 (2:) BPMV coat protein {Bean pod mottle virus}

METNLFKLSLDDVETPKGSMLDLKISQSKIALPKNTVGGTILRSDLLANFLTEGNFRASVDLQRTHRIKGMIKMVATVGIPENTGIALACAMNSSIRGRASSDIYTICSQDCELWNPACTKAMTMSFNPNPCSDAWSLEFLKRTGFHCDIICVTGWTATPMQDVQVTIDWFISSQECVPRTYCVLNPQNPFVLNRWMGKLTFPQGTSRSVKRMPLSIGGGAGAKSAILMNMPNAVLSMWRYFVGDLVFEVSKMTSPYIKCTVSFFIAFGNLADDTINFEAFPHKLVQFGEIQEKVVLKFSQEEFLTAWSTQVRPATTLLADGCPYLYAMVHDSSVSTIPGDFVIGVKLTIIENMCAYGLNPGISGSRLLGTIPQ

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

AVTVVPDPTCCGTLSFKVPKDAKKGKHLGTFDIRQAIMDYGGLHSQEWCAKGIVNPTFTVRMHAPRNAFAGLSIACTFDDYKRIDLPALGNECPPSEMFELPTKVFMLKDADVHEWQFNYGELTGHGLCNWANVATQPTLYFFVASTNQVTMAADWQCIVTMHVDMGPVIDRFELN

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

PTMTWPIQLGDTFAIDRYYEAKEIKLDGSTSMLSISYNFGGPVKHSKKHAISYSRAVMSRNLGWSGTISGSVKSVSSLFCTASFVIFPWECEAPPTLRQVLWGPHQIMHGDGQFEIAIKTRLHSAATTEEGFGRLGILPLSGPIAPDAHVGSYEFIVHINTWRPDSQVHPPM

>d1a6ca3 b.10.1.2 (A:349-513) TRSV capsid protein {Tobacco ringspot virus}

FSSSELYNWFTLTNLKPDANTGVVNFDIPGYIHDFASKDATVTLASNPLSWLVAATGWHYGEVDLCISWSRSKQAQAQEGSVSITTNYRDWGAYWQGQARIYDLRRTEAEIPIFLGSYAGATPSGALGKQNYVRISIVNAKDIVALRVCLRPKSIKFWGRSATLF

>d2tbvc\_ b.10.1.2 (C:) TBSV coat protein {Tomato bushy stunt virus}

IITHVGGVGGSIMAPVAVSRQLVGSKPKFTGRTSGGVTVTSHREYLTQVNNSSGFVVNGGIVGNSLQLNPSNGTLFSWLPALASNFDQYSFNSVVLDYVPLCGTTEVGRVALYFDKDSQDPEPADRVELANFGVLKETAPWAEAMLRIPTDKVKRYCNDSATVDQKLIDLGQLGIATYGGAGADAVGELFLARSVTLYFPQPTNTLLSSKRLDLTGSLADATGPGYLVLTRTPTVLTHTFRATGTFNLSGGLRCLTSLTLGATGAVVINDILAIDNVGTASDYFLNCTVSSLPATVTFTVSGVAAGILLVGRARANVVNLL

>d1cwpa\_ b.10.1.2 (A:) Cowpea chlorotic mottle virus {Host: cowpea (Vigna unguiculta), (L.)}

KAIKAWTGYSVSKWTASCAAAEAKVTSAITISLPNELSSERNKQLKVGRVLLWLGLLPSVSGTVKSCVTETQTTAAASFQVALAVADNSKDVVAAMYPEAFKGITLEQLAADLTIYLYSSAALTEGDVIVHLEVEHVRPTFDDSFTPVY

>d1c8nc\_ b.10.1.2 (C:) TNV coat protein {Tobacco necrosis virus}

GVSRAGGFVTAPVIGAMVTRPTVPRFGMRGNSTVVSNSELILNLTPIALAYTVQSLPLIATQPAWLGTIADNYSKWRWVSLRIIYSPKCPTTTSGTVAMCLSYDRNDVAPGSRVQLSQTYKAINFPPYAGYDGAAILNTDVTPTSAIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNQFCPCTVHIGSDGGPAVAVPPGDIFFKYVIELIEPINPTMN

>d1auyb\_ b.10.1.2 (B:) TYMV coat protein {Turnip yellow mosaic virus}

MEIDKELAPQDRTVTVATVLPAVPGPSPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVSTLTTFYRHASLESLWVTIHPTLQAPTFPTTVGVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTLSPLIVKCPLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLSMHSPLITDTST

>d1e57b\_ b.10.1.2 (B:) PHMV coat protein {Physalis mottle virus}

VVKVKQASIPAPGSILSQPNTEQSPAIVLPFQFEATTFGTAETAAQVSLQTADPITKLTAPYRHAQIVECKAILTPTDLAVSNPLTVYLAWVPANSPATPTQILRVYGGQSFVLGGAISAAKTIEVPLNLDSVNRMLKDSVTYTDTPKLLAYSRAPTNPSKIPTASIQISGRIRLSKPMLIAN

>d1f15b\_ b.10.1.2 (B:) CMV coat protein {Cucumber mosaic virus, strain fny}

DANFRVLSQQLSRLNKTLAAGRPTINHPTFVGSERCRPGYTFTSITLKPPKIDRGSYYGKRLLLPDSVTEYDKKLVSRLQIRVNPLPKFDSTVWVTVRKVPASSDLSVAAISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVYSKDDALETDELVLHVDIEHQRIPTSGVLPV

>d1novc\_ b.10.1.3 (C:) Nodavirus capsid protein {Nodamura virus}

RRRAAPRQQQRQQSNRASNQPRRRRARRTRRQQRMAATNNMLKMSAPGLDFLKCAFASPDFSTDPGKGIPDKFQGLVLPKKHCLTQSITFTPGKQTMLLVAPIPGIACLKAEANVGASFSGVPLASVEFPGFDQLFGTSATDTAANVTAFRYASMAAGVYPTSNLMQFAGSIQVYKIPLKQVLNSYSQTVATVPPTNLAQNTIAIDGLEALDALPNNNYSGSFIEGCYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQASMFTNLTFSGARYTGLGDMDAIAILVTTPTGAVNTAVLKVWACVEYRPNPNSTLYEFARESPANDEYALAAYRKIARDIPIAVACKDN

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

NRRNKARKVVSRSTALVPMAPASQRTGPAPRKPRKRNQALVRNPRLTDAGLAFLKCAFAAPDFSVDPGKGIPDNFHGRTLAIKDCNTTSVVFTPNTDTYIVVAPVPGFAYFRAEVAVGAQPTTFVGVPYPTYATNFGAGSQNGLPAVNNYSKFRYASMACGLYPTSNMMQFSGSVQVWRVDLNLSEAVNPAVTAITPAPGVFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTFAFDKSTDFEWCDFVRSLEFSESNVLGAATAMKLLAPGGGTDTTLTGLGNVNTLVYKISTPTGAVNTAILRTWNCIELQPYTDSALFQFSGVSPPFDPLALECYHNLKMRFPVAVSSRENXSKFWEGVLRVLNQISGTLSVIPGPVGTISAGVHQLTGMYM

>d1dnv\_\_ b.10.1.3 (-) Galleria mellonella densovirus capsid protein {Wax moth (Galleria mellonella), densovirus}

VYIIPRPFSNFGKKLSTYTKSHKFMIFGLANNVIGPTGTGTTAVNRLLTTCLAEIPWQKLPLYMNQSEFDLLPPGSRVVECNVKVIFRTNRIAFETSSTVTKQATLNQISNVQTAIGLNKLGWGINRAFTAFQSDQPMIPTATTAPKYEPVTGDTGYRGMIADYYGADSTNDTAFGNAGNYPHHQVSSFTFLQNYYCMYQQTNQGTGGWPCLAEHLQQFDSKTVNNQCLIDVTYKPKMGLIKSPLNYKIIGQPTVKGTISVGDNLVNMRGAVVTNPPEATQNVAESTHNLTRNFPADLFNIYSDIEKSQVLHKGPWGHENPQIQPSVHIGIQAVPALTTGALLINSSPLNSWTDSMGYIDVMSSCTVMEAQPTHFPFSTEANTNPGNTIYRINLTPNSLTSAFNGLYGNGATLGN

>d1b35a\_ b.10.1.3 (A:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

VMGEDQQIPRNEAQHGVHPISIDTHRISNNWSPQAMCIGEKVVSIRQLIKRFGIFGDANTLQADGSSFVVAPFTVTSPTKTLTSTRNYTQFDYYYYLYAFWRGSMRIKMVAETQDGTGTPRKKTNFTWFVRMFNSLQDSFNSLISTSSSAVTTTVLPSGTINMGPSTQVIDPTVEGLIEVEVPYYNISHITPAVTIDDGTPSMEDYLKGHSPPCLLTFSPRDSISATNHIITASFMRALGDDFSFMYLLGVPPLVNVARA

>d1b35b\_ b.10.1.3 (B:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

ENSHIENEDKRLTSEQKEIVHFVSEGVTPSTTALPDIVNLSTNYLDKNTREDRIHSIKDFLSRPIIIATNLWSVSDPVEKQLYTANFPEVLISNAMYQDKLKGFVGLRATLVVKVQVNSQPFQQGRLMLQYIPYAQYMPNRVTLINETLQGRSGCPRTDLELSVGTEVEMRIPYVSPHLYYNLITGQGSFGSIYVVVYSQLHDQVSGTGSIEYTVWAHLEDVDVQYPTGANIFTGNEAYIKGTSRYDAAQKAHAA

>d1b35c\_ b.10.1.3 (C:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

SKPTVQGKIGECKLRGQGRMANFDGMDMSHKMALSSTNEIETNEGLAGTSLDVMDLSRVLSIPNYWDRFTWKTSDVINTVLWDNYVSPFKVKPYSATITDRFRCTHMGKVANAFTYWRGSMVYTFKFVKTQYHSGRLRISFIPYYYNTTISTGTPDVSRTQKIVVDLRTSTAVSFTVPYIGSRPWLYCIRPESSWLSKDNTDGALMYNCVSGIVRVEVLNQLVAAQNVFSEIDVICEVNGGPDLEFAGPTCPRYVPYAGDFTLADTRKIEAERTQEYSNNED

>d1sida\_ b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

KACPRPAPVPKLLIKGGMEVLDLVTGPDSVTEIEAFLNPRMGQPPTPESLTEGGQYYGWSRGINLATSDTEDSPGNNTLPTWSMAKLQLPMLNEDLTCDTLQMWEAVSVKTEVVGSGSLLDVHGFNKPTDTVNTKGISTPVEGSQYHVFAVGGEPLDLQGLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLNPISKAKLDKDGMYPVEIWHPDPAKNENTRYFGNYTGGTTTPPVLQFTNTLTTVLLDENGVGPLCKGEGLYLSCVDIMGWRVTRNYDVHHWRGLPRYFKITLRKRWVKNPYPMASLISSLFNNMLPQVQGQPMEGENTQVEEVRVYDGTEPVPGDPDMTRYVDRFGKTKTVFPG

>d1fmd2\_ b.10.1.4 (2:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETTLLEDRILTTRNGHTTSTTQSSVGVTFGYATAEDSTSGPNTSALETRVHQAERFFKMALFDWVPSQNFGHMHKVVLPHEPKGVYGGLVKSYAYMRNGWDVEVTAVGNQFNGGCLLVALVPEMGDISDREKYQLTLYPHQFINPRTNMTAHITVPYVGVNRYDQYKQHRPWTLVVMVVAPLTTNTAGAQQIKVYANIAPTNVHVAGELPSKE

>d1qqp1\_ b.10.1.4 (1:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTSAGESADPVTTTVENYGGETQIQRRQHTDVSFIMDRFVKVTPQNQINILDLMQVPSHTLVGALLRASTYYFSDLEIAVKHEGDLTWVPNGAPEKALDNTTNPTAYHKAPLTRLALPYTAPHRVLATVYNGECRYSRNAVPNLRGDLQVLAQKVARTLPTSFNYGAIKATRVTELLYRMKRAETYCPRPLLAIHPTEARHKQKIVAPVK

>d1qqp3\_ b.10.1.4 (3:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGGLVTTDPKTADPVYGKVFNPPRNQLPGRFTNLLDVAEACPTFLRFEGGVPYVTTKTDSDRVLAQFDMSLAAKHMSNTFLAGLAQYYTQYSGTINLHFMFTGPTDAKARYMVAYAPPGMEPPKTPEAAAHCIHAEWDTGLNSKFTFSIPYLSAADYTYTASDVAETTNVQGWVCLFQITHGKADGDALVVLASAGKDFELRLPVDARAE

>d1mvma\_ b.10.1.4 (A:) MVM coat protein {Murine minute virus, strain i}

GVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTVTEQDSGGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVDRDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADVTQGMDREANGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSYGPLTTFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY

>d1hxs1\_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}

GSSSTDNTVRETVGAATSRDALPNTEASGPTHSKEIPALTAVETGATNPLVPSDTVQTRHVVQHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFTYSRFDMELTFVVTANFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWQTSSNPSIFYTYGTAPARISVPYVGISNAYSHFYDGFSKVPLKDQSAALGDSLYGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLKPKHIRVWCPRPPRAVAYYGPGVDYKDGTLTPLSTKDLTTY

>d1pov0\_ b.10.1.4 (0:) Poliovirus {Poliovirus type 1, strain Mahoney}

GAQVSSQKVGAHENSNRAYGGSTINYTTINYYRDSASNAASKQDFSQDPSKFTEPIKDVLIKTAPMLNSPNIEACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQPTEPDVAACRFYTLDTVSWTKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSNTTTMHTSYQNANPGEKGGTFTGTFTPDNNQTSPARRFCPVDYLLGNGTLLGNAFVFPHQIINLRTNNCATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLNFASESSPEIPITLTIAPMCCEFNGLRNITLPRLQ

>d1eah3\_ b.10.1.4 (3:) Poliovirus {Poliovirus type 2, strain Lansing}

GLPVLNTPGSNQYLTADNYQSPCAIPEFDVTPPIDIPGEVRNMMELAEIDTMIPLNLTNQRKNTMDMYRVELNDAAHSDTPILCLSLSPASDPRLAHTMLGEILNYYTHWAGSLKFTFLFCGSMMATGKLLVSYAPPGAEAPKSRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTINDSFTEGGYISMFYQTRVVVPLSTPRKMDILGFVSACNDFSVRLLRDTTHISQEA

>d1aym1\_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 16}

NPVERYVDEVLNEVLVVPNINQSHPTTSNAAPVLDAAETGHTNKIQPEDTIETRYVQSSQTLDEMSVESFLGRSGCIHESVLDIVDNYNDQSFTKWNINLQEMAQIRRKFEMFTYARFDSEITMVPSVAAKDGHIGHIVMQYMYVPPGAPIPTTRDDYAWQSGTNASVFWQHGQPFPRFSLPFLSIASAYYMFYDGYDGDTYKSRYGTVVTNDMGTLCSRIVTSEQLHKVKVVTRIYHKAKHTKAWCPRPPRAVQYSHTHTTNYKLSSEVHNDVAIRPRTNLTTV

>d1bev1\_ b.10.1.4 (1:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

QAAGALVAGTSTSTHSVATDSTPALQAAETGATSTARDESMIETRTIVPTHGIHETSVESFFGRSSLVGMPLLATGTSITHWRIDFREFVQLRAKMSWFTYMRFDVEFTIIATSSTGQNVTTEQHTTYQVMYVPPGAPVPSNQDSFQWQSGCNPSVFADTDGPPAQFSVPFMSSANAYSTVYDGYARFMDTDPDRYGILPSNFLGFMYFRTLEDAAHQVRFRIYAKIKHTSCWIPRAPRQAPYKKRYNLVFSGDSDRICSNRASLTSY

>d1bev3\_ b.10.1.4 (3:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

GLPTKPGPGSYQFMTTDEDCSPCILPDFQPTPEIFIPGKVNNLLEIAQVESILEANNREGVEGVERYVIPVSVQDALDAQIYALRLELGGSGPLSSSLLGTLAKHYTQWSGSVEITCMFTGTFMTTGKVLLAYTPPGGDMPRNREEAMLGTHVIWDFGLQSSITLVIPWISASHFRGVSNDDVLNYQYYAAGHVTIWYQTNMVIPPGFPNTAGIIMMIAAQPNFSFRIQKDREDMTQTAILQ

>d1tme3\_ b.10.1.4 (3:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

SPIAVTVREHKGCFYSTNPDTTVPIYGKTISTPNDYMCGEFSDLLELCKLPTFLGNPNSNNKRYPYFSATNSVPTTSLVDYQVALSCSCMCNSMLAAVARNFNQYRGSLNFLFVFTGAAMVKGKFLIAYTPPGAGKPTTRDQAMQATYAIWDLGLNSSFVFTAPFISPTHYRQTSYTSATIASVDGWVTVWQLTPLTYPSGTPVNSDILTLVSAGDDFTLRMPISPTKWVPQ

>d1tmf1\_ b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

GVDNAEKGKVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNMETTFNYQENDYRLNCLLLTPLPSFCPDSSSGPQKTKAPVQWRWVRSGGVNGANFPLMTKQDYAFLCFSPFTFYKCDLEVTVSALGTDTVASVLRWAPTGAPADVTDQLIGYTPSLGETRNPHMWLVGAGNSQVSFVVPYNSPLSVLPAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCPRPTLFFPWPTPTTTKINADNPVPILELE

>d1tmf2\_ b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

DQNTEEMENLSDRVASDKAGNSATNTQSTVGRLCGYGKSHHGEHPASCADTATDKVLAAERYYTIDLASWTTSQEAFSHIRIPLPHVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASQFHAGSLLVFMAPEFYTGKGTKTGTMEPSDPFTMDTEWRSPQGAPTGYRYDSRTGFFATNHQNQWQWTVYPHQILNLRTNTTVDLEVPYVNVAPSSSWTQHANWTLVVAVLSPLQYATGSSPDVQITASLQPVNPVFNGLRHETVIAQ

>d1dzla\_ b.10.1.4 (A:) L1 protein {Human papillomavirus type 16}

KVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKKPNNNKILVPKVSGLQYRVFRIHLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASAYAANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTQVAVQPGDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGTVGENVPDDLYIKGSGSTANLASSNYFPTPSGSMVTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMSLCAAISTSETTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVTSQAIACQKHTPPAPKEDPLKKYTFWEVNLKEKFSADLDQFPLGRKFLLQLGL

>d1ihma\_ b.10.1.4 (A:) Calcivirus capsid protein {Norwalk virus}

DPLAMDPVAGSSTAVATAGQVNPIDPWIINNFVQAPQGEFTISPNNTPGDVLFDLSLGPHLNPFLLHLSQMYNGWVGNMRVRIMLAGNAFTAGKIIVSCIPPGFGSHNLTIAQATLFPHVIADVRTLDPIEVPLEDVRNVLFHNNDRNQQTMRLVCMLYTPLRTGGGTGDSFVVAGRVMTCPSPDFNFLFLVPPTVEQKTRPFTLPNLPLSSLSNSRAPLPISSMGISPDNVQSVQFQNGRCTLDGRLVGTTPVSLSHVAKIRGTSNGTVINLTELDGTPFHPFEGPAPIGFPDLGGCDWHINMTQFGHSSQTQYDVDTTPDTFVPHLGSIQANGIGSGNYVGVLSWISPPSHPSGSQVDLWKIPNYGSSITEATHLAPSVYPPGFGEVLVFFMSKMPGPGAYNLPCLLPQEYISHLASEQAPTVGEAALLHYVDPDTGRNLGEFKAYPDGFLTCVPNGASSGPQQLPINGVFVFVSWVSRFYQLKPVGTAS

>d1amm\_1 b.11.1.1 (1-85) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GKITFYEDRGFQGHCYECSSDCPNLQPYFSRCNSIRVDSGCWMLYERPNYQGHQYFLRRGDYPDYQQWMGFNDSIRSCRLIPQHT

>d1amm\_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GTFRMRIYERDDFRGQMSEITDDCPSLQDRFHLTEVHSLNVLEGSWVLYEMPSYRGRQYLLRPGEYRRYLDWGAMNAKVGSLRRVMDFY

>d1bd7a\_ b.11.1.1 (A:) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

EHKIILYENPNFTGKKMEIVDDDVPSFHAHGYQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKGDYKDNSDFGAPHPQVQSVRRIRDMQGNPKIIIFEQENFQGHSHELSGPCPNLKETGMEKAGSVLVQAGPWVGYEQANCKGEQFVFEKGEYPRWDSWTSSRRTDSLSSLRPIK

>d1npsa\_ b.11.1.1 (A:) Protein S {Myxococcus xanthus}

ANITVFYNEDFQGKQVDLPPGNYTRAQLAALGIENNTISSVKVPPGVKAILYQNDGFAGDQIEVVANAEELGPLNNNVSSIRVISVPV

>d1hdfa\_ b.11.1.1 (A:) Spherulin 3a (S3a) {Slime mold (Physarum polycephalum)}

SVCKGVSGNPAKGEVFLYKHVNFQGDSWKVTGNVYDFRSVSGLNDVVSSVKVGPNTKAFIFKDDRFNGNFIRLEESSQVTDLTTRNLNDAISSMIVATFE

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

GHKIKGTVVLMRKNVLDVNSVTSVGGIIGQGLDLVGSTLDTLTAFLGRSVSLQLISATKADANGKGKLGKATFLEGIITSLPTLGAGQSAFKINFEWDDGSGIPGAFYIKNFMQTEFFLVSLTLEDIPNHGSIHFVCNSWIYNAKLFKSDRIFFANQTY

>d1lox\_2 b.12.1.1 (2-112) 15-Lipoxygenase {Rabbit (Oryctolagus cuniculus)}

GVYRVCVSTGASIYAGSKNKVELWLVGQHGEVELGSCLRPTRNKEEEFKVNVSKYLGSLLFVRLRKKHFLKEDAWFCNWISVQALGAAEDKYWFPCYRWVVGDGVQSLPVG

>d1pgs\_1 b.13.1.1 (4-140) Peptide:N-glycosidase F, PNGase F {Flavobacterium meningosepticum}

DNTVNIKTFDKVKNAFGDGLSQSAEGTFTFPADVTTVKTIKMFIKNECPNKTCDEWDRYANVYVKNKTTGEWYEIGRFITPYWVGTEKLPRGLEIDVTDFKSLLSGNTELKIYTETWLAKGREYSVDFDIVYGTPDY

>d1pgs\_2 b.13.1.1 (141-314) Peptide:N-glycosidase F, PNGase F {Flavobacterium meningosepticum}

KYSAVVPVIQYNKSSIDGVPYGKAHTLGLKKNIQLPTNTEKAYLRTTISGWGHAKPYDAGSRGCAEWCFRTHTIAINNANTFQHQLGALGCSANPINNQSPGNWTPDRAGWCPGMAVPTRIDVLNNSLTGSTFSYEYKFQSWTNNGTNGDAFYAISSFVIAKSNTPISAPVVTN

>d1phm\_1 b.13.1.2 (45-198) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (Rattus norvegicus)}

NECLGTIGPVTPLDASDFALDIRMPGVTPKESDTYFCMSMRLPVDEEAFVIDFKPRASMDTVHHMLLFGCNMPSSTGSYWFCDEGTCTDKANILYAWARNAPPTRLPKGVGFRVGGETGSKYFVLQVHYGDISAFRDNHKDCSGVSVHLTRVPQ

>d1phm\_2 b.13.1.2 (199-354) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (Rattus norvegicus)}

PLIAGMYLMMSVDTVIPPGEKVVNADISCQYKMYPMHVFAYRVHTHHLGKVVSGYRVRNGQWTLIGRQNPQLPQAFYPVEHPVDVTFGDILAARCVFTGEGRTEATHIGGTSSDEMCNLYIMYYMEAKYALSFMTCTKNVAPDMFRTIPAEANIPI

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

LRNQQAMAANLQARQIVLQQSYPVIQQVETQTFDPANRSVFDVTPANVGIVKGFLVKVTAAITNNHATEAVALTDFGPANLVQRVIYYDPDNQRHTETSGWHLHFVNTAKQGAPFLSSMVTDSPIKYGDVMNVIDAPATIAAGATGELTMYYWVPLAYSETDLTGAVLANVPQSKQRLKLEFANNNTAFAAVGANPLEAIYQGAGAADCEFEEISYTVYQSYLDQLPVGQ

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

NGYILPLIDLSTLYNLENSAQAGLTPNVDFVVQYANLYRYLSTIAVFDNGGSFNAGTDINYLSQRTANFSDTRKLDPKTWAAQTRRRIATDFPKGVYYCDNRDKPIYTLQYGNVGFVVNPKTVNQNARLLMGYEYFTSRT

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

MMPQWSYMHISGQDASEYLSPGLVQFARATETYFSLNNKFRNPTVAPTHDVTTDRSQRLTLRFIPVDREDTAYSYKARFTLAVGDNRVLDMASTYFDIRGVLDRGPTFKPYSGTAYNALAPKGAPNPCEWDEAATALEINLEEEDDDNEDEVDEQAEQQKTHVFGQAPYSGINITKEGIQIGVEGQTPKYADKTFQPEPQIGESQWYETEINHAAGRVLKKTTPMKPCYGSYAKPTNENGGQGILVKQQNGKLESQVEMQFFSTTEATAGNGDNLTPKVVLYSEDVDIETPDTHISYMPTIKEGNSRELMGQQSMPNRPNYIAFRDNFIGLMYYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDPDVRIIENHGTEDELPNYCFPLGGVINTETLTKVKPKTGQENGWEKDATEFSDKNEIRVGNNFAMEINLNANLWRNFLYSNIALYLPDKLKYSPSNVKISDNPNTYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGNDLRVDGASIKFDSICLYATFFPMAHNTASTLEAMLRND

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

TNDQSFNDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWAFTRLKTKETPSLGSGYDPYYTYSGSIPYLDGTFYLNHTFKKVAITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTKDWFLVQMLANYNIGYQGFYIPESYKDRMYSFFRNFQPMSRQVVDDTKYKDYQQVGILHQHNNSGFVGYLAPTMREGQAYPANFPYPLIGKTAVDSITQKKFLCDRTLWRIPFSSNFMSMGALTDLGQNLLYANSAHALDMTFEVDPMDEPTLLYVLFEVFDVVRVHRPHRGVIETVYLRTPFSA

>d1shsa\_ b.15.1.1 (A:) Small heat shock protein {Archaeon Methanococcus jannaschii}

TGIQISGKGFMPISIIEGDQHIKVIAWLPGVNKEDIILNAVGDTLEIRAKRSPLMITESERIIYSEIPEEEEIYRTIKLPATVKEENASAKFENGVLSVILPKAESSIKKGINIE

>d1gmea\_ b.15.1.1 (A:) Small heat shock protein {Wheat (Triticum aestivum)}

SIVRRSNVFDPFADLWADPFDTFRSIVPAISGGGSETAAFANARMDWKETPEAHVFKADLPGVKKEEVKVEVEDGNVLVVSGERTKEKEDKNDKWHRVERSSGKFVRRFRLLEDAKVEEVKAGLENGVLTVTVPKAEVKKPEVKAIQISG

>d1a44\_\_ b.17.1.1 (-) Phosphatidylethanolamine binding protein, PEBP {Cow (Bos taurus)}

PVDLSKWSGPLSLQEVDERPQHPLQVKYGGAEVDELGKVLTPTQVKNRPTSITWDGLDPGKLYTLVLTDPDAPSRKDPKYREWHHFLVVNMKGNNISSGTVLSDYVGSGPPKGTGLHRYVWLVYEQEGPLKCDEPILSNRSGDHRGKFKVASFRKKYELGAPVAGTCYQAEWDDYVPKLYEQLSG

>d1qoua\_ b.17.1.1 (A:) Centroradialis protein Cen {Garden snapdragon (Antirrhinum majus)}

GRVIGDVVDHFTSTVKMSVIYNSNNSIKHVYNGHELFPSAVTSTPRVEVHGGDMRSFFTLIMTDPDVPGPSDPYLREHLHWIVTDIPGTTDSSFGKEVVSYEMPRPNIGIHRFVFLLFKQKKRGQAMLSPPVVCRDGFNTRKFTQENELGLPVAAVFFNCQRET

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

IPEGSLQFLSLRASAPIGSAISRNNWAVTCDSAQSGNECNKAIDGNKDTFWHTFYGANGDPKPPHTYTIDMKTTQNVNGLSMLPRQDGNQNGWIGRHEVYLSSDGTNWGSPVASGSWFADSTTKYSNFETRPARYVRLVAITEANGQPWTSIAEINVFQASS

>d1eut\_2 b.18.1.1 (506-647) Sialidase, C-terminal domain {Micromonospora viridifaciens}

QARMSIADVDSEETAREDGRASNVIDGNPSTFWHTEWSRADAPGYPHRISLDLGGTHTISGLQYTRRQNSANEQVADYEIYTSLNGTTWDGPVASGRFTTSLAPQRAVFPARDARYIRLVALSEQTGHKYAAVAELEVEGQR

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

FFNTIDAEKITQLPVVKAYALSSGASIIEGPGFTGGNLLFLKESSNSIAKFKVTLNSAALLQRYRVRIRYASTTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPVQL

>d1ciy\_1 b.18.1.3 (462-609) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis, CRYIA (A)}

NNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVT

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

NIYAANENGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYTVSNVNTTTNNDGVNDNGARFSDINIGNIVASDNTNVTLDINVTLNSGTPFDLMNIMFVPTNLPPLY

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

RRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQLRSLNGEWRFAWFPAPEAVPESWLECDLPEADTVVVPSNWQMHGYDAPIYTNVTYPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRWVGYGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSGIFRDVSLLHKPT

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

GLQGGMLYPQESPSRECKELDGLWSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQDWRLRHFVGWVWYEREVILPERWTQDLRTRVVLRIGSAHSYAIVWVNGVDTLEHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYPKGYFVQNTYFDFFNYAGLQRSVLLYTTPT

>d1cx1a\_ b.18.1.6 (A:) Cellulose-binding domain {Cellulomonas fimi}

ASLDSEVELLPHTSFAESLGPWSLYGTSEPVFADGRMCVDLPGGQGNPWDAGLVYNGVPVGEGESYVLSFTASATPDMPVRVLVGEGGGAYRTAFEQGSAPLTGEPATREYAFTSNLTFPPDGDAPGQVAFHLGKAGAYEFCISQVSLTTSAT

>d1ulo\_\_ b.18.1.6 (-) Cellulose-binding domain {Cellulomonas fimi}

ASPIGEGTFDDGPEGWVAYGTDGPLDTSTGALCVAVPAGSAQYGVGVVLNGVAIEEGTTYTLRYTATASTDVTVRALVGQNGAPYGTVLDTSPALTSEPRQVTETFTASATYPATPAADDPEGQIAFQLGGFSADAWTLCLDDVALDSEVEL

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

PARQPYGFFLETEETFQPGRWFMRAAQAVTAVVCGPDMIQVSLNAGARGDVQQIFQGRNDPMMIYLVWRRIENFAMAQGNSQQTQAGVTVSVGGVDMRAGRIIAWDGQAALHVHNPTQQNAMVQIQVVFYISMD

>d1ahsa\_ b.19.1.1 (A:) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {African horse sickness virus}

TGPYAGAVEVQQSGRYYVPQGRTRGGYINSNIAEVCMDAGAAGQVNALLAPRRGDAVMIYFVWRPLRIFCDPQGASLESAPGTFVTVDGVNVAAGDVVAWNTIAPVNVGNPGARRSILQFEVLWYT

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

GFTFHKPNIFPYSASFTLNRSQPAHDNLMGTMWLNAGSEIQVAGFDYSCAINAPANTQQFEHIVQLRRVLTTATITLLPDAERFSFPRVITSADGATTWYFNPVILRPNNVEIEFLLNGQIINTYQARFGTIIARNFDTIRLSFQLMRPPNMTPAVAALFPNAQPFEHHATVGLTLRIESAVCE

>d1jsma\_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}

DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDLNGVKPLILRDCSVAGWLLGNPMCDEFLNVPEWSYIVEKDNPVNGLCYPENFNDYEELKHLLSSTNHFEKIRIIPRSSWSNHDASSGVSSACPYNGRSSFFRNVVWLIKKNNAYPTIKRSYNNTNQEDLLILWGIHHPNDAAEQTKLYQNPTTYVSVGTSTLNQRSVPEIATRPKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGGSAIMKSGLEYGNCNTKCQTPMGAINSSMPFHNIHPLTIGECPKYVKSGRLVLATGLRNVP

>d2viua\_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}

STATLCLGHHAVPNGTLVKTITDDQIEVTNATELVQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFITEGFTWTGVIQNGGSNACKRGPGSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYIWGIHHPSTNQEQTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQT

>d1qhva\_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 2}

AITIGNKNDDKLTLWTTPDPSPNCRIHSDNDCKFTLVLTKCGSQVLATVAALAVSGDLSSMTGTVASVSIFLRFDQNGVLMENSSLKKHYWNFRNGNSTNANPYTNAVGFMPNLLAYPKTQSQTAKNNIVSQVYLHGDKTKPMILTITLNGTSESTETSEVSTYSMSFTWSWESGKYTTETFATNSYTFSYIAQE

>d1h7za\_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 3}

KNNTLWTGPKPEANCIIEYGKQNPDSKLTLILVKNGGIVNGYVTLMGASDYVNTLFKNKNVSINVELYFDATGHILPDSSSLKTDLELKYKQTADFSARGFMPSTTAYPFVLPNAGTHNENYIFGQCYYKASDGALFPLEVTVMLNKRLPDSRTSYVMTFLWSLNAGLAPETTQATLITSPFTFSYIREDD

>d1aly\_\_ b.22.1.1 (-) Extracellular domain of CD40 ligand {Human (Homo sapiens)}

GDQNPQIAAHVISEASSKTTSVLQWAEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL

>d1c28a\_ b.22.1.1 (A:) 30 kd adipocyte complement-related protein {Mouse (Mus musculus)}

MYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNGLYADNVNDSTFTGFLLYHDT

>d1tnra\_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}

KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSPKATSSPLYLAHEVQLFSSQYPFHVPLLSSQKMVYPGLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIPHLVLSPSTVFFGAFAL

>d4tsva\_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}

DKPVAHVVANPQAEGQLQWSNRRANALLANGVELRDNQLVVPIEGLFLIYSQVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL

>d1dg6a\_ b.22.1.1 (A:) Apoptosis-2 ligand, apo2l/TRAIL {Human (Homo sapiens)}

QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPAPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG

>d1jtzx\_ b.22.1.1 (X:) TRANCE/RANKL cytokine {Mouse (Mus musculus)}

QPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID

>d1jh5a\_ b.22.1.1 (A:) Soluble part of TALL-1, sTALL-1 {Human (Homo sapiens)}

VTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL

>d1sfp\_\_ b.23.1.1 (-) Acidic seminal fluid protein (ASFP) {Cow (Bos taurus)}

LPRNTNCGGILKEESGVIATYYGPKTNCVWTIQMPPEYHVRVSIQYLQLNCNKESLEIIDGLPGSPVLGKICEGSLMDYRSSGSIMTVKYIREPEHPASFYEVLYFQDPQA

>d1sppb\_ b.23.1.1 (B:) Major seminal plasma glycoprotein PSP-II {Pig (Sus scrofa)}

ARINGPDECGRVIKDTSGSISNTDRQKNLCTWTILMKPDQKVRMAIPYLNLACGKEYVEVFDGLLSGPSYGKLCAGAAIVFLSTANTMTIKYNRISGNSSSPFLIYFYGSSP

>d1cb8a2 b.24.1.1 (A:600-700) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

PKVLANTNQLQAVYHQQLDMVQAIFYTAGKLSVAGIEIETDKPCAVLIKHINGKQVIWAADPLQKEKTAVLSIRDLKTGKTNRVKIDFPQQEFAGATVELK

>d1egua2 b.24.1.1 (A:815-893) Hyaluronate lyase {Streptococcus pneumoniae}

SSLIENNETLQSVYDAKQGVWGIVKYDDSVSTISNQFQVLKRGVYTIRKEGDEYKIAYYNPETQESAPDQEVFKKLEQH

>d1f1sa3 b.24.1.1 (A:920-984) Hyaluronate lyase {Streptococcus agalactiae}

SKQQVIYDKNSQTWAVIKHDNQESLINNQFKMNKAGLYLVQKVGNDYQNVYYQPQTMTKTDQLAI

>d1dd1a\_ b.26.1.1 (A:) Smad4 tumor suppressor C-terminal domain {Human (Homo sapiens)}

NGHLQHHPPMPPHPGHYWPVHNELAFQPPISNHPAPEYWCSIAYFEMDVQVGETFKVPSSCPIVTVDGYVDPSGGDRFCLGQLSNVHRTEAIERARLHIGKGVQLECKGEGDVWVRCLSDHAVFVQSYYLDREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQAAAVAGNIPGPGSVGGIAPAISLSAAAGIGVDDLRRLCILRMSFVKGWGPDYPRQSIKETPCWIEIHLHRALQLLDEVLHTMPI

>d1khxa\_ b.26.1.1 (A:) Smad2 MH2 domain {Human (Homo sapiens)}

PVTYSEPAFWCSIAYYELNQRVGETFHASQPSLTVDGFTDPSNSERFCLGLLSNVNRNATVEMTRRHIGRGVRLYYIGGEVFAECLSDSAIFVQSPNCNQRYGWHPATVCKIPPGCNLKIFNNQEFAALLAQSVNQGFEAVYQLTRMCTIRMSFVKGWGAEYRRQTVTSTPCWIELHLNGPLQWLDKVLTQMGSPSVRCSSMS

>d1k3ja\_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

ATQRFLIEKFSQEQIGENIVCRVICTTGQIPIRDLSADISQVLKEKRSIKKVWTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVGVESDILSLVIFINDKFKQCLEQNKVDRIR

>d1qu5a\_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

EAETREQKLLHSNNTENVKSSKKKGNGRFLTLKPLPDSIIQESLEIQQGVNPFFIGRSEDCNCKIEDNRLSRVHCFIFKKRHAVGKSMYESPAQGLDDIWYCHTGTNVSYLNNNRMIQGTKFLLQDGDEIKIIWDKNNKFVIGFKVEINDTTGLFNEGLGMLQEQRVVLKQTAEEKDLVKKL

>d1nls\_\_ b.29.1.1 (-) Concanavalin A {Jack bean (Canavalia ensiformis)}

ADTIVAVELDTYPNTDIGDPSYPHIGIDIKSVRSKKTAKWNMQNGKVGTAHIIYNSVDKRLSAVVSYPNADSATVSYDVDLDNVLPEWVRVGLSASTGLYKETNTILSWSFTSKLKSNSTHETNALHFMFNQFSKDQKDLILQGDATTGTDGNLELTRVSSNGSPQGSSVGRALFYAPVHIWESSAVVASFEATFTFLIKSPDSHPADGIAFFISNIDSSIPSGSTGRLLGLFPDAN

>d1hqla\_ b.29.1.1 (A:) Legume lectin {Griffonia simplicifolia, lectin I-b4}

SVSFTFPNFWSDVEDSIIFQGDANTTAGTLQLCKTNQYGTPLQWSAGRALYSDPVQLWDNKTESVASFYTEFTFFLKITGNGPADGLAFFLAPPDSDVKDAGEYLGLFNKSTATQPSKNQVVAVEFDTWTNPNFPEPSYRHIGINVNSIVSVATKRWEDSDIFSGKIATARISYDGSAEILTVVLSYPDGSDYILSHSVDMRQNLPESVRVGISASTGNNQFLTVYILSWRFSSNL

>d2pela\_ b.29.1.1 (A:) Legume lectin {Peanut (Arachis hypogaea)}

AETVSFNFNSFSEGNPAINFQGDVTVLSNGNIQLTNLNKVNSVGRVLYAMPVRIWSSATGNVASFLTSFSFEMKDIKDYDPADGIIFFIAPEDTQIPAGSIGGGTLGVSDTKGAGHFVGVEFDTYSNSEYNDPPTDHVGIDVNSVDSVKTVPWNSVSGAVVKVTVIYDSSTKTLSVAVTNDNGDITTIAQVVDLKAKLPERVKFGFSASGSLGGRQIHLIRSWSFTSTLITT

>d1g7ya\_ b.29.1.1 (A:) Legume lectin {Horse gram (Dolichos biflorus), different isoforms}

ADIQSFSFKNFNSSSFILQGDATVSSSKLRLTKVKGNGLPTLSSLGRAFYSSPIQIYDKSTGAVASWATSFTANIFAPNKSSSADGIAFALVPVGSEPKSNSGFLGVFDSDVYDNSAQTVAVEFDTFSNTDWDPTSRHIGIDVNSIKSIRTASWGLANGQNAEILITYNAATSLLVASLVHPSRRTSYIVSERVDITNELPEYVSIGFSATTGLSEGYTETHDVLSWSFASKLPDDSTTEPLDIASYLVRNVL

>d1dhkb\_ b.29.1.1 (B:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris)}

ATETSFIIDAFNKTNLILQGDATVSSNGNLQLSYNSYDSMSRAFYSAPIQIRDSTTGNVASFDTNFTMNIRTHRQANSAVGLDFVLVPVQPESKGDTVTVEFDTFLSRISIDVNNNDIKSVPWDVHDYDGQNAEVRITYNSSTKVFSVSLSNPSTGKSNNVSTTVELEKEVYDWVSVGFSATSGAYQWSYETHDVLSWSFSSKF

>d1gbg\_\_ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus licheniformis}

QTGGSFYEPFNNYNTGLWQKADGYSNGNMFNCTWRANNVSMTSLGEMRLSLTSPSYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPTDGTPWDEIDIEFLGKDTTKVQFNYYTNGVGNHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQLKHTATTQIPQTPGKIMMNLWNGAGVDEWLGSYNGVTPLYAHYNWVRYTKR

>d1dypa\_ b.29.1.2 (A:) kappa-Carrageenase, catalytic {Pseudoalteromonas carrageenovora}

SMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQTENYGVWSWKNENATVSKGKLKLTTKRESHQRTFWDGCNQQQVANYPLYYTSGVAKSRATGNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRESDHDLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDPRNDFHTYGVNVTKDKITWYVDGEIVGEKDNLYWHRQMNLTLSQGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKV

>d1bkza\_ b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}

SNVPHKSSLPEGIRPGTVLRIRGLVPPNASRFHVNLLCGEEQGSDAALHFNPRLDTSEVVFNSKEQGSWGREERGPGVPFQRGQPFEVLIIASDDGFKAVVGDAQYHHFRHRLPLARVRLVEVGGDVQLDSVRIF

>d1hlca\_ b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}

ELEVKNMDMKPGSTLKITGSIADGTDGFVINLGQGTDKLNLHFNPRFSESTIVCNSLDGSNWGQEQREDHLCFSPGSEVKFTVTFESDKFKVKLPDGHELTFPNRLGHSHLSYLSVRGGFNMSSFKLKE

>d1a78a\_ b.29.1.3 (A:) S-lectin, different isoforms {Toad (Bufo arenarum)}

ASAGVAVTNLNLKPGHCVEIKGSIPPDCKGFAVNLGEDASNFLLHFNARFDLHGDVNKIVCNSKEADAWGSEQREEVFPFQQGAEVMVCFEYQTQKIIIKFSSGDQFSFPVRKVLPSIPFLSLEGLAFKSITTE

>d1hdka\_ b.29.1.3 (A:) Charcot-Leyden crystal (CLC) protein {Human (Homo sapiens)}

SLLPVPYTEAASLSTGSTVTIKGRPLVCFLNEPYLQVDFHTEMKEESDIVFHFQVCFGRRVVMNSREYGAWKQQVESKNMPFQDGQEFELSISVLPDKYQVMVNGQSSYTFDHRIKPEAVKMVQVWRDISLTKFNVSYL

>d1a3k\_\_ b.29.1.3 (-) Galectin-3 CRD {Human (Homo sapiens)}

LIVPYNLPLPGGVVPRMLITILGTVKPNANRIALDFQRGNDVAFHFNPRFNENNRRVIVCNTKLDNNWGREERQSVFPFESGKPFKIQVLVEPDHFKVAVNDAHLLQYNHRVKKLNEISKLGISGDIDLTSASYTMI

>d1c1la\_ b.29.1.3 (A:) Congerin I {Conger eel (Conger myriaster)}

GGLQVKNFDFTVGKFLTVGGFINNSPQRFSVNVGESMNSLSLHLDHRFNYGADQNTIVMNSTLKGDNGWETEQRSTNFTLSAGQYFEITLSYDINKFYIDILDGPNLEFPNRYSKEFLPFLSLAGDARLTLVKLE

>d1d2sa\_ b.29.1.4 (A:) Sex hormone-binding globulin {Human (Homo sapiens)}

PPAVHLSNGPGQEPIAVMTFDLTKITKTSSSFEVRTWDPEGVIFYGDTNPKDDWFMLGLRDGRPEIQLHNHWAQLTVGAGPRLDDGRWHQVEVKMEGDSVLLEVDGEEVLRLRQVSGHPIMRIALGGLLFPASNLRLPLVPALDGCLRRDSWLDKQAEISASAPTSLRSC

>d1dyka1 b.29.1.4 (A:2744-2932) Laminin alpha2 chain {Mouse (Mus musculus)}

HGPCVAESEPALLTGSKQFGLSRNSHIAIAFDDTKVKNRLTIELEVRTEAESGLLFYMARINHADFATVQLRNGFPYFSYDLGSGDTSTMIPTKINDGQWHKIKIVRVKQEGILYVDDASSQTISPKKADILDVVGILYVGGLPINYTTRRIGPVTYSLDGCVRNLHMEQAPVDLDQPTSSFHVGTCFA

>d1dyka2 b.29.1.4 (A:2933-3117) Laminin alpha2 chain {Mouse (Mus musculus)}

NAESGTYFDGTGFAKAVGGFKVGLDLLVEFEFRTTRPTGVLLGVSSQKMDGMGIEMIDEKLMFHVDNGAGRFTAIYDAEIPGHMCNGQWHKVTAKKIKNRLELVVDGNQVDAQSPNSASTSADTNDPVFVGGFPGGLNQFGLTTNIRFRGCIRSLKLTKGTGKPLEVNFAKALELRGVQPVSCPT

>d1c4ra\_ b.29.1.4 (A:) Ligand-binding domain of neurexin 1beta {Rat (Rattus norvegicus)}

HAGTTYIFSKGGGQITYKWPPNDRPSTRADRLAIGFSTVQKEAVLVRVDSSSGLGDYLELHIHQGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGRQLTIFNSQATIIIGGKEQGQPFQGQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEV

>d1a8d\_1 b.29.1.6 (1-247) Tetanus neurotoxin {Clostridium tetani}

MKNLDCWVDNEEDIDVILKKSTILNLDINNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNNESSEVIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSVSLKGNNLIWTLKDSAGEVRQITFRDLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNNITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLS

>d1epwa1 b.29.1.6 (A:862-1079) Botulinum neurotoxin {Clostridium botulinum, serotype B}

NIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSY

>d1kit\_1 b.29.1.8 (25-216) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}

ALFDYNATGDTEFDSPAKQGWMQDNTNNGSGVLTNADGMPAWLVQGIGGRAQWTYSLSTNQHAQASSFGWRMTTEMKVLSGGMITNYYANGTQRVLPIISLDSSGNLVVEFEGQTGRTVLATGTAATEYHKFELVFLPGSNPSASFYFDGKLIRDNIQPTASKQNMIVWGNGSSNTDGVAAYRDIKFEIQGD

>d1kit\_2 b.29.1.8 (347-543) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}

DVTDQVKERSFQIAGWGGSELYRRNTSLNSQQDWQSNAKIRIVDGAANQIQVADGSRKYVVTLSIDESGGLVANLNGVSAPIILQSEHAKVHSFHDYELQYSALNHTTTLFVDGQQITTWAGEVSQENNIQFGNADAQIDGRLHVQKIVLTQQGHNLVEFDAFYLAQQTPEVEKDLEKLGWTKIKTGNTMSLYGNAS

>d6cel\_\_ b.29.1.10 (-) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma reesei, Cel7A}

ESACTLQSETHPPLTWQKCSSGGTCTQQTGSVVIDANWRWTHATNSSTNCYDGNTWSSTLCPDNETCAKNCCLDGAAYASTYGVTTSGNSLSIDFVTQSAQKNVGARLYLMASDTTYQEFTLLGNEFSFDVDVSQLPCGLNGALYFVSMDADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQANVEGWEPSSNNANTGIGGHGSCCSQMDIWEANSISEALTPHPCTTVGQEICEGDGCGGTYSDNRYGGTCDPDGCDWNPYRLGNTSFYGPGSSFTLDTTKKLTVVTQFETSGAINRYYVQNGVTFQQPNAELGSYSGNELNDDYCTAEEAEFGGSSFSDKGGLTQFKKATSGGMVLVMSLWDDYYANMLWLDSTYPTNETSSTPGAVRGSCSTSSGVPAQVESQSPNAKVTFSNIKFGPIGSTGNPSG

>d1eg1a\_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma reesei, Endoglucanase I}

EQPGTSTPEVHPKLTTYKCTKSGGCVAQDTSVVLDWNYRWMHDANYNSCTVNGGVNTTLCPDEATCGKNCFIEGVDYAASGVTTSGSSLTMNQYMPSSSGGYSSVSPRLYLLDSDGEYVMLKLNGQELSFDVDLSALPCGENGSLYLSQMDENGGANQYNTAGANYGSGYCDAQCPVQTWRNGTLNTSHQGFCCNEMDILEGNSRANALTPHSCTATACDSAGCGFNPYGSGYKSYYGPGDTVDTSKTFTIITQFNTDNGSPSGNLVSITRKYQQNGVDIPSAQPGGDTISSCPSASAYGGLATMGKALSSGMVLVFSIWNDNSQYMNWLDSGNAGPCSSTEGNPSNILANNPNTHVVFSNIRWGDIGSTT

>d3ovwa\_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Fusarium oxysporum}

ETPDKAKEQHPKLETYRCTKASGCKKQTNYIVADAGIHGIRQKNGAGCGDWGQKPNATACPDEASCAKNCILSGMDSNAYKNAGITTSGNKLRLQQLINNQLVSPRVYLLEENKKKYEMLHLTGTEFSFDVEMEKLPCGMNGALYLSEMPQDGGKSTSRNSKAGAYYGAGYCDAQCYVTPFINGVGNIKGQGVCCNELDIWEANSRATHIAPHPCSKPGLYGCTGDECGSSGICDKAGCGWNHNRINVTDFYGRGKQYKVDSTRKFTVTSQFVANKQGDLIELHRHYIQDNKVIESAVVNISGPPKINFINDKYCAATGANEYMRLGGTKQMGDAMSRGMVLAMSVWWSEGDFMAWLDQGVAGPCDATEGDPKNIVKVQPNPEVTFSNIRIGEIGSTSSV

>d1qh7a\_ b.29.1.11 (A:) Xylanase II {Bacillus agaradhaerens}

EIVTDNSIGNHDGYDYEFWKDSGGSGTMILNHGGTFSAQWNNVNNILFRKGKKFNETQTHQQVGNMSINYGANFQPNGNAYLCVYGWTVDPLVEYYIVDSWGNWRPPGATPKGTITVDGGTYDIYETLRVNQPSIKGIATFKQYWSVRRSKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSSGSANVYSNTLRINGNPLS

>d1bk1\_\_ b.29.1.11 (-) Xylanase II {Aspergillus kawachii}

AGINYVQNYNGNLGDFTYDESAGTFSMYWEDGVSSDFVVGLGWTTGSSNAITYSAEYSASGSSSYLAVYGWVNYPQAEYYIVEDYGDYNPCSSATSLGTVYSDGSTYQVCTDTRTNEPSITGTSTFTQYFSVRESTRTSGTVTVANHFNFWAQHGFGNSDFNYQVMAVEAWSGAGSASVTIS

>d2nlra\_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Streptomyces lividans, CelB2}

DTTICEPFGTTTIQGRYVVQNNRWGSTAPQCVTATDTGFRVTQADGSAPTNGAPKSYPSVFNGCHYTNCSPGTDLPVRLDTVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDGVNQTEIMIWFNRVGPIQPIGSPVGTASVGGRTWEVWSGGNGSNDVLSFVAPSAISGWSFDVMDFVRATVARGLAENDWYLTSVQAGFEPWQNGAGLAVNSFSSTVET

>d1h8va\_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Trichoderma reesei, Cel12A}

ETSCDQWATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGGASWHADWQWSGGQNNVKSYQNSQIAIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVTYSGDYELMIWLGKYGDIGPIGSSQGTVNVGGQSWTLYYGYNGAMQVYSFVAQTNTTNYSGDVKNFFNYLRDNKGYNAAGQYVLSYQFGTEPFTGSGTLNVASWTASIN

>d1oaca1 b.30.2.1 (A:301-724) Copper amine oxidase, domain 3 (catalytic) {Escherichia coli}

PAVKPMQIIEPEGKNYTITGDMIHWRNWDFHLSMNSRVGPMISTVTYNDNGTKRKVMYEGSLGGMIVPYGDPDIGWYFKAYLDSGDYGMGTLTSPIARGKDAPSNAVLLNETIADYTGVPMEIPRAIAVFERYAGPEYKHQEMGQPNVSTERRELVVRWISTVGNADYIFDWIFHENGTIGIDAGATGIEAVKGVKAKTMHDETAKDDTRYGTLIDHNIVGTTHQHIYNFRLDLDVDGENNSLVAMDPVVKPNTAGGPRTSTMQVNQYNIGNEQDAAQKFDPGTIRLLSNPNKENRMGNPVSYQIIPYAGGTHPVAKGAQFAPDEWIYHRLSFMDKQLWVTRYHPGERFPEGKYPNRSTHDTGLGQYSKDNESLDNTDAVVWMTTGTTHVARAEEWPIMPTEWVHTLLKPWNFFDETPTLGALK

>d1ksia1 b.30.2.1 (A:207-647) Copper amine oxidase, domain 3 (catalytic) {Pea seedling (Pisum sativum)}

VSKQSPPFGPKQHSLTSHQPQGPGFQINGHSVSWANWKFHIGFDVRAGIVISLASIYDLEKHKSRRVLYKGYISELFVPYQDPTEEFYFKTFFDSGEFGFGLSTVSLIPNRDCPPHAQFIDTYVHSANGTPILLKNAICVFEQYGNIMWRHTENGIPNESIEESRTEVNLIVRTIVTVGNADNVIDWEFKASGSIKPSIALSGILEIKGTNIKHKDEIKEDLHGKLVSANSIGIYHDHFYIYYLDFDIDGTHNSFEKTSLKTVRIKDGSSKRKSYWTTETQTAKTESDAKITIGLAPAELVVVNPNIKTAVGNEVGYRLIPAIPAHPLLTEDDYPQIRGAFTNYNVWVTAYNRTEKWAGGLYVDHSRGDDTLAVWTKQNREIVNKDIVMWHVVGIHHVPAQEDFPIMPLLSTSFELRPTNFFERNPVLKTLSPRDVAWPGC

>d1av4\_1 b.30.2.1 (212-628) Copper amine oxidase, domain 3 (catalytic) {Arthrobacter globiformis}

PLRTTQKPISITQPEGPSFTVTGGNHIEWEKWSLDVGFDVREGVVLHNIAFRDGDRLRPIINRASIAEMVVPYGDPSPIRSWQNYFDTGEYLVGQYANSLELGCDCLGDITYLSPVISDAFGNPREIRNGICMHEEDWGILAKHSDLWSGINYTRRNRRMVISFFTTIGNADYGFYWYLYLDGTIEFEAKATGVVFTSAFPEGGSDNISQLAPGLGAPFHQHIFSARLDMAIDGFTNRVEEEDVVRQTMGPGNERGNAFSRKRTVLTRESEAVREADARTGRTWIISNPESKNRLNEPVGYKLHAHNQPTLLADPGSSIARRAAFATKDLWVTRYADDERYPTGDFVNQHSGGAGLPSYIAQDRDIDGQDIVVWHTFGLTHFPRVEDWPIMPVDTVGFKLRPEGFFDRSPVLDVPAN

>d1a2va1 b.30.2.1 (A:237-672) Copper amine oxidase, domain 3 (catalytic) {Yeast (Hansenula polymorpha)}

PEAPPINVTQPEGVSFKMTGNVMEWSNFKFHIGFNYREGIVLSDVSYNDHGNVRPIFHRISLSEMIVPYGSPEFPHQRKHALDIGEYGAGYMTNPLSLGCDCKGVIHYLDAHFSDRAGDPITVKNAVCIHEEDDGLLFKHSDFRDNFATSLVTRATKLVVSQIFTAANAEYCLYWVFMQDGAIRLDIRLTGILNTYILGDDEEAGPWGTRVYPNVNAHNHQHLFSLRIDPRIDGDGNSAAACDAKSSPYPLGSPENMYGNAFYSEKTTFKTVKDSLTNYESATGRSWDIFNPNKVNPYSGKPPSYKLVSTQCPPLLAKEGSLVAKRAPWASHSVNVVPYKDNRLYPSGDHVPQWSGDGVRGMREWIGDGSENIDNTDILFFHTFGITHFPAPEDFPLMPAEPITLMLRPRHFFTENPGLDIQPSYAMTTSEAKRAV

>d1cb8a3 b.30.3.1 (A:336-599) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

IEPYHHQFWNGDYVQHLRPAYSFNVRMVSKRTRRSESGNKENLLGRYLSDGATNIQLRGPEYYNIMPVWEWDKIPGITSRDYLTDRPLTKLWGEQGSNDFAGGVSDGVYGASAYALDYDSLQAKKAWFFFDKEIVCLGAGINSNAPENITTTLNQSWLNGPVISTAGKTGRGKITTFKAQGQFWLLHDAIGYYFPEGANLSLSTQSQKGNWFHINNSHSKDEVSGDVFKLWINHGARPENAQYAYIVLPGINKPEEIKKYNGTA

>d1f1sa4 b.30.3.1 (A:620-919) Hyaluronate lyase {Streptococcus agalactiae}

LKSNLSTFNSMDRLAYYNAKKDFGFALSLHSKRTLNYEGMNDENTRGWYTGDGMFYIYNSDQSHYSNHFWPTVNPYKMAGTTEKDAKREDTTKEFMSKHSKDAKEKTGQVTGTSDFVGSVKLNDHFALAAMDFTNWDRTLTAQKGWVILNDKIVFLGSNIKNTNGIGNVSTTIDQRKDDSKTPYTTYVNGKTIDLKQASSQQFTDTKSVFLESKEPGRNIGYIFFKNSTIDIERKEQTGTWNSINRTSKNTSIVSNPFITISQKHDNKGDSYGYMMVPNIDRTSFDKLANSKEVELLENS

>d1ezve1 b.33.1.1 (E:87-215) ISP subunit of the mitochondrial cytochrome bc1-complex, watersoluble domain {Baker's yeast (Saccharomyces cerevisiae)}

DVLAMAKVEVNLAAIPLGKNVVVKWQGKPVFIRHRTPHEIQEANSVDMSALKDPQTDADRVKDPQWLIMLGICTHLGCVPIGEAGDFGGWFCPCHGSHYDISGRIRKGPAPLNLEIPAYEFDGDKVIVG

>d1rfs\_\_ b.33.1.1 (-) ISP subunit from chloroplast cytochrome bf complex {Spinach (Spinacia oleracea)}

TIAKDALGNDVIAAEWLKTHAPGDRTLTQGLKGDPTYLVVESDKTLATFGINAVCTHLGCVVPFNAAENKFICPCHGSQYNNQGRVVRGPAPLSLALAHCDVDDGKVVFVPWTETDFRTGEAPWWSA

>d1g8kb\_ b.33.1.1 (B:) Arsenite oxidase Rieske subunit {Alcaligenes faecalis}

RTTLAYPATAVSVAKNLAANEPVSFTYPDTSSPCVAVKLGAPVPGGVGPDDDIVAYSVLCTHMGCPTSYDSSSKTFSCPCHFTEFDAEKAGQMICGEATADLPRVLLRYDAASDALTAVGVDGLIYGRQANVI

>d1fqta\_ b.33.1.1 (A:) Rieske-type ferredoxin associated with biphenyl dioxygenase {Burkholderia cepacia}

MKFTRVCDRRDVPEGEALKVESGGTSVAIFNVDGELFATQDRCTHGDWSLSDGGYLEGDVVECSLHMGKFCVRTGKVKSPPPCEALKIFPIRIEDNDVLVDFEAGYLAP

>d1byma\_ b.34.1.2 (A:) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

NPIPGLDELGVGNSDAAAPGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLSHNGKDVELLDDLAHTIRIEEL

>d1fx7a3 b.34.1.2 (A:145-230) Iron-dependent regulator IdeR {Mycobacterium tuberculosis}

GADDANLVRLTELPAGSPVAVVVRQLTEHVQGDIDLITRLKDAGVVPNARVTVETTPGGGVTIVIPGHENVTLPHEMAHAVKVEKV

>d1neb\_\_ b.34.2.1 (-) SH3 domain from nebulin {Human (Homo sapiens)}

TAGKIFRAMYDYMAADADEVSFKDGDAIINVQAIDEGWMYGTVQRTGRTGMLPANYVEAI

>d2abl\_1 b.34.2.1 (75-139) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}

MGPSENDPNLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNGQGWVPSNYITPVN

>d1pht\_\_ b.34.2.1 (-) Phosphatidylinositol 3-kinase (p85-alpha subunit, pi3k), SH3 domain {Human (Homo sapiens)}

AEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYIGRKKISPP

>d1g2ba\_ b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}

MDRQGFVPAAYVKKLDSGTGKELVLALYDYQEKSPREVTMKKGDILTLLNSTNKDWWKVEVN

>d1awj\_\_ b.34.2.1 (-) IL-2 inducible T-cell (Itc) kinase {Mouse (Mus musculus)}

KKPLPPTPEDNRRSFQEPEETLVIALYDYQTNDPQELALRCDEEYYLLDSSEIHWWRVQDKNGHEGYAPSSYLVEKS

>d1fmk\_1 b.34.2.1 (82-145) c-src tyrosine kinase {Human (Homo sapiens)}

MVTTFVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLSTGQTGYIPSNYVAPSDSIQA

>d1gl5a\_ b.34.2.1 (A:) tyrosine kinase tec {Mouse (Mus musculus)}

GSEIVVAMYDFQATEAHDLRLERGQEYIILEKNDLHWWRARDKYGSEGYIPSNYVTGKKSNNLDQYD

>d1gria2 b.34.2.1 (A:157-217) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}

QPTYVQALFDFDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPVNRNV

>d1gbra\_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Mouse (Mus musculus)}

GSRRASVGSMEAIAKYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIPKNYIEMKPHPEFIVTD

>d2hsp\_\_ b.34.2.1 (-) Phospholipase C, SH3 domain {Human (Homo sapiens)}

GSPTFKCAVKALFDYKAQREDELTFIKSAIIQNVEKQEGGWWRGDYGGKKQLWFPSNYVEEMVNPEGIHRD

>d1ycsb2 b.34.2.1 (B:457-519) 53BP2 {Human (Homo sapiens)}

IMNKGVIYALWDYEPQNDDELPMKEGDCMTIIHREDEDEIEWWWARLNDKEGYVPRNLLGLYP

>d1bb9\_\_ b.34.2.1 (-) Amphiphysin 2 {Rat (Rattus norvegicus)}

TTGRLDLPPGFMFKVQAQHDYTATDTDELQLKAGDVVLVIPFQNPEEQDEGWLMGVKESDWNQHKELEKCRGVFPENFTERVQ

>d1i07a\_ b.34.2.1 (A:) EPS8 SH3 domain {Mouse (Mus musculus)}

KKYAKSKYDFVARNSSELSVMKDDVLEILDDRRQWWKVRNASGDSGFVPNNILDIMRTP

>d1k1za\_ b.34.2.1 (A:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}

RAQDKKRNELGLPKMEVFQEYYGIPPPPGAFGGFLRLNPGDIVELTKAEAEHNWWEGRNTATNEVGWFPCNRVHPYVH

>d1i1ja\_ b.34.2.1 (A:) Melanoma inhibitory activity protein {Human (Homo sapiens)}

GPMPKLADRKLCADQECSHPISMAVALQDYMAPDCRFLTIHRGQVVYVFSKLKGRGRLFWGGSVQGDYYGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYC

>d1kjwa1 b.34.2.1 (A:430-525) Psd-95 {Rat (Rattus norvegicus)}

GFYIRALFDYDKTKDCGFLSQALSFRFGDVLHVIDAGDEEWWQARRVHSDSETDDIGFIPSKRRVERREWSRLKAKDWGSSSGSQGREDSVLSYET

>d2mysa1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus), pectoral muscle}

AKSSVFVVHPKQSFVKGTIQSKEGGKVTVKTEGGETLTVKEDQVFS

>d1b7ta1 b.34.3.1 (A:29-76) Myosin S1 fragment, N-terminal domain {Bay scallop (Aequipecten irradians)}

DGKKNCWVPDEKEGFASAEIQSSKGDEITVKIVADSSTRTVKKDDIQS

>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}

SKQPDKQRKSQRRAPLHERHKQVRATLSADLREEYGQRNVRVNAGDTVEVLRGDFAGEEGEVINVDLDKAVIHVEDVTLEKTDGEEVPRPLDTSNVRVTDLDLEDEKREARLESEDDSA

>d1jj2p\_ b.34.5.1 (P:) Ribosomal proteins L21e {Archaeon Haloarcula marismortui}

PSSNGPLEGTRGKLKNKPRDRGTSPPQRAVEEFDDGEKVHLKIDPSVPNGRFHPRFDGQTGTVEGKQGDAYKVDIVDGGKEKTIIVTAAHLRRQE

>d1c0ma1 b.34.7.1 (A:217-269) DNA-binding domain of retroviral integrase {Rous sarcoma virus (RSV, avian sarcoma virus)}

VLTEGPPVKIRIETGEWEKGWNVLVWGRGYAAVKNRDTDKVIWVPSRKVKPDI

>d1c6vx\_ b.34.7.1 (X:) DNA-binding domain of retroviral integrase {Simian immunodeficiency virus}

KNSKFKNFRVYYREGRDQLWKGPGELLWKGEGAVLLKVGTDIKVVPRRKAKIIKD

>d1jh2a\_ b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium tuberculosis}

AKVNIKPLEDKILVQANEAETTTASGLVIPDTAKEKPQEGTVVAVGPGRWDEDGEKRIPLDVAEGDTVIYSKYGGTEIKYNGEEYLILSARDVLAVVSK

>d1g31a\_ b.35.1.1 (A:) GP31 co-chaperonin {Bacteriophage T4}

QQLPIRAVGEYVILVSEPAQAGDEEVTESGLIIGKRVQGEVPELCVVHSVGPDVPEGFCEVGDLTSLPVGQIRNVPHPFVALGLKQPKEIKQKFVTCHYKAIPCLYK

>d1e3ia1 b.35.1.2 (A:1-174,A:325-376) Alcohol dehydrogenase {Mouse (Mus musculus), class II}

GTQGKVIKCKAAIAWKTGSPLCIEEIEVSPPKACEVRIQVIATCVCPTDINATDPKKKALFPVVLGHECAGIVESVGPGVTNFKPGDKVIPFFAPQCKRCKLCLSPLTNLCGKLRNFKYPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEANLERVCXKSVDSVPNLVSDYKNKKFDLDLLVTHALPFESINDAIDLMKEGKSIRTILTF

>d1ykfa1 b.35.1.2 (A:1-150,A:315-352) Bacterial secondary alcohol dehydrogenase {Thermoanaerobacter brockii}

MKGFAMLSIGKVGWIEKEKPAPGPFDAIVRPLAVAPCTSDIHTVFEGAIGERHNMILGHEAVGEVVEVGSEVKDFKPGDRVVVPAITPDWRTSEVQRGYHQHSGGMLAGWKFSNVKDGVFGEFFHVNDADMNLAHLPKEIPLEAAVMIPDXDPSKLVTHVFRGFDNIEKAFMLMKDKPKDLIKPVVILA

>d1e3ja1 b.35.1.2 (A:4-150,A:314-351) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}

DNLSAVLYKQNDLRLEQRPIPEPKEDEVLLQMAYVGICGSDVHYYEHGRIADFIVKDPMVIGHEASGTVVKVGKNVKHLKKGDRVAVEPGVPCRRCQFCKEGKYNLCPDLTFCATPPDDGNLARYYVHAADFCHKLPDNVSLEEGALXNVKQLVTHSFKLEQTVDAFEAARKKADNTIKVMISCRQ

>d1qora1 b.35.1.2 (A:2-135,A:266-327) Quinone oxidoreductase {Escherichia coli}

ATRIEFHKHGGPEVLQAVEFTPADPAENEIQVENKAIGINFIDTYIRSGLYPPPSLPSGLGTEAAGIVSKVGSGVKHIKAGDRVVYAQSALGAYSSVHNIIADKAAILPAAISFEQAAASFLKGLTVYYLLRKTXLQGYITTREELTEASNELFSLIASGVIKVDVAEQQKYPLKDAQRAHEILESRATQGSSLLIP

>d1kwaa\_ b.36.1.1 (A:) Cask/Lin-2 {Human (Homo sapiens)}

RSRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMIHRQGTLHVGDEIREINGISVANQTVEQLQKMLREMRGSITFKIVPSYREF

>d1be9a\_ b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}

FLGEEDIPREPRRIVIHRGSTGLGFNIIGGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAAIALKNAGQTVTIIAQYKPEEYSRFEANSRVNSSGRIVTN

>d1qava\_ b.36.1.1 (A:) Syntrophin {Mouse (Mus musculus)}

GSLQRRRVTVRKADAGGLGISIKGGRENKMPILISKIFKGLAADQTEALFVGDAILSVNGEDLSSATHDEAVQALKKTGKEVVLEVKYMK

>d1b8qa\_ b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}

GSHMIEPNVISVRLFKRKVGGLGFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDLSYDSALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQPLGPPTKAV

>d3pdza\_ b.36.1.1 (A:) Phosphatase hPTP1e {Human (Homo sapiens)}

PKPGDIFEVELAKNDNSLGISVTGGVNTSVRHGGIYVKAVIPQGAAESDGRIHKGDRVLAVNGVSLEGATHKQAVETLRNTGQVVHLLLEKGQSPT

>d1g9oa\_ b.36.1.1 (A:) Na+/H+ exchanger regulatory factor, NHERF {Human (Homo sapiens)}

RMLPRLCCLEKGPNGYGFHLHGEKGKLGQYIRLVEPGSPAEKAGLLAGDRLVEVNGENVEKETHQQVVSRIRAALNAVRLLVVDPETDEQL

>d1ihja\_ b.36.1.1 (A:) Inad {Fruit fly (Drosophila melanogaster)}

GELIHMVTLDKTGKKSFGICIVRGEVKDSPNTKTTGIFIKGIVPDSPAHLCGRLKVGDRILSLNGKDVRNSTEQAVIDLIKEADFKIELEIQTF

>d1fc6a3 b.36.1.3 (A:157-248) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}

AGSVTGVGLEITYDGGSGKDVVVLTPAPGGPAEKAGARAGDVIVTVDGTAVKGMSLYDVSDLLQGEADSQVEVVLHAPGAPSNTRTLQLTRQ

>d1k32a1 b.36.1.3 (A:763-853) Tricorn protease {Archaeon Thermoplasma acidophilum}

GRIACDFKLDGDHYVVAKAYAGDYSNEGEKSPIFEYGIDPTGYLIEDIDGETVGAGSNIYRVLSEKAGTSARIRLSGKGGDKRDLMIDILD

>d1g3p\_2 b.37.1.1 (91-217) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}

EYGDTPIPGYTYINPLDGTYPPGTEQNPANPNPSLEESQPLNTFMFQNNRFRNRQGALTVYTGTVTQGTDPVKTYYQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDIFVCEYQGQSSDLPQPPVNA

>d1fgp\_\_ b.37.1.1 (-) N-terminal domains of the minor coat protein g3p {Bacteriophage fd}

ETVESCLAKPHTENSFTNVWKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIPENAAAH

>d1b34a\_ b.38.1.1 (A:) D1 core SNRNP protein {Human (Homo sapiens)}

KLVRFLMKLSHETVTIELKNGTQVHGTITGVDVSMNTHLKAVKMTLKNREPVQLETLSIRGNNIRYFILPDSLPLDTLLV

>d1b34b\_ b.38.1.1 (B:) D2 core SNRNP protein {Human (Homo sapiens)}

TGPLSVLTQSVKNNTQVLINCRNNKKLLGRVKAFDRHCNMVLENVKEMWTEVPKSGKGKKKSKPVNKDRYISKMFLRGDSVIVVLRNPLIAGK

>d1d3ba\_ b.38.1.1 (A:) D3 core SNRNP protein {Human (Homo sapiens)}

GVPIKVLHEAEGHIVTCETNTGEVYRGKLIEAEDNMNCQMSNITVTYRDGRVAQLEQVYIRGCKIRFLILPD

>d1d3bl\_ b.38.1.1 (L:) B core SNRNP protein {Human (Homo sapiens)}

TVGKSSKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFRKIKPKNSKQAEREEKRVLGLVLLRGENLVSMTVEGPPPKDTG

>d1i81a\_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}

RVNVQRPLDALGNSLNSPVIIKLKGDREFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNIVYISP

>d1ltrd\_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}

APQSITELCSEYHNTQIYTINDKILSYTESMAGKREMVIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETKIDKLCVWNNKTPNSIAAISMEKLYAGA

>d1tiid\_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IIB}

GASQFFKDNCNRTTASLVEGVELTKYISDINNNTDGMYVVSSTGGVWRISRAKDYPDNVMTAEMRKIAMAAVLSGMRVNMCASPASSPNVIWAIELEA

>d1c4qa\_ b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}

TPDCVTGKVEYTKYNDDDTFTVKVGDKELATNRANLQSLLLSAQITGMTVTIKTNACHNGGGFSEVIFR

>d1prtb1 b.40.2.1 (B:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella pertussis}

TTRNTGQPATDHYYSNVTATRLLSSTNSRLCAVFVRSGQPVIGACTSPYDGKYWSMYSRLRKMLYLIYVAGISVRVHVSKEEQYYDYEDATFETYALTGISICNPGSSLC

>d1prtd\_ b.40.2.1 (D:) Pertussis toxin S4 subunit {Bordetella pertussis}

DVPYVLVKTNMVVTSVAMKPYEVTPTRMLVCGIAAKLGAAASSPDAHVPFCFGKDLKRPGSSPMEVMLRAVFMQQRPLRMFLGPKQLTFEGKPALELIRMVECSGKQDCP

>d1prtf\_ b.40.2.1 (F:) Pertussis toxin S5 subunit {Bordetella pertussis}

LPTHLYKNFTVQELALKLKGKNQEFCLTAFMSGRSLVRACLSDAGHEHDTWFDTMLGFAISAYALKSRIALTVEDSPYPGTPGDLLELQICPLNGYCE

>d1esfa1 b.40.2.2 (A:1-120) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}

SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT

>d3tss\_1 b.40.2.2 (5-93) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}

NIKDLLDWYSSGSDTFTNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPAFTKGEKVDLNTKRIKKSQHTSEGTWIHFQISGVTNTEK

>d3seb\_1 b.40.2.2 (1-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTEH

>d1enfa1 b.40.2.2 (A:2-101) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}

DLHDKSELTDLALANAYGQYNHPFIKENIKSDEISGEKDLIFRNQGDSGNDLRVKFATADLAQKFKNKNVDIYGASFYYKCEKISENISECLYGGTTLNS

>d1an8\_1 b.40.2.2 (3-95) Streptococcal superantigen Spe-C {Streptococcus pyogenes}

KKDISNVKSDLLYAYTITPYDYKDCRVNFSTTHTLNIDTQKYRGKDYYISSEMSYEASQKFKRDDHVDVFGLFYILNSHTGEYIYGGITPAQN

>d1et9a1 b.40.2.2 (A:1-95) Streptococcal superantigen Spe-H {Streptococcus pyogenes}

NSYNTTNRHNLESLYKHDSNLIEADSIKNSPDIVTSHMLKYSVKDKNLSVFFEKDWISQEFKDKEVDIYALSAQEVCECPGKRYEAFGGITLTNS

>d1eu3a1 b.40.2.2 (A:2A-96) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}

GLEVDNNSLLRNIYSTIVYEYSDIVIDFKTSHNLVTKKLDVRDARDFFINSEMDEYAANDFKTGDKIAVFSVPFDWNYLSKGKVTAYTYGGITPYQK

>d1eova1 b.40.4.1 (A:71-204) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}

AKDNYGKLPLIQSRDSDRTGQKRVKFVDLDEAKDSDKEVLFRARVHNTRQQGATLAFLTLRQQASLIQGLVKANKEGTISKNMVKWAGSLNLESIVLVRGIVKKVDEPIKSATVQNLEIHITKIYTISETPEAL

>d1b8aa1 b.40.4.1 (A:1-103) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus kodakaraensis}

MYRTHYSSEITEELNGQKVKVAGWVWEVKDLGGIKFLWIRDRDGIVQITAPKKKVDPELFKLIPKLRSEDVVAVEGVVNFTPKAKLGFEILPEKIVVLNRAET

>d1c0aa1 b.40.4.1 (A:1-106) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}

MRTEYCGQLRLSHVGQQVTLCGWVNRRRDLGSLIFIDMRDREGIVQVFFDPDRADALKLASELRNEFCIQVTGTVRARDEKNINRDMATGEIEVLASSLTIINRAD

>d1bbua1 b.40.4.1 (A:11-154) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}

VVDLNNELKTRREKLANLREQGIAFPNDFRRDHTSDQLHAEFDGKENEELEALNIEVAVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLPEGVYNEQFKKWDLGDILGAKGKLFKTKTGELSIHCTELRLLTKALRPLPD

>d1cuk\_3 b.40.4.2 (1-64) DNA helicase RuvA subunit, N-terminal domain {Escherichia coli}

MIGRLRGIIIEKQPPLVLIEVGGVGYEVHMPMTCFYELPEAGQEAIVFTHFVVREDAQLLYGFN

>d1bvsa3 b.40.4.2 (A:1-63) DNA helicase RuvA subunit, N-terminal domain {Mycobacterium leprae}

MIFSVRGEVLEVALDHAVIEAAGIGYRVNATPSALATLNQGSQARLVTAMVVREDSMTLYGFS

>d3ulla\_ b.40.4.3 (A:) ssDNA-binding protein {Human (Homo sapiens), mitochondria}

LERSLNRVHLLGRVGQDPVLRQVEGKNPVTIFSLATNEMWRSGDSEVYQLGDVSQKTTWHRISVFRPGLRDVAYQYVKKGSRIYLEGKIDYGEYMDKNNVRRQATTIIADNIIFL

>d1qvca\_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}

ASRGVNKVILVGNLGQDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAEVASEYLRKGSQVYIEGQLRTRKWTDQSGQDRYTTEVVVNVGGTMQMLGGRQGGGAPAGGNIGGGQPQGGWGQPQQPQGGN

>d1ewia\_ b.40.4.3 (A:) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

MVGQLSEGAIAAIMQKGDTNIKPILQVINIRPITTGNSPPRYRLLMSDGLNTLSSFMLATQLNPLVEEEQLSSNCVCQIHRFIVNTLKDGRRVVILMELEVLKSAEAVGVKIGN

>d1fgua1 b.40.4.3 (A:181-298) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

MSKVVPIASLTPYQSKWTICARVTNKSQIRTWSNSRGEGKLFSLELVDESGEIRATAFNEQVDKFFPLIEVNKVYYFSKGTLKIANKQFTAVKNDYEMTFNNETSVMPCEDDHHLPTV

>d1fgua2 b.40.4.3 (A:299-426) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

QFDFTGIDDLENKSKDSLVDIIGICKSYEDATKITVRSNNREVAKRNIYLMDTSGKVVTATLWGEDADKFDGSRQPVLAIKGARVSDFGGRSLSVLSSSTIIANPDIPEAYKLRGWFDAEGQALDGVS

>d1quqa\_ b.40.4.3 (A:) Replication protein A 32 KDa subunit (RPA32) fragment {Human (Homo sapiens)}

HIVPCTISQLLSATLVDEVFRIGNVEISQVTIVGIIRHAEKAPTNIVYKIDDMTAAPMDVRQWVDTDDTSSENTVVPPETYVKVAGHLRSFQNKKSLVAFKIMPLEDMNEFTTHILEVINAHMVLSK

>d1quqb\_ b.40.4.3 (B:) Replication protein A 14 KDa (RPA14) subunit {Human (Homo sapiens)}

DMMDLPRSRINAGMLAQFIDKPVCFVGRLEKIHPTGKMFILSDGEGKNGTIELMEPLDEEISGIVEVVGRVTAKATILCTSYVQFKEDSHPFDLGLYNEAVKIIHDFPQFYPLG

>d1jb7a1 b.40.4.3 (A:36-204) Telomere end binding protein alpha subunit {Oxytricha nova}

YEYVELAKASLTSAQPQHFYAVVIDATFPYKTNQERYICSLKIVDPTLYLKQQKGAGDASDYATLVLYAKRFEDLPIIHRAGDIIRVHRATLRLYNGQRQFNANVFYSSSWALFSTDKRSVTQEINNQDAVSDTTPFSFSSKHATIEKNEISILQNLRKWANQYFSSYS

>d1jb7a2 b.40.4.3 (A:205-328) Telomere end binding protein alpha subunit {Oxytricha nova}

VISSDMYTALNKAQAQKGDFDVVAKILQVHELDEYTNELKLKDASGQVFYTLSLKLKFPHVRTGEVVRIRSATYDETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQDDHSVEVASLKKNV

>d1jb7a3 b.40.4.3 (A:329-495) Telomere end binding protein alpha subunit {Oxytricha nova}

SLNAVVLTEVDKKHAALPSTSLQDLFHHADSDKELQAQDTFRTQFYVTKIEPSDVKEWVKGYDRKTKKSSSLKGASGKGDNIFQVQFLVKDASTQLNNNTYRVLLYTQDGLGANFFNVKADNLHKNADARKKLEDSAELLTKFNSYVDAVVERRNGFYLIKDTKLIY

>d1jb7b\_ b.40.4.3 (B:) Core domain of telomere end binding protein beta subunit {Oxytricha nova}

QQQSAFKQLYTELFNNEGDFSKVSSNLKKPLKCYVKESYPHFLVTDGYFFVAPYFTKEAVNEFHAKFPNVNIVDLTDKVIVINNWSLELRRVNSAEVFTSYANLEARLIVHSFKPNLQERLNPTRYPVNLFRDDEFKTTIQHFRHTALQAAINKTVKGDNLVDISKVADAAGKKGKVDAGIVKASASKGDEFSDFSFKEGNTATLKIADIFVQEKG

>d1jjcb3 b.40.4.4 (B:39-151) Domain B2 of PheRS-beta, PheT {Thermus thermophilus (Thermus aquaticus)}

FPIPRGVVFARVLEAHPIPGTRLKRLVLDAGRTVEVVSGAENARKGIGVALALPGTELPGLGQKVGERVIQGVRSFGMALSPRELGVGEYGGGLLEFPEDALPPGTPLSEAWP

>d1fl0a\_ b.40.4.4 (A:) EMAP II {Human (Homo sapiens)}

IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIKL

>d1gd7a\_ b.40.4.4 (A:) CsaA {Thermus thermophilus}

MTPLEAFQILDLRVGRVLRAEPHEKARKPSYKLWVDLGPLGVKQSSAQITELYRPEDLVGRLVVCAVNLGAKRVAGFLSEVLVLGVPDEAGRVVLLAPDREVPLGGKVF

>d1h95a\_ b.40.4.5 (A:) Y-box protein 1 cold shock domain (YB1-CSD) {Human (Homo sapiens)}

MKKVIATKVLGTVKWFNVRNGYGFINRNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVEGEKGAEAANVTGPG

>d1sro\_\_ b.40.4.5 (-) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase {Escherichia coli}

AEIEVGRVYTGKVTRIVDFGAFVAIGGGKEGLVHISQIADKRVEKVTDYLQMGQEVPVKVLEVDRQGRIRLSIKEA

>d1hh2p1 b.40.4.5 (P:127-198) S1 domain of NusA {Thermotoga maritima}

FEKYSELKGTVTTAEVIRVMGEWADIRIGKLETRLPKKEWIPGEEIKAGDLVKVYIIDVVKTTKGPKILVSR

>d1k0ra1 b.40.4.5 (A:108-183) S1 domain of NusA {Mycobacterium tuberculosis}

STREGEIVAGVIQRDSRANARGLVVVRIGTETKASEGVIPAAEQVPGESYEHGNRLRCYVVGVTRGAREPLITLSR

>d1go3e\_ b.40.4.5 (E:) RNA polymerase II subunit RBP4 (RpoE) {Archaeon Methanococcus jannaschii}

MYKILEIADVVKVPPEEFGKDLKETVKKILMEKYEGRLDKDVGFVLSIVDVKDIGEGKVVHGDGSAYHPVVFETLVYIPEMYELIEGEVVDVVEFGSFVRLGPLDGLIHVSQIMDDYVSYDPKREAIIGKETGKVLEIGDYVRARIVAISLKAERKRGSKIALTMRQPYLGKLEWIEEEKAKKQ

>d1hr0w\_ b.40.4.5 (W:) Translational initiation factor 1, IF1 {Escherichia coli}

AKEKDTIRTEGVVTEALPNATFRVKLDSGPEILAYISGKMRMHYIRILPGDRVVVEITPYDPTRGRIVYRK

>d1jt8a\_ b.40.4.5 (A:) Archaeal initiation factor-1a, aIF1a {Archaeon Methanococcus jannaschii}

MAEQQQEQQIRVRIPRKEENEILGIIEQMLGASRVRVRCLDGKTRLGRIPGRLKNRIWVREGDVVIVKPWEVQGDQKCDIIWRYTKTQVEWLKRKGYLDELL

>d1d7qa\_ b.40.4.5 (A:) Translation initiation factor-1a, eIF1a {Human (Homo sapiens)}

PKNKGKGGKNRRRGKNENESEKRELVFKEDGQEYAQVIKMLGNGRLEAMCFDGVKRLCHIRGKLRKKVWINTSDIILVGLRDYQDNKADVILKYNADEARSLKAYGELPEHAKINETDTFGPGDDDEIQFDDIGDDDEDIDDI

>d1a62\_2 b.40.4.5 (48-125) Rho termination factor, RNA-binding domain {Escherichia coli}

DIFGDGVLEILQDGFGFLRSADSSYLAGPDDIYVSPSQIRRFNLRTGDTISGKIRPPKEGERYFALLKVNEVNFDKPE

>d1bkb\_2 b.40.4.5 (75-139) C-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Pyrobaculum aerophilum}

IIEKFTAQILSVSGDVIQLMDMRDYKTIEVPMKYVEEEAKGRLAPGAEVEVWQILDRYKIIRVKG

>d1jj2a2 b.40.4.5 (A:1-90) N-terminal domain of ribosomal protein L2 {Archaeon Haloarcula marismortui}

GRRIQGQRRGRGTSTFRAPSHRYKADLEHRKVEDGDVIAGTVVDIEHDPARSAPVAAVEFEDGDRRLILAPEGVGVGDELQVGVDAEIAP

>d1fjgl\_ b.40.4.5 (L:) Ribosomal protein S12 {Thermus thermophilus}

PTINQLVRKGREKVRKKSKVPALKGAPFRRGVCTVVRTVTPKKPNSALRKVAKVRLTSGYEVTAYIPGEGHNLQEHSVVLIRGGRVKDLPGVRYHIVRGVYDAAGVKDRKKSRSKYGTKKPKEAA

>d1fjgq\_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}

PKKVLTGVVVSDKMQKTVTVLVERQFPHPLYGKVIKRSKKYLAHDPEEKYKLGDVVEIIESRPISKRKRFRVLRLVESGRMDLVEKYLIRRQNYQSLSKRGGKA

>d1ckma1 b.40.4.6 (A:239-327) RNA guanylyltransferase (mRNA capping enzyme) {Chlorella virus, PBCV-1}

THHTIDFIIMSEDGTIGIFDPNLRKNVPVGKLDGYYNKGSIVECGFADGTWKYIQGRSDKNQANDRLTYEKTLLNIEENITIDELLDLF

>d1a0i\_1 b.40.4.6 (241-349) ATP-dependent DNA ligase {Bacteriophage T7}

PENEADGIIQGLVWGTKGLANEGKVIGFEVLLESGRLVNATNISRALMDEFTETVKEATLSQWGFFSPYGIGDNDACTINPYDGWACQISYMEETPDGSLRHPSFVMFR

>d1fvia1 b.40.4.6 (A:190-293) ATP-dependent DNA ligase {Chlorella virus, PBCV-1}

FKDAEATIISMTALFKNTNTKTKDNFGYSKRSTHKSGKVEEDVMGSIEVDYDGVVFSIGTGFDADQRRDFWQNKESYIGKMVKFKYFEMGSKDCPRFPVFIGIR

>d1dgsa2 b.40.4.6 (A:315-400) NAD+-dependent DNA ligase {Thermus filiformis}

AEEKETRLLDVVFQVGRTGRVTPVGVLEPVFIEGSEVSRVTLHNESYIEELDIRIGDWVLVHKAGGVIPEVLRVLKERRTGKERPI

>d1gvp\_\_ b.40.4.7 (-) Gene V protein {Filamentous bacteriophage (f1, M13)}

MIKVEIKPSQAQFTTRSGVSRQGKPYSLNEQLCYVDLGNEYPVLVKITLDEGQPAYAPGLYTVHLSSFKVGQFGSLMIDRLRLVPAK

>d1pfsa\_ b.40.4.7 (A:) Gene V protein {Pseudomonas bacteriophage pf3}

MNIQITFTDSVRQGTSAKGNPYTFQEGFLHLEDKPHPLQCQFFVESVIPAGSYQVPYRINVNNGRPELAFDFKAMKRA

>d1gpc\_\_ b.40.4.7 (-) Gene 32 protein (gp32) core {Bacteriophage T4}

GFSSEDKGEWKLKLDNAGNGQAVIRFLPSKNDEQAPFAILVNHGFKKNGKWYIETCSSTHGDYDSCPVCQYISKNDLYNTDNKEYSLVKRKTSYWANILVVKDPAAPENEGKVFKYRFGKKIWDKINAMIAVDVEMGETPVDVTCPWEGANFVLKVKQVSGFSNYDESKFLNQSAIPNIDDESFQKELFEQMVDLSEMTSKDKFKSFEELNTKFGQVM

>d1je5a\_ b.40.4.7 (A:) gp2.5 {Bacteriophage T7}

MAKKIFTSALGTAEPYAYIAKPDYGNEERGFGNPRGVYKVDLTIPNKDPRCQRMVDEIVKCHEEAYAAAVEEYEANPPAVARGKKPLKPYEGDMPFFDNGDGTTTFKFKCYASFQDKKTKETKHINLVVVDSKGKKMEDVPIIGGGSKLKVKYSLVPYKWNTAVGASVKLQLESVMLVELATFGGGEDDWADEVEEN

>d1e9ga\_ b.40.5.1 (A:) Inorganic pyrophosphatase {Baker's yeast (Saccharomyces cerevisiae)}

TYTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEITKEETLNPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPIDVLEIGETIAYTGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNDIEDVEKYFPGLLRATNEWFRIYKIPDGKPENQFAFSGEAKNKKYALDIIKETHDSWKQLIAGKSSDSKGIDLTNVTLPDTPTYSKAASDAIPPASLKADAPIDKSIDKWFFISG

>d1i40a\_ b.40.5.1 (A:) Inorganic pyrophosphatase {Escherichia coli}

SLLNVPAGKDLPEDIYVVIEIPANADPIKYEIDKESGALFVDRFMSTAMFYPCNYGYINHTLSLDGDPVDVLVPTPYPLQPGSVTRCRPVGVLKMTDEAGEDAKLVAVPHSKLSKEYDHIKDVNDLPELLKAQIAHFFEHYKDLEKGKWVKVEGWENAEAAKAEIVASFERAKNK

>d1h9ma1 b.40.6.2 (A:1-73) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}

MKISARNVFKGTVSALKEGAVNAEVDILLGGGDKLAAVVTLESARSLQLAAGKEVVAVVKAPWVLLMTDSSGY

>d1h9ra1 b.40.6.2 (A:123-199) C-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}

MQTSARNQWFGTITARDHDDVQQHVDVLLADGKTRLKVAITAQSGARLGLDEGKEVLILLKAPWVGITQDEAVAQNA

>d1h9ra2 b.40.6.2 (A:200-261) C-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}

DNQLPGIISHIERGAEQCEVLMALPDGQTLCATVPVNEATSLQQGQNVTAYFNADSVIIATL

>d1g2913 b.40.6.3 (1:241-301) Maltose transport protein MalK, C-terminal domain {Archaeon Thermococcus litoralis}

GSPPMNFLDAIVTEDGFVDFGEFRLKLLPDQFEVLGELGYVGREVIFGIRPEDLYDAMFAQ

>d1g2914 b.40.6.3 (1:302-372) Maltose transport protein MalK, C-terminal domain {Archaeon Thermococcus litoralis}

VRVPGENLVRAVVEIVENLGSERIVRLRVGGVTFVGSFRSESRVREGVEVDVVFDMKKIHIFDKTTGKAIF

>d1b3qa2 b.40.7.1 (A:540-671) Histidine kinase CheA, C-terminal domain {Thermotoga maritima}

TLAIICALLVKVNNLVYAIPIANIDTILSISKEDIQRVQDRDVIVIRGEVIPVYRLWEVLQIEHKEELEEMEAVIVRVGNRKYGIVVDDLLGQDDIVIKSLGKVFSEVKEFSGAAILGDGSIALIINVSGIV

>d1k0sa\_ b.40.7.1 (A:) Chemotaxis protein CheW {Thermotoga maritima}

MKTLADALKEFEVLSFEIDEQALAFDVDNIEMVIEKSDITPVPKSRHFVEGVINLRGRIIPVVNLAKILGISFDEQKMKSIIVARTKDVEVGFLVDRVLGVLRITENQLDLTNVSDKFGKKSKGLVKTDGRLIIYLDIDKIIEEITVKEGV

>d1bla\_\_ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}

MAEGEITTLPALPEDGGSGAFPPGHFKDPKRLYCKNGGFFLRIHPDGRVDGVREKSDPHIKLQLQAEERGVVSIKGVSANRYLAMKEDGRLLASKSVTDECFFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPGQKAILFLPMSAKS

>d1ihka\_ b.42.1.1 (A:) Fibroblast growth factor 9, FGF9 {Human (Homo sapiens)}

TDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGTRTKRHQKFTHFLPRPVDPDKVPELYKDILSQS

>d1i1b\_\_ b.42.1.2 (-) Interleukin-1beta {Human (Homo sapiens)}

VRSLNCTLRDSQQKSLVMSGPYELKALHLQGQDMEQQVVFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSS

>d1ilr1\_ b.42.1.2 (1:) Interleukin-1 receptor antagonist protein {Human (Homo sapiens)}

SKMQAFRIWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIEPHALFLGIHGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSLTNMPDEGVMVTKFYFQEDE

>d2ila\_\_ b.42.1.2 (-) Interleukin-1alpha {Human (Homo sapiens)}

NVKYNFMRIIKYEFILNDALNQSIIRANAQYLTAAALHNLDEAVKFDMGAYKSSKDDAKITVILRISKTQLYVTAQDEDQPVLLKEMPEIPKTITGSETNLLFFWETHGTKNYFTSVAHPNLFIATKQDYWVCLAGGPPSITDFQILE

>d1abrb1 b.42.2.1 (B:1-140) Plant cytotoxin B-chain (lectin) {Abrus precatorius}

IVEKSKICSSRYEPTVRIGGRDGMCVDVYDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSNGKCLTTYGYAPGSYVMIYDCTSAVAEATYWEIWDNGTIINPKSALVLSAESSSMGGTLTVQTNEYLMRQGWRTGN

>d1ce7b2 b.42.2.1 (B:134-255) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}

TAPREVTIYGFNDLCMESGGGSVTVETCSSGKADKWALYGDGSIRPEQNQAQCLTSGGDSVAGVNIVSCSGAASGQRWVFTNEGAILNLKNGLAMDVANPGGGRIIIYPATGKPNQMWLPVF

>d1hwmb2 b.42.2.1 (B:136-266) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}

DVQPIATLIVGYNEMCLQANGENNNVWMEDCDVTSVQQQWALFDDRTIRVNNSRGLCVTSNGYVSKDLIVIRKCQGLATQRWFFNSDGSVVNLKSTRVMDVKESDVSLQEVIIFPATGNPNQQWRTQVPQI

>d1xyfa1 b.42.2.1 (A:313-436) Endo-1,4-beta-xylanase C-terminal domain {Streptomyces olivaceoviridis}

GQIKGVGSGRCLDVPNASTTDGTQVQLYDCHSATNQQWTYTDAGELRVYGDKCLDAAGTGNGTKVQIYSCWGGDNQKWRLNSDGSIVGVQSGLCLDAVGGGTANGTLIQLYSCSNGSNQRWTRT

>d1jlxa1 b.42.3.1 (A:1-153) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}

AGLPVIMCLKSNNHQKYLRYQSDNIQQYGLLQFSADKILDPLAQFEVEPSKTYDGLVHIKSRYTNKYLVRWSPNHYWITASANEPDENKSNWACTLFKPLYVEEGNMKKVRLLHVQLGHYTQNYTVGGSFVSYLFAESSQIDTGSKDVFHVID

>d1jlxa2 b.42.3.1 (A:154-299) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}

WKSIFQFPKGYVTFKGNNGKYLGVITINQLPCLQFGYDNLNDPKVAHQMFVTSNGTICIKSNYMNKFWRLSTDDWILVDGNDPRETNEAAALFRSDVHDFNVISLLNMQKTWFIKRFTSGKPGFINCMNAATQNVDETAILEIIEL

>d1wba\_\_ b.42.4.1 (-) Winged bean albumin 1 {Goa bean (Psophocarpus tetragonolobus)}

DDPVYDAEGNKLVNRGKYTIVSFSDGAGIDVVATGNENPEDPLSIVKSTRNIMYATSISSEDKTPPQPRNILENMRLKINFATDPHKGDVWSVVDFQPDGQQLKLAGRYPNQVKGAFTIQKGSNTPRTYKLLFCPVGSPCKNIGISTDPEGKKRLVVSYQSDPLVVKFHRH

>d1eyla\_ b.42.4.1 (A:) chymotrypsin inhibitor WCI {Winged bean (Psophocarpus tetragonolobus)}

EFDDDLVDAEGNLVENGGTYYLLPHIWAHGGGIETAKTGNEPCPLTVVRSPNEVSKGEPIRISSQFLSLFIPRGSLVALGFANPPSCAASPWWTVVDSPQGPAVKLSQQKLPEKDILVFKFEKVSHSNIHVYKLLYCQHDEEDVKCDQYIGIHRDRNGNRRLVVTEENPLELVLLKAKS

>d1avac\_ b.42.4.1 (C:) Amylase/subtilisin inhibitor {Barley (Hordeum vulgare), seed}

ADPPPVHDTDGHELRADANYYVLSANRAHGGGLTMAPGHGRHCPLFVSQDPNGQHDGFPVRITPYGVAPSDKIIRLSTDVRISFRAYTTCLQSTEWHIDSELAAGRRHVITGPVKDPSPSGRENAFRIEKYSGAEVHEYKLMSCGDWCQDLGVFRDLKGGAWFLGATEPYHVVVFKKAPPA

>d1a8d\_2 b.42.4.2 (248-452) Tetanus neurotoxin {Clostridium tetani}

ITFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMYLTNAPSYTNGKLNIYYRRLYNGLKFIIKRYTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWYFNHLKDKILGCDWYFVPTDEGWTND

>d3btaa2 b.42.4.2 (A:1079-1295) Botulinum neurotoxin {Clostridium botulinum, serotype A}

NEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL

>d1epwa2 b.42.4.2 (A:1080-1290) Botulinum neurotoxin {Clostridium botulinum, serotype B}

SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE

>d1dfca1 b.42.5.1 (A:1008-1140) Fascin {Human (Homo sapiens)}

EAVQIQFGLINCGNKYLTAEAFGFKVNASASSLKKKQIWTLEQPPDEAGSAAVCLRSHLGRYLAADKDGNVTCEREVPGPDCRFLIVAHDDGRWSLQSEAHRRYFGGTEDRLSCFAQTVSPAEKWSVHIAMHP

>d1dfca2 b.42.5.1 (A:1141-1259) Fascin {Human (Homo sapiens)}

QVNIYSVTRKRYAHLSARPADEIAVDRDVPWGVDSLITLAFQDQRYSVQTADHRFLRHDGRLVARPEPATGYTLEFRSGKVAFRDCEGRYLAPSGPSGTLKAGKATKVGKDELFALEQS

>d1dfca3 b.42.5.1 (A:1260-1382) Fascin {Human (Homo sapiens)}

CAQVVLQAANERNVSTRQGMDLSANQDEETDQETFQLEIDRDTKKCAFRTHTGKYWTLTATGGVQSTASSKNASCYFDIEWRDRRITLRASNGKFVTSKKNGQLAASVETAGDSELFLMKLIN

>d1dfca4 b.42.5.1 (A:1383-1493) Fascin {Human (Homo sapiens)}

RPIIVFRGEHGFIGCRKVTGTLDANRSSYDVFQLEFNDGAYNIKDSTGKYWTVGSDSAVTSSGDTPVDFFFEFCDYNKVAIKVGGRYLKGDHAGVLKASAETVDPASLWEY

>d1i8da1 b.43.4.3 (A:1-93) Riboflavin synthase {Escherichia coli}

MFTGIVQGTAKLVSIDEKPNFRTHVVELPDHMLDGLETGASVAHNGCCLTVTEINGNHVSFDLMKETLRITNLGDLKVGDWVNVERAAKFSDE

>d1i8da2 b.43.4.3 (A:94-206) Riboflavin synthase {Escherichia coli}

IGGHLMSGHIMTTAEVAKILTSENNRQIWFKVQDSQLMKYILYKGFIGIDGISLTVGEVTPTRFCVHLIPETLERTTLGKKKLGARVNIEIDPQTQAVVDTVERVLAARENAM

>d1jb9a1 b.43.4.2 (A:6-162) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Maize (Zea mays), root isoform}

SRSKVSVAPLHLESAKEPPLNTYKPKEPFTATIVSVESLVGPKAPGETCHIVIDHGGNVPYWEGQSYGVIPPGENPKKPGAPQNVRLYSIASTRYGDNFDGRTGSLCVRRAVYYDPETGKEDPSKNGVCSNFLCNSKPGDKIQLTGPSGKIMLLPEE

>d1fdr\_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Escherichia coli}

ADWVTGKVTKVQNWTDALFSLTVHAPVLPFTAGQFTKLGLEIDGERVQRAYSYVNSPDNPDLEFYLVTVPDGKLSPRLAALKPGDEVQVVSEAAGFFVL

>d1a8p\_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Azotobacter vinelandii}

SNLNVERVLSVHHWNDTLFSFKTTRNPSLRFENGQFVMIGLEVDGRPLMRAYSIASPNYEEHLEFFSIKVQNGPLTSRLQHLKEGDELMVSRKPTGTLV

>d1qfja1 b.43.4.2 (A:1-97) NAD(P)H:flavin oxidoreductase {Escherichia coli}

TTLSCKVTSVEAITDTVYRVRIVPDAAFSFRAGQYLMVVMDERDKRPFSMASTPDEKGFIELHIGASEINLYAKAVMDRILKDHQIVVDIPHGEAWL

>d1i7pa1 b.43.4.2 (A:29-153) cytochrome b5 reductase {Rat (Rattus norvegicus)}

HHHMITLENPDIKYPLRLIDKEILSHDTRRFRFALPSPQHILGLPIGQHIYLSTRIDGNLVIRPYTPVSSDDDKGFVDLVVKVYFKETHPKFPAGGKMSQYLENMNIGDTIEFRGPNGLLVYQGK

>d2pia\_1 b.43.4.2 (1-103) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}

TTPQEDGFLRLKIASKEKIARDIWSFELTDPQGAPLPPFEAGANLTVAVPNGSRRTYSLCNDSQERNRYVIAVKRDSNGRGGSISFIDDTSEGDAVEVSLPRN

>d1ep3b1 b.43.4.2 (B:2-102) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}

SQLQEMMTVVSQREVAYNIFEMVLKGTLVDEMDLPGQFLHLAVPNGAMLLRRPISISSWDKRAKTCTILYRIGDETTGTYKLSKLESGAKVDVMGPLGNGF

>d1cqxa2 b.43.4.2 (A:151-261) Flavohemoglobin, central domain {Alcaligenes eutrophus}

WKGWRTFVIREKRPESDVITSFILEPADGGPVVNFEPGQYTSVAIDVPALGLQQIRQYSLSDMPNGRTYRISVKREGGGPQPPGYVSNLLHDHVNVGDQVKLAAPYGSFHI

>d1ja1a1 b.43.4.1 (A:240-518) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}

SSIRQYELVVHEDMDVAKVYTGEMGRLKSYENQKPPFDAKNPFLAAVTANRKLNQGTERHLMHLELDISDSKIRYESGDHVAVYPANDSALVNQIGEILGADLDVIMSLNNLDEESNKKHPFPCPTTYRTALTYYLDITNPPRTNVLYELAQYASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPIDHLCELLPRLQARYYAIASSSKVHPNSVHICAVAVEYEAKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQF

>d1ddga1 b.43.4.1 (A:226-446) Sulfite reductase flavoprotein {Escherichia coli}

IHTSPYSKDAPLVASLSVNQKITGRNSEKDVRHIEIDLGDSGLRYQPGDALGVWYQNDPALVKELVELLWLKGDEPVTVEGKTLPLNEALQWHFELTVNTANIVENYATLTRSETLLPLVGDKAKLQHYAATTPIVDMVRFSPAQLDAEALINLLRPLTPRLYSIASSQAEVENEVHVTVGVVRYDVEGRARAGGASSFLADRVEEEGEVRVFIEHNDNFR

>d1f20a1 b.43.4.1 (A:963-1232) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}

SWKRNKFRLTYVAEAPDLTQGLSNVHKKRVSAARLLSRQNLQSPKSSRSTIFVRLHTNGNQELQYQPGDHLGVFPGNHEDLVNALIERLEDAPPANHVVKVEMLEERNTALGVISNWKDESRLPPCTIFQAFKYYLDITTPPTPLQLQQFASLATNEKEKQRLLVLSKGLQEYEEWKWGKNPTMVEVLEEFPSIQMPATLLLTQLSLLQPRYYSISSSPDMYPDEVHLTVAIVSYHTRDGEGPVHHGVCSSWLNRIQADDVVPCFVRGAP

>d1exma1 b.43.3.1 (A:213-312) Elongation factor Tu (EF-Tu), domain 2 {Thermus thermophilus}

PVRDVDKPFLMPVEDVFTITGRGTVATGRIERGKVKVGDEVEIVGLAPETRKTVVTGVEMHRKTLQEGIAGDNVGVLLRGVSREEVERGQVLAKPGSITP

>d1jnya1 b.43.3.1 (A:228-322) Elongation factor eEF-1alpha, domain 2 {Archaeon Sulfolobus solfataricus}

PVDKPLRIPIQDVYSISGVGTVPVGRVESGVLKVGDKIVFMPAGKVGEVRSIETHHTKMDKAEPGDNIGFNVRGVEKKDIKRGDVVGHPNNPPTV

>d1dar\_1 b.43.3.1 (283-400) Elongation factor G (EF-G), domain II {Thermus thermophilus}

PLDIPPIKGTTPEGEVVEIHPDPNGPLAALAFKIMADPYVGRLTFIRVYSGTLTSGSYVYNTTKGRKERVARLLRMHANHREEVEELKAGDLGAVVGLKETITGDTLVGEDAPRVILE

>d1g7sa1 b.43.3.1 (A:228-328) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

EDSPARGTILEVKEETGLGMTIDAVIYDGILRKDDTIAMMTSKDVISTRIRSLLKPRPLEEMRESRKKFQKVDEVVAAAGIKIVAPGIDDVMAGSPLRVVT

>d1g7sa2 b.43.3.1 (A:460-587) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

IIKPASIRLIPKLVFRQSKPAIGGVEVLTGVIRQGYPLMNDDGETVGTVESMQDKGENLKSASRGQKVAMAIKDAVYGKTIHEGDTLYVDIPENHYHILKEQLSGDLTDEELDLMDKIAEIKRKKNPD

>d1d1na\_ b.43.3.1 (A:) Initiation factor IF2/eIF5b, domains 2 and 4 {Bacillus stearothermophilus}

YEEKVIGQAEVRQTFKVSKVGTIAGCYVTDGKITRDSKVRLIRQGIVVYEGEIDSLKRYKDDVREVAQGYECGLTIKNFNDIKEGDVIEAYVMQEVARA

>d1d2ea2 b.44.1.1 (A:349-451) Elongation factor Tu (EF-Tu) {Cow (Bos taurus), mitochondrial}

HQKVEAQVYILTKEEGGRHKPFVSHFMPVMFSLTWDMACRIILPPGKELAMPGEDLKLTLILRQPMILEKGQRFTLRDGNRTIGTGLVTDTPAMTEEDKNIKW

>d1f60a2 b.44.1.1 (A:335-441) Elongation factor eEF-1alpha, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

CASFNATVIVLNHPGQISAGYSPVLDCHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLGRFAVRDMRQTVAVGVIKSVDK

>d1flma\_ b.45.1.1 (A:) FMN-binding protein {Desulfovibrio vulgaris, strain Miyazaki F}

MLPGTFFEVLKNEGVVAIATQGEDGPHLVNTWNSYLKVLDGNRIVVPVGGMHKTEANVARDERVLMTLGSRKVAGRNGPGTGFLIRGSAAFRTDGPEFEAIARFKWARAALVITVVSAEQTL

>d1ci0a\_ b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Baker's yeast (Saccharomyces cerevisiae)}

FTLNEKQLTDDPIDLFTKWFNEAKEDPRETLPEAITFSSAELPSGRVSSRILLFKELDHRGFTIYSNWGTSRKAHDIATNPNAAIVFFWKDLQRQVRVEGITEHVNRETSERYFKTRPRGSKIGAWASRQSDVIKNREELDELTQKNTERFKDAEDIPCPDYWGGLRIVPLEIEFWQGRPSRLHDRFVYRRKTENDPWKVVRLAP

>d1ejea\_ b.45.1.2 (A:) FMN-binding protein MTH152 {Archaeon Methanobacterium thermoautotrophicum}

GSQAAHMMSMDFEDFPVESAHRILTPRPTVMVTTVDEEGNINAAPFSFTMPVSIDPPVVAFASAPDHHTARNIESTHEFVINITPADIIERMWVTARDIPAGENELEAAGLAWTSSRRVKPPRIVEAPGHLECELLRMFEVGDHNLITGSVVSASVRSGAVKEGLLDVESVKPVLHVGGNKFVVGDHVRHVE

>d1i0ra\_ b.45.1.2 (A:) Ferric reductase {Archaeon Archaeoglobus fulgidus}

MDVEAFYKISYGLYIVTSESNGRKCGQIANTVFQLTSKPVQIAVCLNKENDTHNAVKESGAFGVSVLELETPMEFIGRFGFRKSSEFEKFDGVEYKTGKTGVPLVTQHAVAVIEAKVVKECDVGTHTLFVGEAVDAEVLKDAEVLTYADYHLMKKGKTPRT

>d1k28d1 b.106.1.1 (D:4-200) Baseplate structural protein gp27 {Bacteriophage T4}

LQRPGYPNLSVKLFDSYDAWSNNRFVELAATITTLTMRDSLYGRNEGMLQFYDSKNIHTKMDGNEIIQISVANANDINNVKTRIYGCKHFSVSVDSKGDNIIAIELGTIHSIENLKFGRPFFPDAGESIKEMLGVIYQDRTLLTPAINAINAYVPDIPWTSTFENYLSYVREVALAVGSDKFVFVWQDIMGVNMMDY

>d1k28d2 b.106.1.1 (D:201-376) Baseplate structural protein gp27 {Bacteriophage T4}

DMMINQEPYPMIVGEPSLIGQFIQELKYPLAYDFVWLTKSNPHKRDPMKNATIYAHSFLDSSIPMITTGKGENSIVVSRSGAYSEMTYRNGYEEAIRLQTMAQYDGYAKCSTIGNFNLTPGVKIIFNDSKNQFKTEFYVDEVIHELSNNNSVTHLYMFTNATKLETIDPVKVKNEF

>d1arb\_\_ b.47.1.1 (-) Achromobacter protease {Achromobacter lyticus, strain m497-1}

GVSGSCNIDVVCPEGDGRRDIIRAVGAYSKSGTLACTGSLVNNTANDRKMYFLTAHHCGMGTASTAASIVVYWNYQNSTCRAPNTPASGANGDGSMSQTQSGSTVKATYATSDFTLLELNNAANPAFNLFWAGWDRRDQNYPGAIAIHHPNVAEKRISNSTSPTSFVAWGGGAGTTHLNVQWQPSGGVTEPGSSGSPIYSPEKRVLGQLHGGPSSCSATGTNRSDQYGRVFTSWTGGGAAASRLSDWLDPASTGAQFIDGLDS

>d1qq4a\_ b.47.1.1 (A:) alpha-Lytic protease {Lysobacter enzymogenes, 495}

ANIVGGIEYSINNASLCSVGFSVTRGATKGFVTAGHCGTVNATARIGGAVVGTFAARVFPGNDRAWVSLTSAQTLLPRVANGSSFVTVRGSTEAAVGAAVCHSGRTTGYQCGTITAKNVTANYAEGAVRGLTQSNACMGRGDSGGSWITSAGQAQGVMSGGNVQSNGNNCGIPASQRSSLFERLQPILSQYGLSLVTG

>d2sfa\_\_ b.47.1.1 (-) Serine proteinase {Streptomyces fradiae}

IAGGEAIYAAGGGRCSLGFNVRSSSGATYALTAGHCTEIASTWYTNSGQTSLLGTRAGTSFPGNDYGLIRHSNASAADGRVYLYNGSYRDITGAGNAYVGQTVQRSGSTTGLHSGRVTGLNATVNYGGGDIVSGLIQTNVCAEPGDSGGALFAGSTALGLTSGGSGNCRTGGTTFFQPVTEALSAYGVSIL

>d1qtfa\_ b.47.1.1 (A:) Exfoliative toxin B {Staphylococcus aureus}

KEYSAEEIRKLKQKFEVPPTDKELYTHITDNARSPYNSVGTVFVKGSTLATGVLIGKNTIVTNYHVAREAAKNPSNIIFTPAQNRDAEKNEFPTPYGKFEAEEIKESPYGQGLDLAIIKLKPNEKGESAGDLIQPANIPDHIDIAKGDKYSLLGYPYNYSAYSLYQSQIEMFNDSQYFGYTEVGNSGSGIFNLKGELIGIHSGKGGQHNLPIGVFFNRKISSLYSVDNTFGDTLGNDLKKRAKLDK

>d1gdna\_ b.47.1.2 (A:) Trypsin(ogen) {Mold (Fusarium oxysporum)}

IVGGTSASAGDFPFIVSISRNGGPWCGGSLLNANTVLTAAHCVSGYAQSGFQIRAGSLSRTSGGITSSLSSVRVHPSYSGNNNDLAILKLSTSIPSGGNIGYARLAASGSDPVAGSSATVAGWGATSEGGSSTPVNLLKVTVPIVSRATCRAQYGTSAITNQMFCAGVSSGGKDSCQGDSGGPIVDSSNTLIGAVSWGNGCARPNYSGVYASVGALRSFIDTYA

>d1eq9a\_ b.47.1.2 (A:) (alpha,gamma)-chymotrypsin(ogen) {Red fire ant (Solenopsis invicta)}

IVGGKDAPVGKYPYQVSLRLSGSHRCGASILDNNNVLTAAHCVDGLSNLNRLKVHVGTNYLSESGDVYDVEDAVVNKNYDDFLLRNDVALVHLTNPIKFNDLVQPIKLSTNDEDLESNPCTLTGWGSTRLGGNTPNALQEIELIVHPQKQCERDQWRVIDSHICTLTKRGEGACHGDSGGPLVANGAQIGIVSFGSPCALGEPDVYTRVSSFVSWINANLKK

>d1azza\_ b.47.1.2 (A:) Crab collagenase {Atlantic sand fiddler crab (Uca pugilator)}

IVGGVEAVPNSWPHQAALFIDDMYFCGGSLISPEWILTAAHCMDGAGFVDVVLGAHNIREDEATQVTIQSTDFTVHENYNSFVISNDIAVIRLPVPVTLTAAIATVGLPSTDVGVGTVVTPTGWGLPSDSALGISDVLRQVDVPIMSNADCDAVYGIVTDGNICIDSTGGKGTCNGDSGGPLNYNGLTYGITSFGAAAGCEAGYPDAFTRVTYFLDWIQTQTGITP

>d2hlca\_ b.47.1.2 (A:) HL collagenase {Common cattle grub (Hypoderma lineatum)}

IINGYEAYTGLFPYQAGLDITLQDQRRVWCGGSLIDNKWILTAAHCVHDAVSVVVYLGSAVQYEGEAVVNSERIISHSMFNPDTYLNDVALIKIPHVEYTDNIQPIRLPSGEELNNKFENIWATVSGWGQSNTDTVILQYTYNLVIDNDRCAQEYPPGIIVESTICGDTSDGKSPCFGDSGGPFVLSDKNLLIGVVSFVSGAGCESGKPVGFSRVTSYMDWIQQNTGIKF

>g1jou.1 b.47.1.2 (A:,B:) Thrombin {Human (Homo sapiens)}

SEYQTFFNPRTFGSGEADCGLRPLFEKKSLEDKTERELLESYIDGXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDAGGPFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQKVIDQFGE

>d1pytc\_ b.47.1.2 (C:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (Bos taurus)}

SRPSSRVVNGEDAVPYSWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLQGSEQVIPINAGDLFVHPLWNSNCVACGNDIALVKLSRSAQLGDKVQLANLPPAGDILPNEAPCYISGWGRLYTGGPLPDKLQEALLPVVDYEHCSQYDWWGITVKKTMVCAGGDTRSGCDGDSGGPLNCPAADGSWQVHGVTSFVSAFGCNTIKKPTVFTRVSAFIDWINETIASN

>d1a7s\_\_ b.47.1.2 (-) Heparin binding protein, HBP {Human (Homo sapiens)}

IVGGRKARPRQFPFLASIQNQGRHFCGGALIHARFVMTAASCFPGVSTVVLGAYDLRRRERQSRQTFSISSMSENGYDPQQNLNDLMLLQLDREANLTSSVTILPLPLQNATVEAGTRCQVAGWGSQRSGGRLSRFPRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLVCEGLAHGVASFSLGPCGRGPDFFTRVALFRDWIDGVLNNPGPGPA

>d1a0la\_ b.47.1.2 (A:) beta-Tryptase {Human (Homo sapiens)}

IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPKK

>d1danh\_ b.47.1.2 (H:) Coagulation factor VIIa {Human (Homo sapiens)}

IVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP

>d1dlea\_ b.47.1.2 (A:) Factor B {Human (Homo sapiens)}

ADPDESQSLSLCGMVWEHRKGTDYHKQPWQAKISVIRPSKGHESCMGAVVSEYFVLTAAHCFTVDDKEHSIKVSVGGEKRDLEIEVVLFHPNYNINGKKEAGIPEFYDYDVALIKLKNKLKYGQTIRPICLPCTEGTTRALRLPPTTTCQQQKEELLPAQDIKALFVSEEEKKLTRKEVYIKNGDKKGSCERDAQYAPGYDKVKDISEVVTPRFLCTGGVSPYADPNTCRGDSGGPLIVHKRSRFIQVGVISWGVVDVCKNQKRQKQVPAHARDFHINLFQVLPWLKEKLQDEDLGFL

>d1bio\_\_ b.47.1.2 (-) Factor D {Human (Homo sapiens)}

ILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHSLSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQLSEKATLGPAVRPLPWQRVDRDVAPGTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCAESNRRDSCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTRVASYAAWIDSVLA

>d1a5ia\_ b.47.1.2 (A:) Single chain tissue plasminogen activator {Vampire bat (Desmodus rotundus)}

TCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCFQESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNDIALLQLKSDSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPKFLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGEKDVPGVYTKVTNYLGWIRDNMHL

>d1bqya\_ b.47.1.2 (A:) Plasminogen activator from snake venom, TSV-PA {Chinese green tree viper (Trimeresurus stejnejeri)}

VFGGDECNINEHRSLVVLFNSNGFLCGGTLINQDWVVTAAHCDSNNFQLLFGVHSKKILNEDEQTRDPKEKFFCPNRKKDDEVDKDIMLIKLDSSVSNSEHIAPLSLPSSPPSVGSVCRIMGWGKTIPTKEIYPDVPHCANINILDHAVCRTAYSWRQVANTTLCAGILQGGRDTCHFDSGGPLICNGIFQGIVSWGGHPCGQPGEPGVYTKVFDYLDWIKSIIAGNKDATCPP

>d1ao5a\_ b.47.1.2 (A:) Kallikrein-13 {Mouse (Mus musculus)}

VVGGFNCEKNSQPWQVAVYYQKEHICGGVLLDRNWVLTAAHCYVDQYEVWLGKNKLFQEEPSAQHRLVSKSFPHPGFNMSLLMLQTIPPGADFSDDLMLLRLSKPADITDVVKPIALPTKEPKPGSKCLASGWGSITPTRWQKPDDLQCVFITLLPNENCAKVYLQKVTDVMLCAGEMGGGKDTCRDDSGGPLICDGILQGTTSYGPVPCGKPGVPAIYTNLIKFNSWIKDTMMKNA

>d1elva1 b.47.1.2 (A:410-668) Complement C1S protease, catalytic domain {Human (Homo sapiens)}

CGVPREPFEEKQRIIGGSDADIKNFPWQVFFDNPWAGGALINEYWVLTAAHVVEGNREPTMYVGSTSVQTSRLAKSKMLTPEHVFIHPGWKLLAVPEGRTNFDNDIALVRLKDPVKMGPTVSPICLPGTSSDYNLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKCKEVKVEKPTADAEAYVFTPNMICAGGEKGMDSCKGDSGGAFAVQDPNDKTKFYAAGLVSWGPQCGTYGLYTRVKNYVDWIMKTMQENS

>d1fi8a\_ b.47.1.2 (A:) Granzyme B {Rat (Rattus norvegicus)}

IIGGHEAKPHSRPYMAYLQIMDEYSGSKKCGGFLIREDFVLTAAHCSGSKIQVTLGAHNIKEQEKMQQIIPVVKIIPHPAYNSKTISNDIMLLKLKSKAKRSSAVKPLNLPRRNVKVKPGDVCYVAGWGKLGPMGKYSDTLQEVELTVQEDQKCESYLKNYFDKANEICAGDPKIKRASFRGDSGGPLVCKKVAAGIVSYGQNDGSTPRAFTKVSTFLSWIKKTMKK

>g1fiz.1 b.47.1.2 (L:,A:) Beta-acrosin {Pig (Sus scrofa)}

ATCDGPCGLRFRQXVVGGMSAEPGAWPWMVSLQIFMYHNNRRYHTCGGILLNSHWVLTAAHCFKNKKKVTDWRLIFGANEVVWGSNKPVKPPLQERFVEEIIIHEKYVSGLEINDIALIKITPPVPCGPFIGPGCLPQFKAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLELCNSTRWYNGRIRSTNVCAGYPRGKIDTCQGDSGGPLMCRDRAENTFVVVGITSWGVGCARAKRPGVYTSTWPYLNWIASKIGSNALQMVQLGTPPR

>d1eaxa\_ b.47.1.2 (A:) Matriptase MTSP1 {Human (Homo sapiens)}

VVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENTGV

>d1svpa\_ b.47.1.3 (A:) Viral capsid protein {Sindbis virus}

ALKLEADRLFDVKNEDGDVIGHALAMEGKVMKPLHVKGTIDHPVLSKLKFTKSSAYDMEFAQLPVNMRSEAFTYTSEHPEGFYNWHHGAVQYSGGRFTIPRGVGGRGDAGRPIMDNSGRVVAIVLGGADEGTRTALSVVTWNSKGKTIKTTPEGTEEWSA

>d1cu1a1 b.47.1.3 (A:705-720,A:3-186) NS3 protease {Human hepatitis C virus (HCV), different isolates}

GSVVIVGRIILSGSGSXITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRSPVFTD

>d1befa\_ b.47.1.3 (A:) NS3 protease {Dengue virus serotype 2}

WDVPSPPPVGKAELEDGAYRIKQKGILGYSQIGAGVYKEGTFHTMWHVTRGAVLMHKGKRIEPSWADVKKDLVSCGGGWKLEGEWKEGEEVQVLALEPGKNPRAVQTKPGLFKTNAGTIGAVSLDFSPGTSGSPIIDKKGKVVGIYGNGVVTRSGAYVSAIAQTEKSIEDNPEIEDD

>d1cqqa\_ b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human rhinovirus type 2}

GPEEEFGMSLIKHNSCVITTENGKFTGLGVYDRFVVVPTHADPGKEIQVDGITTKVIDSYDLYNKNGIKLEITVLKLDRNEKFRDIRRYIPNNEDDYPNCNLALLANQPEPTIINVGDVVSYGNILLSGNQTARMLKYSYPTKSGYCGGVLYKIGQVLGIHVGGNGRDGFSAMLLRSYFT

>d1hava\_ b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human hepatitis A virus}

STLEIAGLVRKNLVQFGVGEKNGSVRWVMNALGVKDDWLLVPSHAYKFEKDYEMMEFYFNRGGTYYSISAGNVVIQSLDVGFQDVVLMKVPTIPKFRDITQHFIKKGDVPRALNRLATLVTTVNGTPMLISEGPLKMEEKATYVHKKNDGTTVDLTVDQAWRGKGEGLPGMCGGALVSSNQSIQNAILGIHVAGGNSILVAKLVTQEMFQNIDKKI

>d2hrva\_ b.47.1.4 (A:) 2A cysteine proteinase {Human rhinovirus 2}

GPSDMYVHVGNLIYRNLHLFNSEMHESILVSYSSDLIIYRTNTVGDDYIPSCDCTQATYYCKHKNRYFPITVTSHDWYEIQESEYYPKHIQYNLLIGEGPCEPGDCGGKLLCKHGVIGIVTAGGDNHVAFIDLRHFHCA

>d1maba2 b.49.1.1 (A:10-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (Rattus norvegicus)}

SSILEERILGADTSVDLEETGRVLSIGDGIARVHGLRNVQAEEMVEFSSGLKGMSLNLEPDNVGVVVFGNDKLIKEGDIVKRTGAI

>d1skye2 b.49.1.1 (E:1-82) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

MTRGRVIQVMGPVVDVKFENGHLPAIYNALKIQHKARNENEVDIDLTLEVALHLGDDTVRTIAMASTDGLIRGMEVIDTGAP

>d1bd0a1 b.49.2.1 (A:2-11,A:245-382) Alanine racemase {Bacillus stearothermophilus}

NDFHRDTWAEXFSLHSRLVHVKKLQPGEKVSYGATYTAQTEEWIGTIPIGYADGWLRRLQHFHVLVDGQKAPIVGRICMDQCMIRLPGPLPVGTKVTLIGRQGDEVISIDDVARHLETINYEVPCTISYRVPRIFFRHKRIMEVRNAIG

>d1d7ka1 b.49.2.1 (A:7-43,A:284-427) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}

EEFDCHFLDEGFTAKDILDQKINEVSSSDDKDAFYVAXFTLAVNIIAKKIVLKEQTGSDDEDESSEQTFMYYVNDGVYGSFNCILYDHAHVKPLLQKRPKPDERYYSSSIWGPTCDGLDRIVERCDLPEMHVGDWMLFENMGAYTVAAASTFNGFQRPTIYYVMSGPAWQLMQQFQNPDFPP

>d1hvc\_\_ b.50.1.1 (-) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGKWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFGGSSGPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF

>d4fiv\_\_ b.50.1.1 (-) Feline immunodeficiency virus (FIV) protease {Feline immunodeficiency virus}

VGTTTTLEKRPEILIFVNGYPIKFLLDTGADITILNRRDFQVKNSIENGRQNMIGVGGGKRGTNYINVHLEIRDENYKTQCIFGNVCVLEDNSLIQPLLGRDNMIKFNIRLVM

>d1baia\_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}

LAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDTGADDTVISEEDWPTDWPVMEAANPQIHGIGGGIPVRKSRDMIELGVINRDGSLERPLLLFPLVAMTPVNILGRDCLQGLGLRLTNL

>d1fmb\_\_ b.50.1.1 (-) EIAV protease {Equine infectious anemia virus}

VTYNLEKRPTTIVLINDTPLNVLLDTGADTSVLTTAHYNRLKYRGRKYQGTGIGGVGGNVETFSTPVTIKKKGRHIKTRMLVADIPVTILGRDILQDLGAKLVL

>d2er7e\_ b.50.1.2 (E:) Endothiapepsin {Chestnut blight fungus (Endothia parasitica)}

STGSATTTPIDSLDDAYITPVQIGTPAQTLNLDFDTGSSDLWVFSSETTASEVDGQTIYTPSKSTTAKLLSGATWSISYGDGSSSSGDVYTDTVSVGGLTVTGQAVESAKKVSSSFTEDSTIDGLLGLAFSTLNTVSPTQQKTFFDNAKASLDSPVFTADLGYHAPGTYNFGFIDTTAYTGSITYTAVSTKQGFWEWTSTGYAVGSGTFKSTSIDGIADTGTTLLYLPATVVSAYWAQVSGAKSSSSVGGYVFPCSATLPSFTFGVGSARIVIPGDYIDFGPISTGSSSCFGGIQSSAGIGINIFGDVALKAAFVVFNGATTPTLGFASK

>d2apr\_\_ b.50.1.2 (-) Acid protease {Bread mold (Rhizopus chinensis)}

AGVGTVPMTDYGNDIEYYGQVTIGTPGKKFNLDFDTGSSDLWIASTLCTNCGSGQTKYDPNQSSTYQADGRTWSISYGDGSSASGILAKDNVNLGGLLIKGQTIELAKREAASFASGPNDGLLGLGFDTITTVRGVKTPMDNLISQGLISRPIFGVYLGKAKNGGGGEYIFGGYDSTKFKGSLTTVPIDNSRGWWGITVDRATVGTSTVASSFDGILDTGTTLLILPNNIAASVARAYGASDNGDGTYTISCDTSAFKPLVFSINGASFQVSPDSLVFEEFQGQCIAGFGYGNWGFAIIGDTFLKNNYVVFNQGVPEVQIAPVAE

>d1eaga\_ b.50.1.2 (A:) Acid protease {Yeast (Candida albicans)}

QAVPVTLHNEQVTYAADITVGSNNQKLNVIVDTGSSDLWVPDVNVDCQVTYSDQTADFCKQKGTYDPSGSSASQDLNTPFKIGYGDGSSSQGTLYKDTVGFGGVSIKNQVLADVDSTSIDQGILGVGYKTNEAGGSYDNVPVTLKKQGVIAKNAYSLYLNSPDAATGQIIFGGVDNAKYSGSLIALPVTSDRELRISLGSVEVSGKTINTDNVDVLLDSGTTITYLQQDLADQIIKAFNGKLTQDSNGNSFYEVDCNLSGDVVFNFSKNAKISVPASEFAASLQGDDGQPYDKCQLLFDVNDANILGDNFLRSAYIVYDLDDNEISLAQVKYTSASSISALT

>g1htr.1 b.50.1.2 (P:,B:) Pepsin(ogen) {Human (Homo sapiens), progastricsin (pepsinogen C)}

AVVKVPLKKFKSIRETMKEKGLLGEFLRTHKYDPAWKYRFGDLXSVTYEPMAYMDAAYFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYGSGSLTGFFGYDTLTVQSIQVPNQEFGLSENEPGTNFVYAQFDGIMGLAYPALSVDEATTAMQGMVQEGALTSPVFSVYLSNQQGSSGGAVVFGGVDSSLYTGQIYWAPVTQELYWQIGIEEFLIGGQASGWCSEGCQAIVDTGTSLLTVPQQYMSALLQATGAQEDEYGQFLVNCNSIQNLPSLTFIINGVEFPLPPSSYILSNNGYCTVGVEPTYLSSQNGQPLWILGDVFLRSYYSVYDLGNNRVGFATAA

>d1mpp\_\_ b.50.1.2 (-) Pepsin {Mucor pusillus}

GSVDTPGLYDFDLEEYAIPVSIGTPGQDFYLLFDTGSSDTWVPHKGCDNSEGCVGKRFFDPSSSSTFKETDYNLNITYGTGGANGIYFRDSITVGGATVKQQTLAYVDNVSGPTAEQSPDSELFLDGIFGAAYPDNTAMEAEYGDTYNTVHVNLYKQGLISSPVFSVYMNTNDGGGQVVFGGVNNTLLGGDIQYTDVLKSRGGYFFWDAPVTGVKIDGSDAVSFDGAQAFTIDTGTNFFIAPSSFAEKVVKAALPDATESQQGYTVPCSKYQDSKTTFSLVLQKSGSSSDTIDVSVPISKMLLPVDKSGETCMFIVLPDGGNQFIVGNLFLRFFVNVYDFGKNRIGFAPLASGYEND

>d1hrna\_ b.50.1.2 (A:) Chymosin (synonim: renin) {Human (Homo sapiens)}

GNTTSSVILTNYMDTQYYGEIGIGTPPQTFKVVFDTGSSNVWVPSSKCSRLYTACVYHKLFDASDSSSYKHNGTELTLRYSTGTVSGFLSQDIITVGGITVTQMFGEVTEMPALPFMLAEFDGVVGMGFIEQAIGRVTPIFDNIISQGVLKEDVFSFYYNRDSENSQSLGGQIVLGGSDPQHYEGNFHYINLIKTGVWQIQMKGVSVGSSTLLCEDGCLALVDTGASYISGSTSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGKEYTLTSADYVFQESYSSKKLCTLAIHAMDIPPPTGPTWALGATFIRKFYTEFDRRNNRIGFALAR

>d1fkna\_ b.50.1.2 (A:) beta-secretase (memapsin) {Human (Homo sapiens)}

RRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYN

>d1pfza\_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}

HLTIGFKVENAHDRILKTIKTHKLKNYIKESVNFLNSGLTKTNYLGSSNDNIELVDFQNIMFYGDAEVGDNQQPFTFILDTGSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEKDGTKVEMNYVSGTVSGFFSKDLVTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKDLSIGSVDPIVVELKNQNKIENALFTFYLPVHDKHTGFLTIGGIEERFYEGPLTYEKLNHDLYWQITLDAHVGNIMLEKANCIVDSGTSAITVPTDFLNKMLQNLDVIKVPFLPFYVTLCNNSKLPTFEFTSENGKYTLEPEYYLQHIEDVGPGLCMLNIIGLDFPVPTFILGDPFMRKYFTVFDYDNHSVGIALAKKNL

>d1ile\_2 b.51.1.1 (198-386) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

KEIQDPSVYVRFPLKEPKKLGLEKASLLIWTTTPWTLPGNVAAAVHPEYTYAAFQVGDEALILEEGLGRKLLGEGTQVLKTFPGKALEGLPYTPPYPQALEKGYFVVLADYVSQEDGTGIVHQAPAFGAEDLETARVYGLPLLKTVDEEGKLLVEPFKGLYFREANRAILRDLRGRGLLFKEESYLHSY

>d1ffya2 b.51.1.1 (A:201-394) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

HDKRSASIYVAFNVKDDKGVVDADAKFIIWTTTPWTIPSNVAITVHPELKYGQYNVNGEKYIIAEALSDAVAEALDWDKASIKLEKEYTGKELEWVVAQHPFLDRESLVINGDHVTTDAGTGCVHTAPGHGEDDYIVGQQYELPVISPIDDKGVFTEEGGQFEGMFYDKANKAVTDLLTEKGALLKLDFITHSY

>d1gaxa2 b.51.1.1 (A:190-342) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

TEPTPGKLYTLRYEVEGGGFIEIATVRPETVFADQAIAVHPEDERYRHLLGKRARIPLTEVWIPILADPAVEKDFGTGALKVTPAHDPLDYEIGERHGLKPVSVINLEGRMEGERVPEALRGLDRFEARRKAVELFREAGHLVKEEDYTIALA

>d1gmua1 b.107.1.1 (A:1-70) Urease metallochaperone UreE, N-terminal domain {Klebsiella aerogenes}

MLYLTQRLEIPAAATASVTLPIDVRVKSRVKVTLNDGRDAGLLLPRGLLLRGGDVLSNEEGTEFVQVIAA

>d1eara1 b.107.1.1 (A:1-74) Urease metallochaperone UreE, N-terminal domain {Bacillus pasteurii}

MVITKIVGHIDDLSHQIKKVDWLEVEWEDLNKRILRKETENGTDIAIKLENSGTLRYGDVLYESDDTLIAIRTK

>d1aa6\_1 b.52.2.2 (565-715) Formate dehydrogenase H {Escherichia coli}

PIDKLTDEYPMVLSTVREVGHYSCRSMTGNCAALAALADEPGYAQINTEDAKRLGIEDEALVWVHSRKGKIITRAQVSDRPNKGAIYMTYQWWIGACNELVTENLSPITKTPEYKYCAVRVEPIADQRAAEQYVIDEYNKLKTRLREAALA

>d1tmo\_1 b.52.2.2 (632-798) Trimethylamine N-oxide reductase {Shewanella massilia}

ERSHGGPGSDKHPIWLQSCHPDKRLHSQMCESREYRETYAVNGREPVYISPVDAKARGIKDGDIVRVFNDRGQLLAGAVVSDNFPKGIVRIHEGAWYGPVGKDGSTEGGAEVGALCSYGDPNTLTLDIGTSKLAQACSAYTCLVEFEKYQGKVPKVSSFDGPIEVEI

>d1g8ka1 b.52.2.2 (A:683-825) Arsenite oxidase large subunit {Alcaligenes faecalis}

LPATVQQQKDKYRFWLNNGRNNEVWQTAYHDQYNSLMQERYPMAYIEMNPDDCKQLDVTGGDIVEVYNDFGSTFAMVYPVAEIKRGQTFMLFGYVNGIQGDVTTDWTDRDIIPYYKGTWGDIRKVGSMSEFKRTVSFKSRRFG

>d2napa1 b.52.2.2 (A:601-723) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}

AAEEPDAEYPLYLTSMRVIDHWHTATMTGKVPELQKANPIAFVEINEEDAARTGIKHGDSVIVETRRDAMELPARVSDVCRPGLIAVPFFDPKKLVNKLFLDATDPVSREPEYKICAARVRKA

>d1qcsa1 b.52.2.3 (A:0-85) N-terminal domain of NSF-N, NSF-Nn {Hamster (Cricetulus griseus)}

NMAGRSMQAARCPTDELSLSNCAVVSEKDYQSGQHVIVRTSPNHKYIFTLRTHPSVVPGSVAFSLPQRKWAGLSIGQEIEVALYSF

>d1cr5a1 b.52.2.3 (A:26-107) N-terminal domain of NSF-N, NSF-Nn {Baker's yeast (Saccharomyces cerevisiae), sec18p}

TRHLKVSNCPNNSYALANVAAVSPNDFPNNIYIIIDNLFVFTTRHSNDIPPGTIGFNGNQRTWGGWSLNQDVQAKAFDLFKY

>d1cz4a1 b.52.2.3 (A:1-91) N-terminal domain of VAT-N, VAT-Nn {Archaeon Thermoplasma acidophilum}

MESNNGIILRVAEANSTDPGMSRVRLDESSRRLLDAEIGDVVEIEKVRKTVGRVYRARPEDENKGIVRIDSVMRNNCGASIGDKVKVRKVR

>d1e32a1 b.52.2.3 (A:21-106) Membrane fusion atpase p97 N-terminal domain , P97-Nn {Mouse (Mus musculus)}

NRPNRLIVDEAINEDNSVVSLSQPKMDELQLFRGDTVLLKGKKRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVISIQPCP

>d1dfup\_ b.53.1.1 (P:) Ribosomal protein L25 {Escherichia coli}

MFTINAEVRKEQGKGASRRLRAANKFPAIIYGGKEAPLAIELDHDKVMNMQAKAEFYSEVLTIVVDGKEIKVKAQDVQRHPYKPKLQHIDFVRA

>d1feua\_ b.53.1.1 (A:) Ribosomal protein TL5 (general stress protein CTC) {Thermus thermophilus}

MEYRLKAYYREGEKPSALRRAGKLPGLMYNRHLNRKVYVDLVEFDKVFRQASIHHVIVLELPDGQSLPTLVRQVNLDKRRRRPEHVDFFVLSDEPVEMYVPLRFVGTPAGVRAGGVLQEIHRDILVKVSPRNIPEFIEVDVSGLEIGDSLHASDLKLPPGVELAVSPEETIAAVVPPEDVEKLAE

>d1mai\_\_ b.55.1.1 (-) Phospholipase C delta-1 {Rat (Rattus norvegicus)}

GLQDDPDLQALLKGSQLLKVKSSSWRRERFYKLQEDCKTIWQESRKVMRSPESQLFSIEDIQEVRMGHRTEGLEKFARDIPEDRCFSIVFKDQRNTLDLIAPSPADAQHWVQGLRKIIH

>d1dro\_\_ b.55.1.1 (-) beta-spectrin {Fruit fly (Drosophila melanogaster)}

GSGTGAGEGHEGYVTRKHEWDSTTKKASNRSWDKVYMAAKAGRISFYKDQKGYKSNPELTFRGEPSYDLQNAAIEIASDYTKKKHVLRVKLANGALFLLQAHDDTEMSQWVTSLKAQSDSTA

>d1dyna\_ b.55.1.1 (A:) Dynamin {Human (Homo sapiens)}

ILVIRKGWLTINNIGIMKGGSKEYWFVLTAENLSWYKDDEEKEKKYMLSVDNLKLRDVEKGFMSSKHIFALFNTEQRNVYKDYRQLELACETQEEVDSWKASFLRAGVYPERV

>d1btka\_ b.55.1.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}

AAVILESIFLKRSQQKKKTSPLNFKKCLFLLTVHKLSYYEYDFERGRRGSKKGSIDVEKITCVETVVPEKNPPPERQIPRRGEESSEMEQISIIERFPYPFQVVYDEGPLYVFSPTEELRKRWIHQLKNVIRYNSDLVQKYHPCFWIDGQYLCCSQTAKNAMGCQILEN

>d1pls\_\_ b.55.1.1 (-) Pleckstrin, N-terminal domain {Human (Homo sapiens)}

MEPKRIREGYLVKKGSVFNTWKPMWVVLLEDGIEFYKKKSDNSPKGMIPLKGSTLTSPCQDFGKRMFVFKITTTKQQDHFFQAAFLEERDAWVRDINKAIKCIEGLEHHHHHH

>d1dbha2 b.55.1.1 (A:418-550) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

AIKKMNEIQKNIDGWEGKDIGQCCNEFIMEGTLTRVGAKHERHIFLFDGLMICCKSNHGQPRLPGASNAEYRLKEKFFMRKVQINDKDDTNEYKHAFEIILKDENSVIFSAKSAEEKNNWMAALISLQYRSTL

>d1foea2 b.55.1.1 (A:1240-1401) GEF of TIAM1 (T-Lymphoma invasion and metastasis indusing protein 1) {Mouse (Mus musculus)}

EFGAVFDQLIAEQTGEKKEVADLSMGDLLLHTSVIWLNPPASLGKWKKEPELAAFVFKTAVVLVYKDGSKQKKKLVGSHRLSIYEEWDPFRFRHMIPTEALQVRALPSADAEANAVCEIVHVKSESEGRPERVFHLCCSSPESRKDFLKSVHSILRDKHRRQ

>d1bak\_\_ b.55.1.1 (-) G-protein coupled receptor kinase 2 (beta-adrenergic receptor kinase 1) {Human (Homo sapiens)}

GSHMGKDCIMHGYMSKMGNPFLTQWQRRYFYLFPNRLEWRGEGEAPQSLLTMEEIQSVEETQIKERKCLLLKIRGGKQFILQCDSDPELVQWKKELRDAYREAQQLVQRVPKMKNKPRS

>d1faoa\_ b.55.1.1 (A:) Dual adaptor of phosphotyrosine and 3-phosphoinositides DAPP1/PHISH {Human (Homo sapiens)}

PSLGTKEGYLTKQGGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDLTECSAVQFDYSQERVNCFCLVFPFRTFYLCAKTGVEADEWIKILRWKLSQI

>d1fgya\_ b.55.1.1 (A:) Grp1 {Mouse (Mus musculus)}

TFFNPDREGWLLKLGGRVKTWKRRWFILTDNCLYYFEYTTDKEPRGIIPLENLSIREVLDPRKPNCFELYNPSHKGQVIKACKTEADGRVVEGNHVVYRISAPSPEEKEEWMKSIKASISRDPFYDM

>d1fhoa\_ b.55.1.1 (A:) UNC-89 {Nematode (Caenorhabditis elegans)}

MGDTGKLGRIIRHDAFQVWEGDEPPKLRYVFLFRNKIMFTEQDASTSPPSYTHYSSIRLDKYNIRQHTTDEDTIVLQPQEPGLPSFRIKPKDFETSEYVRKAWLRDIAEEQEKYAAERD

>d1aqca\_ b.55.1.2 (A:) X11 {Human (Homo sapiens)}

MEDLIDGIIFAANYLGSTQLLSDKTPSKNVRMMQAQEAVSRIKMAQKLAKSRKKAPEGESQPMTEVDLFILTQRIKVLNADTQETMMDHPLRTISYIADIGNIVVLMARRRIPRSNSQENVEASHPSQDGKRQYKMICHVFESEDAQLIAQSIGQAFSVAYQEFLR

>d1qqga1 b.55.1.2 (A:12-114) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

DVRKVGYLRKPKSMHKRFFVLRAASEAGGPARLEYYENEKKWRHKSSAPKRSIPLESCFNINKRADSKNKHLVALYTRDEHFAIAADSEAEQDSWYQALLQLH

>d1qqga2 b.55.1.2 (A:159-262) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

AFKEVWQVILKPKGLGQTKNLIGIYRLCLTSKTISFVKLNSEAAAVVLQLMNIRRCGHSENFFFIEVGRSAVTGPGEFWMQVDDSVVAQNMHETILEAMRAMSD

>d1shca\_ b.55.1.2 (A:) Shc adaptor protein {Human (Homo sapiens)}

GSHMGQLGGEEWTRHGSFVNKPTRGWLHPNDKVMGPGVSYLVRYMGCVEVLQSMRALDFNTRTQVTREAISLVCEAVPGAKGATRRRKPCSRPLSSILGRSNLKFAGMPITLTVSTSSLNLMAADCKQIIANHHMQSISFASGGDPDTAEYVAYVAKDPVNQRACHILECPEGLAQDVISTIGQAFELRFKQYLR

>d1ddma\_ b.55.1.2 (A:) Numb {Fruit fly (Drosophila melanogaster)}

HQWQADEEAVRSATCSFSVKYLGCVEVFESRGMQVCEEALKVLRQSRRRPVRGLLHVSGDGLRVVDDETKGLIVDQTIEKVSFCAPDRNHERGFSYICRDGTTRRWMCHGFLACKDSGERLSHAVGCAFAVCLER

>d1egxa\_ b.55.1.4 (A:) Vasodilator-stimulated phosphoprotein (VASP) {Human (Homo sapiens)}

MSETVICSSRATVMLYDDGNKRWLPAGTGPQAFSRVQIYHNPTANSFRVVGRKMQPDQQVVINCAIVRGVKYNQATPNFHQWRDARQVWGLNFGSKEDAAQFAAGMASALEALEG

>d1ddwa\_ b.55.1.4 (A:) Homer {Rat (Rattus norvegicus)}

MGEQPIFSTRAHVFQIDPNTKKNWVPTSKHAVTVSYFYDSTRNVYRIISLDGSKAIINSTITPNMTFTKTSQKFGQWADSRANTVYGLGFSSEHHLSKFAEKFQEFKEAAR

>d1e5wa2 b.55.1.5 (A:199-346) Moesin {Human (Homo sapiens)}

EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVFYAPRLRINKRILALCMGNHELYMRRRKPDTIEVQQMKAQAREEKHQKQMERAMLENEKKKREMAEKEKEKIEREKEE

>d1gg3a2 b.55.1.5 (A:188-279) Erythroid membrane protein 4.1R {Human (Homo sapiens)}

GVDLHKAKDLEGVDIILGVCSSGLLVYKDKLRINRFPWPKVLKISYKRSSFFIKIRPGEQEQYESTIGFKLPSYRAAKKLWKVCVEHHTFFR

>d1ytfc1 b.56.1.1 (C:) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

ENLMLCLYDKVTRTKARWKCSLKDGVVTINRNDYTFQKAQVEAEWV

>d1ytfd2 b.56.1.1 (D:55-119) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

NTQSKLTVKGNLDTYGFCDDVWTFIVKNCQVTVEDSHRDASQNGSGDSQSVISVDKLRIVACNSK

>d1iega\_ b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}

QAVAPVYVGGFLARYDQSPDEAELLLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVAAMQSVRDGLFCLGCVTSPRFLEIVRRASEKSELVSRGPVSPLQPDKVVEFLSGSYAGLSLASRRCDDVEQATSLSGSETTPFKAVALCSVGRRRGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQRCGSTAVDASGDPFRSDSYGLLGNSVDALYIRERLPKLRYDKQLVGVTERESYVKA

>d1at3a\_ b.57.1.1 (A:) HSV-2 protease {Herpes simplex virus type 2}

RAVPIYVAGFLALYDSGDPGELALDPDTVRAALPPENPLPINVDHRARCEVGRVLAVVNDPRGPFFVGLIACVQLERVLETAASAAIFERRGPALSREERLLYLITNYLPSVSLSTKRRGDEVPPDRTLFAHVALCAIGRRLGTIVTYDTSLDAAIAPFRHLDPATREGVRREAAEAELALAGRTWAPGVEALTHTLLSTAVNNMMLRDRWSLVAERRRQAGIAGHTYLQA

>d1fl1a\_ b.57.1.1 (A:) KSHV protease {Kaposi's sarcoma-associated herpes virus}

AQGLYVGGFVDVVSCPKLEQELYLDPDQVTDYLPVTEPLPITIEHLPETEVGWTLGLFQVSHGIFCTGAITSPAFLELASRLADTSHVARAPVKNLPKEPLLEILHTWLPGLSLSSIHPRELSQTPSGPVFQHVSLCALGRRRGTVAVYGHDAEWVVSRFSSVSKSERAHILQHVSSCRLEDLSTPNFVSPLETLMAKAIDAGFIRDRLDLLKTDRGVASILSPVYLKA

>d1a49a1 b.58.1.1 (A:116-217) Pyruvate kinase (PK) {Rabbit (Oryctolagus cuniculus)}

PEIRTGLIKGSGTAEVELKKGATLKITLDNAYMEKCDENILWLDYKNICKVVDVGSKVYVDDGLISLQVKQKGPDFLVTEVENGGFLGSKKGVNLPGAAVDL

>d1e0ta1 b.58.1.1 (A:70-167) Pyruvate kinase (PK) {Escherichia coli}

PEIRTMKLEGGNDVSLKAGQTFTFTTDKSVIGNSEMVAVTYEGFTTDLSVGNTVLVDDGLIGMEVTAIEGNKVICKVLNNGDLGENKGVNLPGVSIAL

>d1i2da1 b.58.1.2 (A:2-170) ATP sulfurylase N-terminal domain {Fungus (Penicillium chrysogenum)}

ANAPHGGVLKDLLARDAPRQAELAAEAESLPAVTLTERQLCDLELIMNGGFSPLEGFMNQADYDRVCEDNRLADGNVFSMPITLDASQEVIDEKKLQAGSRITLRDFRDDRNLAILTIDDIYRPDKTKEAKLVFGGDPEHPAIVYLNNTVKEFYIGGKIEAVNKLNHYD

>d1jhda1 b.58.1.2 (A:1-173) ATP sulfurylase N-terminal domain {unnamed symbiont of Riftia pachyptila}

MIKPVGSDELKPLFVYDPEEHHKLSHEAESLPSVVISSQAAGNAVMMGAGYFSPLQGFMNVADAMGAAEKMTLSDGSFFPVPVLCLLENTDAIGDAKRIALRDPNVEGNPVLAVMDIEAIEEVSDEQMAVMTDKVYRTTDMDHIGVKTFNSQGRVAVSGPIQVLNFSYFQADF

>d1hbq\_\_ b.60.1.1 (-) Retinol binding protein {Cow (Bos taurus)}

ERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGQMSATAKGRVRLLNNWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDHWIIDTDYETFAVQYSCRLLNLDGTCADSYSFVFARDPSGFSPEVQKIVRQRQEELCLARQYRLIPHNGYCNGK

>d1hn2a\_ b.60.1.1 (A:) Odorant-binding protein {Cow (Bos taurus)}

AQEEEAEQNLSELSGPWRTVYIGSTNPEKIQENGPFRTYFRELVFDDEKGTVDFYFSVKRDGKWKNVHVKATKQDDGTYVADYEGQNVFKIVSLSRTHLVAHNINVDKHGQTTELTELFVKLNVEDEDLEKFWKLTEDKGIDKKNVVNFLENENHPHPE

>d1bj7\_\_ b.60.1.1 (-) Lipocalin allergen {Cow (Bos taurus), bos d 2}

IDPSKIPGEWRIIYAAADNKDKIVEGGPLRNYYRRIECINDCESLSITFYLKDQGTCLLLTEVAKRQEGYVYVLEFYGTNTLEVIHVSENMLVTYVENYDGERITKMTEGLAKGTSFTPEELEKYQQLNSERGVPNENIENLIKTDNCPP

>d1ew3a\_ b.60.1.1 (A:) Lipocalin allergen {Horse (Equus caballus), equ c 1}

VAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFVDVIRALDNSSLYAEYQTKVNGECTEFPMVFDKTEEDGVYSLNYDGYNVFRISEFENDEHIILYLVNFDKDRPFQLFEFYAREPDVSPEIKEEFVKIVQKRGIVKENIIDLTKIDRCFQLRG

>d1e5pa\_ b.60.1.1 (A:) Aphrodisin, a sex pheromone {Golden hamster (Mesocricetus auratus)}

FAELQGKWYTIVIAADNLEKIEEGGPLRFYFRHIDCYKNCSEMEITFYVITNNQCSKTTVIGYLKGNGTYETQFEGNNIFQPLYITSDKIFFTNKNMDRAGQETNMIVVAGKGNALTPEENEILVQFAHEKKIPVENILNILATDTCPE

>d1exsa\_ b.60.1.1 (A:) beta-Lactoglobulin {Pig (Sus scrofa)}

VEVTPIMTELDTQKVAGTWHTVAMAVSDVSLLDAKSSPLKAYVEGLKPTPEGDLEILLQKRENDKCAQEVLLAKKTDIPAVFKINALDENQLFLLDTDYDSHLLLCMENSASPEHSLVCQSLARTLEVDDQIREKFEDALKTLSVPMRILPAQLEEQCRV

>d1epba\_ b.60.1.1 (A:) Retinoic acid-binding protein {Rat (Rattus norvegicus), albino}

VKDFDISKFLGFWYEIAFASKMGTPGLAHKEEKMGAMVVELKENLLALTTTYYSEDHCVLEKVTATEGDGPAKFQVTRLSGKKEVVVEATDYLTYAIIDITSLVAGAVHRTMKLYSRSLDDNGEALYNFRKITSDHGFSETDLYILKHDLTCVKVLQSAA

>d1qqsa\_ b.60.1.1 (A:) Neutrophil gelatinase-associated lipocalin (NGAL) {Human (Homo sapiens)}

TSDLIPAPPLSKVPLQQNFQDNQFQGKWYVVGLAGNAILREDKDPQKMYATIYEEKEDASYNVTSVLFRKKKCDYAIRTFVPGCQPGEFTLGNIKSYPGLTSYLVRVVSTNYNQHAMVFFKKVSQNREYFKITLYGRTKELTSELKNNFIRFSKSLGLPENHIVFPVPIDQCID

>d1bbpa\_ b.60.1.1 (A:) Bilin-binding protein {Cabbage butterfly (Pieris brassicae)}

NVYHDGACPEVKPVDNFDWSNYHGKWWEVAKYPNSVEKYGKCGWAEYTPEGKSVKVSNYHVIHGKEYFIEGTAYPVGDSKIGKIYHKLTYGGVTKENVFNVLSTDNKNYIIGYYCKYDEDKKGHQDFVWVLSRSKVLTGEAKTAVENYLIGSPVVDSQKLVYSDFSEAACKVN

>d1i4ua\_ b.60.1.1 (A:) Alpha-crustacyanin {European lobster (Homarus gammarus)}

DKIPDFVVPGKCASVDRNKLWAEQTPNRNSYAGVWYQFALTNNPYQLIEKCVRNEYSFDGKQFVIESTGIAYDGNLLKRNGKLYPNPFGEPHLSIDYENSFAAPLVILETDYSNYACLYSCIDYNFGYHSDFSFIFSRSANLADQYVKKCEAAFKNINVDTTRFVKTVQGSSCPYDTQKTL

>d1qfta\_ b.60.1.1 (A:) Histamine binding protein {Brown ear tick (Rhipicephalus appendiculatus)}

NQPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLEIAAA

>d1np1a\_ b.60.1.1 (A:) Nitrophorin 1 {Rhodnius prolixus}

KCTKNALAQTGFNKDKYFNGDVWYVTDYLDLEPDDVPKRYCAALAAGTASGKLKEALYHYDPKTQDTFYDVSELQEESPGKYTANFKKVEKNGNVKVDVTSGNYYTFTVMYADDSSALIHTCLHKGNKDLGDLYAVLNRNKDTNAGDKVKGAVTAASLKFSDFISTKDNKCEYDNVSLKSLLTK

>d1ifc\_\_ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}

AFDGTWKVDRNENYEKFMEKMGINVVKRKLGAHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSLADGTELTGTWTMEGNKLVGKFKRVDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE

>d1b56\_\_ b.60.1.2 (-) Epidermal fatty acid binding protein {Human (Homo sapiens)}

TVQQLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTTQFSCTLGEKFEETTADGRKTQTVCNFTDGALVQHQEWDGKESTITRKLKDGKLVVECVMNNVTCTRIYEKVE

>d1mdc\_\_ b.60.1.2 (-) Fatty acid-binding protein {Tobacco hornworm (Manduca sexta)}

SYLGKVYSLVKQENFDGFLKSAGLSDDKIQALVSDKPTQKMEANGDSYSNTSTGGGGAKTVSFKSGVEFDDVIGAGDSVKSMYTVDGNVVTHVVKGDAGVATFKKEYNGDDLVVTITSSNWDGVARRYYKA

>d1ftpa\_ b.60.1.2 (A:) Fatty acid-binding protein {Desert locust (Schistocerca gregaria)}

VKEFAGIKYKLDSQTNFEEYMKAIGVGAIERKAGLALSPVIELEILDGDKFKLTSKTAIKNTEFTFKLGEEFDEETLDGRKVKSTITQDGPNKLVHEQKGDHPTIIIREFSKEQCVITIKLGDLVATRIYKAQ

>d1cbs\_\_ b.60.1.2 (-) Cellular retinoic-acid-binding protein (CRABP) {Human (Homo sapiens), CRABP-II}

PNFSGNWKIIRSENFEELLKVLGVNVMLRKIAVAAASKPAVEIKQEGDTFYIKTSTTVRTTEINFKVGEEFEEQTVDGRPCKSLVKWESENKMVCEQKLLKGEGPKTSWTRELTNDGELILTMTADDVVCTRVYVRE

>d1ggla\_ b.60.1.2 (A:) Cellular retinol-binding protein III {Human (Homo sapiens)}

PPNLTGYYRFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQKGEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVH

>d1lfo\_\_ b.60.1.2 (-) Liver fatty acid binding protein {Rat (Rattus norvegicus)}

MNFSGKYQVQSQENFEPFMKAMGLPEDLIQKGKDIKGVSEIVHEGKKVKLTITYGSKVIHNEFTLGEECELETMTGEKVKAVVKMEGDNKMVTTFKGIKSVTEFNGDTITNTMTLGDIVYKRVSKRI

>d1eal\_\_ b.60.1.2 (-) Ileal lipid binding protein {Pig (Sus scrofa)}

AFTGKYEIESEKNYDEFMKRLALPSDAIDKARNLKIISEVKQDGQNFTWSQQYPGGHSITNTFTIGKECDIETIGGKKFKATVQMEGGKVVVNSPNYHHTAEIVDGKLVEVSTVGGVSYERVSKKLA

>d1swga\_ b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}

SRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASGGGSAEAGITGTWYNQLGSTFIVTAGADGALTGTYESA

>d1ij8a\_ b.61.1.1 (A:) Avidin {Chicken (Gallus gallus)}

KCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYTTAVTATSNEIKESPLHGTENTINKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGINIFTRL

>d1smpi\_ b.61.2.1 (I:) Metalloprotease inhibitor {Erwinia chrysanthemi}

SSLRLPSAAELSGQWVLSGAEQHCDIRLNTDVLDGTTWKLAGDTACLQKLLPEAPVGWRPTPDGLTLTQADGSAVAFFSRNRDRYEHKLVDGSVRTLKKK

>d1jiwi\_ b.61.2.1 (I:) Metalloprotease inhibitor {Pseudomonas aeruginosa, aprin}

SSLILLSASDLAGQWTLQQDEAPAICHLELRDSEVAEASGYDLGGDTACLTRWLPSEPRAWRPTPAGIALLERGGLTLMLLGRQGEGDYRVQKGDGGQLVLRRAT

>d1ei5a1 b.61.3.1 (A:336-417) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum anthropi}

EVSRVEADSAWFGSWLDDETGLVLSLEDAGHGRMKARFGTSPEMMDVVSANEARSAVTTIRRDGETIELVRASENLRLSMKR

>d1ei5a2 b.61.3.1 (A:418-520) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum anthropi}

VKGEAKHDIIGRYHSDELDADLLLVSEGGAIYGAFEGFLGKSDMYPLYSVGSDVWLLPVQRSMDAPSPGEWKLVFRRDDKGEITGLSVGCWLARGVEYRRVQP

>d1jjua5 b.61.4.1 (A:166-273) Quinohemoprotein amine dehydrogenase A chain, domain 3 {Paracoccus denitrificans}

PDAYADDASGAYVLAGRQPGRGDYTGRLVLKKAGEDYEVTMTLDFADGSRSFSGTGRILGAGEWRATLSDGTVTIRQIFALQDGRFSGRWHDADSDVIGGRLAAVKAD

>d1jmxa5 b.61.4.1 (A:163-281) Quinohemoprotein amine dehydrogenase A chain, domain 3 {Pseudomonas putida}

ESAAWAEWQKARPKADALPGQWAFSGHMLAKGDVRGVMSVTPDQGDTFKVEVKGAYADGTPFNGSGSAILYNGYEWRGNVKVGDANLRQVFAALDGEMKGRMFEAEHDERGLDFTAVKE

>d1ihga2 b.62.1.1 (A:2-196) Cyclophilin 40 isomerase domain {Cow (Bos taurus)}

SHPSPQAKPSNPSNPRVFFDVDIGGERVGRIVLELFADIVPKTAENFRALCTGEKGIGPTTGKPLHFKGCPFHRIIKKFMIQGGDFSNQNGTGGESIYGEKFEDENFHYKHDKEGLLSMANAGSNTNGSQFFITTVPTPHLDGKHVVFGQVIKGMGVAKILENVEVKGEKPAKLCVIAECGELKEGDDWGIFPKD

>d1clh\_\_ b.62.1.1 (-) Bacterial cyclophilin {Escherichia coli}

AKGDPHVLLTTSAGNIELELDKQKAPVSVQNFVDYVNSGFYNNTTFHRVIPGFMIQGGGFTEQMQQKKPNPPIKNEADNGLRNTRGTIAMARTADKDSATSQFFINVADNAFLDHGQRDFGYAVFGKVVKGMDVADKISQVPTHDVGPYQNVPSKPVVILSAKVLP

>d1c39a\_ b.64.1.1 (A:) Cation-dependent mannose 6-phosphate receptor, extracytoplasmic domain {Cow (Bos taurus)}

EKTCDLVGEKGKESEKELALLKRLTPLFQKSFESTVGQSPDMYSYVFRVCREAGQHSSGAGLVQIQKSNGKETVVGRFNETQIFQGSNWIMLIYKGGDEYDNHCGREQRRAVVMISCNRHTLADNFNPVSEERGKVQDCFYLFEMDSSLACS

>d1e6fa\_ b.64.1.1 (A:) Cation-independent mannose-6-phosphate receptor (MIR-receptor) {Human (Homo sapiens)}

DDCQVTNPSTGHLFDLSSLSGRAGFTAAYSEKGLVYMSICGENENCPPGVGACFGQTRISVGKANKRLRYVDQVLQLVYKDGSPCPSKSGLSYKSVISFVCRPEAGPTNRPMLISLDKQTCTLFFSWHTPLACE

>d1f3ua\_ b.65.1.1 (A:) TFIIF beta subunit, Rap30 {Human (Homo sapiens)}

AERGELDLTGAKQNTGVWLVKVPKYLSQQWAKASGRGEVGKLRIAKTQGRTEVSFTLNEDLANIHDIGGKPASVSAPREHPFVLQSVGGQTLTVFTESSSDKLSLEGIVVQRAECRPA

>d1f3ud\_ b.65.1.1 (D:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}

SSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRN

>d1hxn\_\_ b.66.1.1 (-) Hemopexin {Rabbit (Oryctolagus cuniculus)}

ESTRCDPDLVLSAMVSDNHGATYVFSGSHYWRLDTNRDGWHSWPIAHQWPQGPSTVDAAFSWEDKLYLIQDTKVYVFLTKGGYTLVNGYPKRLEKELGSPPVISLEAVDAAFVCPGSSRLHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKPLGPNSCSTSGPNLYLIHGPNLYCYRHVDKLNAAKNLPQPQRVSRLLGCTH

>d1qhua1 b.66.1.1 (A:24-215) Hemopexin {Rabbit (Oryctolagus cuniculus)}

IEQCSDGWSFDATTLDDNGTMLFFKDEFVWKSHRGIRELISERWKNFIGPVDAAFRHGHTSVYLIKGDKVWVYTSEKNEKVYPKSLQDEFPGIPFPLDAAVECHRGECQDEGILFFQGNRKWFWDLTTGTKKERSWPAVGNCTSALRWLGRYYCFQGNQFLRFNPVSGEVPPGYPLDVRDYFLSCPGRGHRS

>d1gen\_\_ b.66.1.1 (-) Gelatinase A (MMP-2), C-terminal domain {Human (Homo sapiens)}

LGPVTPEICKQDIVFDGIAQIRGEIFFFKDRFIWRTVTPRDKPMGPLLVATFWPELPEKIDAVYEAPQEEKAVFFAGNEYWIYSASTLERGYPKPLTSLGLPPDVQRVDAAFNWSKNKKTYIFAGDKFWRYNEVKKKMDPGFPKLIADAWNAIPDNLDAVVDLQGGGHSYFFKGAYYLKLENQSLKSVKFGSIKSDWLGC

>d1fbl\_1 b.66.1.1 (272-466) Collagenase, C-terminal domain {Pig (Sus scrofa)}

PQTPQVCDSKLTFDAITTLRGELMFFKDRFYMRTNSFYPEVELNFISVFWPQVPNGLQAAYEIADRDEVRFFKGNKYWAVRGQDVLYGYPKDIHRSFGFPSTVKNIDAAVFEEDTGKTYFFVAHECWRYDEYKQSMDTGYPKMIAEEFPGIGNKVDAVFQKDGFLYFFHGTRQYQFDFKTKRILTLQKANSWFNC

>d3sil\_\_ b.68.1.1 (-) Salmonella sialidase {Salmonella typhimurium, strain lt2}

EKSVVFKAEGEHFTDQKGNTIVGSGSGGTTKYFRIPAMCTTSKGTIVVFADARHNTASDQSFIDTAAARSTDGGKTWNKKIAIYNDRVNSKLSRVMDPTCIVANIQGRETILVMVGKWNNNDKTWGAYRDKAPDTDWDLVLYKSTDDGVTFSKVETNIHDIVTKNGTISAMLGGVGSGLQLNDGKLVFPVQMVRTKNITTVLNTSFIYSTDGITWSLPSGYCEGFGSENNIIEFNASLVNNIRNSGLRRSFETKDFGKTWTEFPPMDKKVDNRNHGVQGSTITIPSGNKLVAAHSSAQNKNNDYTRSDISLYAHNLYSGEVKLIDDFYPKVGNASGAGYSCLSYRKNVDKETLYVVYEANGSIEFQDLSRHLPVIKSYN

>d1f8ea\_ b.68.1.1 (A:) Influenza neuraminidase {Influenza A virus, different strains}

RDFNNLTKGLCTINSWHIYGKDNAVRIGEDSDVLVTREPYVSCDPDECRFYALSQGTTIRGKHSNGTIHDRSQYRALISWPLSSPPTVYNSRVECIGWSSTSCHDGKTRMSICISGPNNNASAVIWYNRRPVTEINTWARNILRTQESECVCHNGVCPVVFTDGSATGPAETRIYYFKEGKILKWEPLAGTAKHIEECSCYGERAEITCTCRDNWQGSNRPVIRIDPVAMTHTSQYICSPVLTDNPRPNDPTVGKCNDPYPGNNNNGVKGFSYLDGVNTWLGRTISIASRSGYEMLKVPNALTDDKSKPTQGQTIVLNTDWSGYSGSFMDYWAEGECYRACFYVELIRGRPKEDKVWWTSNSIVSMCSSTEFLGQWDWPDGAKIEYFL

>d1inv\_\_ b.68.1.1 (-) Influenza neuraminidase {Influenza B virus, different strains}

EPEWTYPRLSCQGSTFQKALLISPHRFGEIKGNSAPLIIREPFVACGPKECRHFALTHYAAQPGGYYNGTRKDRNKLRHLVSVKLGKIPTVENSIFHMAAWSGSACHDGREWTYIGVDGPDNDALVKIKYGEAYTDTYHSYAHNILRTQESACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEILPTGRVEHTEECTCGFASNKTIECACRDNSYTAKRPFVKLNVETDTAEIRLMCTKTYLDTPRPDDGSIAGPCESNGDKWLGGIKGGFVHQRMASKIGRWYSRTMSKTNRMGMELYVRYDGDPWTDSDALTLSGVMVSIEEPGWYSFGFEIKDKKCDVPCIGIEMVHDGGKDTWHSAATAIYCLMGSGQLLWDTVTGVDMAL

>d1e8ua\_ b.68.1.1 (A:) Paramyxovirus hemagglutinin-neuraminidase head domain {Newcastle disease virus}

GAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDMSATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSVSATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYPGVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKPGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSYFSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYRNHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKTYCLSIAEISNTLFGEFRIVPLLVEILKND

>d1eur\_\_ b.68.1.1 (-) Micromonospora sialidase, N-terminal domain {Micromonospora viridifaciens}

GEPLYTEQDLAVNGREGFPNYRIPALTVTPDGDLLASYDGRPTGIDAPGPNSILQRRSTDGGRTWGEQQVVSAGQTTAPIKGFSDPSYLVDRETGTIFNFHVYSQRQGFAGSRPGTDPADPNVLHANVATSTDGGLTWSHRTITADITPDPGWRSRFAASGEGIQLRYGPHAGRLIQQYTIINAAGAFQAVSVYSDDHGRTWRAGEAVGVGMDENKTVELSDGRVLLNSRDSARSGYRKVAVSTDGGHSYGPVTIDRDLPDPTNNASIIRAFPDAPAGSARAKVLLFSNAASQTSRSQGTIRMSCDDGQTWPVSKVFQPGSMSYSTLTALPDGTYGLLYEPGTGIRYANFNLAWLGGICAP

>d2sli\_2 b.68.1.1 (277-759) Leech intramolecular trans-sialidase, C-terminal domain {North american leech (Macrobdella decora)}

GENIFYAGDVTESNYFRIPSLLTLSTGTVISAADARYGGTHDSKSKINIAFAKSTDGGNTWSEPTLPLKFDDYIAKNIDWPRDSVGKNVQIQGSASYIDPVLLEDKLTKRIFLFADLMPAGIGSSNASVGSGFKEVNGKKYLKLRWHKDAGRAYDYTIREKGVIYNDATNQPTEFRVDGEYNLYQHDTNLTCKQYDYNFSGNNLIESKTDVDVNMNIFYKNSVFKAFPTNYLAMRYSDDEGASWSDLDIVSSFKPEVSKFLVVGPGIGKQISTGENAGRLLVPLYSKSSAELGFMYSDDHGDNWTYVEADNLTGGATAEAQIVEMPDGSLKTYLRTGSNCIAEVTSIDGGETWSDRVPLQGISTTSYGTQLSVINYSQPIDGKPAIILSSPNATNGRKNGKIWIGLVNDTGNTGIDKYSVEWKYSYAVDTPQMGYSYSCLAELPDGQVGLLYEKYDSWSRNELHLKDILKFEKYSISELTGQA

>d1kit\_3 b.68.1.1 (217-346,544-781) Vibrio cholerae sialidase {Vibrio cholerae}

VIFRGPDRIPSIVASSVTPGVVTAFAEKRVGGGDPGALSNTNDIITRTSRDGGITWDTELNLTEQINVSDEFDFSDPRPIYDPSSNTVLVSYARWPTDAAQNGDRIKPWMPNGIFYSVYDVASGNWQAPIXVNPGPGHGITLTRQQNISGSQNGRLIYPAIVLDRFFLNVMSIYSDDGGSNWQTGSTLPIPFRWKSSSILETLEPSEADMVELQNGDLLLTARLDFNQIVNGVNYSPRQQFLSKDGGITWSLLEANNANVFSNISTGTVDASITRFEQSDGSHFLLFTNPQGNPAGTNGRQNLGLWFSFDEGVTWKGPIQLVNGASAYSDIYQLDSENAIVIVETDNSNMRILRMPITLLKQKLTLSQN

>d1jjub\_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Paracoccus denitrificans}

RDYILAPARPDKLVVIDTEKMAVDKVITIADAGPTPMVPMVAPGGRIAYATVNKSESLVKIDLVTGETLGRIDLSTPEERVKSLFGAALSPDGKTLAIYESPVRLELTHFEVQPTRVALYDAETLSRRKAFEAPRQITMLAWARDGSKLYGLGRDLHVMDPEAGTLVEDKPIQSWEAETYAQPDVLAVWNQHESSGVMATPFYTARKDIDPADPTAYRTGLLTMDLETGEMAMREVRIMDVFYFSTAVNPAKTRAFGAYNVLESFDLEKNASIKRVPLPHSYYSVNVSTDGSTVWLGGALGDLAAYDAETLEKKGQVDLPGNASMSLASVRLFTRDE

>d1jmxb\_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Pseudomonas putida}

GPALKAGHEYMIVTNYPNNLHVVDVASDTVYKSCVMPDKFGPGTAMMAPDNRTAYVLNNHYGDIYGIDLDTCKNTFHANLSSVPGEVGRSMYSFAISPDGKEVYATVNPTQRLNDHYVVKPPRLEVFSTADGLEAKPVRTFPMPRQVYLMRAADDGSLYVAGPDIYKMDVKTGKYTVALPLRNWNRKGYSAPDVLYFWPHQSPRHEFSMLYTIARFKDDKQDPATADLLYGYLSVDLKTGKTHTQEFADLTELYFTGLRSPKDPNQIYGVLNRLAKYDLKQRKLIKAANLDHTYYCVAFDKKGDKLYLGGTFNDLAVFNPDTLEKVKNIKLPGGDMSTTTPQVFIR

>d1tbga\_ b.69.4.1 (A:) beta1-subunit of the signal-transducing G protein heterotrimer {Cow (Bos taurus)}

MSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVGRIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTREGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIETGQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGMCRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQELMTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRAGVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN

>d1erja\_ b.69.4.1 (A:) Tup1, C-therminal domain {Baker's yeast (Saccharomyces cerevisiae)}

HYLVPYNQRANHSKPIPPFLLDLDSQSVPDALKKQTNDYYILYNPALPREIDVELHKSLDHTSVVCCVKFSNDGEYLATGCNKTTQVYRVSDGSLVARLSDDSAANKDPENLNTSSSPSSDLYIRSVCFSPDGKFLATGAEDRLIRIWDIENRKIVMILQGHEQDIYSLDYFPSGDKLVSGSGDRTVRIWDLRTGQCSLTLSIEDGVTTVAVSPGDGKYIAAGSLDRAVRVWDSETGFLVERLDSENESGTGHKDSVYSVVFTRDGQSVVSGSLDRSVKLWNLQNANNKSDSKTPNSGTCEVTYIGHKDFVLSVATTQNDEYILSGSKDRGVLFWDKKSGNPLLMLQGHRNSVISVAVANGSSLGPEYNVFATGSGDCKARIWKYKKI

>d1k8kc\_ b.69.4.1 (C:) Arp2/3 complex 41 kDa subunit ARPC1 {Cow (Bos taurus)}

AYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGNKWVQVHELKEHNGQVTGVDWAPDSNRIVTCGTDRNAYVWTLKGRTWKPTLVILRINRAARCVRWAPNEKKFAVGSGSRVISICYFEQENDWWVCKHIKKPIRSTVLSLDWHPNSVLLAAGSCDFKCRIFSAYIKEVEERPAPTPWGSKMPFGELMFESSSSCGWVHGVCFSANGSRVAWVSHDSTVCLADADKKMAVATLASETLPLLAVTFITESSLVAAGHDCFPVLFTYDSAAGKLSFGGRLDVPKQSSQRGLTARERFQNLDKKASSEGSAAAGAGLDSLHKNSVSQISVLSGGKAKCSQFCTTGMDGGMSIWDVRSLESALKDLKIV

>d1h4ia\_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylobacterium extorquens}

NDKLVELSKSDDNWVMPGKNYDSNNFSDLKQINKGNVKQLRPAWTFSTGLLNGHEGAPLVVDGKMYIHTSFPNNTFALGLDDPGTILWQDKPKQNPAARAVACCDLVNRGLAYWPGDGKTPALILKTQLDGNVAALNAETGETVWKVENSDIKVGSTLTIAPYVVKDKVIIGSSGAELGVRGYLTAYDVKTGEQVWRAYATGPDKDLLLASDFNIKNPHYGQKGLGTGTWEGDAWKIGGGTNWGWYAYDPGTNLIYFGTGNPAPWNETMRPGDNKWTMTIFGRDADTGEAKFGYQKTPHDEWDYAGVNVMMLSEQKDKDGKARKLLTHPDRNGIVYTLDRTDGALVSANKLDDTVNVFKSVDLKTGQPVRDPEYGTRMDHLAKDICPSAMGYHNQGHDSYDPKRELFFMGINHICMDWEPFMLPYRAGQFFVGATLNMYPGPKGDRQNYEGLGQIKAYNAITGDYKWEKMERFAVWGGTMATAGDLVFYGTLDGYLKARDSDTGDLLWKFKIPSGAIGYPMTYTHKGTQYVAIYYGVGGWPGVGLVFDLADPTAGLGAVGAFKKLANYTQMGGGVVVFSLDGKGPYDDPNVGEWK

>d1flga\_ b.70.1.1 (A:) Ethanol dehydrogenase {Pseudomonas aeruginosa}

KDVTWEDIANDDKTTGDVLQYGMGTHAQRWSPLKQVNADNVFKLTPAWSYSFGDEKQRGQESQAIVSDGVIYVTASYSRLFALDAKTGKRLWTYNHRLPDDIRPCCDVVNRGAAIYGDKVFFGTLDASVVALNKNTGKVVWKKKFADHGAGYTMTGAPTIVKDGKTGKVLLIHGSSGDEFGVVGRLFARDPDTGEEIWMRPFVEGHMGRLNGKDSTVTGDVKAPSWPDDRNSPTGKVESWSHGGGAPWQSASFDAETNTIIVGAGNPGPWNTWARTAKGGNPHDYDSLYTSGQVGVDPSSGEVKWFYQHTPNDAWDFSGNNELVLFDYKAKDGKIVKATAHADRNGFFYVVDRSNGKLQNAFPFVDNITWASHIDLKTGRPVEREGQRPPLPEPGQKHGKAVEVSPPFLGGKNWNPMAYSQDTGLFYVPANHWKEDYWTEEVSYTKGSAYLGMGFRIKRMYDDHVGSLRAMDPVSGKVVWEHKEHLPLWAGVLATAGNLVFTGTGDGYFKAFDAKSGKELWKFQTGSGIVSPPITWEQDGEQYLGVTVGYGGAVPLWGGDMADLTRPVAQGGSFWVFKLPSW

>d1kb0a2 b.70.1.1 (A:1-573) Quinoprotein alcohol dehydrogenase, N-terminal domain {Comamonas testosteroni}

TGPAAQAAAAVQRVDGDFIRANAARTPDWPTIGVDYAETRYSRLDQINAANVKDLGLAWSYNLESTRGVEATPVVVDGIMYVSASWSVVHAIDTRTGNRIWTYDPQIDRSTGFKGCCDVVNRGVALWKGKVYVGAWDGRLIALDAATGKEVWHQNTFEGQKGSLTITGAPRVFKGKVIIGNGGAEYGVRGYITAYDAETGERKWRWFSVPGDPSKPFEDESMKRAARTWDPSGKWWEAGGGGTMWDSMTFDAELNTMYVGTGNGSPWSHKVRSPKGGDNLYLASIVALDPDTGKYKWHYQETPGDNWDYTSTQPMILADIKIAGKPRKVILHAPKNGFFFVLDRTNGKFISAKNFVPVNWASGYDKHGKPIGIAAARDGSKPQDAVPGPYGAHNWHPMSFNPQTGLVYLPAQNVPVNLMDDKKWEFNQAGPGKPQSGTGWNTAKFFNAEPPKSKPFGRLLAWDPVAQKAAWSVEHVSPWNGGTLTTAGNVVFQGTADGRLVAYHAATGEKLWEAPTGTGVVAAPSTYMVDGRQYVSVAVGWGGVYGLAARATERQGPGTVYTFVVGGKARMPE

>d1e43a1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus licheniformis}

YAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR

>d1g94a1 b.71.1.1 (A:355-448) Bacterial alpha-Amylase {Pseudoalteromonas haloplanctis (Alteromonas haloplanctis)}

NWAVTNWWDNTNNQISFGRGSSGHMAINKEDSTLTATVQTDMASGQYCNVLKGELSADAKSCSGEVITVNSDGTINLNIGAWDAMAIHKNAKLN

>d1bag\_1 b.71.1.1 (348-425) Bacterial alpha-Amylase {Bacillus subtilis}

QPEELSNPNGNNQIFMNQRGSHGVVLANAGSSSVSINTATKLPDGRYDNKAGAGSFQVNDGKLTGTINARSVAVLYPD

>d1gjwa1 b.71.1.1 (A:573-636) Maltosyltransferase {Thermotoga maritima}

GKFENLTTKDLVMYSYEKNGQKIVIAANVGKEPKEITGGRVWNGKWSDEEKVVLKPLEFALVVQ

>d1pama3 b.71.1.1 (A:407-496) Cyclodextrin glycosyltransferase {Bacillus sp., strain 1011}

GSTHERWINNDVIIYERKFGNNVAVVAINRNMNTPASITGLVTSLPRGSYNDVLGGILNGNTLTVGAGGAASNFTLAPGGTAVWQYTTDA

>d1smd\_1 b.71.1.1 (404-496) Animal alpha-amylase {Human (Homo sapiens)}

QPFTNWYDNGSNQVAFGRGNRGFIVFNNDDWTFSLTLQTGLPAGTYCDVISGDKINGNCTGIKIYVSDDGKAHFSISNSAEDPFIAIHAESKL

>d2taaa1 b.71.1.1 (A:382-478) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}

YKNPYIKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSLSGASYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSDSS

>d1smaa2 b.71.1.1 (A:506-588) Maltogenic amylase {Thermus sp.}

GDVAFLTADDEVNHLVYAKTDGNETVMIIINRSNEAAEIPMPIDARGKWLVNLLTGERFAAEAETLCVSLPPYGFVLYAVESW

>d1bvza2 b.71.1.1 (A:503-585) Maltogenic amylase {Thermoactinomyces vulgaris, TVAII}

GNVRSWHADKQANLYAFVRTVQDQHVGVVLNNRGEKQTVLLQVPESGGKTWLDCLTGEEVHGKQGQLKLTLRPYQGMILWNGR

>d1eh9a2 b.71.1.1 (A:491-557) Glycosyltrehalose trehalohydrolase {Archaeon Sulfolobus solfataricus, km1}

CDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFPQHIEEGKYEFDKGFALYK

>d1bf2\_2 b.71.1.1 (638-750) Isoamylase {Pseudomonas amyloderamosa}

YSGSQLTWYQPSGAVADSNYWNNTSNYAIAYAINGPSLGDSNSIYVAYNGWSSSVTFTLPAPPSGTQWYRVTDTCDWNDGASTFVAPGSETLIGGAGTTYGQCGQSLLLLISK

>d1gcya1 b.71.1.1 (A:358-418) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase) {Pseudomonas stutzeri}

RADSAISFHSGYSGLVATVSGSQQTLVVALNSDLGNPGQVASGSFSEAVNASNGQVRVWRS

>d1avaa1 b.71.1.1 (A:347-403) Plant alpha-amylase {Barley (Hordeum vulgare), seeds, AMY2 isozyme}

HNESKLQIIEADADLYLAEIDGKVIVKLGPRYDVGNLIPGGFKVAAHGNDYAVWEKI

>d1uok\_1 b.71.1.1 (480-558) Oligo-1,6-glucosidase {Bacillus cereus}

GSYDLILENNPSIFAYVRTYGVEKLLVIANFTAEECIFELPEDISYSEVELLIHNYDVENGPIENITLRPYEAMVFKLK

>d1g5aa1 b.71.1.1 (A:555-628) Amylosucrase {Neisseria polysaccharea}

RLVTFNTNNKHIIGYIRNNALLAFGNFSEYPQTVTAHTLQAMPFKAHDLIGGKTVSLNQDLTLQPYQVMWLEIA

>d1eg3a3 b.72.1.1 (A:47-84) Dystrophin {Human (Homo sapiens)}

PASQHFLSTSVQGPWERAISPNKVPYYINHETQTTCWD

>d1i5hw\_ b.72.1.1 (W:) Ubiquitin ligase NEDD4 WWIII domain {Rat (Rattus norvegicus)}

GSPVDSNDLGPLPPGWEERTHTDGRVFFINHNIKKTQWEDPRMQNVAITG

>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}

MGDCANANVYPNWVSKDWAGGQPTHNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQVGSCN

>d1ed7a\_ b.72.2.1 (A:) Chitin-binding domain of chitinase A1 {Bacillus circulans}

AWQVNTAYTAGQLVTYNGKTYKCLQPHTSLAGWEPSNVPALWQLQ

>d1flja\_ b.74.1.1 (A:) Carbonic anhydrase {Rat (Rattus norvegicus), isozyme III}

AKEWGYASHNGPEHWHELYPIAKGDNQSPIELHTKDIRHDPSLQPWSVSYDPGSAKTILNNGKTCRVVFDDTFDRSMLRGGPLSGPYRLRQFHLHWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTFGEALKQPDGIAVVGIFLKIGREKGEFQILLDALDKIKTKGKEAPFNHFDPSCLFPACRDYWTYHGSFTTPPCEECIVWLLLKEPMTVSSDQMAKLRSLFASAENEPPVPLVGNWRPPQPIKGRVVRASFK

>d1znca\_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme IV}

WCYEVQAESSNYPCLVPVKWGGNCQKDRQSPINIVTTKAKVDKKLGRFFFSGYDKKQTWTVQNNGHSVMMLLENKASISGGGLPAPYQAKQLHLHWSDLPYKGSEHSLDGEHFAMEMHIVHEKEKGTSRNVKEAQDPEDEIAVLAFLVEAGTQVNEGFQPLVEALSNIPKPEMSTTMAESSLLDLLPKEEKLRHYFRYLGSLTTPTCDEKVVWTVFREPIQLHREQILAFSQKLYYDKEQTVSMKDNVRPLQQLGQRTVIKS

>d1jd0a\_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme XII}

KWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNSDLYPDASTASNKSEGLAVLAVLIEMGSFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREMINNFRQVQKFDERLVYTSFS

>d1koqa\_ b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}

THWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFLTVNGRTYTLKQFHFHVPSENQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLNQPFDASTLLPKRLKYYRFAGSLTTPPCTEGVSWLVLKTYDHIDQAQAEKFTRAVGSENNRPVQPLNARVVIE

>d1ji6a2 b.77.2.1 (A:291-502) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis, CRY3bb1}

LYSKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLQGIEFHTRLQPGYFGKDSFNYWSGNYVETRPSIGSSKTITSPFYGDKSTEPVQKLSFDGQKVYRTIANTDVAAWPNGKVYLGVTKVDFSQYDDQKNETSTQTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRRGTIPFFTWTHRSVD

>d1ciy\_2 b.77.2.1 (256-461) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis, CRYIA (A)}

PIRTVSQLTREIYTNPVLENFDGSFRGMAQRIEQNIRQPHLMDILNSITIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTNLPSTIYRQRGTVDSLDVIPPQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLRAPTFSWQHRSAEF

>d1i5pa2 b.77.2.1 (A:264-472) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

YQSLMVSSGANLYASGSGPQQTQSFTAQNWPFLYSLFQVNSNYILSGISGTRLSITFPNIGGLPGSTTTHSLNSARVNYSGGVSSGLIGATNLNHNFNCSTVLPPLSTPFVRSWLDSGTDRAGVATSTNWQTESFQTTLSLRCGAFSARGNSNYFPDYFIRNISGVPLVIRNEDLTRPLHYNQIRNIESPSGTPGGARAYLVSVHNRKN

>g1jot.2 b.77.3.1 (B:,A:) Lectin MPA {Osage orange (Maclura pomifera)}

RNGKSQSIIVGPWGDRXGVTFDDGAYTGIREINFEYNSETAIGGLRVTYDLNGMPFVAEDHKSFITGFKPVKISLEFPSEYIVEVSGYVGKVEGYTVIRSLTFKTNKQTYGPYGVTNGTPFSLPIENGLIVGFKGSIGYWLDYFSIYLSL

>d1c3ma\_ b.77.3.1 (A:) Heltuba lectin {Jerusalem artishoke (Helianthus tuberosus)}

ASDIAVQAGPWGGNGGKRWLQTAHGGKITSIIIKGGTCIFSIQFVYKDKDNIEYHSGKFGVLGDKAETITFAEDEDITAISGTFGAYYHMTVVTSLTFQTNKKVYGPFGTVASSSFSLPLTKGKFAGFFGNSGDVLDSIGGVVVP

>d1jpc\_\_ b.78.1.1 (-) Lectin (agglutinin) {Snowdrop (Galanthus nivalis)}

DNILYSGETLSTGEFLNYGSFVFIMQEDCNLVLYDVDKPIWATNTGGLSRSCFLSMQTDGNLVVYNPSNKPIWASNTGGQNGNYVCILQKDRNVVIYGTDRWATGTHT

>d1dlpa2 b.78.1.1 (A:116-235) Fetuin-binding protein Scafet precursor {Bluebell (Scilla campanulata)}

GSVVVANNGNSILYSTQGNDNHPQTLHATQSLQLSPYRLSMETDCNLVLFDRDDRVWSTNTAGKGTGCRAVLQPNGRMDVLTNQNIAVWTSGNSRSAGRYVFVLQPDRNLAIYGGALWTT

>d1air\_\_ b.80.1.1 (-) Pectate lyase {Erwinia chrysanthemi, type C}

ATDTGGYAATAGGNVTGAVSKTATSMQDIVNIIDAARLDANGKKVKGGAYPLVITYTGNEDSLINAAAANICGQWSKDPRGVEIKEFTKGITIIGANGSSANFGIWIKKSSDVVVQNMRIGYLPGGAKDGDMIRVDDSPNVWVDHNELFAANHECDGTPDNDTTFESAVDIKGASNTVTVSYNYIHGVKKVGLDGSSSSDTGRNITYHHNYYNDVNARLPLQRGGLVHAYNNLYTNITGSGLNVRQNGQALIENNWFEKAINPVTSRYDGKNFGTWVLKGNNITKPADFSTYSITWTADTKPYVNADSWTSTGTFPTVAYNYSPVSAQCVKDKLPGYAGVGKNLATLTSTAC

>d1pcl\_\_ b.80.1.1 (-) Pectate lyase {Erwinia chrysanthemi, type E}

AVETDAATTGWATQNGGTTGGAKAAKAVEVKNISDFKKALNGTDSSAKIIKVTGPIDISGGKAYTSFDDQKARSQISIPSNTTIIGVGSNGKFTNGSLVIKGVKNVILRNLYIETPVDVAPHYESGDGWNAEWDAAVIDNSTNVWVDHVTISDGSFTDDKYTTKDGEKYVQHDGALDIKKGSDYVTISYSRFELHDKTILIGHSDSNGSQDSGKLRVTFHNNVFDRVTERAPRVRFGSIHAYNNVYLGDVKHSVYPYLYSFGLGTSGSILSESNSFTLSNLKSIDGKNPECSIVKQFNSKVFSDKGSLVNGSTTTKLDTCGLTAYKPTLPYKYSAQTMTSSLATSINNNAGYGKL

>d1bn8a\_ b.80.1.1 (A:) Pectate lyase {Bacillus subtilis}

ADLGHQTLGSNDGWGAYSTGTTGGSKASSSNVYTVSNRNQLVSALGKETNTTPKIIYIKGTIDMNVDDNLKPLGLNDYKDPEYDLDKYLKAYDPSTWGKKEPSGTQEEARARSQKNQKARVMVDIPANTTIVGSGTNAKVVGGNFQIKSDNVIIRNIEFQDAYDYFPQWDPTDGSSGNWNSQYDNITINGGTHIWIDHCTFNDGSRPDSTSPKYYGRKYQHHDGQTDASNGANYITMSYNYYHDHDKSSIFGSSDSKTSDDGKLKITLHHNRYKNIVQRAPRVRFGQVHVYNNYYEGSTSSSSYPFSYAWGIGKSSKIYAQNNVIDVPGLSAAKTISVFSGGTALYDSGTLLNGTQINASAANGLSSSVGWTPSLHGSIDASANVKSNVINQAGAGKLN

>d1ee6a\_ b.80.1.1 (A:) Pectate lyase {Bacillus sp., strain ksmp15}

APTVVHETIRVPAGQTFDGKGQTYVANPNTLGDGSQAENQKPIFRLEAGASLKNVVIGAPAADGVHCYGDCTITNVIWEDVGEDALTLKSSGTVNISGGAAYKAYDKVFQINAAGTINIRNFRADDIGKLVRQNGGTTYKVVMNVENCNISRVKDAILRTDSSTSTGRIVNTRYSNVPTLFKGFKSGNTTASGNTQY

>d1rmg\_\_ b.80.1.3 (-) Rhamnogalacturonase A {Aspergillus aculeatus}

QLSGSVGPLTSASTKGATKTCNILSYGAVADNSTDVGPAITSAWAACKSGGLVYIPSGNYALNTWVTLTGGSATAIQLDGIIYRTGTASGNMIAVTDTTDFELFSSTSKGAVQGFGYVYHAEGTYGARILRLTDVTHFSVHDIILVDAPAFHFTMDTCSDGEVYNMAIRGGNEGGLDGIDVWGSNIWVHDVEVTNKDECVTVKSPANNILVESIYCNWSGGCAMGSLGADTDVTDIVYRNVYTWSSNQMYMIKSNGGSGTVSNVLLENFIGHGNAYSLDIDGYWSSMTAVAGDGVQLNNITVKNWKGTEANGATRPPIRVVCSDTAPCTDLTLEDIAIWTESGSSELYLCRSAYGSGYCLKDSSSHTSYTTTSTVTAAPSGYSATTMAADLATAFGLTASIPIPTIPTSFYPGLTPYSALAG

>d1bhe\_\_ b.80.1.3 (-) Polygalacturonase {Erwinia carotovora, subsp. carotovora}

SDSRTVSEPKTPSSCTTLKADSSTATSTIQKALNNCDQGKAVRLSAGSTSVFLSGPLSLPSGVSLLIDKGVTLRAVNNAKSFENAPSSCGVVDKNGKGCDAFITAVSTTNSGIYGPGTIDGQGGVKLQDKKVSWWELAADAKVKKLKQNTPRLIQINKSKNFTLYNVSLINSPNFHVVFSDGDGFTAWKTTIKTPSTARNTDGIDPMSSKNITIAYSNIATGDDNVAIKAYKGRAETRNISILHNDFGTGHGMSIGSETMGVYNVTVDDLKMNGTTNGLRIKSDKSAAGVVNGVRYSNVVMKNVAKPIVIDTVYEKKEGSNVPDWSDITFKDVTSETKGVVVLNGENAKKPIEVTMKNVKLTSDSTWQIKNVNVKK

>d1hg8a\_ b.80.1.3 (A:) Polygalacturonase {Fusarium moniliforme}

DPCSVTEYSGLATAVSSCKNIVLNGFQVPTGKQLDLSSLQNDSTVTFKGTTTFATTADNDFNPIVISGSNITITGASGHVIDGNGQAYWDGKGSNSNSNQKPDHFIVVQKTTGNSKITNLNIQNWPVHCFDITGSSQLTISGLILDNRAGDKPNAKSGSLPAAHNTDGFDISSSDHVTLDNNHVYNQDDCVAVTSGTNIVVSNMYCSGGHGLSIGSVGGKSDNVVDGVQFLSSQVVNSQNGCRIKSNSGATGTINNVTYQNIALTNISTYGVDVQQDYLNGGPTGKPTNGVKISNIKFIKVTGTVASSAQDWFILCGDGSCSGFTFSGNAITGGGKTSSCNYPTNTCPS

>d1xat\_\_ b.81.1.3 (-) Xenobiotic acetyltransferase {Pseudomonas aeruginosa}

NYFESPFRGKLLSEQVSNPNIRVGRYSYYSGYYHGHSFDDCARYLMPDRDDVDKLVIGSFCSIGSGAAFIMAGNQGHRAEWASTFPFHFMHEEPAFAGAVNGYQPAGDTLIGHEVWIGTEAMFMPGVRVGHGAIIGSRALVTGDVEPYAIVGGNPARTIRKRFSDGDIQNLLEMAWWDWPLADIEAAMPLLCTGDIPALYQHWKQRQA

>d1kk6a\_ b.81.1.3 (A:) Xenobiotic acetyltransferase {Enterococcus faecium, VAT(D)}

MGPNPMKMYPIEGNKSVQFIKPILEKLENVEVGEYSYYDSKNGETFDKQILYHYPILNDKLKIGKFCSIGPGVTIIMNGANHRMDGSTYPFNLFGNGWEKHMPKLDQLPIKGDTIIGNDVWIGKDVVIMPGVKIGDGAIVAANSVVVKDIAPYMLAGGNPANEIKQRFDQDTINQLLDIKWWNWPIDIINENIDKILDNSIIREVIW

>d1fxja1 b.81.1.4 (A:252-329) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Escherichia coli}

VMLRDPARFDLRGTLTHGRDVEIDTNVIIEGNVTLGHRVKIGTGCVIKNSVIGDDCEISPYTVVEDANLAAACTIGPF

>d1hm9a1 b.81.1.4 (A:252-459) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Streptococcus pneumoniae}

VSFVNPEATYIDIDVEIAPEVQIEANVILKGQTKIGAETVLTNGTYVVDSTIGAGAVITNSMIEESSVADGVTVGPYAHIRPNSSLGAQVHIGNFVEVKGSSIGENTKAGHLTYIGNCEVGSNVNFGAGTITVNYDGKNKYKTVIGDNVFVGSNSTIIAPVELGDNSLVGAGSTITKDVPADAIAIGRGRQINKDEYATRLPHHPKNQ

>d1fi2a\_ b.82.1.2 (A:) Germin {Barley (Hordeum vulgare)}

TDPDPLQDFCVADLDGKAVSVNGHTCKPMSEAGDDFLFSSKLTKAGNTSTPNGSAVTELDVAEWPGTNTLGVSMNRVDFAPGGTNPPHIHPRATEIGMVMKGELLVGILGSLDSGNKLYSRVVRAGETFVIPRGLMHFQFNVGKTEAYMVVSFNSQNPGIVFVPLTLFGSDPPIPTPVLTKALRVEAGVVELLKSKFAGGS

>d2phla1 b.82.1.2 (A:11-210) Seed storage 7S protein {French bean (Phaseolus vulgaris), phaseolin}

DNPFYFNSDNSWNTLFKNQYGHIRVLQRFDQQSKRLQNLEDYRLVEFRSKPETLLLPQQADAELLLVVRSGSAILVLVKPDDRREYFFLTSDNPIFSDHQKIPAGTIFYLVNPDPKEDLRIIQLAMPVNNPQIHEFFLSSTEAQQSYLQEFSKHILEASFNSKFEEINRVLFEEEGQQEGVIVNIDSEQIKELSKHAKSS

>d2phla2 b.82.1.2 (A:220-381) Seed storage 7S protein {French bean (Phaseolus vulgaris), phaseolin}

NTIGNEFGNLTERTDNSLNVLISSIEMEEGALFVPHYYSKAIVILVVNEGEAHVELVGPKGNKETLEYESYRAELSKDDVFVIPAAYPVAIKATSNVNFTGFGINANNNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSGDEVMKLINKQSGSYFVDAH

>g1dgr.3 b.82.1.2 (M:,N:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}

QLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVSDLTFPGSGEEVEELLENQKESYFVDGQPXDKPFNLRSRDPIYSNNYGKLYEITPEKNSQLRDLDILLNCLQMNEGALFVPHYNSRATVILVANEGRAEVELVGLE

>d1fxza1 b.82.1.2 (A:10-248) Seed storage 7S protein {Soybean (Glycine max), proglycinin}

NECQIQKLNALKPDNRIESEGGLIETWNPNNKPFQCAGVALSRCTLNRNALRRPSYTNGPQEIYIQQGKGIFGMIYPGCPSTFEEPQQPQQRGQSSRPQDRHQKIYNFREGDLIAVPTGVAWWMYNNEDTPVVAVSIIDTNSLENQLDQMPRRFYLAGNQEQEFLKYQQEQGGHQSQKGKHQQEEENEGGSILSGFTLEFLEHAFSVDKQIAKNLQGENEGEDKGAIVTVKGGLSVIKP

>d1fxza2 b.82.1.2 (A:297-470) Seed storage 7S protein {Soybean (Glycine max), proglycinin}

ICTMRLRHNIGQTSSPDIYNPQAGSVTTATSLDFPALSWLRLSAEFGSLRKNAMFVPHYNLNANSIIYALNGRALIQVVNCNGERVFDGELQEGRVLIVPQNFVVAARSQSDNFEYVSFKTNDTPMIGTLAGANSLLNALPEEVIQHTFNLKSQQARQIKNNNPFKFLVPPQES

>d1qjea\_ b.82.2.1 (A:) Isopenicillin N synthase {Emericella nidulans}

SKANVPKIDVSPLFGDDQAAKMRVAQQIDAASRDTGFFYAVNHGINVQRLSQKTKEFHMSITPEEKWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRIQAKTPTHEVNVWPDETKHPGFQDFAEQYYWDVFGLSSALLKGYALALGKEENFFARHFKPDDTLASVVLIRYPYLDPYPEAAIKTAADGTKLSFEWHEDVSLITVLYQSNVQNLQVETAAGYQDIEADDTGYLINCGSYMAHLTNNYYKAPIHRVKWVNAERQSLPFFVNLGYDSVIDPFDPREPNGKSDREPLSYGDYLQNGLVSLINKNGQT

>d1dcs\_\_ b.82.2.1 (-) Deacetoxycephalosporin C synthase {Streptomyces clavuligerus}

MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFERIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGGNYVNIRRTSKA

>d1gp6a\_ b.82.2.1 (A:) Anthocyanidin synthase {Mouse-ear cress (Arabidopsis thaliana)}

VAVERVESLAKSGIISIPKEYIRPKEELESINDVFLEEKKEDGPQVPTIDLKNIESDDEKIRENCIEELKKASLDWGVMHLINHGIPADLMERVKKAGEEFFSLSVEEKEKYANDQATGKIQGYGSKLANNASGQLEWEDYFFHLAYPEEKRDLSIWPKTPSDYIEATSEYAKCLRLLATKVFKALSVGLGLEPDRLEKEVGGLEELLLQMKINYYPKCPQPELALGVEAHTDVSALTFILHNMVPGLQLFYEGKWVTAKCVPDSIVMHIGDTLEILSNGKYKSILHRGLVNKEKVRISWAVFCEPPKDKIVLKPLPEMVSVESPAKFPPRTFAQHIEHKLFGKEQEEL

>d1hw5a2 b.82.3.2 (A:1-137) Catabolite gene activator protein, N-terminal domain {Escherichia coli}

VLGKPQTDPTLEWFLSHCHIHKYPSKSTLIHQGEKAETLYYIVKGSVAVLIKDEEGKEMILSYLNQGDFIGELGLFEEGQERSAWVRAKTACEVAEISYKKFRQLIQVNPDILMRLSAQMARRLQVLAEKVGNLAFL

>d1cx4a1 b.82.3.2 (A:130-265) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}

RIIHPKTDDQRNRLQEACKDILLFKNLDPEQMSQVLDAMFEKLVKEGEHVIDQGDDGDNFYVIDRGTFDIYVKCDGVGRCVGNYDNRGSFGELALMYNTPRAATITATSPGALWGLDRVTFRRIIVKNNAKKRKMY

>d1cx4a2 b.82.3.2 (A:266-412) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}

ESFIESLPFLKSLEVSERLKVVDVIGTKVYNDGEQIIAQGDSADSFFIVESGEVRITMKRKGKSDIEENGAVEIARCLRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALFGTNMDIV

>d1ig3a1 b.82.6.1 (A:179-263) Thiamin pyrophosphokinase, substrate-binding domain {Mouse (Mus musculus)}

DSLIYLLQPGKHRLHVDTGMEGSWCGLIPVGQPCNQVTTTGLKWNLTNDVLGFGTLVSTSNTYDGSGLVTVETDHPLLWTMAIKS

>d1ig0a1 b.82.6.1 (A:224-319) Thiamin pyrophosphokinase, substrate-binding domain {Baker's yeast (Saccharomyces cerevisiae)}

TDLIFLIKKNGTLIEYDPQFRNTCIGNCGLLPIGEATLVKETRGLKWDVKNWPTSVVTGRVSSSNRFVGDNCCFIDTKDDIILNVEIFVDKLIDFL

>d1bdo\_\_ b.84.1.1 (-) Biotinyl domain of acetyl-CoA carboxylase {Escherichia coli}

EISGHIVRSPMVGTFYRTPSPDAKAFIEVGQKVNVGDTLCIVEAMKMMNQIEADKSGTVKAILVESGQPVEFDEPLVVIE

>d1dd2a\_ b.84.1.1 (A:) Biotin carboxyl carrier domain of transcarboxylase (TC 1.3S) {Propionibacterium freudenreichii, subsp. shermanii}

AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKIG

>d1htp\_\_ b.84.1.1 (-) Protein H of glycine cleavage system {Pea (Pisum sativum)}

SNVLDGLKYAPSHEWVKHEGSVATIGITDHAQDHLGEVVFVELPEPGVSVTKGKGFGAVESVKATSDVNSPISGEVIEVNTGLTGKPGLINSSPYEDGWMIKIKPTSPDELESLLGAKEYTKFCEEEDAAH

>d1gjxa\_ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Neisseria meningitidis}

ALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLETDKATMDVPAEVAGVVKEVKVKVGDKISEGGLIVVVEAEGTA

>d1fyc\_\_ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Human (Homo sapiens)}

GSNMSYPPHMQVLLPALSPTMTMGTVQRWEKKVGEKLSEGDLLAEIETDKATIGFEVQEEGYLAKILVPEGTRDVPLGTPLCIIVEKEADISAFADYRPTEVTDLK

>d1pmr\_\_ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Escherichia coli}

SSVDILVPDLPESVADATVATWHKKPGDAVVRDEVLVEIETDKVVLEVPASADGILDAVLEDEGTTVTSRQILGRLREGN

>d1k8ma\_ b.84.1.1 (A:) Lipoyl domain of the mitochondrial branched-chain alpha-ketoacid dehydrogenase {Human (Homo sapiens)}

MGQVVQFKLSDIGEGIREVTVKEWYVKEGDTVSQFDSICEVQSDKASVTITSRYDGVIKKLYYNLDDIAYVGKPLVDIETEALKDLE

>d1dv1a1 b.84.2.1 (A:331-446) Biotin carboxylase subunit of acetyl-CoA carboxylase, C-terminal domain {Escherichia coli}

RGHAVECRINAEDPNTFLPSPGKITRFHAPGGFGVRWESHIYAGYTVPPYYDSMIGKLICYGENRDVAIARMKNALQELIIDGIKTNVDLQIRIMNDENFQHGGTNIHYLEKKLGL

>d1gsoa1 b.84.2.1 (A:328-426) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}

ERASLGVVMAAGGYPGDYRTGDVIHGLPLEEVAGGKVFHAGTKLADDEQVVTNGGRVLCVTALGHTVAEAQKRAYALMTDIHWDDCFCRKDIGWRAIER

>d1b6ra1 b.84.2.1 (A:277-355) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

NNPSVMINLIGSDVNYDWLKLPLVHLHWYDKEVRPGRKVGHLNLTDSDTSRLTATLEALIPLLPPEYASGVIWAQSKFG

>d1eyza1 b.84.2.1 (A:319-392) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

GPAASAVILPQLTSQNVTFDNVQNAVGADLQIRLFGKPEIDGSRRLGVALATAESVVDAIERAKHAAGQVKVQG

>d2gpr\_\_ b.84.3.1 (-) Glucose permease IIa domain, IIa-glc {Mycoplasma capricolum}

MWFFNKNLKVLAPCDGTIITLDEVEDEVFKERMLGDGFAINPKSNDFHAPVSGKLVTAFPTKHAFGIQTKSGVEILLHIGLDTVSLDGNGFESFVTQDQEVNAGDKLVTVDLKSVAKKVPSIKSPIIFTNNGGKTLEIVKMGEVKQGDVVAILK

>d1glaf\_ b.84.3.1 (F:) Glucose-specific factor III (glsIII) {Escherichia coli}

GLFDKLKSLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEKIVGDGIAIKPTGNKMVAPVDGTIGKIFETNHAFSIESDSGVELFVHFGIDTVELKGEGFKRIAEEGQRVKVGDTVIEFDLPLLEEKAKSTLTPVVISNMDEIKELIKLSGSVTVGETPVIRIKK

>d1euwa\_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Escherichia coli}

MMKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIADPSLAAMMLPRSGLGHKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMIFVPVVQAEFNLVEDF

>d1f7ra\_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline immunodeficiency virus}

MIIEGDGILDKRSEDAGYDLLAAKEIHLLPGEVKVIPTGVKLMLPKGYWGLIIGKSSIGSKGLDVLGGVIDEGYRGEIGVIMINVSRKSITLMERQKIAQLIILPCKHEVLEQGKVVMDSERGDNGYGSTGVF

>d1dfaa1 b.86.1.2 (A:1-180,A:416-454) PI-Scei intein {Baker's yeast (Saccharomyces cerevisiae)}

CFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGRETMYSVVQKSQHRAHKSDSSREVPELLKFTCNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELVKEVSKSYPISEGPERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAXCRGFYFELQELKEDDYYGITLSDDSDHQFLLANQVVVHN

>d1dq3a1 b.86.1.2 (A:1-128,A:415-454) PI-Pfui intein {Archaeon Pyrococcus furiosus}

CIDGKAKIIFENEGEEHLTTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPESKRVVKGKVNVIWKYELGKDVTKYEIITNKGTKILTSPWHPFFVLTPDFKIVEKRADELKEGDILIGGMXGLEVVRHITTTNEPRTFYDLTVENYQNYLAGENGMIFVHN

>d1am2\_\_ b.86.1.2 (-) GyrA intein {Mycobacterium xenopi}

ASITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYAVRTVEGLRVTGTANHPLLCLVDVAGVPTLLWKLIDEIKPGDYAVIQRSAFSVDCAGFARGKPEFAPTTYTVGVPGLVRFLEAHHRDPDAKAIADELTDGRFYYAKVASVTDAGVQPVYSLRVDTADHAFITNGFVSHN

>d1umua\_ b.87.1.1 (A:) UmuD' {Escherichia coli}

DYVEQRIDLNQLLIQHPSATYFVKASGDSMIDGGISDGDLLIVDSAITASHGDIVIAAVDGEFTVKKLQLRPTVQLIPMNSAYSPITISSEDTLDVFGVVIHVVK

>d1jhfa2 b.87.1.1 (A:73-198) LexA C-terminal domain {Escherichia coli}

EEGLPLVGRVAADEPLLAQQHIEGHYQVDPSLFKPNADFLLRVSGMSMKDIGIMDGDLLAVHKTQDVRNGQVVVARIDDEVTVKRLKKQGNKVELLPENSEFKPIVVDLRQQSFTIEGLAVGVIRN

>d1f39a\_ b.87.1.1 (A:) lambda repressor C-terminal domain {Bacteriophage lambda virus}

ASASAFWLEVEGNSMTAPTGSKPSFPDGMLILVDPEQAVEPGDFCIARLGGDEFTFKKLIRDSGQVFLQPLNPQYPMIPCNESCSVVGKVIASQWPEETFG

>d1aqt\_2 b.93.1.1 (2-86) Epsilon subunit of F1F0-ATP synthase N-terminal domain {Escherichia coli}

STYHLDVVSAEQQMFSGLVEKIQVTGSEGELGIYPGHAPLLTAIKPGMIRIVKQHGHEEFIYLSGGILEVQPGNVTVLADTAIRG

>d1e79h2 b.93.1.1 (H:15-100) Epsilon subunit of F1F0-ATP synthase N-terminal domain {Cow (Bos taurus)}

QMSFTFASPTQVFFNSANVRQVDVPTQTGAFGILAAHVPTLQVLRPGLVVVHAEDGTTSKYFVSSGSVTVNADSSVQLLAEEAVTL

>d1trea\_ c.1.1.1 (A:) Triosephosphate isomerase {Escherichia coli}

MRHPLVMGNWKLNGSRHMVHELVSNLRKELAGVAGCAVAIAPPEMYIDMAKREAEGSHIMLGAQNVNLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETEAENEAGKTEEVCARQIDAVLKTQGAAAFEGAVIAYEPVWAIGTGKSATPAQAQAVHKFIRDHIAKVDANIAEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA

>d1hg3a\_ c.1.1.1 (A:) Triosephosphate isomerase {Archaeon Pyrococcus woesei}

AKLKEPIIAINFKTYIEATGKRALEIAKAAEKVYKETGVTIVVAPQLVDLRMIAESVEIPVFAQHIDPIKPGSHTGHVLPEAVKEAGAVGTLLNHSENRMILADLEAAIRRAEEVGLMTMVCSNNPAVSAAVAALNPDYVAVEPPELIGTGIPVSKAKPEVITNTVELVKKVNPEVKVLCGAGISTGEDVKKAIELGTVGVLLASGVTKAKDPEKAIWDLVSGI

>d1qo2a\_ c.1.2.1 (A:) Phosphoribosylformimino-5-aminoimidazole carboxamide ribotite isomerase HisA {Thermotoga maritima}

MLVVPAIDLFRGKVARMIKGRKENTIFYEKDPVELVEKLIEEGFTLIHVVDLSNAIENSGENLPVLEKLSEFAEHIQIGGGIRSLDYAEKLRKLGYRRQIVSSKVLEDPSFLKSLREIDVEPVFSLDTRGGRVAFKGWLAEEEIDPVSLLKRLKEYGLEEIVHTEIEKDGTLQEHDFSLTKKIAIEAEVKVLAAGGISSENSLKTAQKVHTETNGLLKGVIVGRAFLEGILTVEVMKRYAR

>d1thfd\_ c.1.2.1 (D:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}

MLAKRIIACLDVKDGRVVKGSNFENLRDSGDPVELGKFYSEIGIDELVFLDITASVEKRKTMLELVEKVAEQIDIPFTVGGGIHDFETASELILRGADKVSINTAAVENPSLITQIAQTFGSQAVVVAIDAKRVDGEFMVFTYSGKKNTGILLRDWVVEVEKRGAGEILLTSIDRDGTKSGYDTEMIRFVRPLTTLPIIASGGAGKMEHFLEAFLAGADAALAASVFHFREIDVRELKEYLKKHGVNVRLEGL

>d1jvna1 c.1.2.1 (A:230-552) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}

DYSNYGLTRRIIACLDVRTNDQGDLVVTKGDQYDVREKSDGKGVRNLGKPVQLAQKYYQQGADEVTFLNITSFRDCPLKDTPMLEVLKQAAKTVFVPLTVGGGIKDIVDVDGTKIPALEVASLYFRSGADKVSIGTDAVYAAEKYYELGNRGDGTSPIETISKAYGAQAVVISVDPKRVYVNSQADTKNKVFETEYPGPNGEKYCWYQCTIKGGRESRDLGVWELTRACEALGAGEILLNCIDKDGSNSGYDLELIEHVKDAVKIPVIASSGAGVPEHFEEAFLKTRADACLGAGMFHRGEFTVNDVKEYLLEHGLKVRMDEE

>d1dbta\_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Bacillus subtilis}

MKNNLPIIALDFASAEETLAFLAPFQQEPLFVKVGMELFYQEGPSIVKQLKERNCELFLDLKLHDIPTTVNKAMKRLASLGVDLVNVHAAGGKKMMQAALEGLEEGTPAGKKRPSLIAVTQLTSTSEQIMKDELLIEKSLIDTVVHYSKQAEESGLDGVVCSVHEAKAIYQAVSPSFLTVTPGIRMSEDAANDQVRVATPAIAREKGSSAIVVGRSITKAEDPVKAYKAVRLEWEGI

>d1dvja\_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}

MDVMNRLILAMDLMNRDDALRVTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRFGCRIIADFKVADIPETNEKICRATFKAGADAIIVHGFPGADSVRACLNVAEEMGREVFLLTEMSHPGAEMFIQGAADEIARMGVDLGVKNYVGPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSIYLADNPAAAAAGIIESIKDLLIPEDPAANKARKEAELAAATA

>d1dqwa\_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Baker's yeast (Saccharomyces cerevisiae)}

MHKATYKERAATHPSPVAAKLFNIMHEKQTNLCASLDVRTTKELLELVEALGPKICLLKTHVDILTDFSMEGTVKPLKALSAKYNFLLFEDRKFADIGNTVKLQYSAGVYRIAEWADITNAHGVVGPGIVSGLKQAAEEVTKEPRGLLMLAELSCKGSLSTGEYTKGTVDIAKSDKDFVIGFIAQRDMGGRDEGYDWLIMTPGVGLDDKGDALGQQYRTVDDVVSTGSDIIIVGRGLFAKGRDAKVEGERYRKAGWEAYLRRCGQQD

>d1pii\_2 c.1.2.4 (255-452) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Escherichia coli}

GENKVCGLTRGQDAKAAYDAGAIYGGLIFVATSPRCVNVEQAQEVMAAAPLQYVGVFRNHDIADVVDKAKVLSLAAVQLHGNEEQLYIDTLREALPAHVAIWKALSVGETLPAREFQHVDKYVLDNGQGGSGQRFDWSLLNGQSLGNVLLAGGLGADNCVEAAQTGCAGLDFNSAVESQPGIKDARLLASVFQTLRAY

>d1nsj\_\_ c.1.2.4 (-) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Thermotoga maritima}

MVRVKICGITNLEDALFSVESGADAVGFVFYPKSKRYISPEDARRISVELPPFVFRVGVFVNEEPEKILDVASYVQLNAVQLHGEEPIELCRKIAERILVIKAVGVSNERDMERALNYREFPILLDTKTPEYGGSGKTFDWSLILPYRDRFRYLVLSGGLNPENVRSAIDVVRPFAVDVSSGVEAFPGKKDHDSIKMFIKNAKGL

>d1pii\_1 c.1.2.4 (1-254) Indole-3-glycerophosphate synthase, IPGS {Escherichia coli}

MQTVLAKIVADKAIWVEARKQQQPLASFQNEVQPSTRHFYDALQGARTAFILECKKASPSKGVIRDDFDPARIAAIYKHYASAISVLTDEKYFQGSFNFLPIVSQIAPQPILCKDFIIDPYQIYLARYYQADACLLMLSVLDDDQYRQLAAVAHSLEMGVLTEVSNEEEQERAIALGAKVVGINNRDLRDLSIDLNRTRELAPKLGHNVTVISESGINTYAQVRELSHFANGFLIGSALMAHDDLHAAVRRVLL

>d1a53\_\_ c.1.2.4 (-) Indole-3-glycerophosphate synthase, IPGS {Archaeon Sulfolobus solfataricus}

PRYLKGWLKDVVQLSLRRPSFRASRQRPIISLNERILEFNKRNITAIIAEYKRKSPSGLDVERDPIEYSKFMERYAVGLSILTEEKYFNGSYETLRKIASSVSIPILMKDFIVKESQIDDAYNLGADTVLLIVKILTERELESLLEYARSYGMEPLIEINDENDLDIALRIGARFIGINSRDLETLEINKENQRKLISMIPSNVVKVAESGISERNEIEELRKLGVNAFLIGSSLMRNPEKIKEFIL

>d1qopa\_ c.1.2.4 (A:) Trp synthase alpha-subunit {Salmonella typhimurium}

MERYENLFAQLNDRREGAFVPFVTLGDPGIEQSLKIIDTLIDAGADALELGVPFSDPLADGPTIQNANLRAFAAGVTPAQCFEMLAIIREKHPTIPIGLLMYANLVFNNGIDAFYARCEQVGVDSVLVADVPVEESAPFRQAALRHNIAPIFICPPNADDDLLRQVASYGRGYTYLLSRSGVTGAENRGALPLHHLIEKLKEYHAAPALQGFGISSPEQVSAAVRAGAAGAISGSAIVKIIEKNLASPKQMLAELRSFVSAMKAASR

>d1geqa\_ c.1.2.4 (A:) Trp synthase alpha-subunit {Archaeon Pyrococcus furiosus}

MFKDGSLIPYLTAGDPDKQSTLNFLLALDEYAGAIELGIPFSDPIADGKTIQESHYRALKNGFKLREAFWIVKEFRRHSSTPIVLMTYYNPIYRAGVRNFLAEAKASGVDGILVVDLPVFHAKEFTEIAREEGIKTVFLAAPNTPDERLKVIDDMTTGFVYLVSLYGTTGAREEIPKTAYDLLRRAKRICRNKVAVGFGVSKREHVVSLLKEGANGVVVGSALVKIIGEKGREATEFLKKKVEELLGI

>d2dora\_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme A}

MLNTTFANAKFANPFMNASGVHCMTIEDLEELKASQAGAYITKSSTLEKREGNPLPRYVDLELGSINSMGLPNLGFDYYLDYVLKNQKENAQEGPIFFSIAGMSAAENIAMLKKIQESDFSGITELNLSCPNVPGKPQLAYDFEATEKLLKEVFTFFTKPLGVKLPPYFDLVHFDIMAEILNQFPLTYVNSVNSIGNGLFIDPEAESVVIKPKDGFGGIGGAYIKPTALANVRAFYTRLKPEIQIIGTGGIETGQDAFEHLLCGATMLQIGTALHKEGPAIFDRIIKELEEIMNQKGYQSIADFHGKLKSL

>d1ep3a\_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme B}

MTENNRLSVKLPGLDLKNPIIPASGCFGFGEEYAKYYDLNKLGSIMVKATTLHPRFGNPTPRVAETASGMLNAIGLQNPGLEVIMTEKLPWLNENFPELPIIANVAGSEEADYVAVCAKIGDAANVKAIELNISCPNVKHGGQAFGTDPEVAAALVKACKAVSKVPLYVKLSPNVTDIVPIAKAVEAAGADGLTMINTLMGVRFDLKTRQPILANITGGLSGPAIKPVALKLIHQVAQDVDIPIIGMGGVANAQDVLEMYMAGASAVAVGTANFADPFVCPKIIDKLPELMDQYRIESLESLIQEVKEGKK

>d1d3ga\_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Human (Homo sapiens)}

MATGDERFYAEHLMPTLQGLLDPESAHRLAVRFTSLGLLPRARFQDSDMLEVRVLGHKFRNPVGIAAGFDKHGEAVDGLYKMGFGFVEIGSVTPKPQEGNPRPRVFRLPEDQAVINRYGFNSHGLSVVEHRLRARQQKQAKLTEDGLPLGVNLGKNKTSVDAAEDYAEGVRVLGPLADYLVVNVSSPNTAGLRSLQGKAELRRLLTKVLQERDGLRRVHRPAVLVKIAPDLTSQDKEDIASVVKELGIDGLIVTNTTVSRPAGLQGALRSETGGLSGKPLRDLSTQTIREMYALTQGRVPIIGVGGVSSGQDALEKIRAGASLVQLYTALTFWGPPVVGKVKRELEALLKEQGFGGVTDAIGADHRR

>d1oyb\_\_ c.1.4.1 (-) Old yellow enzyme (OYE) {Brewer's yeast (Saccharomyces carlsbergensis)}

SFVKDFKPQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRALHPGNIPNRDWAVEYYTQRAQRPGTMIITEGAFISPQAGGYDNAPGVWSEEQMVEWTKIFNAIHEKKSFVWVQLWVLGWAAFPDNLARDGLRYDSASDNVFMDAEQEAKAKKANNPQHSLTKDEIKQYIKEYVQAAKNSIAAGADGVEIHSANGYLLNQFLDPHSNTRTDEYGGSIENRARFTLEVVDALVEAIGHEKVGLRLSPYGVFNSMSGGAETGIVAQYAYVAGELEKRAKAGKRLAFVHLVEPRVTNPFLTEGEGEYEGGSNDFVYSIWKGPVIRAGNFALHPEVVREEVKDKRTLIGYGRFFISNPDLVDRLEKGLPLNKYDRDTFYQMSAHGYIDYPTYEEALKLGWDKK

>d1huva\_ c.1.4.1 (A:) Membrane-associated (S)-mandelate dehydrogenase {Pseudomonas putida}

NLFNVEDYRKLAQKRLPKMVYDYLEGGAEDEYGVKHNRDVFQQWRFKPKRLVDVSRRSLQAEVLGKRQSMPLLIGPTGLNGALWPKGDLALARAATKAGIPFVLSTASNMSIEDLARQCDGDLWFQLYVIHREIAQGMVLKALHTGYTTLVLTTDVAVNGYRERDLHNRFKIPPFLTLKNFEGIDLGKMDKANLEMQAALMSRQMDASFNWEALRWLRDLWPHKLLVKGLLSAEDADRCIAEGADGVILSNHGGRQLDCAISPMEVLAQSVAKTGKPVLIDSGFRRGSDIVKALALGAEAVLLGRATLYGLAARGETGVDEVLTLLKADIDRTLAQIGCPDITSLSPDYLQNE

>d1h61a\_ c.1.4.1 (A:) Pentaerythritol tetranirate reductase {Enterobacter cloacae}

SAEKLFTPLKVGAVTAPNRVFMAPLTRLRSIEPGDIPTPLMGEYYRQRASAGLIISEATQISAQAKGYAGAPGLHSPEQIAAWKKITAGVHAEDGRIAVQLWHTGRISHSSIQPGGQAPVSASALNANTRTSLRDENGNAIRVDTTTPRALELDEIPGIVNDFRQAVANAREAGFDLVELHSAHGYLLHQFLSPSSNQRTDQYGGSVENRARLVLEVVDAVCNEWSADRIGIRVSPIGTFQNVDNGPNEEADALYLIEELAKRGIAYLHMSETDLAGGKPYSEAFRQKVRERFHGVIIGAGAYTAEKAEDLIGKGLIDAVAFGRDYIANPDLVARLQKKAELNPQRPESFYGGGAEGYTDYPSL

>d1djna1 c.1.4.1 (A:1-340) Trimethylamine dehydrogenase, N-terminal domain {Methylophilus methylotrophus, w3a1}

ARDPKHDILFEPIQIGPKTLRNRFYQVPHCIGAGSDKPGFQSAHRSVKAEGGWAALNTEYCSINPESDDTHRLSARIWDEGDVRNLKAMTDEVHKYGALAGVELWYGGAHAPNMESRATPRGPSQYASEFETLSYCKEMDLSDIAQVQQFYVDAAKRSRDAGFDIVYVYGAHSYLPLQFLNPYYNKRTDKYGGSLENRARFWLETLEKVKHAVGSDCAIATRFGVDTVYGPGQIEAEVDGQKFVEMADSLVDMWDITIGDIAEWGEDAGPSRFYQQGHTIPWVKLVKQVSKKPVLGVGRYTDPEKMIEIVTKGYADIIGCARPSIADPFLPQKVEQGRYD

>d1ltda1 c.1.4.1 (A:98-511) Flavocytochrome b2, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

APGETKEDIARKEQLKSLLPPLDNIINLYDFEYLASQTLTKQAWAYYSSGANDEVTHRENHNAYHRIFFKPKILVDVRKVDISTDMLGSHVDVPFYVSATALCKLGNPLEGEKDVARGCGQGVTKVPQMISTLASCSPEEIIEAAPSDKQIQWYQLYVNSDRKITDDLVKNVEKLGVKALFVTVDAPSLGQREKDMKLKFSNTKAGPKAMKKTNVEESQGASRALSKFIDPSLTWKDIEELKKKTKLPIVIKGVQRTEDVIKAAEIGVSGVVLSNHGGRQLDFSRAPIEVLAETMPILEQRNLKDKLEVFVDGGVRRGTDVLKALCLGAKGVGLGRPFLYANSCYGRNGVEKAIEILRDEIEMSMRLLGVTSIAELKPDLLDLSTLKARTVGVPNDVLYNEVYEGPTLTEFEDA

>d1h7wa2 c.1.4.1 (A:533-844) Dihydropyrimidine dehydrogenase, domain 4 {Pig (Sus scrofa)}

ISVEMAGLKFINPFGLASAAPTTSSSMIRRAFEAGWGFALTKTFSLDKDIVTNVSPRIVRGTTSGPMYGPGQSSFLNIELISEKTAAYWCQSVTELKADFPDNIVIASIMCSYNKNDWMELSRKAEASGADALELNLSCPHGMGERGMGLACGQDPELVRNICRWVRQAVQIPFFAKLTPNVTDIVSIARAAKEGGADGVTATNTVSGLMGLKADGTPWPAVGAGKRTTYGGVSGTAIRPIALRAVTTIARALPGFPILATGGIDSAESGLQFLHSGASVLQVCSAVQNQDFTVIQDYCTGLKALLYLKSIE

>d1ea0a2 c.1.4.1 (A:423-1193) Alpha subunit of glutamate synthase, central and FMN domains {Azospirillum brasilense}

TTHLDELVKTASLKGEPSDMDKAELRRRQQAFGLTMEDMELILHPMVEDGKEAIGSMGDDSPIAVLSDKYRGLHHFFRQNFSQVTNPPIDSLRERRVMSLKTRLGNLGNILDEDETQTRLLQLESPVLTTAEFRAMRDYMGDTAAEIDATFPVDGGPEALRDALRRIRQETEDAVRGGATHVILTDEAMGPARAAIPAILATGAVHTHLIRSNLRTFTSLNVRTAEGLDTHYFAVLIGVGATTVNAYLAQEAIAERHRRGLFGSMPLEKGMANYKKAIDDGLLKIMSKMGISVISSYRGGGNFEAIGLSRALVAEHFPAMVSRISGIGLNGIQKKVLEQHATAYNEEVVALPVGGFYRFRKSGDRHGWEGGVIHTLQQAVTNDSYTTFKKYSEQVNKRPPMQLRDLLELRSTKAPVPVDEVESITAIRKRFITPGMSMGALSPEAHGTLNVAMNRIGAKSDSGEGGEDPARFRPDKNGDNWNSAIKQVASGRFGVTAEYLNQCRELEIKVAQGAKPGEGGQLPGFKVTEMIARLRHSTPGVMLISPPPHHDIYSIEDLAQLIYDLKQINPDAKVTVKLVSRSGIGTIAAGVAKANADIILISGNSGGTGASPQTSIKFAGLPWEMGLSEVHQVLTLNRLRHRVRLRTDGGLKTGRDIVIAAMLGAEEFGIGTASLIAMGCIMVRQCHSNTCPVGVCVQDDKLRQKFVGTPEKVVNLFTFLAEEVREILAGLGFRSLNEVIGRTDLLHQVSRGAEHLDDLDLNPRLAQVDPG

>d1eepa\_ c.1.5.1 (A:) Inosine monophosphate dehydrogenase (IMPDH) {Lyme disease spirochete (Borrelia burgdorferi)}

NKITKEALTFDDVSLIPRKSSVLPSEVSLKTQLTKNISLNIPFLSSAMDTVTESQMAIAIAKEGGIGIIHKNMSIEAQRKEIEKVKTYKFQKTINTNGDTNEQKPEIFTAKQHLEKSDAYKNAEHKEDFPNACKDLNNKLRVGAAVSIDIDTIERVEELVKAHVDILVIDSAHGHSTRIIELIKKIKTKYPNLDLIAGNIVTKEAALDLISVGADCLKVGIGPGSICTTRIVAGVGVPQITAICDVYEACNNTNICIIADGGIRFSGDVVKAIAAGADSVMIGNLFAGTKESPSEEIIYNGKKFKSYVGMGSISAMKRGSKSRYFQLENNEPKKLVPEGIEGMVPYSGKLKDILTQLKGGLMSGMGYLGAATISDLKINSKFVKISHS

>d1ak5\_1 c.1.5.1 (2-101,222-483) Inosine monophosphate dehydrogenase (IMPDH) {Tritrichomonas foetus}

AKYYNEPCHTFNEYLLIPGLSTVDCIPSNVNLSTPLVKFQKGQQSEINLKIPLVSAIMQSVSGEKMAIALAREGGISFIFGSQSIESQAAMVHAVKNFKAXHNELVDSQKRYLVGAGINTRDFRERVPALVEAGADVLCIDSSDGFSEWQKITIGWIREKYGDKVKVGAGNIVDGEGFRYLADAGADFIKIGIGGGSICITREQKGIGRGQATAVIDVVAERNKYFEETGIYIPVCSDGGIVYDYHMTLALAMGADFIMLGRYFARFEESPTRKVTINGSVMKEYWGEGSSRARNWQRYDLGGKQKLSFEEGVDSYVPYAGKLKDNVEASLNKVKSTMCNCGALTIPQLQSKAKITLVSSVSI

>d1jr1a1 c.1.5.1 (A:17-112,A:233-514) Inosine monophosphate dehydrogenase (IMPDH) {Chinese hamster (Cricetulus griseus)}

GLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKITLKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQXYPLASKDAKKQLLCGAAIGTHEDDKYRLDLLALAGVDVVVLDSSQGNSIFQINMIKYMKEKYPNLQVIGGNVVTAAQAKNLIDAGVDALRVGMGCGSICITQEVLACGRPQATAVYKVSEYARRFGVPVIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVRAMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF

>d1bd0a2 c.1.6.1 (A:12-244) Alanine racemase {Bacillus stearothermophilus}

VDLDAIYDNVENLRRLLPDDTHIMAVVKANAYGHGDVQVARTALEAGASRLAVAFLDEALALREKGIEAPILVLGASRPADAALAAQQRIALTVFRSDWLEEASALYSGPFPIHFHLKMDTGMGRLGVKDEEETKRIVALIERHPHFVLEGLYTHFATADEVNTDYFSYQYTRFLHMLEWLPSRPPLVHCANSAASLRFPDRTFNMVRFGIAMYGLAPSPGIKPLLPYPLKEA

>d1d7ka2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}

DLGDILKKHLRWLKALPRVTPFYAVKCNDSKAIVKTLAATGTGFDCASKTEIQLVQSLGVPPERIIYANPCKQVSQIKYAANNGVQMMTFDSEVELMKVARAHPKAKLVLRIATDDSKAVCRLSVKFGATLRTSRLLLERAKELNIDVVGVSFHVGSGCTDPETFVQAISDARCVFDMGAEVGFSMYLLDIGGGFPGSEDVKLKFEEITGVINPALDKYFPSDSGVRIIAEPGRYYVASA

>d1exba\_ c.1.7.1 (A:) Voltage-dependent K+ channel beta subunit {Rat (Rattus norvegicus)}

LQFYRNLGKSGLRVSCLGLGTWVTFGGQITDEMAEHLMTLAYDNGINLFDTAEVYAAGKAEVVLGNIIKKKGWRRSSLVITTKIFWGGKAETERGLSRKHIIEGLKASLERLQLEYVDVVFANRPDPNTPMEETVRAMTHVINQGMAMYWGTSRWSSMEIMEAYSVARQFNLIPPICEQAEYHMFQREKVEVQLPELFHKIGVGAMTWSPLACGIVSGKYDSGIPPYSRASLKGYQWLKDKILSEEGRRQQAKLKELQAIAERLGCTLPQLAIAWCLRNEGVSSVLLGASNAEQLMENIGAIQVLPKLSSSIVHEIDSILGNKPYS

>d2alr\_\_ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}

AASCVLLHTGQKMPLIGLGTWKSEPGQVKAAVKYALSVGYRHIDCAAIYGNEPEIGEALKEDVGPGKAVPREELFVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYAFERGDNPFPKNADGTICYDSTHYKETWKALEALVAKGLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNELIAHCQARGLEVTAYSPLGSSDRAWRDPDEPVLLEEPVVLALAEKYGRSPAQILLRWQVQRKVICIPKSITPSRILQNIKVFDFTFSPEEMKQLNALNKNWRYIVPMLTVDGKRVPRDAGHPLYPFNDPY

>d1afsa\_ c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Rat (Rattus norvegicus)}

MDSISLRVALNDGNFIPVLGFGTTVPEKVAKDEVIKATKIAIDNGFRHFDSAYLYEVEEEVGQAIRSKIEDGTVKREDIFYTSKLWSTFHRPELVRTCLEKTLKSTQLDYVDLYIIHFPMALQPGDIFFPRDEHGKLLFETVDICDTWEAMEKCKDAGLAKSIGVSNFNCRQLERILNKPGLKYKPVCNQVECHLYLNQSKMLDYCKSKDIILVSYCTLGSSRDKTWVDQKSPVLLDDPVLCAIAKKYKQTPALVALRYQLQRGVVPLIRSFNAKRIKELTQVFEFQLASEDMKALDGLNRNFRYNNAKYFDDHPNHPF

>d1hw6a\_ c.1.7.1 (A:) 2,5-diketo-D-gluconic acid reductase A {Corynebacterium sp.}

TVPSIVLNDGNSIPQLGYGVFKVPPADTQRAVEEALEVGYRHIDTAAIYGNEEGVGAAIAASGIARDDLFITTKLWNDRHDGDEPAAAIAESLAKLALDQVDLYLVHWPTPAADNYVHAWEKMIELRAAGLTRSIGVSNHLVPHLERIVAATGVVPAVNQIELHPAYQQREITDWAAAHDVKIESWGPLGQGKYDLFGAEPVTAAAAAHGKTPAQAVLRWHLQKGFVVFPKSVRRERLEENLDVFDFDLTDTEIAAIDAMDP

>d1e43a2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus amyloliquefaciens/Bacillus licheniformis chimera}

VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYDLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKAWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKARKQ

>d1g94a2 c.1.8.1 (A:1-354) Bacterial alpha-amylase {Pseudoalteromonas haloplanctis (Alteromonas haloplanctis)}

TPTTFVHLFEWNWQDVAQECEQYLGPKGYAAVQVSPPNEHITGSQWWTRYQPVSYELQSRGGNRAQFIDMVNRCSAAGVDIYVDTLINHMAAGSGTGTAGNSFGNKSFPIYSPQDFHESCTINNSDYGNDRYRVQNCELVGLADLDTASNYVQNTIAAYINDLQAIGVKGFRFDASKHVAASDIQSLMAKVNGSPVVFQEVIDQGGEAVGASEYLSTGLVTEFKYSTELGNTFRNGSLAWLSNFGEGWGFMPSSSAVVFVDNHDNQRGHGGAGNVITFEDGRLYDLANVFMLAYPYGYPKVMSSYDFHGDTDAGGPNVPVHNNGNLECFASNWKCEHRWSYIAGGVDFRNNTAD

>d1bag\_2 c.1.8.1 (1-347) Bacterial alpha-amylase {Bacillus subtilis}

LTAPSIKSGTILHAWNWSFNTLKHNMKDIHDAGYTAIQTSPINQVKEGNQGDKSMSNWYWLYQPTSYQIGNRYLGTEQEFKEMCAAAEEYGIKVIVDAVINHTTFDYAAISNEVKSIPNWTHGNTQIKNWSDRWDVTQNSLLGLYDWNTQNTQVQSYLKRFLERALNDGADGFRFDAAKHIELPDDGSYGSQFWPNITNTSAEFQYGQILQDSASRDAAYANYMDVTASNYGHSIRSALKNRNLGVSNISHYASDVSADKLVTWVESHDTYANDDEESTWMSDDDIRLGWAVIASRSGSTPLFFSRPEGGGNGVRFPGKSQIGDRGSALFEDQAITAVNRFHNVMAG

>d1gjwa2 c.1.8.1 (A:1-572) Maltosyltransferase {Thermotoga maritima}

MLLREINRYCKEKATGKRIYAVPKLWIPGFFKKFDEKSGRCFVDPYELGAEITDWILNQSREWDYSQPLSFLKGEKTPDWIKRSVVYGSLPRTTAAYNHKGSGYYEENDVLGFREAGTFFKMMLLLPFVKSLGADAIYLLPVSRMSDLFKKGDAPSPYSVKNPMELDERYHDPLLEPFKVDEEFKAFVEACHILGIRVILDFIPRTAARDSDLIREHPDWFYWIKVEELADYTPPRAEELPFKVPDEDELEIIYNKENVKRHLKKFTLPPNLIDPQKWEKIKREEGNILELIVKEFGIITPPGFSDLINDPQPTWDDVTFLRLYLDHPEASKRFLDPNQPPYVLYDVIKASKFPGKEPNRELWEYLAGVIPHYQKKYGIDGARLDMGHALPKELLDLIIKNVKEYDPAFVMIAEELDMEKDKASKEAGYDVILGSSWYFAGRVEEIGKLPDIAEELVLPFLASVETPDTPRIATRKYASKMKKLAPFVTYFLPNSIPYVNTGQEIGEKQPMNLGLDTDPNLRKVLSPTDEFFGKLAFFDHYVLHWDSPDRGVLNFIKKLIKVRHEFLDFVLN

>d1qhoa4 c.1.8.1 (A:1-407) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}

SSSASVKGDVIYQIIIDRFYDGDTTNNNPAKSYGLYDPTKSKWKMYWGGDLEGVRQKLPYLKQLGVTTIWLSPVLDNLDTLAGTDNTGYHGYWTRDFKQIEEHFGNWTTFDTLVNDAHQNGIKVIVDFVPNHSTPFKANDSTFAEGGALYNNGTYMGNYFDDATKGYFHHNGDISNWDDRYEAQWKNFTDPAGFSLADLSQENGTIAQYLTDAAVQLVAHGADGLRIDAVKHFNSGFSKSLADKLYQKKDIFLVGEWYGDDPGTANHLEKVRYANNSGVNVLDFDLNTVIRNVFGTFTQTMYDLNNMVNQTGNEYKYKENLITFIDNHDMSRFLSVNSNKANLHQALAFILTSRGTPSIYYGTEQYMAGGNDPYNRGMMPAFDTTTTAFKEVSTLAGLRRNNAAIQY

>d1hx0a2 c.1.8.1 (A:1-403) Animal alpha-amylase {Pig (Sus scrofa)}

EYAPQTQSGRTSIVHLFEWRWVDIALECERYLGPKGFGGVQVSPPNENIVVTNPSRPWWERYQPVSYKLCTRSGNENEFRDMVTRCNNVGVRIYVDAVINHMCGSGAAAGTGTTCGSYCNPGNREFPAVPYSAWDFNDGKCKTASGGIESYNDPYQVRDCQLVGLLDLALEKDYVRSMIADYLNKLIDIGVAGFRIDASKHMWPGDIKAVLDKLHNLNTNWFPAGSRPFIFQEVIDLGGEAIKSSEYFGNGRVTEFKYGAKLGTVVRKWSGEKMSYLKNWGEGWGFMPSDRALVFVDNHDNQRGHGAGGSSILTFWDARLYKIAVGFMLAHPYGFTRVMSSYRWARNFVNGEDVNDWIGPPNNNGVIKEVTINADTTCGNDWVCEHRWREIRNMVWFRNVVDG

>d2aaa\_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus niger, acid amylase}

LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVPDHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTETAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDCPYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPRFAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYTWIATTNAIRKLAIAADSAYIT

>d1smaa3 c.1.8.1 (A:124-505) Maltogenic amylase, central domain {Thermus sp.}

DLFQAPDWVKDTVWYQIFPERFANGNPAISPKGARPWGSEDPTPTSFFGGDLQGIIDHLDYLADLGITGIYLTPIFRAPSNHKYDTADYFEIDPHFGDKETLKTLVKRCHEKGIRVMLDAVFNHCGYEFAPFQDVLKNGAASRYKDWFHIREFPLQTEPRPNYDTFAFVPHMPKLNTAHPEVKRYLLDVATYWIREFDIDGWRLDVANEIDHQFWREFRQAVKALKPDVYILGEIWHDAMPWLRGDQFDAVMNYPLADAALRFFAKEDMSASEFADRLMHVLHSYPKQVNEAAFNLLGSHDTPRLLTVCGGDVRKVKLLFLFQLTFTGSPCIYYGDEIGMTGGNDPECRKCMVWDPEKQNKELYEHVKQLIALRKQYRALRR

>d1eh9a3 c.1.8.1 (A:91-490) Glycosyltrehalose trehalohydrolase, central domain {Archaeon Sulfolobus solfataricus, km1}

FNNETFLKKEDLIIYEIHVGTFTPEGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIVIAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKTHGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSWKIDEEIFSFYKILIKMRKELSIA

>d1bf2\_3 c.1.8.1 (163-637) Isoamylase, central domain {Pseudomonas amyloderamosa}

PSTQSTGTKPTRAQKDDVIYEVHVRGFTEQDTSIPAQYRGTYYGAGLKASYLASLGVTAVEFLPVQETQNDANDVVPNSDANQNYWGYMTENYFSPDRRYAYNKAAGGPTAEFQAMVQAFHNAGIKVYMDVVYNHTAEGGTWTSSDPTTATIYSWRGLDNATYYELTSGNQYFYDNTGIGANFNTYNTVAQNLIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYNFDAADSNVAINRILREFTVRPAAGGSGLDLFAEPWAIGGNSYQLGGFPQGWSEWNGLFRDSLRQAQNELGSMTIYVTQDANDFSGSSNLFQSSGRSPWNSINFIDVHDGMTLKDVYSCNGANNSQAWPYGPSDGGTSTNYSWDQGMSAGTGAAVDQRRAARTGMAFEMLSAGTPLMQGGDEYLRTLQCNNNAYNLDSSANWLTYSWTTDQSNFYTFAQRLIAFRKAHPALRPSSW

>d1gcya2 c.1.8.1 (A:1-357) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase) {Pseudomonas stutzeri}

DQAGKSPNAVRYHGGDEIILQGFHWNVVREAPNDWYNILRQQAATIAADGFSAIWMPVPWRDFSSWSDGSKSGGGEGYFWHDFNKNGRYGSDAQLRQAASALGGAGVKVLYDVVPNHMNRGYPDKEINLPAGQGFWRNDCADPGNYPNDCDDGDRFIGGDADLNTGHPQVYGMFRDEFTNLRSQYGAGGFRFDFVRGYAPERVNSWMTDSADNSFCVGELWKGPSEYPNWDWRNTASWQQIIKDWSDRAKCPVFDFALKERMQNGSIADWKHGLNGNPDPRWREVAVTFVDNHDTGYSPGQNGGQHHWALQDGLIRQAYAYILTSPGTPVVYWDHMYDWGYGDFIRQLIQVRRAAGV

>d1avaa2 c.1.8.1 (A:1-346) Plant alpha-amylase {Barley (Hordeum vulgare), seeds, AMY2 isozyme}

QVLFQGFNWESWKHNGGWYNFLMGKVDDIAAAGITHVWLPPASQSVAEQGYMPGRLYDLDASKYGNKAQLKSLIGALHGKGVKAIADIVINHRTAEHKDGRGIYCIFEGGTPDARLDWGPHMICRDDRPYADGTGNPDTGADFGAAPDIDHLNLRVQKELVEWLNWLKADIGFDGWRFDFAKGYSADVAKIYIDRSEPSFAVAEIWTSLAYGGDGKPNLNQDQHRQELVNWVDKVGGKGPATTFDFTTKGILNVAVEGELWRLRGTDGKAPGMIGWWPAKAVTFVDNHDTGSTQHMWPFPSDRVMQGYAYILTHPGTPCIFYDHFFDWGLKEEIDRLVSVRTRHGI

>d1uok\_2 c.1.8.1 (1-479) Oligo-1,6, glucosidase {Bacillus cereus}

MEKQWWKESVVYQIYPRSFMDSNGDGIGDLRGIISKLDYLKELGIDVIWLSPVYESPNDDNGYDISDYCKIMNEFGTMEDWDELLHEMHERNMKLMMDLVVNHTSDEHNWFIESRKSKDNKYRDYYIWRPGKEGKEPNNWGAAFSGSAWQYDEMTDEYYLHLFSKKQPDLNWDNEKVRQDVYEMMKFWLEKGIDGFRMDVINFISKEEGLPTVETEEEGYVSGHKHFMNGPNIHKYLHEMNEEVLSHYDIMTVGEMPGVTTEEAKLYTGEERKELQMVFQFEHMDLDSGEGGKWDVKPCSLLTLKENLTKWQKALEHTGWNSLYWNNHDQPRVVSRFGNDGMYRIESAKMLATVLHMMKGTPYIYQGEEIGMTNVRFESIDEYRDIETLNMYKEKVMERGEDIEKVMQSIYIKGRDNARTPMQWDDQNHAGFTTGEPWITVNPNYKEINVKQAIQNKDSIFYYYKKLIELRKNNEIVVY

>d1g5aa2 c.1.8.1 (A:1-554) Amylosucrase {Neisseria polysaccharea}

SPNSQYLKTRILDIYTPEQRAGIEKSEDWRQFSRRMDTHFPKLMNELDSVYGNNEALLPMLEMLLAQAWQSYSQRNSSLKDIDIARENNPDWILSNKQVGGVCYVDLFAGDLKGLKDKIPYFQELGLTYLHLMPLFKCPEGKSDGGYAVSSYRDVNPALGTIGDLREVIAALHEAGISAVVDFIFNHTSNEHEWAQRCAAGDPLFDNFYYIFPDRRMPDQYDRTLREIFPDQHPGGFSQLEDGRWVWTTFNSFQWDLNYSNPWVFRAMAGEMLFLANLGVDILRMDAVAFIWKQMGTSCENLPQAHALIRAFNAVMRIAAPAVFFKSEAIVHPDQVVQYIGQDECQIGYNPLQMALLWNTLATREVNLLHQALTYRHNLPEHTAWVNYVRSHDDIGWTFADEDAAYLGISGYDHRQFLNRFFVNRFDGSFARGVPFQYNPSTGDCRVSGTAAALVGLAQDDPHAVDRIKLLYSIALSTGGLPLIYLGDEVGTLNDDDWSQDSNKSDDSRWAHRPRYNEALYAQRNDPSTAAGQIYQDLRHMIAVRQSNPRFDGG

>d1eswa\_ c.1.8.1 (A:) Amylomaltase MalQ {Thermus aquaticus}

MELPRAFGLLLHPTSLPGPYGVGVLGREARDFLRFLKEAGGRYWQVLPLGPTGYGDSPYQSFSAFAGNPYLIDLRPLAERGYVRLEDPGFPQGRVDYGLLYAWKWPALKEAFRGFKEKASPEEREAFAAFREREAWWLEDYALFMALKGAHGGLPWNRWPLPLRKREEKALREAKSALAEEVAFHAFTQWLFFRQWGALKAEAEALGIRIIGDMPIFVAEDSAEVWAHPEWFHLDEEGRPTVVAGVPPDYFSETGQRWGNPLYRWDVLEREGFSFWIRRLEKALELFHLVRIDHFRGFEAYWEIPASCPTAVEGRWVKAPGEKLFQKIQEVFGEVPVLAEDLGVITPEVEALRDRFGLPGMKVLQFAFDDGMENPFLPHNYPAHGRVVVYTGTHDNDTTLGWYRTATPHEKAFMARYLADWGITFREEEEVPWALMHLGMKSVARLAVYPVQDVLALGSEARMNYPGRPSGNWAWRLLPGELSPEHGARLRAMAEATERL

>d1b1ya\_ c.1.8.2 (A:) beta-Amylase {Barley (Hordeum vulgare)}

MKGNYVQVYVMLPLDAVSVNNRFEKGDELRAQLRKLVEAGVDGVMVDVWWGLVEGKGPKAYDWSAYKQLFELVQKAGLKLQAIMSFHQCGGNVGDAVNIPIPQWVRDVGTRDPDIFYTDGHGTRNIEYLTLGVDNQPLFHGRSAVQMYADYMTSFRENMKDFLDAGVIVDIEVGLGPAGELRYPSYPQSHGWSFPGIGEFICYDKYLQADFKAAAAAVGHPEWEFPNDAGQYNDTPERTQFFRDNGTYLSEKGRFFLAWYSNNLIKHGDRILDEANKVFLGYKVQLAIKIAGVHWWYKVPSHAAELTAGYYNLHDRDGYRTIARMLKRHRASINFTCAEMRDSEQPPDAMSAPEELVQQVLSAGWREGLNVSCENALPRYDPTAYNTILRNARPHGINQSGPPEHKLFGFTYLRLSNQLVEGQNYVNFKTFVDRMHANLPRDPYVDPMAPLPRSGPEISIEMILQAAQPKIQPFPFQEHTDLPVGPTGGMGGQAEGPTCG

>d1b9za2 c.1.8.2 (A:1-417) Bacterial beta-amylase, catalytic domain {Bacillus cereus}

AVNGKGMNPDYKAYLMAPLKKIPEVTNWETFENDLRWAKQNGFYAITVDFWWGDMEKNGDQQFDFSYAQRFAQSVKNAGMKMIPIISTHQCGGNVGDDCNVPIPSWVWNQKSDDSLYFKSETGTVNKETLNPLASDVIRKEYGELYTAFAAAMKPYKDVIAKIYLSGGPAGELRYPSYTTSDGTGYPSRGKFQAYTEFAKSKFRLWVLNKYGSLNEVNKAWGTKLISELAILPPSDGEQFLMNGYLSMYGKDYLEWYQGILENHTKLIGELAHNAFDTTFQVPIGAKIAGVHWQYNNPTIPHGAEKPAGYNDYSHLLDAFKSAKLDVTFTCLEMTDKGSYPEYSMPKTLVQNIATLANEKGIVLNGENALSIGNEEEYKRVAEMAFNYNFAGFTLLRYQDVMYNNSLMGKFKDLLGV

>d1xyza\_ c.1.8.3 (A:) Xylanase {Clostridium thermocellum, XynZ}

NALRDYAEARGIKIGTCVNYPFYNNSDPTYNSILQREFSMVVCENEMKFDALQPRQNVFDFSKGDQLLAFAERNGMQMRGHTLIWHNQNPSWLTNGNWNRDSLLAVMKNHITTVMTHYKGKIVEWDVANECMDDSGNGLRSSIWRNVIGQDYLDYAFRYAREADPDALLFYNDYNIEDLGPKSNAVFNMIKSMKERGVPIDGVGFQCHFINGMSPEYLASIDQNIKRYAEIGVIVSFTEIDIRIPQSENPATAFQVQANNYKELMKICLANPNCNTFVMWGFTDKYTWIPGTFPGYGNPLIYDSNYNPKPAYNAIKEALM

>d1hiza\_ c.1.8.3 (A:) Xylanase {Bacillus stearothermophilus, Xt6}

SYAKKPHISALNAPQLDQRYKNEFTIGAAVEPYQLQNEKDVQMLKRHFNSIVAENVMKPISIQPEEGKFNFEQADRIVKFAKANGMDIRFHTLVWHSQVPQWFFLDKEGKPMVNETDPVKREQNKQLLLKRLETHIKTIVERYKDDIKYWDVVNEVVGDDGKLRNSPWYQIAGIDYIKVAFQAARKYGGDNIKLYMNDYNTEVEPKRTALYNLVKQLKEEGVPIDGIGHQSHIQIGWPSEAEIEKTINMFAALGLDNQITELDVSMYGWPPRAYPTYDAIPKQKFLDQAARYDRLFKLYEKLSDKISNVTFWGIADNHTWLDSRADVYYDANGNVVVDPNAPYAKVEKGKGKDAPFVFGPDYKVKPAYWAIIDHK

>d1bg4\_\_ c.1.8.3 (-) Xylanase {Penicillium simplicissimum}

EASVSIDAKFKAHGKKYLGTIGDQYTLTKNTKNPAIIKADFGQLTPENSMKWDATEPNRGQFTFSGSDYLVNFAQSNGKLIRGHTLVWHSQLPGWVSSITDKNTLISVLKNHITTVMTRYKGKIYAWDVLNEIFNEDGSLRNSVFYNVIGEDYVRIAFETARSVDPNAKLYINDYNLDSAGYSKVNGMVSHVKKWLAAGIPIDGIGSQTHLGAGAGSAVAGALNALASAGTKEIAITELDIAGASSTDYVNVVNACLNQAKCVGITVWGVADPDSWRSSSSPLLFDGNYNPKAAYNAIANAL

>d1edg\_\_ c.1.8.3 (-) Endoglucanase CelA {Clostridium cellulolyticum}

MYDASLIPNLQIPQKNIPNNDGMNFVKGLRLGWNLGNTFDAFNGTNITNELDYETSWSGIKTTKQMIDAIKQKGFNTVRIPVSWHPHVSGSDYKISDVWMNRVQEVVNYCIDNKMYVILNTHHDVDKVKGYFPSSQYMASSKKYITSVWAQIAARFANYDEHLIFEGMNEPRLVGHANEWWPELTNSDVVDSINCINQLNQDFVNTVRATGGKNASRYLMCPGYVASPDGATNDYFRMPNDISGNNNKIIVSVHAYCPWNFAGLAMADGGTNAWNINDSKDQSEVTWFMDNIYNKYTSRGIPVIIGECGAVDKNNLKTRVEYMSYYVAQAKARGILCILWDNNNFSGTGELFGFFDRRSCQFKFPEIIDGMVKYAFGLIN

>d1ceo\_\_ c.1.8.3 (-) Endoglucanase CelC {Clostridium thermocellum}

MVSFKAGINLGGWISQYQVFSKEHFDTFITEKDIETIAEAGFDHVRLPFDYPIIESDDNVGEYKEDGLSYIDRCLEWCKKYNLGLVLDMHHAPGYRFQDFKTSTLFEDPNQQKRFVDIWRFLAKRYINEREHIAFELLNQVVEPDSTRWNKLMLECIKAIREIDSTMWLYIGGNNYNSPDELKNLADIDDDYIVYNFHFYNPFFFTHQKAHWSESAMAYNRTVKYPGQYEGIEEFVKNNPKYSFMMELNNLKLNKELLRKDLKPAIEFREKKKCKLYCGEFGVIAIADLESRIKWHEDYISLLEEYDIGGAVWNYKKMDFEIYNEDRKPVSQELVNILAR

>d1cz1a\_ c.1.8.3 (A:) Exo-beta-(1,3)-glucanase {Yeast (Candida albicans)}

AWDYDNNVIRGVNLGGWFVLEPYMTPSLFEPFQNGNDQSGVPVDEYHWTQTLGKEAALRILQKHWSTWITEQDFKQISNLGLNFVRIPIGYWAFQLLDNDPYVQGQVQYLEKALGWARKNNIRVWIDLHGAPGSQNGFDNSGLRDSYNFQNGDNTQVTLNVLNTIFKKYGGNEYSDVVIGIELLNEPLGPVLNMDKLKQFFLDGYNSLRQTGSVTPVIIHDAFQVFGYWNNFLTVAEGQWNVVVDHHHYQVFSGGELSRNINDHISVACNWGWDAKKESHWNVAGEWSAALTDCAKWLNGVNRGARYEGAYDNAPYIGSCQPLLDISQWSDEHKTDTRRYIEAQLDAFEYTGGWVFWSWKTENAPEWSFQTLTYNGLFPQPVTDRQFPNQCGFH

>d1ecea\_ c.1.8.3 (A:) Endocellulase E1 {Acidothermus cellulolyticus}

AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLWSRDYRSMLDQIKSLGYNTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGLRIILDRHRPDCSGQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEPHDPACWGCGDPSIDWRLAAERAGNAVLSVNPNLLIFVEGVQSYNGDSYWWGGNLQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTWFSDPTFPNNMPGIWNKNWGYLFNQNIAPVWLGEFGTTLQSTTDQTWLKTLVQYLRPTAQYGADSFQWTFWSWNPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPV

>d7a3ha\_ c.1.8.3 (A:) Endoglucanase Cel5a {Bacillus agaradhaerens}

SVVEEHGQLSISNGELVNERGEQVQLKGMSSHGLQWYGQFVNYESMKWLRDDWGINVFRAAMYTSSGGYIDDPSVKEKVKEAVEAAIDLDIYVIIDWHILSDNDPNIYKEEAKDFFDEMSELYGDYPNVIYEIANEPNGSDVTWGNQIKPYAEEVIPIIRNNDPNNIIIVGTGTWSQDVHHAADNQLADPNVMYAFHFYAGTHGQNLRDQVDYALDQGAAIFVSEWGTSAATGDGGVFLDEAQVWIDFMDERNLSWANWSLTHKDESSAALMPGANPTGGWTEAELSPSGTFVREKIRES

>d1g0ca\_ c.1.8.3 (A:) Alkaline cellulase K catalytic domain {Bacillus sp.}

PAGMQAVKSPSEAGALQLVELNGQLTLAGEDGTPVQLRGMSTHGLQWFGEIVNENAFVALSNDWGSNMIRLAMYIGENGYATNPEVKDLVYEGIELAFEHDMYVIVDWHVHAPGDPRADVYSGAYDFFEEIADHYKDHPKNHYIIWELANEPSPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILVGNPNWSQRPDLSADNPIDAENIMYSVHFYTGSHGASHIGYPEGTPSSERSNVMANVRYALDNGVAVFATEWGTSQANGDGGPYFDEADVWLNFLNKHNISWANWSLTNKNEISGAFTPFELGRTDATDLDPGANQVWAPEELSLSGEYVRARIKGIEYTPIDRTK

>d1bqca\_ c.1.8.3 (A:) Beta-mannanase {Thermomonospora fusca}

ATGLHVKNGRLYEANGQEFIIRGVSHPHNWYPQHTQAFADIKSHGANTVRVVLSNGVRWSKNGPSDVANVISLCKQNRLICMLEVHDTTGYGEQSGASTLDQAVDYWIELKSVLQGEEDYVLINIGNEPYGNDSATVAAWATDTSAAIQRLRAAGFEHTLVVDAPNWGQDWTNTMRNNADQVYASDPTGNTVFSIHMYGVYSQASTITSYLEHFVNAGLPLIIGEFGHDHSDGNPDEDTIMAEAERLKLGYIGWSWSGNGGGVEYLDMVYNFDGDNLSPWGERIFYGPNGIASTAKEAVIFG

>d1qnra\_ c.1.8.3 (A:) Beta-mannanase {Trichoderma reesei}

ASSFVTISGTQFNIDGKVGYFAGTNCYWCSFLTNHADVDSTFSHISSSGLKVVRVWGFNDVNTQPSPGQIWFQKLSATGSTINTGADGLQTLDYVVQSAEQHNLKLIIPFVNNWSDYGGINAYVNAFGGNATTWYTNTAAQTQYRKYVQAVVSRYANSTAIFAWELGNEPRCNGCSTDVIVQWATSVSQYVKSLDSNHLVTLGDEGLGLSTGDGAYPYTYGEGTDFAKNVQIKSLDFGTFHLYPDSWGTNYTWGNGWIQTHAAACLAAGKPCVFEEYGAQQNPCTNEAPWQTTSLTTRGMGGDMFWQWGDTFANGAQSNSDPYTVWYNSSNWQCLVKNHVDAIN

>d1j9ya\_ c.1.8.3 (A:) Mannanase 26A {Pseudomonas fluorescens, subsp. cellulosa}

PVTVKLVDSQATMETRSLFAFMQEQRRHSIMFGHQHETTQGLTITRTDGTQSDTFNAVGDFAAVYGWDTLSIVAPKAEGDIVAQVKKAYARGGIITVSSHFDNPKTDTQKGVWPVGTSWDQTPAVVDSLPGGAYNPVLNGYLDQVAEWANNLKDEQGRLIPVIFRLYHENTGSWFWWGDKQSTPEQYKQLFRYSVEYLRDVKGVRNFLYAYSPNNFWDVTEANYLERYPGDEWVDVLGFDTYGPVADNADWFRNVVANAALVARMAEARGKIPVISEIGIRAPDIEAGLYDNQWYRKLISGLKADPDAREIAFLLVWRNAPQGVPGPNGTQVPHYWVPANRPENINNGTLEDFQAFYADEFTAFNRDIEQVYQRPT

>d1ghsa\_ c.1.8.3 (A:) Plant beta-glucanases {Barley (Hordeum vulgare), 1,3-beta-glucanase}

IGVCYGVIGNNLPSRSDVVQLYRSKGINGMRIYFADGQALSALRNSGIGLILDIGNDQLANIAASTSNAASWVQNNVRPYYPAVNIKYIAAGNEVQGGATQSILPAMRNLNAALSAAGLGAIKVSTSIRFDEVANSFPPSAGVFKNAYMTDVARLLASTGAPLLANVYPYFAYRDNPGSISLNYATFQPGTTVRDQNNGLTYTSLFDAMVDAVYAALEKAGAPAVKVVVSESGWPSAGGFAASAGNARTYNQGLINHVGGGTPKKREALETYIFAMFNENQKTGDATERSFGLFNPDKSPAYNIQF

>d1jz8a5 c.1.8.3 (A:334-625) beta-Galactosidase, domain 3 {Escherichia coli}

EVRIENGLLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHYPNHPLWYTLCDRYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQRDRNHPSVIIWSLGNESGHGANHDALYRWIKSVDPSRPVQYEGGGADTTATDIICPMYARVDEDQPFPAVPKWSIKKWLSLPGETRPLILCQYAHAMGNSLGGFAKYWQAFRQYPRLQGGFVWDWVDQSLIKYDENGNPWSAYGGDFGDTPNDRQFCMNGLVFADRTPHPALTEAKHQQQ

>d1bhga3 c.1.8.3 (A:329-632) beta-Glucuronidase, domain 3 {Human (Homo sapiens)}

VAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWLGANAFRTSHYPYAEEVMQMCDRYGIVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVVRRDKNHPAVVMWSVANEPASHLESAGYYLKMVIAHTKSLDPSRPVTFVSNSNYAADKGAPYVDVICLNSYYSWYHDYGHLELIQLQLATQFENWYKKYQKPIIQSEYGAETIAGFHQDPPLMFTEEYQKSLLEQYHLGLDQKRRKYVVGELIWNFADFMTEQSPTRVLGNKKGIFTRQRQPKSAAFLLRERYWKIANE

>d1clxa\_ c.1.8.3 (A:) Xylanase A, catalytic core {Pseudomonas fluorescens}

GLASLADFPIGVAVAASGGNADIFTSSARQNIVRAEFNQITAENIMKMSYMYSGSNFSFTNSDRLVSWAAQNGQTVHGHALVWHPSYQLPNWASDSNANFRQDFARHIDTVAAHFAGQVKSWDVVNEALFDSADDPDGRGSANGYRQSVFYRQFGGPEYIDEAFRRARAADPTAELYYNDFNTEENGAKTTALVNLVQRLLNNGVPIDGVGFQMHVMNDYPSIANIRQAMQKIVALSPTLKIKITELDVRLNNPYDGNSSNDYTNRNDCAVSCAGLDRQKARYKEIVQAYLEVVPPGRRGGITVWGIADPDSWLYTHQNLPDWPLLFNDNLQPKPAYQGVVEALS

>d1e4mm\_ c.1.8.4 (M:) Plant beta-glucosidase (myrosinase) {White mustard (Sinapis alba)}

EITCQENLPFTCGNTDALNSSSFSSDFIFGVASSAYQIEGTIGRGLNIWDGFTHRYPNKSGPDHGNGDTTCDSFSYWQKDIDVLDELNATGYRFSIAWSRIIPRGKRSRGVNEKGIDYYHGLISGLIKKGITPFVTLFHWDLPQTLQDEYEGFLDPQIIDDFKDYADLCFEEFGDSVKYWLTINQLYSVPTRGYGSALDAPGRCSPTVDPSCYAGNSSTEPYIVAHHQLLAHAKVVDLYRKNYTHQGGKIGPTMITRWFLPYNDTDRHSIAATERMKEFFLGWFMGPLTNGTYPQIMIDTVGERLPSFSPEESNLVKGSYDFLGLNYYFTQYAQPSPNPVNSTNHTAMMDAGAKLTYINASGHYIGPLFEKDKADSTDNIYYYPKGIYSVMDYFKNKYYNPLIYVTENGISTPGDENRNQSMLDYTRIDYLCSHLCFLNKVIKEKDVNVKGYLAWALGDNYEFNKGFTVRFGLSYIDWNNVTDRDLKKSGQWYQSFISP

>d1pbga\_ c.1.8.4 (A:) 6-phospho-beta-D-galactosidase, PGAL {Lactococcus lactis}

MTKTLPKDFIFGGATAAYQAEGATHTDGKGPVAWDKYLEDNYWYTAEPASDFYHKYPVDLELAEEYGVNGIRISIAWSRIFPTGYGEVNEKGVEFYHKLFAECHKRHVEPFVTLHHFDTPEALHSNGDFLNRENIEHFIDYAAFCFEEFPEVNYWTTFNEIGPIGDGQYLVGKFPPGIKYDLAKVFQSHHNMMVSHARAVKLYKDKGYKGEIGVVHALPTKYPYDPENPADVRAAELEDIIHNKFILDATYLGHYSDKTMEGVNHILAENGGELDLRDEDFQALDAAKDLNDFLGINYYMSDWMQAFDGETEIIHNGKGEKGSSKYQIKGVGRRVAPDYVPRTDWDWIIYPEGLYDQIMRVKNDYPNYKKIYITENGLGYKDEFVDNTVYDDGRIDYVKQHLEVLSDAIADGANVKGYFIWSLMDVFSWSNGYEKRYGLFYVDFDTQERYPKKSAHWYKKLAETQVIE

>d1qoxa\_ c.1.8.4 (A:) Beta-glucosidase A {Bacillus circulans, subsp. alkalophilus}

SIHMFPSDFKWGVATAAYQIEGAYNEDGRGMSIWDTFAHTPGKVKNGDNGNVACDSYHRVEEDVQLLKDLGVKVYRFSISWPRVLPQGTGEVNRAGLDYYHRLVDELLANGIEPFCTLYHWDLPQALQDQGGWGSRITIDAFAEYAELMFKELGGKIKQWITFNEPWCMAFLSNYLGVHAPGNKDLQLAIDVSHHLLVAHGRAVTLFRELGISGEIGIAPNTSWAVPYRRTKEDMEACLRVNGWSGDWYLDPIYFGEYPKFMLDWYENLGYKPPIVDGDMELIHQPIDFIGINYYTSSMNRYNPGEAGGMLSSEAISMGAPKTDIGWEIYAEGLYDLLRYTADKYGNPTLYITENGACYNDGLSLDGRIHDQRRIDYLAMHLIQASRAIEDGINLKGYMEWSLMDNFEWAEGYGMRFGLVHVDYDTLVRTPKDSFYWYKGVISRGWLDL

>d1gowa\_ c.1.8.4 (A:) beta-Glycosidase {Archaeon Sulfolobus solfataricus}

MYSFPNSFRFGWSQAGFQSEMGTPGSEDPNTDWYKWVHDPENMAAGLVSGDLPENGPGYWGNYKTFHDNAQKMGLKIARLNSEWSRQFPNPLPRPQNFDESKQDVTEVEINENELKRLDEYANKDALNHYREIFKDLKSRGLYFIQNMYHWPLPLWLHDPIRVRRGDFTGPSGWLSTRTVYEFARFSAYTAWKFDDLVDEYSTMNEPNVVGGLGYVGVKSGFPPGYLSFELSRRAMYNIIQAHARAYDGIKSVSKKPVGIIYANSSFQPLTDKDMEAVEMAENDNRWWFFDAIIRGEITRGNEKIVRDDLKGRLDWIGVNYYTRTVVKRTEKGYVSLGGYGHGCERNSVSLAGLPTSDFGWEFFPEGLYDVLTKYWNRYHLYMYVTENGIADDADYQRPYYLVSHVYQVHRAINSGADVRGYLHWSLADNYEWASGFSMRFGLLKVDYNTKRLYWRPSALVYREIATNGAITDEIEHLNSVPPVKPLRH

>d1nar\_\_ c.1.8.5 (-) Seed storage protein {Vicia narbonensis, Narbonin}

PKPIFREYIGVKPNSTTLHDFPTEIINTETLEFHYILGFAIESYYESGKGTGTFEESWDVELFGPEKVKNLKRRHPEVKVVISIGGRGVNTPFDPAEENVWVSNAKESLKLIIQKYSDDSGNLIDGIDIHYEHIRSDEPFATLMGQLITELKKDDDLNINVVSIAPSENNSSHYQKLYNAKKDYINWVDYQFSNQQKPVSTDDAFVEIFKSLEKDYHPHKVLPGFSTDPLDTKHNKITRDIFIGGCTRLVQTFSLPGVFFWNANDSVIPKRDGDKPFIVELTLQQLLAA

>d1cnv\_\_ c.1.8.5 (-) Seed storage protein {Jack bean (Canavalia ensiformis), Concanavalin B}

DISSTEIAVYWGQREDGLLRDTCKTNNYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVALDGIHFDIQKPVDELNWDNLLEELYQIKDVYQSTFLLSAAPGCLSPDEYLDNAIQTRHFDYIFVRFYNDRSCQYSTGNIQRIRNAWLSWTKSVYPRDKNLFLELPASQATAPGGGYIPPSALIGQVLPYLPDLQTRYAGIALWNRQADKETGYSTNIIRYL

>d2ebn\_\_ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {Flavobacterium meningosepticum, endoglycosidase F1}

TTKANIKLFSFTEVNDTNPLNNLNFTLKNSGKPLVDMVVLFSANINYDAANDKVFVSNNPNVQHLLTNRAKYLKPLQDKGIKVILSILGNHDRSGIANLSTARAKAFAQELKNTCDLYNLDGVFFDDEYSAYQTPPPSGFVTPSNNAAARLAYETKQAMPNKLVTVYVYSRTSSFPTAVDGVNAGSYVDYAIHDYGGSYDLATNYPGLAKSGMVMSSQEFNQGRYATAQALRNIVTKGYGGHMIFAMDPNRSNFTSGQLPALKLIAKELYGDELVYSNTPYSKDW

>d1eoka\_ c.1.8.5 (A:) Endo-beta-N-acetylglucosaminidase {Flavobacterium meningosepticum, endoglycosidase F3}

NGVCIAYYITDGRNPTFKLKDIPDKVDMVILFGLKYWSLQDTTKLPGGTGMMGSFKSYKDLDTQIRSLQSRGIKVLQNIDDDVSWQSSKPGGFASAAAYGDAIKSIVIDKWKLDGISLDIEHSGAKPNPIPTFPGYAATGYNGWYSGSMAATPAFLNVISELTKYFGTTAPNNKQLQIASGIDVYAWNKIMENFRNNFNYIQLQSYGANVSRTQLMMNYATGTNKIPASKMVFGAYAEGGTNQANDVEVAKWTPTQGAKGGMMIYTYNSNVSYANAVRDAVK

>d1edt\_\_ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {Streptomyces plicatus, endoglycosidase H}

KQGPTSVAYVEVNNNSMLNVGKYTLADGGGNAFDVAVIFAANINYDTGTKTAYLHFNENVQRVLDNAVTQIRPLQQQGIKVLLSVLGNHQGAGFANFPSQQAASAFAKQLSDAVAKYGLDGVDFDDEYAEYGNNGTAQPNDSSFVHLVTALRANMPDKIISLYNIGPAASRLSYGGVDVSDKFDYAWNPYYGTWQVPGIALPKAQLSPAAVEIGRTSRSTVADLARRTVDEGYGVYLTYNLDGGDRTADVSAFTRELYGSEAVRT

>d1edqa2 c.1.8.5 (A:133-443,A:517-563) Chitinase A, catalytic domain {Serratia marcescens}

TDGSHLAPLKEPLLEKNKPYKQNSGKVVGSYFVEWGVYGRNFTVDKIPAQNLTHLLYGFIPICGGNGINDSLKEIEGSFQALQRSCQGREDFKVSIHDPFAALQKAQKGVTAWDDPYKGNFGQLMALKQAHPDLKILPSIGGWTLSDPFFFMGDKVKRDRFVGSVKEFLQTWKFFDGVDIDWEFPGGKGANPNLGSPQDGETYVLLMKELRAMLDQLSVETGRKYELTSAISAGKDKIDKVAYNVAQNSMDHIFLMSYDFYGAFDLKNLGHQTALNAPAWKPDTAYTTVNGVNALLAQGVKPGKIVVGTAMXDARSVQAKGKYVLDKQLGGLFSWEIDADNGDILNSMNASLGNSAGVQ

>d1goia2 c.1.8.5 (A:3-291,A:380-446) Chitinase B, catalytic domain {Serratia marcescens}

TRKAVIGYYFIPTNQINNYTETDTSVVPFPVSNITPAKAKQLTHINFSFLDINSNLECAWDPATNDAKARDVVNRLTALKAHNPSLRIMFSIGGWYYSNDLGVSHANYVNAVKTPASRAKFAQSCVRIMKDYGFDGVNIDWEYPQAAEVDGFIAALQEIRTLLNQQTITDGRQALPYQLTIAGAGGAFFLSRYYSKLAQIVAPLDYINLMTYDLAGPWEKVTNHQAALFGDAAGPTFYNALREANLGWSWEELTRAFPSPFSLTVDAAVQQHLMMEGVPSAKIVMGVPFXDDAESFKYKAKYIKQQQLGGVMFWHLGQDNRNGDLLAALDRYFNAADYDDSQLDMGTGLRYTGVGPG

>d1d2ka1 c.1.8.5 (A:36-292,A:355-427) Chitinase 1 {Fungus (Coccidioides immitis)}

GGFRSVVYFVNWAIYGRGHNPQDLKADQFTHILYAFANIRPSGEVYLSDTWADTDKHYPGDKWDEPGNNVYGCIKQMYLLKKNNRNLKTLLSIGGWTYSPNFKTPASTEEGRKKFADTSLKLMKDLGFDGIDIDWEYPEDEKQANDFVLLLKACREALDAYSAKHPNGKKFLLTIASPAGPQNYNKLKLAEMDKYLDFWNLMAYDFSGSWDKVSGHMSNVFPSTTKPESTPFSSDKAVKDYIKAGVPANKIVLGMPLXDTVKIAGKKAEYITKNGMGGGMWWESSSDKTGNESLVGTVVNGLGGTGKLEQRENELSYPESVYDNLKNGMPS

>d1e9la1 c.1.8.5 (A:22-266,A:337-393) Chitinase-like lectin ym1, saccharide binding domain {Mouse (Mus musculus)}

YQLMCYYTSWAKDRPIEGSFKPGNIDPCLCTHLIYAFAGMQNNEITYTHEQDLRDYEALNGLKDKNTELKTLLAIGGWKFGPAPFSAMVSTPQNRQIFIQSVIRFLRQYNFDGLNLDWQYPGSRGSPPKDKHLFSVLVKEMRKAFEEESVEKDIPRLLLTSTGAGIIDVIKSGYKIPELSQSLDYIQVMTYDLHDPKDGYTGENSPLYKSPYDIGKSADLNVDSIISYWKDHGAASEKLIVGFPAXDNVRSFKLKAQWLKDNNLGGAVVWPLDMDDFSGSFCHQRHFPLTSTLKGDLNIHSAS

>d1qba\_3 c.1.8.6 (338-780) Bacterial chitobiase (beta-N-acetylhexosaminidase) {Serratia marcescens}

FPYRGIFLDVARNFHKKDAVLRLLDQMAAYKLNKFHFHLSDDEGWRIEIPGLPELTEVGGQRCHDLSETTCLLPQYGQGPDVYGGFFSRQDYIDIIKYAQARQIEVIPEIDMPAHARAAVVSMEARYKKLHAAGKEQEANEFRLVDPTDTSNTTSVQFFNRQSYLNPCLDSSQRFVDKVIGEIAQMHKEAGQPIKTWHFGGDEAKNIRLGAGYTDKAKPEPGKGIIDQGNEDKPWAKSQVCQTMIKEGKVADMEHLPSYFGQEVSKLVKAHGIDRMQAWQDGLKDAESSKAFATSRVGVNFWDTLYWGGFDSVNDWANKGYEVVVSNPDYVYMDFPYEVNPDERGYYWGTRFSDERKVFSFAPDNMPQNAETSVDRDGNHFNAKSDKPWPGAYGLSAQLWSETQRTDPQMEYMIFPRALSVAERSWHRAGWEQDYRAGREYKG

>d1jaka1 c.1.8.6 (A:151-506) beta-N-acetylhexosaminidase {Streptomyces plicatus}

YAWRSAMLDVSRHFFGVDEVKRYIDRVARYKYNKLHLHLSDDQGWRIAIDSWPRLATYGGSTEVGGGPGGYYTKAEYKEIVRYAASRHLEVVPEIDMPGHTNAALASYAELNCDGVAPPLYTGTKVGFSSLCVDKDVTYDFVDDVIGELAALTPGRYLHIGGDEAHSTPKADFVAFMKRVQPIVAKYGKTVVGWHQLAGAEPVEGALVQYWGLDRTGDAEKAEVAEAARNGTGLILSPADRTYLDMKYTKDTPLGLSWAGYVEVQRSYDWDPAGYLPGAPADAVRGVEAPLWTETLSDPDQLDYMAFPRLPGVAELGWSPASTHDWDTYKVRLAAQAPYWEAAGIDFYRSPQVPWT

>d1i0da\_ c.1.9.3 (A:) Phosphotriesterase {Pseudomonas diminuta}

DRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQFFLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGEQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASASALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIPLRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS

>d1bf6a\_ c.1.9.3 (A:) Phosphotriesterase homology protein {Escherichia coli}

SFDPTGYTLAHEHLHIDLSGFKNNVDCRLDQYAFICQEMNDLMTRGVRNVIEMTNRYMGRNAQFMLDVMRETGINVVACTGYYQDAFFPEHVATRSVQELAQEMVDEIEQGIDGTELKAGIIAEIGTSEGKITPLEEKVFIAAALAHNQTGRPISTHTSFSTMGLEQLALLQAHGVDLSRVTVGHCDLKDNLDNILKMIDLGAYVQFDTIGKNSYYPDEKRIAMLHALRDRGLLNRVMLSMDITRRSHLKANGGYGYDYLLTTFIPQLRQSGFSQADVDVMLRENPSQFFQ

>d1jcla\_ c.1.10.1 (A:) Deoxyribose-phosphate aldolase DeoC {Escherichia coli}

HMTDLKASSLRALKLMDLTTLNDDDTDEKVIALCHQAKTPVGNTAAICIYPRFIPIARKTLKEQGTPEIRIATVTNFPHGNDDIDIALAETRAAIAYGADEVDVVFPYRALMAGNEQVGFDLVKACKEACAAANVLLKVIIETGELKDEALIRKASEISIKAGADFIKTSTGKVAVNATPESARIMMEVIRDMGVEKTVGFKPAGGVRTAEDAQKYLAIADELFGADWADARHYRFGASSLLASLLKALGHG

>d1nal1\_ c.1.10.1 (1:) N-acetylneuraminate lyase {Escherichia coli}

NLRGVMAALLTPFDQQQALDKASLRRLVQFNIQQGIDGLYVGGSTGEAFVQSLSEREQVLEIVAEEGKGKIKLIAHVGCVTTAESQQLAASAKRYGFDAVSAVTPFYYPFSFEEHCDHYRAIIDSADGLPMVVYNIPALSGVKLTLDQINTLVTLPGVGALKQTSGDLYQMEQIRREHPDLVLYNGYDEIFASGLLAGADGGIGSTYNIMGWRYQGIVKALKEGDIQTAQKLQTECNKVIDLLIKTGVFRGLKTVLHYMDVVSVPLCRKPFGPVDEKYQPELKALAQQLMQ

>d1f74a\_ c.1.10.1 (A:) N-acetylneuraminate lyase {Haemophilus influenzae}

MRDLKGIFSALLVSFNEDGTINEKGLRQIIRHNIDKMKVDGLYVGGSTGENFMLSTEEKKEIFRIAKDEAKDQIALIAQVGSVNLKEAVELGKYATELGYDCLSAVTPFYYKFSFPEIKHYYDTIIAETGSNMIVYSIPFLTGVNMGIEQFGELYKNPKVLGVKFTAGDFYLLERLKKAYPNHLIWAGFDEMMLPAASLGVDGAIGSTFNVNGVRARQIFELTKAGKLKEALEIQHVTNDLIEGILANGLYLTIKELLKLEGVDAGYCREPMTSKATAEQVAKAKDLKAKFLS

>d1dhpa\_ c.1.10.1 (A:) Dihydrodipicolinate synthase {Escherichia coli}

MFTGSIVAIVTPMDEKGNVCRASLKKLIDYHVASGTSAIVSVGTTGESATLNHDEHADVVMMTLDLADGRIPVIAGTGANATAEAISLTQRFNDSGIVGCLTVTPYYNRPSQEGLYQHFKAIAEHTDLPQILYNVPSRTGCDLLPETVGRLAKVKNIIGIKEATGNLTRVNQIKELVSDDFVLLSGDDASALDFMQLGGHGVISVTANVAARDMAQMCKLAAEGHFAEARVINQRLMPLHNKLFVEPNPIPVKWACKELGLVATDTLRLPMTPITDSGRETVRAALKHAGLL

>d1adoa\_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), muscle isozyme}

PHSHPALTPEQKKELSDIAHRIVAPGKGILAADESTGSIAKRLQSIGTENTEENRRFYRQLLLTADDRVNPCIGGVILFHETLYQKADDGRPFPQVIKSKGGVVGIKVDKGVVPLAGTNGETTTQGLDGLSERCAQYKKDGADFAKWRCVLKIGEHTPSALAIMENANVLARYASICQQNGIVPIVEPEILPDGDHDLKRCQYVTEKVLAAVYKALSDHHIYLEGTLLKPNMVTPGHACTQKYSHEEIAMATVTALRRTVPPAVTGVTFLSGGQSEEEASINLNAINKCPLLKPWALTFSYGRALQASALKAWGGKKENLKAAQEEYVKRALANSLACQGKYTSSGQAGAAASESLFISNHAY

>d1euaa\_ c.1.10.1 (A:) KDPG aldolase {Escherichia coli}

MKNWKTSAESILTTGPVVPVIVVKKLEHAVPMAKALVAGGVRVLEVTLRTECAVDAIRAIAKEVPEAIVGAGTVLNPQQLAEVTEAGAQFAISPGLTEPLLKAATEGTIPLIPGISTVSELMLGMDYGLKEFKFFPAEANGGVKALQAIAGPFSQVRFCPTGGISPANYRDYLALKSVLCIGGSWLVPADALEAGDYDRITKLAREAVEGAKL

>d1qfea\_ c.1.10.1 (A:) Type I 3-dehydroquinate dehydratase {Salmonella typhi}

MKTVTVKNLIIGEGMPKIIVSLMGRDINSVKAEALAYREATFDILEWRVDHFMDIASTQSVLTAARVIRDAMPDIPLLFTFRSAKEGGEQTITTQHYLTLNRAAIDSGLVDMIDLELFTGDADVKATVDYAHAHNVYVVMSNHDFHQTPSAEEMVSRLRKMQALGADIPKIAVMPQSKHDVLTLLTATLEMQQHYADRPVITMSMAKEGVISRLAGEVFGSAATFGAVKQASAPGQIAVNDLRSVLMILHNA

>d1f05a\_ c.1.10.1 (A:) Transaldolase {Human (Homo sapiens)}

MESALDQLKQFTTVVADTGDFHAIDEYKPQDATTNPSLILAAAQMPAYQELVEEAIAYGRKLGGSQEDQIKNAIDKLFVLFGAEILKKIPGRVSTEVDARLSFDKDAMVARARRLIELYKEAGISKDRILIKLSSTWEGIQAGKELEEQHGIHCNMTLLFSFAQAVACAEAGVTLISPFVGRILDWHVANTDKKSYEPLEDPGVKSVTKIYNYYKKFSYKTIVMGASFRNTGEIKALAGCDFLTISPKLLGELLQDNAKLVPVLSAKAAQASDLEKIHLDEKSFRWLHNEDQMAVEKLSDGIRKFAADAVKLERMLTERMFN

>d1h7na\_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Baker's yeast (Saccharomyces cerevisiae)}

MHTAEFLETEPTEISSVLAGGYNHPLLRQWQSERQLTKNMLIFPLFISDNPDDFTEIDSLPNINRIGVNRLKDYLKPLVAKGLRSVILFGVPLIPGTKDPVGTAADDPAGPVIQGIKFIREYFPELYIICDVCLCEYTSHGHCGVLYDDGTINRERSVSRLAAVAVNYAKAGAHCVAPSDMIDGRIRDIKRGLINANLAHKTFVLSYAAKFSGNLYGPFRDAACSAPSNGDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPSTFYLDIMRDASEICKDLPICAYHVSGEYAMLHAAAEKGVVDLKTIAFESHQGFLRAGARLIITYLAPEFLDWLDE

>d1b4ka\_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Pseudomonas aeruginosa}

YPYTRLRRNRRDDFSRRLVRENVLTVDDLILPVFVLDGVNQRESIPSMPGVERLSIDQLLIEAEEWVALGIPALALFPVTPVEKKSLDAAEAYNPEGIAQRATRALRERFPELGIITDVALDPFTTHGQDGILDDDGYVLNDVSIDVLVRQALSHAEAGAQVVAPSDMMDGRIGAIREALESAGHTNVRIMAYSAKYASAYYGPFRDAVGSASNLGKGNKATYQMDPANSDEALHEVAADLAEGADMVMVKPGMPYLDIVRRVKDEFRAPTFVYQVSGEYAMHMGAIQNGWLAESVILESLTAFKRAGADGILTYFAKQAAEQLRR

>d1gg1a\_ c.1.10.4 (A:) 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (DAHP synthase, AroG) {Escherichia coli}

DLRIKEIKELLPPVALLEKFPATENAANTVAHARKAIHKILKGNDDRLLVVIGPCSIHDPVAAKEYATRLLALREELKDELEIVMRVYFEKPRTTVGWKGLINDPHMDNSFQINDGLRIARKLLLDINDSGLPAAGEFLDMITPQYLADLMSWGAIGARTTESQVHRELASGLSCPVGFKNGTDGTIKVAIDAINAAGAPHCFLSVTKWGHSAIVNTSGNGDCHIILRGGKEPNYSAKHVAEVKEGLNKAGLPAQVMIDFSHANSSKQFKKQMDVCADVCQQIAGGEKAIIGVMVESHLVEGNQSLESGEPLAYGKSITDACIGWEDTDALLRQLANAVKARR

>d1d9ea\_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Escherichia coli}

MKQKVVSIGDINVANDLPFVLFGGMNVLESRDLAMRICEHYVTVTQKLGIPYVFKASFDKANRSSIHSYRGPGLEEGMKIFQELKQTFGVKIITDVHEPSQAQPVADVVDVIQLPAFLARQTDLVEAMAKTGAVINVKKPQFVSPGQMGNIVDKFKEGGNEKVILCDRGANFGYDNLVVDMLGFSIMKKVSGNSPVIFDVTHALQCRDPFGAASGGRRAQVAELARAGMAVGLAGLFIEAHPDPEHAKCDGPSALPLAKLEPFLKQMKAIDDLVKGFEELDTSK

>d1ec7a1 c.1.11.2 (A:138-446) D-glucarate dehydratase {Escherichia coli}

DGQQRSEVEMLGYLFFVGNRKATPLPYQSQPDDSCDWYRLRHEEAMTPDAVVRLAEAAYEKYGFNDFKLKGGVLAGEEEAESIVALAQRFPQARITLDPNGAWSLNEAIKIGKYLKGSLAYAEDPCGAEQGFSGREVMAEFRRATGLPTATNMIATDWRQMGHTLSLQSVDIPLADPHFWTMQGSVRVAQMCHEFGLTWGSHSNNHFDISLAMFTHVAAAAPGKITAIDTHWIWQEGNQRLTKEPFEIKGGLVQVPEKPGLGVEIDMDQVMKAHELYQKHGLGARDDAMGMQYLIPGWTFDNKRPCMVR

>d1fhua1 c.1.11.2 (A:100-320) O-succinylbenzoate synthase {Escherichia coli}

QAANYRAAPLCNGDPDDLILKLADMPGEKVAKVKVGLYEAVRDGMVVNLLLEAIPDLHLRLDANRAWTPLKGQQFAKYVNPDYRDRIAFLEEPCKTRDDSRAFARETGIAIAWDESLREPDFAFVAEEGVRAVVIKPTLTGSLEKVREQVQAAHALGLTAVISSSIESSLGLTQLARIAAWLTPDTIPGLDTLDLMQAQQVRRWPGSTLPVVEVDALERLL

>d2mnr\_1 c.1.11.2 (133-359) Mandelate racemase {Pseudomonas putida}

PVQAYDSHSLDGVKLATERAVTAAELGFRAVKTKIGYPALDQDLAVVRSIRQAVGDDFGIMVDYNQSLDVPAAIKRSQALQQEGVTWIEEPTLQHDYEGHQRIQSKLNVPVQMGENWLGPEEMFKALSIGACRLAMPDAMKIGGVTGWIRASALAQQFGIPMSSHLFQEISAHLLAATPTAHWLERLDLAGSVIEPTLTFEGGNAVIPDLPGVGIIWREKEIGKYLV

>d2chr\_1 c.1.11.2 (127-370) Chlormuconate cycloisomerase {Alcaligenes eutrophus}

PLRSAIPIAWTLASGDTKRDLDSAVEMIERRRHNRFKVKLGFRSPQDDLIHMEALSNSLGSKAYLRVDVNQAWDEQVASVYIPELEALGVELIEQPVGRENTQALRRLSDNNRVAIMADESLSTLASAFDLARDRSVDVFSLKLCNMGGVSATQKIAAVAEASGIASYGGTMLDSTIGTSVALQLYSTVPSLPFGCELIGPFVLADTLSHEPLEIRDYELQVPTGVGHGMTLDEDKVRQYARVS

>d1jpdx1 c.1.11.2 (X:114-321) L-Ala-D/L-Glu epimerase {Escherichia coli}

TLPETVITAQTVVIGTPDQMANSASTLWQAGAKLLKVKLDNHLISERMVAIRTAVPDATLIVDANESWRAEGLAARCQLLADLGVAMLEQPLPAQDDAALENFIHPLPICADESCHTRSNLKALKGRYEMVNIKLDKTGGLTEALALATEARAQGFSLMLGCMLCTSRAISAALPLVPQVSFADLDGPTWLAVDVEPALQFTTGELHL

>d1jpma1 c.1.11.2 (A:126-359) L-Ala-D/L-Glu epimerase {Bacillus subtilis}

YRDTLETDYTVSVNSPEEMAADAENYLKQGFQTLKIKVGKDDIATDIARIQEIRKRVGSAVKLRLDANQGWRPKEAVTAIRKMEDAGLGIELVEQPVHKDDLAGLKKVTDATDTPIMADESVFTPRQAFEVLQTRSADLINIKLMKAGGISGAEKINAMAEACGVECMVGSMIETKLGITAAAHFAASKRNITRFDFDAPLMLKTDVFNGGITYSGSTISMPGKPGLGIIGAAL

>d1kcza1 c.1.11.2 (A:161-413) beta-Methylaspartase {Clostridium tetanomorphum}

GAEINAVPVFAQSGDDRYDNVDKMIIKEADVLPHALINNVEEKLGLKGEKLLEYVKWLRDRIIKLRVREDYAPIFHIDVYGTIGAAFDVDIKAMADYIQTLAEAAKPFHLRIEGPMDVEDRQKQMEAMRDLRAELDGRGVDAELVADEWCNTVEDVKFFTDNKAGHMVQIKTPDLGGVNNIADAIMYCKANGMGAYCGGTCNETNRSAEVTTNIGMACGARQVLAKPGMGVDEGMMIVKNEMNRVLALVGRRK

>d1dqua\_ c.1.12.6 (A:) Isocitrate lyase {Aspergillus nidulans}

SYIEEEDQRYWDEVAAVKNWWKDSRWRYTKRPFTAEQIVAKRGNLKIEYPSNVQAKKLWGILERNFKNKEASFTYGCLDPTMVTQMAKYLDTVYVSGWQSSSTASSTDEPSPDLADYPMNTVPNKVNHLWMAQLFHDRKQREERMTTPKDQRHKVANVDYLRPIIADADTGHGGLTAVMKLTKLFVERGAAGIHIEDQAPGTKKCGHMAGKVLVPISEHINRLVAIRAQADIMGTDLLAIARTDSEAATLITSTIDHRDHPFIIGSTNPDIQPLNDLMVMAEQAGKNGAELQAIEDEWLAKAGLKLFNDAVVDAINNSPLPNKKAAIEKYLTQSKGKSNLEARAIAKEIAGTDIYFDWEAPRTREGYYRYQGGTQCAINRAVAYAPFADLIWMESKLPDYKQAKEFADGVHAVWPEQKLAYNLSPSFNWKKAMPRDEQETYIKRLGALGYAWQFITLAGLHTTALISDTFAKAYAKQGMRAYGELVQEPEMANGVDVVTHQKWSGANYVDNMLKMITGG

>d1f8ma\_ c.1.12.6 (A:) Isocitrate lyase {Mycobacterium tuberculosis}

ASVVGTPKSAEQIQQEWDTNPRWKDVTRTYSAEDVVALQGSVVEEHTLARRGAEVLWEQLHDLEWVNALGALTGNMAVQQVRAGLKAIYLSGWQVAGDANLSGHTYPDQSLYPANSVPQVVRRINNALQRADQIAKIEGDTSVENWLAPIVADGEAGFGGALNVYELQKALIAAGVAGSHWEDQLASEKKCGHLGGKVLIPTQQHIRTLTSARLAADVADVPTVVIARTDAEAATLITSDVDERDQPFITGERTREGFYRTKNGIEPCIARAKAYAPFADLIWMETGTPDLEAARQFSEAVKAEYPDQMLAYNCSPSFNWKKHLDDATIAKFQKELAAMGFKFQFITLAGFHALNYSMFDLAYGYAQNQMSAYVELQEREFAAEERGYTATKHQREVGAGYFDRIATTVDPNSSTTALTGSTEEGQF

>d1bura1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

FQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEALYKAQAETGEIKGHYLNATAGTCEDMMKRAVFARELGVPIVMHDYLTGGFTANTTLSHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGGDHIHSGTVVGKLEGERDITLGFVDLLRDDYTEKDRSRGIYFTQSWVSTPGVLPVASGGIHVWHMPALTEIFGDDSVLQFGGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAREGNTIIREATKWSPELAAACEVWKEIKFEFPAMDTV

>d5ruba1 c.1.14.1 (A:138-457) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Rhodospirillum rubrum}

GPSVNISALWKVLGRPEVDGGLVVGTIIKPKLGLRPKPFAEACHAFWLGGDFIKNDEPQGNQPFAPLRDTIALVADAMRRAQDETGEAKLFSANITADDPFEIIARGEYVLETFGENASHVALLVDGYVAGAAAITTARRRFPDNFLHYHRAGHGAVTSPQSKRGYTAFVHCKMARLQGASGIHTGTMGFGKMEGESSDRAIAYMLTQDEAQGPFYRQSWGGMKACTPIISGGMNALRMPGFFENLGNANVILTAGGGAFGHIDGPVAGARSLRQAWQAWRDGVPVLDYAREHKELARAFESFPGDADQIYPGWRKALGV

>d1geha1 c.1.14.1 (A:137-443) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Archaeon Thermococcus kodakaraensis}

DGPAFGIEGVRKMLEIKDRPIYGVVPKPKVGYSPEEFEKLAYDLLSNGADYMKDDENLTSPWYNRFEERAEIMAKIIDKVENETGEKKTWFANITADLLEMEQRLEVLADLGLKHAMVDVVITGWGALRYIRDLAADYGLAIHGHRAMHAAFTRNPYHGISMFVLAKLYRLIGIDQLHVGTAGAGKLEGGKWDVIQNARILRESHYKPDENDVFHLEQKFYSIKAAFPTSSGGLHPGNIQPVIEALGTDIVLQLGGGTLGHPDGPAAGARAVRQAIDAIMQGIPLDEYAKTHKELARALEKWGHVTP

>d4xiaa\_ c.1.15.3 (A:) D-xylose isomerase {Arthrobacter, strain b3728}

VQPTPADHFTFGLWTVGWTGADPFGVATRANLDPVEAVHKLAELGAYGITFHDNDLIPFDATAAEREKILGDFNQALADTGLKVPMVTTNLFSHPVFKDGGFTSNDRSIRRFALAKVLHNIDLAAEMGAETFVMWGGREGSEYDGSKDLAAALDRMREGVDTAAGYIKDKGYNLRIALEPKPNEPRGDIFLPTVGHGLAFIEQLEHGDIVGLNPETGHEQMAGLNFTHGIAQALWAEKLFHIDLNGQRGIKYDQDLVFGHGDLTSAFFTVDLLENGFPNGGPKYTGPRHFDYKPSRTDGYDGVWDSAKANMSMYLLLKERALAFRADPEVQEAMKTSGVFELGETTLNAGESAADLMNDSASFAGFDAEAAAERNFAFIRLNQLAIEHLLGSR

>d1a0ea\_ c.1.15.3 (A:) D-xylose isomerase {Thermotoga neapolitana}

AEFFPEIPKVQFEGKESTNPLAFKFYDPEEIIDGKPLKDHLKFSVAFWHTFVNEGRDPFGDPTADRPWNRYTDPMDKAFARVDALFEFCEKLNIEYFCFHDRDIAPEGKTLRETNKILDKVVERIKERMKDSNVKLLWGTANLFSHPRYMHGAATTCSADVFAYAAAQVKKALEITKELGGEGYVFWGGREGYETLLNTDLGFELENLARFLRMAVDYAKRIGFTGQFLIEPKPKEPTKHQYDFDVATAYAFLKSHGLDEYFKFNIEANHATLAGHTFQHELRMARILGKLGSIDANQGDLLLGWDTDQFPTNVYDTTLAMYEVIKAGGFTKGGLNFDAKVRRASYKVEDLFIGHIAGMDTFALGFKVAYKLVKDGVLDKFIEEKYRSFREGIGRDIVEGKVDFEKLEEYIIDKETIELPSGKQEYLESLINSYIVKTILELR

>d1luca\_ c.1.16.1 (A:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}

MKFGNFLLTYQPPELSQTEVMKRLVNLGKASEGCGFDTVWLLEHHFTEFGLLGNPYVAAAHLLGATETLNVGTAAIVLPTAHPVRQAEDVNLLDQMSKGRFRFGICRGLYDKDFRVFGTDMDNSRALMDCWYDLMKEGFNEGYIAADNEHIKFPKIQLNPSAYTQGGAPVYVVAESASTTEWAAERGLPMILSWIINTHEKKAQLDLYNEVATEHGYDVTKIDHCLSYITSVDHDSNRAKDICRNFLGHWYDSYVNATKIFDDSDQTKGYDFNKGQWRDFVLKGHKDTNRRIDYSYEINPVGTPEECIAIIQQDIDATGIDNICCGFEANGSEEEIIASMKLFQSDVMPYLKEKQ

>d1lucb\_ c.1.16.1 (B:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}

MKFGLFFLNFMNSKRSSDQVIEEMLDTAHYVDQLKFDTLAVYENHFSNNGVVGAPLTVAGFLLGMTKNAKVASLNHVITTHHPVRVAEEACLLDQMSEGRFAFGFSDCEKSADMRFFNRPTDSQFQLFSECHKIINDAFTTGYCHPNNDFYSFPKISVNPHAFTEGGPAQFVNATSKEVVEWAAKLGLPLVFRWDDSNAQRKEYAGLYHEVAQAHGVDVSQVRHKLTLLVNQNVDGEAARAEARVYLEEFVRESYSNTDFEQKMGELLSENAIGTYEESTQAARVAIECCGAADLLMSFESMEDKAQQRAVIDVVNANIV

>d2ptd\_\_ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Bacillus cereus}

ASSVNELENWSKWMQPIPDSIPLARISIPGTHDSGTFKLQNPIKQVWGMTQEYDFRYQMDHGARIFDIRGRLTDDNTIVLHHGPLYLYVTLHEFINEAKQFLKDNPSETIIMSLKKEYEDMKGAEDSFSSTFEKKYFVDPIFLKTEGNIKLGDARGKIVLLKRYSGSNEPGGYNNFYWPDNETFTTTVNQNANVTVQEKYKVSYDEKVKSIKDTMDETMNNSEDLNHLYINFTSLSSGGTAWNSPYYYASYINPEIANYIKQKNPARVGWVIQDYINEKWSPLLYQEVIRANKSLI

>d2plc\_\_ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Listeria monocytogenes}

VTTKQWMSALPDTTNLAALSIPGTHDTMSYNGDITWTLTKPLAQTQTMSLYQQLEAGIRYIDIRAKDNLNIYHGPIFLNASLSGVLETITQFLKKNPKETIIMRLKDEQNSNDSFDYRIQPLINIYKDYFYTTPRTDTSNKIPTLKDVRGKILLLSENHTKKPLVINSRKFGMQFGAPNQVIQDDYNGPSVKTKFKEIVQTAYQASKADNKLFLNHISATSLTFTPRQYAAALNNKVEQFVLNLTSEKVRGLGILIMDFPEKQTIKNIIKNNKF

>d7reqa1 c.1.19.1 (A:4-560) Methylmalonyl-CoA mutase, alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

LPRFDSVDLGNAPVPADAARRFEELAAKAGTGEAWETAEQIPVGTLFNEDVYKDMDWLDTYAGIPPFVHGPYATMYAFRPWTIRQYAGFSTAKESNAFYRRNLAAGQKGLSVAFDLPTHRGYDSDNPRVAGDVGMAGVAIDSIYDMRELFAGIPLDQMSVSMTMNGAVLPILALYVVTAEEQGVKPEQLAGTIQNDILKEFMVRNTYIYPPQPSMRIISEIFAYTSANMPKWNSISISGYHMQEAGATADIEMAYTLADGVDYIRAGESVGLNVDQFAPRLSFFWGIGMNFFMEVAKLRAARMLWAKLVHQFGPKNPKSMSLRTHSQTSGWSLTAQDVYNNVVRTCIEAMAATQGHTQSLHTNSLDEAIALPTDFSARIARNTQLFLQQESGTTRVIDPWSGSAYVEELTWDLARKAWGHIQEVEKVGGMAKAIEKGIPKMRIEEAAARTQARIDSGRQPLIGVNKYRLEHEPPLDVLKVDNSTVLAEQKAKLVKLRAERDPEKVKAALDKITWAAGNPDDKDPDRNLLKLCIDAGRAMATVGEMSDALEKVFGRYT

>d7reqb1 c.1.19.1 (B:16-475) Methylmalonyl-CoA mutase, alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

LTPTTLSLAGDFPKATEEQWEREVEKVLNRGRPPEKQLTFAECLKRLTVHTVDGIDIVPMYRPKDAPKKLGYPGVAPFTRGTTVRNGDMDAWDVRALHEDPDEKFTRKAILEGLERGVTSLLLRVDPDAIAPEHLDEVLSDVLLEMTKVEVFSRYDQGAAAEALVSVYERSDKPAKDLALNLGLDPIGFAALQGTEPDLTVLGDWVRRLAKFSPDSRAVTIDANIYHNAGAGDVAELAWALATGAEYVRALVEQGFTATEAFDTINFRVTATHDQFLTIARLRALREAWARIGEVFGVDEDKRGARQNAITSWRELTREDPYVNILRGSIATFSASVGGAESITTLPFTQALGLPEDDFPLRIARNTGIVLAEEVNIGRVNDPAGGSYYVESLTRSLADAAWKEFQEVEKLGGMSKAVMTEHVTKVLDACNAERAKRLANRKQPITAVSEFPMIGARSIE

>d1aj2\_\_ c.1.21.1 (-) Dihydropteroate synthetase {Escherichia coli}

MKLFAQGTSLDLSHPHVMGILNVTPDSFSDGGTHNSLIDAVKHANLMINAGATIIDVGGESTRPGAAEVSVEEELQRVIPVVEAIAQRFEVWISVDTSKPEVIRESAKVGAHIINDIRSLSEPGALEAAAETGLPVCLMHMQGNPKTMQEAPKYDDVFAEVNRYFIEQIARCEQAGIAKEKLLLDPGFGFGKNLSHNYSLLARLAEFHHFNLPLLVGMSRKSMIGQLLNVGPSERLSGSLACAVIAAMQGAHIIRVHDVKETVEAMRVVEATLSAKENKRYE

>d1ad1a\_ c.1.21.1 (A:) Dihydropteroate synthetase {Staphylococcus aureus}

TKTKIMGILNVTPDSFSDGGKFNNVESAVTRVKAMMDEGADIIDVGGVSTRPGHEMITVEEELNRVLPVVEAIVGFDVKISVDTFRSEVAEACLKLGVDIINDQWAGLYDHRMFQVVAKYDAEIVLMHNGNGNRDEPVVEEMLTSLLAQAHQAKIAGIPSNKIWLDPGIGFAKTRNEEAEVMARLDELVATEYPVLLATSRKRFTKEMMGYDTTPVERDEVTAATTAYGIMKGVRAVRVHNVELNAKLAKGIDFLKENENARHN

>d1uroa\_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Human (Homo sapiens)}

GFPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAAQDFFSTCRSPEACCELTLQPLRRFPLDAAIIFSDILVVPQALGMEVTMVPGKGPSFPEPLREEQDLERLRDPEVVASELGYVFQAITLTRQRLAGRVPLIGFAGAPWTLMTYMVEGGGSSTMAQAKRWLYQRPQASHQLLRILTDALVPYLVGQVVAGAQALQLFESHAGHLGPQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAGYEVVGLDWTVAPKKARECVGKTVTLQGNLDPCALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPDMDPEHVGAFVDAVHKHSRLLRQ

>d1j93a\_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Tobacco (Nicotiana tabacum), UROD-III}

TQPLLLDAVRGKEVERPPVWLMRQAGRYMKSYQLLCEKYPLFRDRSENVDLVVEISLQPWKVFRPDGVILFSDILTPLSGMNIPFDIIKGKGPVIFDPLRTAADVEKVREFIPEKSVPYVGEALTILRKEVNNQAAVLGFVGAPFTLASYVVEGGSSKNFTKIKRLAFAEPKVLHALLQKFATSMAKYIRYQADSGAQAVQIFDSWATELSPVDFEEFSLPYLKQIVDSVKLTHPNLPLILYASGSGGLLERLPLTGVDVVSLDWTVDMADGRRRLGPNVAIQGNVDPGVLFGSKEFITNRINDTVKKAGKGKHILNLGHGIKVGTPEENFAHFFEIAKGLRY

>d1heta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Horse (Equus caballus)}

GFSTGYGSAVKVAKVTQGSTCAVFGLGGVGLSVIMGCKAAGAARIIGVDINKDKFAKAKEVGATECVNPQDYKKPIQEVLTEMSNGGVDFSFEVIGRLDTMVTALSCCQEAYGVSVIVGVPPDSQNLSMNPMLLLSGRTWKGAIFGGFKS

>d1keva2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase {Clostridium beijerinckii}

MMTTGFHGAELADIQMGSSVVVIGIGAVGLMGIAGAKLRGAGRIIGVGSRPICVEAAKFYGATDILNYKNGHIVDQVMKLTNGKGVDRVIMAGGGSETLSQAVSMVKPGGIISNINYHGSGDALLIPRVEWGCGMAHKTIKGGLCPGGRLRAEMLRDMVVYNRV

>d1e3ja2 c.2.1.1 (A:151-313) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}

LEPLSVGVHACRRAGVQLGTTVLVIGAGPIGLVSVLAAKAYGAFVVCTARSPRRLEVAKNCGADVTLVVDPAKEEESSIIERIRSAIGDLPNVTIDCSGNEKCITIGINITRTGGTLMLVGMGSQMVTVPLVNACAREIDIKSVFRYCNDYPIALEMVASGRC

>d1qora2 c.2.1.1 (A:136-265) Quinone oxidoreductase {Escherichia coli}

YEIKPDEQFLFHAAAGGVGLIACQWAKALGAKLIGTVGTAQKAQSALKAGAWQVINYREEDLVERLKEITGGKKVRVVYDSVGRDTWERSLDCLQRRGLMVSFGNSSGAVTGVNLGILNQKGSLYVTRPS

>d1ek6a\_ c.2.1.2 (A:) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Human (Homo sapiens)}

MAEKVLVTGGAGYIGSHTVLELLEAGYLPVVIDNFHNAFRGGGSLPESLRRVQELTGRSVEFEEMDILDQGALQRLFKKYSFMAVIHFAGLKAVGESVQKPLDYYRVNLTGTIQLLEIMKAHGVKNLVFSSSATVYGNPQYLPLDEAHPTGGCTNPYGKSKFFIEEMIRDLCQADKTWNAVLLRYFNPTGAHASGCIGEDPQGIPNNLMPYVSQVAIGRREALNVFGNDYDTEDGTGVRDYIHVVDLAKGHIAALRKLKEQCGCRIYNLGTGTGYSVLQMVQAMEKASGKKIPYKVVARREGDVAACYANPSLAQEELGWTAALGLDRMCEDLWRWQKQNPSGFGT

>d1kewa\_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}

MKILITGGAGFIGSAVVRHIIKNTQDTVVNIDKLTYAGNLESLSDISESNRYNFEHADICDSAEITRIFEQYQPDAVMHLAAESHVDRSITGPAAFIETNIVGTYALLEVARKYWSALGEDKKNNFRFHHISTDEVYGDLPHPDEVENSVTLPLFTETTAYAPSSPYSASKASSDHLVRAWRRTYGLPTIVTNCSNNYGPYHFPEKLIPLVILNALEGKPLPIYGKGDQIRDWLYVEDHARALHMVVTEGKAGETYNIGGHNEKKNLDVVFTICDLLDEIVPKATSYREQITYVADRPGHDRRYAIDAGKISRELGWKPLETFESGIRKTVEWYLANTQWVNNVKSGAYQSWIEQNYEGRQ

>d1e6ua\_ c.2.1.2 (A:) GDP-4-keto-6-deoxy-d-mannose epimerase/reductase (GDP-fucose synthetase) {Escherichia coli}

AKQRVFIAGHRGMVGSAIRRQLEQRGDVELVLRTRDELNLLDSRAVHDFFASERIDQVYLAAAKVGGIVANNTYPADFIYQNMMIESNIIHAAHQNDVNKLLFLGSSCIYPKLAKQPMAESELLQGTLEPTNEPYAIAKIAGIKLCESYNRQYGRDYRSVMPTNLYGPHDNFHPSNSHVIPALLRRFHEATAQKAPDVVVWGSGTPMREFLHVDDMAAASIHVMELAHEVWLENTQPMLSHINVGTGVDCTIRELAQTIAKVVGYKGRVVFDASKPDGTPRKLLDVTRLHQLGWYHEISLEAGLASTYQWFLENQ

>d1db3a\_ c.2.1.2 (A:) GDP-mannose 4,6-dehydratase {Escherichia coli}

SKVALITGVTGQDGSYLAEFLLEKGYEVHGIKRRASSFNTERVDHIYQDPHTCNPKFHLHYGDLSDTSNLTRILREVQPDEVYNLGAMSHVAVSFESPEYTADVDAMGTLRLLEAIRFLGLEKKTRFYQASTSELYGLVQEIPQKETTPFYPRSPYAVAKLYAYWITVNYRESYGMYACNGILFNHESPRRGETFVTRKITRAIANIAQGLESCLYLGNMDSLRDWGHAKDYVKMQWMMLQQEQPEDFVIATGVQYSVRQFVEMAAAQLGIKLRFEGTGVEEKGIVVSVTGHDAPGVKPGDVIIAVDPRYFRPAEVETLLGDPTKAHEKLGWKPEITLREMVSEMVANDLEAAKKHS

>d1eq2a\_ c.2.1.2 (A:) ADP-L-glycero-D-mannoheptose 6-epimerase {Escherichia coli}

MIIVTGGAGFIGSNIVKALNDKGITDILVVDNLKDGTKFVNLVDLNIADYMDKEDFLIQIMAGEEFGDVEAIFHEGACSSTTEWDGKYMMDNNYQYSKELLHYCLEREIPFLYASSAATYGGRTSDFIESREYEKPLNVYGYSKFLFDEYVRQILPEANSQIVGFRYFNVYGPREGHKGSMASVAFHLNTQLNNGESPKLFEGSENFKRDFVYVGDVADVNLWFLENGVSGIFNLGTGRAESFQAVADATLAYHKKGQIEYIPFPDKLKGRYQAFTQADLTNLRAAGYDKPFKTVAEGVTEYMAWLN

>d1qrra\_ c.2.1.2 (A:) Sulfolipid biosynthesis protein SQD1 {Thale cress (Arabidopsis thaliana)}

KRVMVIGGDGYCGWATALHLSKKNYEVCIVDNLVRRLFDHQLGLESLTPIASIHDRISRWKALTGKSIELYVGDICDFEFLAESFKSFEPDSVVHFGEQRSAPYSMIDRSRAVYTQHNNVIGTLNVLFAIKEFGEECHLVKLGTMGEYGTPNIDIEEGYITITHNGRTDTLPYPKQASSFYHLSKVHDSHNIAFTCKAWGIRATDLNQGVVYGVKTDETEMHEELRNRLDYDAVFGTALNRFCVQAAVGHPLTVYGKGGQTRGYLDIRDTVQCVEIAIANPAKAGEFRVFNQFTEQFSVNELASLVTKAGSKLGLDVKKMTVPNPRVEAEEHYYNAKHTKLMELGLEPHYLSDSLLDSLLNFAVQFKDRVDTKQIMPSVSWKKIGVKTKS

>d1k6xa\_ c.2.1.2 (A:) Negative transcriptional regulator NmrA {Aspergillus nidulans}

QQKKTIAVVNATGRQAASLIRVAAAVGHHVRAQVHSLKGLIAEELQAIPNVTLFQGPLLNNVPLMDTLFEGAHLAFINTTSQAGDEIAIGKDLADAAKRAGTIQHYIYSSMPDHSLYGPWPAVPMWAPKFTVENYVRQLGLPSTFVYAGIYNNNFTSLPYPLFQMELMPDGTFEWHAPFDPDIPLPWLDAEHDVGPALLQIFKDGPQKWNGHRIALTFETLSPVQVCAAFSRALNRRVTYVQVPKVEIKVNIPVGYREQLEAIEVVFGEHKAPYFPLPEFSRPAAGSPKGLGPANGKGAGAGMMQGPGGVISQRVTDEARKLWSGWRDMEEYAREVFPIEEEANGLDWML

>d1cyda\_ c.2.1.2 (A:) Carbonyl reductase {Mouse (Mus musculus)}

LNFSGLRALVTGAGKGIGRDTVKALHASGAKVVAVTRTNSDLVSLAKECPGIEPVCVDLGDWDATEKALGGIGPVDLLVNNAALVIMQPFLEVTKEAFDRSFSVNLRSVFQVSQMVARDMINRGVPGSIVNVSSMVAHVTFPNLITYSSTKGAMTMLTKAMAMELGPHKIRVNSVNPTVVLTDMGKKVSADPEFARKLKERHPLRKFAEVEDVVNSILFLLSDRSASTSGGGILVDAGYLAS

>d1oaa\_\_ c.2.1.2 (-) Sepiapterin reductase {Mouse (Mus musculus)}

ADGLGCAVCVLTGASRGFGRALAPQLARLLSPGSVMLVSARSESMLRQLKEELGAQQPDLKVVLAAADLGTEAGVQRLLSAVRELPRPEGLQRLLLINNAATLGDVSKGFLNVNDLAEVNNYWALNLTSMLCLTSGTLNAFQDSPGLSKTVVNISSLCALQPYKGWGLYCAGKAARDMLYQVLAAEEPSVRVLSYAPGPLDNDMQQLARETSKDPELRSKLQKLKSDGALVDCGTSAQKLLGLLQKDTFQSGAHVDFYD

>d1hdr\_\_ c.2.1.2 (-) Dihydropteridin reductase (pteridine reductase) {Human (Homo sapiens)}

EARRVLVYGGRGALGSRCVQAFRARNWWVASVDVVENEEASASIIVKMTDSFTEQADQVTAEVGKLLGEEKVDAILCVAGGWAGGNAKSKSLFKNCDLMWKQSIWTSTISSHLATKHLKEGGLLTLAGAKAALDGTPGMIGYGMAKGAVHQLCQSLAGKNSGMPPGAAAIAVLPVTLDTPMNRKSMPEADFSSWTPLEFLVETFHDWITGKNRPSSGSLIQVVTTEGRTELTPAYF

>d1e7wa\_ c.2.1.2 (A:) Dihydropteridin reductase (pteridine reductase) {Leishmania major}

TVPVALVTGAAKRLGRSIAEGLHAEGYAVCLHYHRSAAEANALSATLNARRPNSAITVQADLSNVATAPVSGADGSAPVTLFTRCAELVAACYTHWGRCDVLVNNASSFYPTPLLRNDEDGHEPCVGDREAMETATADLFGSNAIAPYFLIKAFAHRVAGTPAKHRGTNYSIINMVDAMTNQPLLGYTIYTMAKGALEGLTRSAALELAPLQIRVNGVGPGLSVLVDDMPPAVWEGHRSKVPLYQRDSSAAEVSDVVIFLCSSKAKYITGTCVKVDGGYSLTRA

>d1fds\_\_ c.2.1.2 (-) Human estrogenic 17beta-hydroxysteroid dehydrogenase {Human (Homo sapiens)}

ARTVVLITGCSSGIGLHLAVRLASDPSQSFKVYATLRDLKTQGRLWEAARALACPPGSLETLQLDVRDSKSVAAARERVTEGRVDVLVCNAGLGLLGPLEALGEDAVASVLDVNVVGTVRMLQAFLPDMKRRGSGRVLVTGSVGGLMGLPFNDVYCASKFALEGLCESLAVLLLPFGVHLSLIECGPVHTAFMEKVLGSPEEVLDRTDIHTFHRFYQYLAHSKQVFREAAQNPEEVAEVFLTALRAPKPTLRYFTTERFLPLLRMRLDDPSGSNYVTAMHREVFGDV

>d1fmca\_ c.2.1.2 (A:) 7-alpha-hydroxysteroid dehydrogenase {Escherichia coli}

MFNSDNLRLDGKCAIITGAGAGIGKEIAITFATAGASVVVSDINADAANHVVDEIQQLGGQAFACRCDITSEQELSALADFAISKLGKVDILVNNAGGGGPKPFDMPMADFRRAYELNVFSFFHLSQLVAPEMEKNGGGVILTITSMAAENKNINMTSYASSKAAASHLVRNMAFDLGEKNIRVNGIAPGAILTDALKSVITPEIEQKMLQHTPIRRLGQPQDIANAALFLCSPAASWVSGQILTVSGGGVQELN

>d1hdca\_ c.2.1.2 (A:) 3-alpha,20-beta-hydroxysteroid dehydrogenase {Streptomyces hydrogenans}

NDLSGKTVIITGGARGLGAEAARQAVAAGARVVLADVLDEEGAATARELGDAARYQHLDVTIEEDWQRVVAYAREEFGSVDGLVNNAGISTGMFLETESVERFRKVVEINLTGVFIGMKTVIPAMKDAGGGSIVNISSAAGLMGLALTSSYGASKWGVRGLSKLAAVELGTDRIRVNSVHPGMTYTPMTAETGIRQGEGNYPNTPMGRVGEPGEIAGAVVKLLSDTSSYVTGAELAVDGGWTTGPTVKYVMGQ

>d1fjha\_ c.2.1.2 (A:) 3-alpha-hydroxysteroid dehydrogenase {Comamonas testosteroni}

MSIIVISGCATGIGAATRKVLEAAGHQIVGIDIRDAEVIADLSTAEGRKQAIADVLAKCSKGMDGLVLCAGLGPQTKVLGNVVSVNYFGATELMDAFLPALKKGHQPAAVVISSVASAHLAFDKNPLALALEAGEEAKARAIVEHAGEQGGNLAYAGSKNALTVAVRKRAAAWGEAGVRLNTIAPGATETPLLQAGLQDPRYGESIAKFVPPMGRRAEPSEMASVIAFLMSPAASYVHGAQIVIDGGIDAVMRPTQF

>d1bdb\_\_ c.2.1.2 (-) Cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase {Pseudomonas sp., lb400}

MKLKGEAVLITGGASGLGRALVDRFVAEGAKVAVLDKSAERLAELETDHGDNVLGIVGDVRSLEDQKQAASRCVARFGKIDTLIPNAGIWDYSTALVDLPEESLDAAFDEVFHINVKGYIHAVKACLPALVASRGNVIFTISNAGFYPNGGGPLYTAAKHAIVGLVRELAFELAPYVRVNGVGSGGINSDLRGPSSLGMGSKAISTVPLADMLKSVLPIGRMPEVEEYTGAYVFFATRGDAAPATGALLNYDGGLGVRGFFSGAGGNDLLEQLNIH

>d1b16a\_ c.2.1.2 (A:) Drosophila alcohol dehydrogenase {Fruit fly (Drosophila lebanonensis)}

MDLTNKNVIFVAALGGIGLDTSRELVKRNLKNFVILDRVENPTALAELKAINPKVNITFHTYDVTVPVAESKKLLKKIFDQLKTVDILINGAGILDDHQIERTIAINFTGLVNTTTAILDFWDKRKGGPGGIIANICSVTGFNAIHQVPVYSASKAAVVSFTNSLAKLAPITGVTAYSINPGITRTPLVHTFNSWLDVEPRVAELLLSHPTQTSEQCGQNFVKAIEANKNGAIWKLDLGTLEAIEWTKHWDSHI

>d1gcoa\_ c.2.1.2 (A:) Glucose dehydrogenase {Bacillus megaterium}

MYKDLEGKVVVITGSSTGLGKSMAIRFATEKAKVVVNYRSKEDEANSVLEEIKKVGGEAIAVKGDVTVESDVINLVQSAIKEFGKLDVMINNAGLENPVSSHEMSLSDWNKVIDTNLTGAFLGSREAIKYFVENDIKGTVINMSSVHEKIPWPLFVHYAASKGGMKLMTETLALEYAPKGIRVNNIGPGAINTPINAEKFADPEQRADVESMIPMGYIGEPEEIAAVAAWLASSEASYVTGITLFADGGMTQYPSFQAGRG

>d1gega\_ c.2.1.2 (A:) meso-2,3-butanediol dehydrogenase {Klebsiella pneumoniae}

KKVALVTGAGQGIGKAIALRLVKDGFAVAIADYNDATAKAVASEINQAGGHAVAVKVDVSDRDQVFAAVEQARKTLGGFDVIVNNAGVAPSTPIESITPEIVDKVYNINVKGVIWGIQAAVEAFKKEGHGGKIINACSQAGHVGNPELAVYSSSKFAVRGLTQTAARDLAPLGITVNGYCPGIVKTPMWAEIDRQVSEAAGKPLGYGTAEFAKRITLGRLSEPEDVAACVSYLASPDSDYMTGQSLLIDGGMVFN

>d1h5qa\_ c.2.1.2 (A:) Mannitol dehydrogenase {Mushroom (Agaricus bisporus)}

PGFTISFVNKTIIVTGGNRGIGLAFTRAVAAAGANVAVIYRSAADAVEVTEKVGKEFGVKTKAYQCDVSNTDIVTKTIQQIDADLGPISGLIANAGVSVVKPATELTHEDFAFVYDVNVFGVFNTCRAVAKLWLQKQQKGSIVVTSSMSSQIINQSSLNGSLTQVFYNSSKAACSNLVKGLAAEWASAGIRVNALSPGYVNTDQTAHMDKKIRDHQASNIPLNRFAQPEEMTGQAILLLSDHATYMTGGEYFIDGGQLIW

>d1i01a\_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Escherichia coli}

MNFEGKIALVTGASRGIGRAIAETLAARGAKVIGTATSENGAQAISDYLGANGKGLMLNVTDPASIESVLEKIRAEFGEVDILVNNAGITRDNLLMRMKDEEWNDIIETNLSSVFRLSKAVMRAMMKKRHGRIITIGSVVGTMGNGGQANYAAAKAGLIGFSKSLAREVASRGITVNVVAPGFIETDMTRALSDDQRAGILAQVPAGRLGGAQEIANAVAFLASDEAAYITGETLHVNGGM

>d1eno\_\_ c.2.1.2 (-) Enoyl-ACP reductase {Oil seed rape (Brassica napus)}

LPIDLRGKRAFIAGIADDNGYGWAVAKSLAAAGAEILVGTWVPALNIFETSLRRGKFDQSRVLPDGSLMEIKKVYPLDAVFDNPEDVPEDVKANKRYAGSSNWTVQEAAECVRQDFGSIDILVHSLANGPEVSKPLLETSRKGYLAAISASSYSFVSLLSHFLPIMNPGGASISLTYIASERIIPGYGGGMSSAKAALESDTRVLAFEAGRKQNIRVNTISAGPLGSRAAKAIGFIDTMIEYSYNNAPIQKTLTADEVGNAAAFLVSPLASAITGATIYVDNGLNSMGVALDSPVFK

>d1eny\_\_ c.2.1.2 (-) Enoyl-ACP reductase {Mycobacterium tuberculosis, TB, gene InhA}

AGLLDGKRILVSGIITDSSIAFHIARVAQEQGAQLVLTGFDRLRLIQRITDRLPAKAPLLELDVQNEEHLASLAGRVTEAIGAGNKLDGVVHSIGFMPQTGMGINPFFDAPYADVSKGIHISAYSYASMAKALLPIMNPGGSIVGMDFDPSRAMPAYNWMTVAKSALESVNRFVAREAGKYGVRSNLVAAGPIRTLAMSAIVGGALGEEAGAQIQLLEEGWDQRAPIGWNMKDATPVAKTVCALLSDWLPATTGDIIYADGGAHTQLL

>d1qg6a\_ c.2.1.2 (A:) Enoyl-ACP reductase {Escherichia coli}

GFLSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKLKGRVEEFAAQLGSDIVLQCDVAEDASIDTMFAELGKVWPKFDGFVHSIGFAPGDQLDGDYVNAVTREGFKIAHDISSYSFVAMAKACRSMLNPGSALLTLSYLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEGVRVNAISAGPIRTLAASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGISGEVVHVDGGFSIAAMNE

>d2ae2a\_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (Datura stramonium), II}

AGRWNLEGCTALVTGGSRGIGYGIVEELASLGASVYTCSRNQKELNDCLTQWRSKGFKVEASVCDLSSRSERQELMNTVANHFHGKLNILVNNAGIVIYKEAKDYTVEDYSLIMSINFEAAYHLSVLAHPFLKASERGNVVFISSVSGALAVPYEAVYGATKGAMDQLTRCLAFEWAKDNIRVNGVGPGVIATSLVEMTIQDPEQKENLNKLIDRCALRRMGEPKELAAMVAFLCFPAASYVTGQIIYVDGGLMANCGF

>d1g0oa\_ c.2.1.2 (A:) 1,3,8-trihydroxynaphtalene reductase (THNR, naphtol reductase) {Rice blast fungus (Magnaporthe grisea)}

KYDAIPGPLGPQSASLEGKVALVTGAGRGIGREMAMELGRRGCKVIVNYANSTESAEEVVAAIKKNGSDAACVKANVGVVEDIVRMFEEAVKIFGKLDIVCSNSGVVSFGHVKDVTPEEFDRVFTINTRGQFFVAREAYKHLEIGGRLILMGSITGQAKAVPKHAVYSGSKGAIETFARCMAIDMADKKITVNVVAPGGIKTDMYHAVCREYIPNGENLSNEEVDEYAAVQWSPLRRVGLPIDIARVVCFLASNDGGWVTGKVIGIDGGACM

>d1hdoa\_ c.2.1.2 (A:) Biliverdin IX beta reductase {Human (Homo sapiens)}

MAVKKIAIFGATGQTGLTTLAQAVQAGYEVTVLVRDSSRLPSEGPRPAHVVVGDVLQAADVDKTVAGQDAVIVLLGTRNDLSPTTVMSEGARNIVAAMKAHGVDKVVACTSAFLLWDPTKVPPRLQAVTDDHIRMHKVLRESGLKYVAVMPPHIGDQPLTGAYTVTLDGRGPSRVISKHDLGHFMLRCLTTDEYDGHSTYPSHQY

>d1e6wa\_ c.2.1.2 (A:) 3-hydroxyacyl-CoA dehydrogenase {Rat (Rattus norvegicus)}

SVKGLVAVITGGASGLGLSTAKRLVGQGATAVLLDVPNSEGETEAKKLGGNCIFAPANVTSEKEVQAALTLAKEKFGRIDVAVNCAGIAVAIKTYHEKKNQVHTLEDFQRVINVNLIGTFNVIRLVAGVMGQNEPDQGGQRGVIINTASVAAFEGQVGQAAYSASKGGIVGMTLPIARDLAPIGIRVVTIAPGLFATPLLTTLPDKVRNFLASQVPFPSRLGDPAEYAHLVQMVIENPFLNGEVIRLDGAIRMQP

>d1hu4a\_ c.2.1.2 (A:) Carbonyl reductase/20beta-hydroxysteroid dehydrogenase {Pig (Sus scrofa)}

SSNTRVALVTGANKGIGFAIVRDLCRQFAGDVVLTARDVARGQAAVKQLQAEGLSPRFHQLDIIDLQSIRALCDFLRKEYGGLDVLVNNAAIAFQLDNPTPFHIQAELTMKTNFMGTRNVCTELLPLIKPQGRVVNVSSTEGVRALNECSPELQQKFKSETITEEELVGLMNKFVEDTKNGVHRKEGWSDSTYGVTKIGVSVLSRIYARKLREQRAGDKILLNACCPGWVRTDMGGPKAPKSPEVGAETPVYLALLPSDAEGPHGQFVTDKKVVEWGVPPESYPWVNA

>d1b7go1 c.2.1.3 (O:1-138,O:301-340) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Sulfolobus solfataricus}

MVNVAVNGYGTIGKRVADAIIKQPDMKLVGVAKTSPNYEAFIAHRRGIRIYVPQQSIKKFEESGIPVAGTVEDLIKTSDIVVDTTPNGVGAQYKPIYLQLQRNAIFQGGEKAEVADISFSALCNYNEALGKKYIRVVSXESIVVPENIDAIRASMKLMSAEDSMRITNESLGILKGYLI

>d1ggaa1 c.2.1.3 (A:1-164,A:334-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Trypanosoma brucei brucei, glycosome}

TIKVGINGFGRIGRMVFQALCDDGLLGNEIDVVAVVDMNTDARYFAYQMKYDSVHGKFKHSVSTTKSKPSVAKDDTLVVNGHRILCVKAQRNPADLPWGKLGVEYVIESTGLFTVKSAAEGHLRGGARKVVISAPASGGAKTFVMGVNHNNYNPREQHVVSNASXNEWGYSHRVVDLVRHMAARDRAAKL

>d1gl3a1 c.2.1.3 (A:1-133,A:355-367) Aspartate beta-semialdehyde dehydrogenase {Escherichia coli}

MKNVGFIGWRGMVGSVLMQRMVEERDFDAIRPVFFSTSQLGQAAPSFGGTTGTLQDAFDLEALKALDIIVTCQGGDYTNEIYPKLRESGWQGYWIDAASSLRMKDDAIIILDPVNQDVITDGLNNGIRTFVGGXAAEPLRRMLRQLA

>d1ebfa1 c.2.1.3 (A:2-150,A:341-359) Homoserine dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

STKVVNVAVIGAGVVGSAFLDQLLAMKSTITYNLVLLAEAERSLISKDFSPLNVGSDWKAALAASTTKTLPLDDLIAHLKTSPKPVILVDNTSSAYIAGFYTKFVENGISIATPNKKAFSSDLATWKALFSNKPTNGFVYHEATVGAGLXAAVTAAGVLGDVIKIAQRL

>d1e5qa1 c.2.1.3 (A:2-124,A:392-450) Saccharopine reductase {Rice blast fungus (Magnaporthe grisea)}

ATKSVLMLGSGFVTRPTLDVLTDSGIKVTVACRTLESAKKLSAGVQHSTPISLDVNDDAALDAEVAKHDLVISLIPYTFHATVIKSAIRQKKHVVTTSYVSPAMMELDQAAKDAGITVMNEIGXYSAMAKLVGVPCAVAVKFVLDGTISDRGVLAPMNSKINDPLMKELKEKYGIECKEKVVA

>d1f06a1 c.2.1.3 (A:1-118,A:269-320) Diaminopimelic acid dehydrogenase (DAPDH) {Corynebacterium glutamicum}

MTNIRVAIVGYGNLGRSVEKLIAKQPDMDLVGIFSRRATLDTKTPVFDVADVDKHADDVDVLFLCMGSATDIPEQAPKFAQFACTVDTYDNHRDIPRHRQVMNEAATAAGNVALVSTGXRNPDFTASSQIAFGRAAHRMKQQGQSGAFTVLEVAPYLLSPENLDDLIARDV

>d1dih\_1 c.2.1.3 (2-130,241-273) Dihydrodipicolinate reductase {Escherichia coli}

HDANIRVAIAGAGGRMGRQLIQAALALEGVQLGAALEREGSSLLGSDAGELAGAGKTGVTVQSSLDAVKDDFDVFIDFTRPEGTLNHLAFCRQHGKGMVIGTTGFDEAGKQAIRDAAADIAIVFAANFSXMTFANGAVRSALWLSGKESGLFDMRDVLDLNNL

>d1k5ha2 c.2.1.3 (A:1-125,A:275-300) 1-deoxy-D-xylulose-5-phosphate reductoisomerase {Escherichia coli}

MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEASAKLLKTMLQQQGSRTEVLSGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKTILLANKXDMRTPIAHTMAWPNRVNSGVKPLDFC

>d1gcua1 c.2.1.3 (A:1-128,A:247-292) Biliverdin reductase {Rat (Rattus norvegicus)}

MDAEPKRKFGVVVVGVGRAGSVRLRDLKDPRSAAFLNLIGFVSRRELGSLDEVRQISLEDALRSQEIDVAYICSESSSHEDYIRQFLQAGKHVLVEYPMTLSFAAAQELWELAAQKGRVLHEEHVELLXKNIFLKDQDIFVQKLLDQVSAEDLAAEKKRIMHCLGLASDIQKLCH

>d1h6da1 c.2.1.3 (A:51-212,A:375-433) Glucose-fructose oxidoreductase, N-terminal domain {Zymomonas mobilis}

QAATLPAGASQVPTTPAGRPMPYAIRPMPEDRRFGYAIVGLGKYALNQILPGFAGCQHSRIEALVSGNAEKAKIVAAEYGVDPRKIYDYSNFDKIAKDPKIDAVYIILPNSLHAEFAIRAFKAGKHVMCEKPMATSVADCQRMIDAAKAANKKLMIGYRCHYXNQFSAQLDHLAEAVINNKPVRSPGEEGMQDVRLIQAIYEAARTGRPVNTDWGYVRQGGY

>d1dpga1 c.2.1.3 (A:1-181,A:413-426) Glucose 6-phosphate dehydrogenase, N-terminal domain {Leuconostoc mesenteroides}

VSEIKTLVTFFGGTGDLAKRKLYPSVFNLYKKGYLQKHFAIVGTARQALNDDEFKQLVRDCIKDFTDDQAQAEAFIEHFSYRAHDVTDAASYAVLKEAIEEAADKFDIDGNRIFYMSVAPRFFGTIAKYLKSEGLLADTGYNRLMIEKPFGTSYDTAAELQNDLENAFDDNQLFRIDHYLGXEPYERMIHDTMNGD

>d1qkia1 c.2.1.3 (A:12-199,A:435-449) Glucose 6-phosphate dehydrogenase, N-terminal domain {Human (Homo sapiens)}

VCGILREELFQGDAFHQSDTHIFIIMGASGDLAKKKIYPTIWWLFRDGLLPENTFIVGYARSRLTVADIRKQSEPFFKATPEEKLKLEDFFARNSYVAGQYDDAASYQRLNSHMNALHLGSQANRLFYLALPPTVYEAVTKNIHESCMSQIGWNRIIVEKPFGRDLQSSDRLSNHISSLFREDQIYRIXDAYERLILDVFCGSQ

>d2naca1 c.2.1.4 (A:148-335) Formate dehydrogenase {Pseudomonas sp., strain 101}

ISVAEHVVMMILSLVRNYLPSHEWARKGGWNIADCVSHAYDLEAMHVGTVAAGRIGLAVLRRLAPFDVHLHYTDRHRLPESVEKELNLTWHATREDMYPVCDVVTLNCPLHPETEHMINDETLKLFKRGAYIVNTARGKLCDRDAVARALESGRLAGYAGDVWFPQPAPKDHPWRTMPYNGMTPHISG

>d1qp8a1 c.2.1.4 (A:83-263) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}

ADAVAEFALALLLAPYKRIIQYGEKMKRGDYGRDVEIPLIQGEKVAVLGLGEIGTRVGKILAALGAQVRGFSRTPKEGPWRFTNSLEEALREARAAVCALPLNKHTRGLVKYQHLALMAEDAVFVNVGRAEVLDRDGVLRILKERPQFIFASDVWWGRNDFAKDAEFFSLPNVVATPWVAG

>d1dxy\_1 c.2.1.4 (101-299) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}

SPAAIAEFALTDTLYLLRNMGKVQAQLQAGDYEKAGTFIGKELGQQTVGVMGTGHIGQVAIKLFKGFGAKVIAYDPYPMKGDHPDFDYVSLEDLFKQSDVIDLHVPGIEQNTHIINEAAFNLMKPGAIVINTARPNLIDTQAMLSNLKSGKLAGVGIDTYEYETEDLLNLAKHGSFKDPLWDELLGMPNVVLSPHIAYY

>d1gdha1 c.2.1.4 (A:101-291) D-glycerate dehydrogenase {Hyphomicrobium methylovorum}

VTVATAEIAMLLLLGSARRAGEGEKMIRTRSWPGWEPLELVGEKLDNKTLGIYGFGSIGQALAKRAQGFDMDIDYFDTHRASSSDEASYQATFHDSLDSLLSVSQFFSLNAPSTPETRYFFNKATIKSLPQGAIVVNTARGDLVDNELVVAALEAGRLAYAGFDVFAGEPNINEGYYDLPNTFLFPHIGSA

>d1psda1 c.2.1.4 (A:108-295) Phosphoglycerate dehydrogenase {Escherichia coli}

NTRSVAELVIGELLLLLRGVPEANAKAHRGVWNKLAAGSFEARGKKLGIIGYGHIGTQLGILAESLGMYVYFYDIENKLPLGNATQVQHLSDLLNMSDVVSLHVPENPSTKNMMGAKEISLMKPGSLLINASRGTVVDIPALCDALASKHLAGAAIDVFPTEPATNSDPFTSPLCEFDNVLLTPHIGG

>d1pjca1 c.2.1.4 (A:136-303) L-alanine dehydrogenase {Phormidium lapideum}

AGRLSVQFGARFLERQQGGRGVLLGGVPGVKPGKVVILGGGVVGTEAAKMAVGLGAQVQIFDINVERLSYLETLFGSRVELLYSNSAEIETAVAEADLLIGAVLVPGRRAPILVPASLVEQMRTGSVIVDVAVDQGGCVETLHPTSHTQPTYEVFGVVHYGVPNMPGA

>d1f8ga1 c.2.1.4 (A:144-326) Nicotinamide nucleotide transhydrogenase dI component {Rhodospirillum rubrum}

AGYRAVIDGAYEFARAFPMMMTAAGTVPPARVLVFGVGVAGLQAIATAKRLGAVVMATDVRAATKEQVESLGGKFITVDDEAMKTAETAGGYAKEMGEEFRKKQAEAVLKELVKTDIAITTALIPGKPAPVLITEEMVTKMKPGSVIIDLAVEAGGNCPLSEPGKIVVKHGVKIVGHTNVPSR

>d1b3ra1 c.2.1.4 (A:190-352) S-adenosylhomocystein hydrolase {Rat (Rattus norvegicus)}

NLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEIDPINALQAAMEGYEVTTMDEACKEGNIFVTTTGCVDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNENAVEKVNIKPQVDRYLLKNGHRIILLAEGRLVNLGCAMGH

>d1civa1 c.2.1.5 (A:12-193) Malate dehydrogenase {Flaveria bidentis, chloroplast}

LPAKQKPECFGVFCLTYDLKAEEETKSWKKIINVAVSGAAGMISNHLLFKLASGEVFGPDQPISLKLLGSERSFAALEGVAMELEDSLYPLLRQVSIGIDPYEIFQDAEWALLIGAKPRGPGMERADLLDINGQIFAEQGKALNAVASPNVKVMVVGNPCNTNALICLKNAPNIPPKNFHAL

>d2cmd\_1 c.2.1.5 (1-145) Malate dehydrogenase {Escherichia coli}

MKVAVLGAAGGIGQALALLLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVKIKGFSGEDATPALEGADVVLISAGVRRKPGMDRSDLFNVNAGIVKNLVQQVAKTCPKACIGIITNPVNTTVAIAAEVLKKAGVYDKNKLFG

>d2hlpa1 c.2.1.5 (A:22-162) Malate dehydrogenase {Archaeon Haloarcula marismortui}

TKVSVVGAAGTVGAAAGYNIALRDIADEVVFVDIPDKEDDTVGQAADTNHGIAYDSNTRVRQGGYEDTAGSDVVVITAGIPRQPGQTRIDLAGDNAPIMEDIQSSLDEHNDDYISLTTSNPVDLLNRHLYEAGDRSREQVIG

>d1hyha1 c.2.1.5 (A:21-166) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus confusus}

ARKIGIIGLGNVGAAVAHGLIAQGVADDYVFIDANEAKVKADQIDFQDAMANLEAHGNIVINDWAALADADVVISTLGNIKLQQDNPTGDRFAELKFTSSMVQSVGTNLKESGFHGVLVVISNPVDVITALFQHVTGFPAHKVIGT

>d5ldh\_1 c.2.1.5 (1-162) Lactate dehydrogenase {Pig (Sus scrofa)}

ATLKEKLIAPVAQQETTIPDNKITVVGVGQVGMACAISILGKSLTDELALVDVLEDKLKGEMMDLQHGSLFLQTPKIVANKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPNCIIIVVSNPVDILTYVAWKLSGLPKHRVIG

>d1ceqa1 c.2.1.5 (A:19-163) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}

PKAKIVLVGSGMIGGVMATLIVQKNLGDVVLFDIVKNMPHGKALDTSHTNVMAYSNCKVSGSNTYDDLAGSDVVIVTAGFTKAPGKSDKEWNRDDLLPLNNKIMIEIGGHIKKNCPNAFIIVVTNPVDVMVQLLHQHSGVPKNKIIGL

>d1ldna1 c.2.1.5 (A:15-162) Lactate dehydrogenase {Bacillus stearothermophilus}

MKNNGGARVVVIGAGFVGASYVFALMNQGIADEIVLIDANESKAIGDAMDFNHGKVFAPKPVDIWHGDYDDCRDADLVVICAGANQKPGETRLDLVDKNIAIFRSIVESVMASGFQGLFLVATNPVDILTYATWKFSGLPHERVIGSG

>d1llda1 c.2.1.5 (A:7-149) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}

PTKLAVIGAGAVGSTLAFAAAQRGIAREIVLEDIAKERVEAEVLDMQHGSSFYPTVSIDGSDDPEICRDADMVVITAGPRQKPGQSRLELVGATVNILKAIMPNLVKVAPNAIYMLITNPVDIATHVAQKLTGLPENQIFGSG

>d1hyea1 c.2.1.5 (A:1-145) MJ0490, lactate/malate dehydrogenase {Archaeon Methanococcus jannaschii}

MKVTIIGASGRVGSATALLLAKEPFMKDLVLIGREHSINKLEGLREDIYDALAGTRSDANIYVESDENLRIIDESDVVIITSGVPRKEGMSRMDLAKTNAKIVGKYAKKIAEICDTKIFVITNPVDVMTYKALVDSKFERNQVFG

>d1qmga2 c.2.1.6 (A:82-307) Acetohydroxy acid isomeroreductase, ketoacid reductoisomerase (KARI) {Spinach (Spinacia oleracea)}

SATTFDFDSSVFKKEKVTLSGHDEYIVRGGRNLFPLLPDAFKGIKQIGVIGWGSQAPAQAQNLKDSLTEAKSDVVVKIGLRKGSNSFAEARAAGFSEENGTLGDMWETISGSDLVLLLISDSAQADNYEKVFSHMKPNSILGLSHGFLLGHLQSLGQDFPKNISVIAVCPKGMGPSVRRLYVQGKEVNGAGINSSFAVHQDVDGRATDVALGWSIALGSPFTFATT

>d1pgja2 c.2.1.6 (A:1-178) 6-phosphogluconate dehydrogenase {Trypanosoma brucei}

SMDVGVVGLGVMGANLALNIAEKGFKVAVFNRTYSKSEEFMKANASAPFAGNLKAFETMEAFAASLKKPRKALILVQAGAATDSTIEQLKKVFEKGDILVDTGNAHFKDQGRRAQQLEAAGLRFLGMGISGGEEGARKGPAFFPGGTLSVWEEIRPIVEAAAAKADDGRPCVTMNGSG

>d1f0ya2 c.2.1.6 (A:12-203) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (Homo sapiens)}

KIIVKHVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAKSKKGIEESLRKVAKKKFAENPKAGDEFVEKTLSTIATSTDAASVVHSTDLVVEAIVENLKVKNELFKRLDKFAAEHTIFASNTSSLQITSIANATTRQDRFAGLHFFNPVPVMKLVEVIKTPMTSQKTFESLVDFSKALGKHPVSCKDTP

>d1dlja2 c.2.1.6 (A:1-196) UDP-glucose dehydrogenase (UDPGDH) {Streptococcus pyogenes}

MKIAVAGSGYVGLSLGVLLSLQNEVTIVDILPSKVDKINNGLSPIQDEYIEYYLKSKQLSIKATLDSKAAYKEAELVIIATPTNYNSRINYFDTQHVETVIKEVLSVNSHATLIIKSTIPIGFITEMRQKFQTDRIIFSPEFLRESKALYDNLYPSRIIVSCEENDSPKVKADAEKFALLLKSAAKKNNVPVLIMG

>d1bg6\_2 c.2.1.6 (4-187) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}

SKTYAVLGLGNGGHAFAAYLALKGQSVLAWDIDAQRIKEIQDRGAIIAEGPGLAGTAHPDLLTSDIGLAVKDADVILIVVPAIHHASIAANIASYISEGQLIILNPGATGGALEFRKILRENGAPEVTIGETSSMLFTCRSERPGQVTVNAIKGAMDFACLPAAKAGWALEQIGSVLPQYVAVE

>d1evya2 c.2.1.6 (A:9-188) Glycerol-3- phosphate dehydrogenase {Trypanosome (Leishmania mexicana)}

KDELLYLNKAVVFGSGAFGTALAMVLSKKCREVCVWHMNEEEVRLVNEKRENVLFLKGVQLASNITFTSDVEKAYNGAEIILFVIPTQFLRGFFEKSGGNLIAYAKEKQVPVLVCTKGIERSTLKFPAEIIGEFLPSPLLSVLAGPSFAIEVATGVFTCVSIASADINVARRLQRIMSTG

>d1ks9a2 c.2.1.6 (A:1-167) Ketopantoate reductase PanE {Escherichia coli}

MKITVLGCGALGQLWLTALCKQGHEVQGWLRVPQPYCSVNLVETDGSIFNESLTANDPDFLATSDLLLVTLKAWQVSDAVKSLASTLPVTTPILLIHNGMGTIEELQNIQQPLLMGTTTHAARRDGNVIIHVANGITHIGPARQQDGDYSYLADILQTVLPDVAWHN

>d1jaya\_ c.2.1.6 (A:) Coenzyme F420H2:NADP+ oxidoreductase (FNO) {Archaeon Archaeoglobus fulgidus}

MRVALLGGTGNLGKGLALRLATLGHEIVVGSRREEKAEAKAAEYRRIAGDASITGMKNEDAAEACDIAVLTIPWEHAIDTARDLKNILREKIVVSPLVPVSRGAKGFTYSSERSAAEIVAEVLESEKVVSALHTIPAARFANLDEKFDWDVPVCGDDDESKKVVMSLISEIDGLRPLDAGPLSNSRLVESLTPLILNIMRFNGMGELGIKFL

>d1bgva1 c.2.1.7 (A:195-449) Glutamate dehydrogenase {Clostridium symbiosum}

KARSFGGSLVRPEATGYGSVYYVEAVMKHENDTLVGKTVALAGFGNVAWGAAKKLAELGAKAVTLSGPDGYIYDPEGITTEEKINYMLEMRASGRNKVQDYADKFGVQFFPGEKPWGQKVDIIMPCATQNDVDLEQAKKIVANNVKYYIEVANMPTTNEALRFLMQQPNMVVAPSKAVNAGGVLVSGFEMSQNSERLSWTAEEVDSKLHQVMTDIHDGSAAAAERYGLGYNLVAGANIVGFQKIADAMMAQGIAW

>d1gtma1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}

GGSLGRIEATARGASYTIREAAKVLGWDTLKGKTIAIQGYGNAGYYLAKIMSEDFGMKVVAVSDSKGGIYNPDGLNADEVLKWKNEHGSVKDFPGATNITNEELLELEVDVLAPAAIEEVITKKNADNIKAKIVAEVANGPVTPEADEILFEKGILQIPDFLCNAGGVTVSYFEWVQNITGYYWTIEEVRERLDKKMTKAFYDVYNIAKEKNIHMRDAAYVVAVQRVYQAMLDRGWVKH

>d1hwxa1 c.2.1.7 (A:209-501) Glutamate dehydrogenase {Cow (Bos taurus)}

HGRISATGRGVFHGIENFIENASYMSILGMTPGFGDKTFAVQGFGNVGLHSMRYLHRFGAKCVAVGESDGSIWNPDGIDPKELEDFKLQHGTILGFPKAKIYEGSILEVDCDILIPAASEKQLTKSNAPRVKAKIIAEGANGPTTPQADKIFLERNIMVIPDLYLNAGGVTVSYFQILKNLNHVSYGRLTFKYERDSNYHLLMSVQESLERKFGKHGGTIPIVPTAEFQDRISGASEKDIVHSGLAYTMERSARQIMRTAMKYNLGLDLRTAAYVNAIEKVFRVYNEAGVTFT

>d1leha1 c.2.1.7 (A:135-364) Leucine dehydrogenase {Bacillus sphaericus}

GISPAFGSSGNPSPVTAYGVYRGMKAAAKEAFGSDSLEGLAVSVQGLGNVAKALCKKLNTEGAKLVVTDVNKAAVSAAVAEEGADAVAPNAIYGVTCDIFAPCALGAVLNDFTIPQLKAKVIAGSADNQLKDPRHGKYLHELGIVYAPDYVINAGGVINVADELYGYNRTRAMKRVDGIYDSIEKIFAISKRDGVPSYVAADRMAEERIAKVAKARSQFLQDQRNILNGR

>d1c1da1 c.2.1.7 (A:149-349) Phenylalanine dehydrogenase {Rhodococcus sp., M4}

SAFTTAVGVFEAMKATVAHRGLGSLDGLTVLVQGLGAVGGSLASLAAEAGAQLLVADTDTERVAHAVALGHTAVALEDVLSTPCDVFAPCAMGGVITTEVARTLDCSVVAGAANNVIADEAASDILHARGILYAPDFVANAGGAIHLVGREVLGWSESVVHERAVAIGDTLNQVFEISDNDGVTPDEAARTLAGRRAREAS

>d1a4ia1 c.2.1.7 (A:127-296) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}

LTSINAGRLARGDLNDCFIPCTPKGCLELIKETGVPIAGRHAVVVGRSKIVGAPMHDLLLWNNATVTTCHSKTAHLDEEVNKGDILVVATGQPEMVKGEWIKPGAIVIDCGINYVPDDKKPNGRKVVGDVAYDEAKERASFITPVPGGVGPMTVAMLMQSTVESAKRFLE

>d1edza1 c.2.1.7 (A:149-319) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}

PCTPLAIVKILEFLKIYNNLLPEGNRLYGKKCIVINRSEIVGRPLAALLANDGATVYSVDVNNIQKFTRGESLKLNKHHVEDLGEYSEDLLKKCSLDSDVVITGVPSENYKFPTEYIKEGAVCINFACTKNFSDDVKEKASLYVPMTGKVTIAMLLRNMLRLVRNVELSKE

>d1do8a1 c.2.1.7 (A:280-573) Mitochondrial NAD(P)-dependenent malic enzyme {Human (Homo sapiens)}

IQGTAAVALAGLLAAQKVISKPISEHKILFLGAGEAALGIANLIVMSMVENGLSEQEAQKKIWMFDKYGLLVKGRKAKIDSYQEPFTHSAPESIPDTFEDAVNILKPSTIIGVAGAGRLFTPDVIRAMASINERPVIFALSNPTAQAECTAEEAYTLTEGRCLFASGSPFGPVKLTDGRVFTPGQGNNVYIFPGVALAVILCNTRHISDSVFLEAAKALTSQLTDEELAQGRLYPPLANIQEVSINIAIKVTEYLYANKMAFRYPEPEDKAKYVKERTWRSEYDSLLPDVYEWP

>d1djna2 c.3.1.1 (A:490-645) Trimethylamine dehydrogenase, C-terminal domain {Methylophilus methylotrophus, w3a1}

RWNTDGTNCLTHDPIPGADASLPDQLTPEQVMDGKKKIGKRVVILNADTYFMAPSLAEKLATAGHEVTIVSGVHLANYMHFTLEYPNMMRRLHELHVEELGDHFCSRIEPGRMEIYNIWGDGSKRTYRGPGVSPRDANTSHRWIEFDSLVLVTGRH

>d1cjca1 c.3.1.1 (A:107-331) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}

HQALDIPGEELPGVFSARAFVGWYNGLPENRELAPDLSCDTAVILGQGNVALDVARILLTPPDHLEKTDITEAALGALRQSRVKTVWIVGRRGPLQVAFTIKELREMIQLPGTRPMLDPADFLGLQDRIKEAARPRKRLMELLLRTATEKPGVEEAARRASASRAWGLRFFRSPQQVLPSPDGRRAAGIRLAVTRLEGIGEATRAVPTGDVEDLPCGLVLSSIGY

>d1h7wa3 c.3.1.1 (A:288-440) Dihydropyrimidine dehydrogenase, domain 3 {Pig (Sus scrofa)}

PKTDDIFQGLTQDQGFYTSKDFLPLVAKSSKAGMCACHSPLPSIRGAVIVLGAGDTAFDCATSALRCGARRVFLVFRKGFVNIRAVPEEVELAKEEKCEFLPFLSPRKVIVKGGRIVAVQFVRTEQDETGKWNEDEDQIVHLKADVVISAFGS

>d1coy\_1 c.3.1.2 (4-318,451-506) Cholesterol oxidase {Brevibacterium sterolicum}

RTLADGDRVPALVIGSGYGGAVAALRLTQAGIPTQIVEMGRSWDTPGSDGKIFCGMLNPDKRSMWLADKTDQPVSNFMGFGINKSIDRYVGVLDSERFSGIKVYQGRGVGGGSLVNGGMAVTPKRNYFEEILPSVDSNEMYNKYFPRANTGLGVNNIDQAWFESTEWYKFARTGRKTAQRSGFTTAFVPNVYDFEYMKKEAAGQVTKSGLGGEVIYGNNAGKKSLDKTYLAQAAATGKLTITTLHRVTKVAPATGSGYSVTMEQIDEQGNVVATKVVTADRVFFAAGSVGTSKLLVSMKAQGHLPNLSSQVGEGWXGVLLNKATDNFGRLPEYPGLYVVDGSLVPGNVGVNPFVTITALAERNMDKIISSDI

>d1k0ia1 c.3.1.2 (A:1-173,A:276-394) p-Hydroxybenzoate hydroxylase, PHBH {Pseudomonas aeruginosa}

MKTQVAIIGAGPSGLLLGQLLHKAGIDNVILERQTPDYVLGRIRAGVLEQGMVDLLREAGVDRRMARDGLVHEGVEIAFAGQRRRIDLKRLSGGKTVTVYGQTEVTRDLMEAREACGATTVYQAAEVRLHDLQGERPYVTFERDGERLRLDCDYIAGCDGFHGISRQSIPAERXMQHGRLFLAGDAAHIVPPTGAKGLNLAASDVSTLYRLLLKAYREGRGELLERYSAICLRRIWKAERFSWWMTSVLHRFPDTDAFSQRIQQTELEYYLGSEAGLATIAENYVGLPYEEIE

>d1el8a1 c.3.1.2 (A:1-217,A:322-385) Sarcosine oxidase {Bacillus sp., strain b0618}

STHFDVIVVGAGSMGMAAGYQLAKQGVKTLLVDAFDPPHTNGSHHGDTRIIRHAYGEGREYVPLALRSQELWYELEKETHHKIFTKTGVLVFGPKGESAFVAETMEAAKEHSLTVDLLEGDEINKRWPGITVPENYNAIFEPNSGVLFSENCIRAYRELAEARGAKVLTHTRVEDFDISPDSVKIETANGSYTADKLIVSMGAWNSKLLSKLNLDIPXDEHFIIDLHPEHSNVVIAAGFSGHGFKFSSGVGEVLSQLALTGKTEHDISIFSINRPALKESLQ

>d1foha5 c.3.1.2 (A:1-240,A:342-461) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}

TKYSESYCDVLIVGAGPAGLMAARVLSEYVRQKPDLKVRIIDKRSTKVYNGQADGLQCRTLESLKNLGLADKILSEANDMSTIALYNPDENGHIRRTDRIPDTLPGISRYHQVVLHQGRIERHILDSIAEISDTRIKVERPLIPEKMEIDSSKAEDPEAYPVTMTLRYMSDHESTPLQFGHKTENSLFHSNLQTQEEEDANYRLPEGKEAGEIETVHCKYVIGCDGGHSWVRRTLGFEMIXVTEKFSKDERVFIAGDACHTHSPKAGQGMNTSMMDTYNLGWKLGLVLTGRAKRDILKTYEEERHAFAQALIDFDHQFSRLFSGRPAKDVADEMGVSMDVFKEAFVKGNEFASGTAINYDE

>d1gpea1 c.3.1.2 (A:1-328,A:525-587) Glucose oxidase {Penicillium amagasakiense}

YLPAQQIDVQSSLLSDPSKVAGKTYDYIIAGGGLTGLTVAAKLTENPKIKVLVIEKGFYESNDGAIIEDPNAYGQIFGTTVDQNYLTVPLINNRTNNIKAGKGLGGSTLINGDSWTRPDKVQIDSWEKVFGMEGWNWDNMFEYMKKAEAARTPTAAQLAAGHSFNATCHGTNGTVQSGARDNGQPWSPIMKALMNTVSALGVPVQQDFLCGHPRGVSMIMNNLDENQVRVDAARAWLLPNYQRSNLEILTGQMVGKVLFKQTASGPQAVGVNFGTNKAVNFDVFAKHEVLLAAGSAISPLILEYSGIGLKSVLDQANVTQLLDLPVGIXCSMMSRELGGVVDATAKVYGTQGLRVIDGSIPPTQVSSHVMTIFYGMALKVADAILDDYAKSA

>d1b5qa1 c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (Zea mays)}

PRVIVVGAGMSGISAAKRLSEAGITDLLILEATDHIGGRMHKTNFAGINVELGANWVEGVNGGKMNPIWPIVNSTLKLRNFRSDFDYLAQNVYKEDGGVYDEDYVQKRIELADSVEEMGEKLSATLHASGRDDMSILAMQRLNEHQPNGPATPVDMVVDYYKFDYEFAEPPRVTSLQNTVPLATFSDFGDDVYFVADQRGYEAVVYYLAGQYLKTDDKSGKIVDPRLQLNKVVREIKYSPGGVTVKTEDNSVYSADYVMVSASLGVLQSDLIQFKPKLPTWKVRAIYQFXWPVGVNRYEYDQLRAPVGRVYFTGEHTSEHYNGYVHGAYLSGIDSAEILINCAQKKMC

>d1f8ra1 c.3.1.2 (A:4-319,A:433-486) L-amino acid oxidase {Malayan pit viper (Calloselasma rhodostoma)}

RNPLAECFQENDYEEFLEIARNGLKATSNPKHVVIVGAGMAGLSAAYVLAGAGHQVTVLEASERPGGRVRTYRNEEAGWYANLGPMRLPEKHRIVREYIRKFDLRLNEFSQENDNAWYFIKNIRKKVGEVKKDPGLLKYPVKPSEAGKSAGQLYEESLGKVVEELKRTNCSYILNKYDTYSTKEYLIKEGDLSPGAVDMIGDLLNEDSGYYVSFIESLKHDDIFAYEKRFDEIVDGMDKLPTAMYRDIQDKVHFNAQVIKIQQNDQKVTVVYETLSKETPSVTADYVIVCTTSRAVRLIKFNPPLLPKKAHALRSVXFTPYQFQHFSDPLTASQGRIYFAGEYTAQAHGWIDSTIKSGLRAARDVNLASEN

>d1gosa1 c.3.1.2 (A:4-289,A:402-500) Monoamine oxidase B {Human (Homo sapiens)}

KCDVVVVGGGISGMAAAKLLHDSGLNVVVLEARDRVGGRTYTLRNQKVKYVDLGGSYVGPTQNRILRLAKELGLETYKVNEVERLIHHVKGKSYPFRGPFPPVWNPITYLDHNNFWRTMDDMGREIPSDAPWKAPLAEEWDNMTMKELLDKLCWTESAKQLATLFVNLCVTAETHEVSALWFLWYVKQCGGTTRIISTTNGGQERKFVGGSGQVSERIMDLLGDRVKLERPVIYIDQTRENVLVETLNHEMYEAKYVISAIPPTLGMKIHFNPPLPMMRNQMITRVXFPPGILTQYGRVLRQPVDRIYFAGTETATHWSGYMEGAVEAGERAAREILHAMGKIPEDEIWQSEPESVDVPAQPITTTFLERHLPSVPGLLRLIGLTT

>d1chua2 c.3.1.4 (A:2-237,A:354-422) L-aspartate oxidase {Escherichia coli}

NTLPEHSCDVLIIGSGAAGLSLALRLADQHQVIVLSKGPVTEGSTFYAQGGIAAVFDETDSIDSHVEDTLIAGAGICDRHAVEFVASNARSCVQWLIDQGVLFDTHIQPNGEESYHLTREGGHSHRRILHAADATGREVETTLVSKALNHPNIRVLERTNAVDLIVSDKIGLPGTRRVVGAWVWNRNKETVETCHAKAVVLATGGASKVYQYTTNPDISSGDGIAMAWRAGCRVANXCGGVMVDDHGRTDVEGLYAIGEVSYTGLHGANRMASNSLLECLVYGWSAAEDITRRMPYAHDISTLPPW

>d1fuma2 c.3.1.4 (A:1-225,A:358-442) Fumarate reductase flavoprotein subunit {Escherichia coli}

QTFQADLAIVGAGGAGLRAAIAAAQANPNAKIALISKVYPMRSHTVAAEGGSAAVAQDHDSFEYHFHDTVAGGDWLCEQDVVDYFVHHCPTEMTQLELWGCPWSRRPDGSVNVRRFGGMKIERTWFAADKTGFHMLHTLFQTSLQFPQIQRFDEHFVLDILVDDGHVRGLVAMNMMEGTLVQIRANAVVMATGGAGRVYRYNTNGGIVTGDGMGMALSHGVPLRDXMGGIETDQNCETRIKGLFAVGECSSVGLHGANRLGSNSLAELVVFGRLAGEQATERAATAGNGNEAAIEAQAAGVEQRLKDLVNQ

>d1qlaa2 c.3.1.4 (A:1-250,A:372-457) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}

MKVQYCDSLVIGGGLAGLRAAVATQQKGLSTIVLSLIPVKRSHSAAAQGGMQASLGNSKMSDGDNEDLHFMDTVKGSDWGCDQKVARMFVNTAPKAIRELAAWGVPWTRIHKGDRMAIINAQKTTITEEDFRHGLIHSRDFGGTKKWRTCYTADATGHTMLFAVANECLKLGVSIQDRKEAIALIHQDGKCYGAVVRDLVTGDIIAYVAKGTLIATGGYGRIYKNTTNAVVCEGTGTAIALETGIAQLGNXMGGIRTDYRGEAKLKGLFSAGEAACWDMHGFNRLGGNSVSEAVVAGMIVGEYFAEHCANTQVDLETKTLEKFVKGQEAYMKSLVES

>d1d4ca2 c.3.1.4 (A:103-359,A:506-570) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}

KFVPVDADKAAQDKAIAAGVKETTDVVIIGSGGAGLAAAVSARDAGAKVILLEKEPIPGGNTKLAAGGMNAAETKPQAKLGIEDKKQIMIDDTMKGGRNINDPELVKVLANNSSDSIDWLTSMGADMTDVGRMGGASVNRSHRPTGGAGVGAHVAQVLWDNAVKRGTDIRLNSRVVRILEDASGKVTGVLVKGEYTGYYVIKADAVVIAAGGFAKNNERVSKYDPKLKGFKATNHPGATGDGLDVALQAGAATRDLEXMGGLVIDTKAEVKSEKTGKPITGLYAAGEVTGGVHGANRLGGNAISDIVTYGRIAGASAAKFAKD

>d1jnra2 c.3.1.4 (A:2-256,A:402-502) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

VYYPKKYELYKADEVPTEVVETDILIIGGGFSGCGAAYEAAYWAKLGGLKVTLVEKAAVERSGAVAQGLSAINTYIDLTGRSERQNTLEDYVRYVTLDMMGLAREDLVADYARHVDGTVHLFEKWGLPIWKTPDGKYVREGQWQIMIHGESYKPIIAEAAKMAVGEENIYERVFIFELLKDNNDPNAVAGAVGFSVREPKFYVFKAKAVILATGGATLLFRPRSTGEAAGRTWYAIFDTGSGYYMGLKAGAMLTQXAGFWVCGPEDLMPEEYAKLFPLKYNRMTTVKGLFAIGDCAGANPHKFSSGSFTEGRIAAKAAVRFILEQKPNPEIDDAVVEELKKKAYAPMERFMQYKDLS

>d3grs\_1 c.3.1.5 (18-165,291-363) Glutathione reductase {Human (Homo sapiens)}

VASYDYLVIGGGSGGLASARRAAELGARAAVVESHKLGGTCVNVGCVPKKVMWNTAVHSEFMHDHADYGFPSCEGKFNWRVIKEKRDAYVSRLNAIYQNNLTKSHIEIIRGHAAFTSDPKPTIEVSGKKYTAPHILIATGGMPSTPHEXRVPNTKDLSLNKLGIQTDDKGHIIVDEFQNTNVKGIYAVGDVCGKALLTPVAIAAGRKLAHRLFEYKEDSKLD

>d3grs\_2 c.3.1.5 (166-290) Glutathione reductase {Human (Homo sapiens)}

SQIPGASLGITSDGFFQLEELPGRSVIVGAGYIAVEMAGILSALGSKTSLMIRHDKVLRSFDSMISTNCTEELENAGVEVLKFSQVKEVKKTLSGLEVSMVTAVPGRLPVMTMIPDVDCLLWAIG

>d1feca1 c.3.1.5 (A:1-169,A:287-357) Trypanothione reductase {Crithidia fasciculata}

SRAYDLVVIGAGSGGLEAGWNAASLHKKRVAVIDLQKHHGPPHYAALGGTCVNVGCVPKKLMVTGANYMDTIRESAGFGWELDRESVRPNWKALIAAKNKAVSGINDSYEGMFADTEGLTFHQGFGALQDNHTVLVRESADPNSAVLETLDTEYILLATGSWPQHLGIEXVPRSQTLQLEKAGVEVAKNGAIKVDAYSKTNVDNIYAIGDVTDRVMLTPVAINEGAAFVDTVFANKPRATD

>d1feca2 c.3.1.5 (A:170-286) Trypanothione reductase {Crithidia fasciculata}

GDDLCITSNEAFYLDEAPKRALCVGGGYISIEFAGIFNAYKARGGQVDLAYRGDMILRGFDSELRKQLTEQLRANGINVRTHENPAKVTKNADGTRHVVFESGAEADYDVVMLAIGR

>d1h6va1 c.3.1.5 (A:10-170,A:293-366) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

SYDFDLIIIGGGSGGLAAAKEAAKFDKKVMVLDFVTPTPLGTNWGLGGTCVNVGCIPKKLMHQAALLGQALKDSRNYGWKLEDTVKHDWEKMTESVQNHIGSLNWGYRVALREKKVVYENAYGKFIGPHKIMATNNKGKEKVYSAERFLIATGERPRYLGIXRDSCTRTIGLETVGVKINEKTGKIPVTDEEQTNVPYIYAIGDILEGKLELTPVAIQAGRLLAQRLYGGSTVKCD

>d1h6va2 c.3.1.5 (A:171-292) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

PGDKEYCISSDDLFSLPYCPGKTLVVGASYVALECAGFLAGIGLDVTVMVRSILLRGFDQDMANKIGEHMEEHGIKFIRQFVPTKIEQIEAGTPGRLKVTAKSTNSEETIEDEFNTVLLAVG

>d1vdc\_1 c.3.1.5 (1-117,244-316) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}

LETHNTRLCIVGSGPAAHTAAIYAARAELKPLLFEGWMANDIAPGGQLTTTTDVENFPGFPEGILGVELTDKFRKQSERFGTTIFTETVTKVDFSSKPFKLFTDSKAILADAVILAIGAVAKXGHEPATKFLDGGVELDSDGYVVTKPGTTQTSVPGVFAAGDVQDKKYRQAITAAGTGCMAALDAEHYLQEI

>d1vdc\_2 c.3.1.5 (118-243) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}

RLSFVGSGEVLGGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANFLTKYGSKVYIIHRRDAFRASKIMQQRALSNPKIDVIWNSSVVEAYGDGERDVLGGLKVKNVVTGDVSDLKVSGLFFAI

>d1hyua1 c.3.1.5 (A:199-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Salmonella typhimurium}

AEKRAAEALNKRDAYDVLIVGSGPAGAAAAVYSARKGIRTGLMGERFGGQVLDTVDIENYISVPKTEGQKLAGALKAHVSDYDVDVIDSQSASKLVPAATEGGLHQIETASGAVLKARSIIIATGAKXLPNTHWLEGALERNRMGEIIIDAKCETSVKGVFAAGDCTTVPYKQIIIATGEGAKASLSAFDYLIRTKIA

>d1fl2a2 c.3.1.5 (A:326-451) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Escherichia coli}

WRNMNVPGEDQYRTKGVTYCPHCDGPLFKGKRVAVIGGGNSGVEAAIDLAGIVEHVTLLEFAPEMKADQVLQDKLRSLKNVDIILNAQTTEVKGDGSKVVGLEYRDRVSGDIHNIELAGIFVQIGL

>d1nhp\_1 c.3.1.5 (1-119,243-321) NADH peroxidase {Enterococcus faecalis}

MKVIVLGSSHGGYEAVEELLNLHPDAEIQWYEKGDFISFLSAGMQLYLEGKVKDVNSVRYMTGEKMESRGVNVFSNTEITAIQPKEHQVTVKDLVSGEERVENYDKLIISPGAVPFELDXGVRPNTAWLKGTLELHPNGLIKTDEYMRTSEPDVFAVGDATLIKYNPADTEVNIALATNARKQGRFAVKNLEEPVKPFP

>d1nhp\_2 c.3.1.5 (120-242) NADH peroxidase {Enterococcus faecalis}

IPGKDLDNIYLMRGRQWAIKLKQKTVDPEVNNVVVIGSGYIGIEAAEAFAKAGKKVTVIDILDRPLGVYLDKEFTDVLTEEMEANNITIATGETVERYEGDGRVQKVVTDKNAYDADLVVVAV

>d1d7ya1 c.3.1.5 (A:5-115,A:237-308) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}

ALKAPVVVLGAGLASVSFVAELRQAGYQGLITVVGDEAERPYDRPPLSKDFMAHGDAEKIRLDCKRAPEVEWLLGVTAQSFDPQAHTVALSDGRTLPYGTLVLATGAAPRAXVLANDALARAAGLACDDGIFVDAYGRTTCPDVYALGDVTRQRNPLSGRFERIETWSNAQNQGIAVARHLVDP

>d1d7ya2 c.3.1.5 (A:116-236) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}

LPTLQGATMPVHTLRTLEDARRIQAGLRPQSRLLIVGGGVIGLELAATARTAGVHVSLVETQPRLMSRAAPATLADFVARYHAAQGVDLRFERSVTGSVDGVVLLDDGTRIAADMVVVGIG

>d1lvl\_1 c.3.1.5 (1-150,266-335) Dihydrolipoamide dehydrogenase {Pseudomonas putida}

QQTIQTTLLIIGGGPGGYVAAIRAGQLGIPTVLVEGQALGGTCLNIGCIPSKALIHVAEQFHQASRFTEPSPLGISVASPRLDIGQSVAWKDGIVDRLTTGVAALLKKHGVKVVHGWAKVLDGKQVEVDGQRIQCEHLLLATGSSSVELPXRRPRTKGFNLECLDLKMNGAAIAIDERCQTSMHNVWAIGDVAGEPMLAHRAMAQGEMVAEIIAGKARRFE

>d1lpfa2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}

PAPLSDDIIVDSTGALEFQAVPKKLGVIGAGVIGLELGSVWARLGAEVTVLEALDKFLPAADEQIAKEALKVLTKQGLNIRLGARVTASEVKKKQVTVTFTDANGEQKETFDKLIVAVG

>d1ojt\_1 c.3.1.5 (117-275,401-470) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

GSADAEYDVVVLGGGPGGYSAAFAAADEGLKVAIVERYKTLGGVCLNVGCIPSKALLHNAAVIDEVRHLAANGIKYPEPELDIDMLRAYKDGVVSRLTGGLAGMAKSRKVDVIQGDGQFLDPHHLEVSLTAGDAYEQAAPTGEKKIVAFKNCIIAAGSRXAPNGKLISAEKAGVAVTDRGFIEVDKQMRTNVPHIYAIGDIVGQPMLAHKAVHEGHVAAENCAGHKAYFD

>d1ojt\_2 c.3.1.5 (276-400) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

VTKLPFIPEDPRIIDSSGALALKEVPGKLLIIGGGIIGLEMGTVYSTLGSRLDVVEMMDGLMQGADRDLVKVWQKQNEYRFDNIMVNTKTVAVEPKEDGVYVTFEGANAPKEPQRYDAVLVAAGR

>d1jeha1 c.3.1.5 (A:1-160,A:283-355) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

TINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGKLGGTCLNVGCIPSKALLNNSHLFHQMHTEAQKRGIDVNGDIKINVANFQKAKDDAVKQLTGGIELLFKKNKVTYYKGNGSFEDETKIRVTPVDGLEGTVKEDHILDVKNIIVATGSEVTPFXVGRRPYIAGLGAEKIGLEVDKRGRLVIDDQFNSKFPHIKVVGDVTFGPMLAHKAEEEGIAAVEMLKTGHGHVN

>d1dxla2 c.3.1.5 (A:153-275) Dihydrolipoamide dehydrogenase {Garden pea (Pisum sativum)}

SLPGVTIDEKKIVSSTGALALSEIPKKLVVIGAGYIGLEMGSVWGRIGSEVTVVEFASEIVPTMDAEIRKQFQRSLEKQGMKFKLKTKVVGVDTSGDGVKLTVEPSAGGEQTIIEADVVLVSA

>d1fcda1 c.3.1.5 (A:1-114,A:256-327) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}

AGRKVVVVGGGTGGATAAKYIKLADPSIEVTLIEPNTDYYTCYLSNEVIGGDRKLESIKHGYDGLRAHGIQVVHDSATGIDPDKKLVKTAGGAEFGYDRCVVAPGIELIYDKIEXQRAGKIAQIAGLTNDAGWCPVDIKTFESSIHKGIHVIGDASIANPMPKSGYSANSQGKVAAAAVVVLLKGEE

>d1fcda2 c.3.1.5 (A:115-255) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}

GYSEEAAAKLPHAWKAGEQTAILRKQLEDMADGGTVVIAPPAAPFRCPPGPYERASQVAYYLKAHKPMSKVIILDSSQTFSKQSQFSKGWERLYGFGTENAMIEWHPGPDSAVVKVDGGEMMVETAFGDEFKADVINLIPP

>d1djna3 c.4.1.1 (A:341-489,A:646-729) Trimethylamine dehydrogenase, middle domain {Methylophilus methylotrophus, w3a1}

DIRVCIGCNVCISRWEIGGPPMICTQNATAGEEYRRGWHPEKFRQTKNKDSVLIVGAGPSGSEAARVLMESGYTVHLTDTAEKIGGHLNQVAALPGLGEWSYHRDYRETQITKLLKKNKESQLALGQKPMTADDVLQYGADKVIIATGAXSECTLWNELKARESEWAENDIKGIYLIGDAEAPRLIADATFTGHRVAREIEEANPQIAIPYKRETIAWGTPHMPGGNFKIEYKV

>d1cjca2 c.4.1.1 (A:6-106,A:332-460) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}

TPQICVVGSGPAGFYTAQHLLKHHSRAHVDIYEKQLVPFGLVRFGVAPDHPEVKNVINTFTQTARSDRCAFYGNVEVGRDVTVQELQDAYHAVVLSYGAEDXKSRPIDPSVPFDPKLGVVPNMEGRVVDVPGLYCSGWVKRGPTGVITTTMTDSFLTGQILLQDLKAGHLPSGPRPGSAFIKALLDSRGVWPVSFSDWEKLDAEEVSRGQASGKPREKLLDPQEMLRLLGH

>d1h7wa4 c.4.1.1 (A:184-287,A:441-532) Dihydropyrimidine dehydrogenase, domain 2 {Pig (Sus scrofa)}

EAYSAKIALLGAGPASISCASFLARLGYSDITIFEKQEYVGGLSTSEIPQFRLPYDVVNFEIELMKDLGVKIICGKSLSENEITLNTLKEEGYKAAFIGIGLPEXVLRDPKVKEALSPIKFNRWDLPEVDPETMQTSEPWVFAGGDIVGMANTTVESVNDGKQASWYIHKYIQAQYGASVSAKPELPLFYTPVDLVD

>d1an9a1 c.4.1.2 (A:1-194,A:288-340) D-amino acid oxidase, N-terminal domain {Pig (Sus scrofa)}

MRVVVIGAGVIGLSTALCIHERYHSVLQPLDVKVYADRFTPFTTTDVAAGLWQPYTSEPSNPQEANWNQQTFNYLLSHIGSPNAANMGLTPVSGYNLFREAVPDPYWKDMVLGFRKLTPRELDMFPDYRYGWFNTSLILEGRKYLQWLTERLTERGVKFFLRKVESFEEVARGGADVIINCTGVWAGVLQPDPLXQVRLEREQLRFGSSNTEVIHNYGHGGYGLTIHWGCALEVAKLFGKVLEERNLL

>d1c0pa1 c.4.1.2 (A:999-1193,A:1289-1361) D-amino acid oxidase, N-terminal domain {Yeast (Rhodotorula gracilis)}

LMMHSQKRVVVLGSGVIGLSSALILARKGYSVHILARDLPEDVSSQTFASPWAGANWTPFMTLTDGPRQAKWEESTFKKWVELVPTGHAMWLKGTRRFAQNEDGLLGHWYKDITPNYRPLPSSECPPGAIGVTYDTLSVHAPKYCQYLARELQKLGATFERRTVTSLEQAFDGADLVVNATGLGAKSIAGIDDQAXRGGPRVEAERIVLPLDRTKSPLSLGRGSARAAKEKEVTLVHAYGFSSAGYQQSWGAAEDVAQLVDEAFQRYHG

>d1tml\_\_ c.6.1.1 (-) Cellulase E2 {Thermomonospora fusca, strain yx}

NDSPFYVNPNMSSAEWVRNNPNDPRTPVIRDRIASVPQGTWFAHHNPGQITGQVDALMSAAQAAGKIPILVVYNAPGRDCGNHSSGGAPSHSAYRSWIDEFAAGLKNRPAYIIVEPDLISLMSSCMQHVQQEVLETMAYAGKALKAGSSQARIYFDAGHSAWHSPAQMASWLQQADISNSAHGIATNTSNYRWTADEVAYAKAVLSAIGNPSLRAVIDTSRNGNGPAGNEWCDPSGRAIGTPSTTNTGDPMIDAFLWIKLPGEADGCIAGAGQFVPQAAYEMAIAA

>d1qjwa\_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Trichoderma reesei, Cel6a}

ATYSGNPFVGVTPWANAYYASEVSSLAIPSLTGAMATAAAAVAKVPSFMWLDTLDKTPLMEQTLADIRTANKNGGNYAGQFVVFDLPDRDCAALASNGEYSIADGGVAKYKNYIDTIRQIVVEYSDIRTLLVIEPDSLANLVTNLGTPKCANAQSAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQDPAAQLFANVYKNASSPRALRGLATNVANYNGWNITSPPSYTQGNAVYNEKLYIHAIGPLLANHGWSNAFFITDQGRSGKQPTGQQQWGDWCNVIGTGFGIRPSANTGDSLLDSFVWVKPGGECDGTSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

>d1dysa\_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6b}

GNPFSGRTLLVNSDYSSKLDQTRQAFLSRGDQTNAAKVKYVQEKVGTFYWISNIFLLRDIDVAIQNARAAKARGENPIVGLVLYNLPDRDCSAGESSGELKLSQNGLNRYKNEYVNPFAQKLKAASDVQFAVILEPDAIGNMVTGTSAFCRNARGPQQEAIGYAISQLQASHIHLYLDVANGGWLGWADKLEPTAQEVATILQKAGNNAKIRGFSSNVSNYNPYSTSNPPPYTSGSPSPDESRYATNIANAMRQRGLPTQFIIDQSRVALSGARSEWGQWCNVNPAGFGQPFTTNTNNPNVDAIVWVKPGGESDGQCGMGGAPAAGMWFDAYAQMLTQNAHDEIA

>d1e8ca1 c.98.1.1 (A:3-87) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

RNLRDLLAPWVPDAPSRALREMTLDSRVAAAGDLFVAVVGHQADGRRYIPQAIAQGVAAIIAEAKDEATDGEIREMHGVPVIYLS

>d1gg4a3 c.98.1.1 (A:1-81) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

MISVTLSQLTDILNGELQGADITLDAVTTDTRKLTPGCLFVALKGERFDAHDFADQAKAGGAGALLVSRPLDIDLPQLIVK

>d1igra1 c.10.2.5 (A:1-149) L1 and L2 domains of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

EICGPGIDIRNDYQQLKRLENCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECG

>d1igra2 c.10.2.5 (A:300-478) L1 and L2 domains of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

KVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRHSHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLCVSEIYRMEEVTGTKGRQSKGDINTRNNGERASCESDVDDDDKEQKLISEEDLN

>d1jj2k\_ c.12.1.1 (K:) Ribosomal protein L15 (L15p) {Archaeon Haloarcula marismortui}

TSKKKRQRGSRTHGGGSHKNRRGAGHRGGRGDAGRDKHEFHNHEPLGKSGFKRPQKVQEEAATIDVREIDENVTLLAADDVAEVEDGGFRVDVRDVVEEADDADYVKVLGAGQVRHELTLIADDFSEGAREKVEGAGGSVELTDLGEERQ

>d1jj2n\_ c.12.1.1 (N:) Ribosomal protein L18e {Archaeon Haloarcula marismortui}

SKTNPRLSSLIADLKSAARSSGGAVWGDVAERLEKPRRTHAEVNLGRIERYAQEDETVVVPGKVLGSGVLQKDVTVAAVDFSGTAETKIDQVGEAVSLEQAIENNPEGSHVRVIR

>d1h4xa\_ c.13.2.1 (A:) Anti-sigma factor antagonist SpoIIaa {Bacillus sphaericus}

AFQLEMVTRETVVIRLFGELDHHAVEQIRAKISTAIFQGAVTTIIWNFERLSFMDSSGVGLVLGRMRELEAVAGRTILLNPSPTMRKVFQFSGLGPWMMDATEEEAIDRVR

>d1auz\_\_ c.13.2.1 (-) Anti-sigma factor antagonist SpoIIaa {Bacillus subtilis}

SLGIDMNVKESVLCIRLTGELDHHTAETLKQKVTQSLEKDDIRHIVLNLEDLSFMDSSGLGVILGRYKQIKQIGGEMVVCAISPAVKRLFDMSGLFKIIRFEQSEQQALLTLGVAS

>d1fc6a4 c.14.1.2 (A:78-156,A:249-463) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}

VTSEQLLFLEAWRAVDRAYVDKSFNGQSWFKLRETYLKKEPMDRRAQTYDAIRKMLAVLDDPFTRFLEPSRLAALRRGTXKVTINPVTFTTCSNVAAAALPPGAAKQQLGYVRLATFNSNTTAAAQQAFTELSKQGVAGLVLDIRNNGGGLFPAGVNVARMLVDRGDLVLIADSQGIRDIYSADGNSIDSATPLVVLVNRGTASASEVLAGALKDSKRGLIAGERTFGKGLIQTVVDLSDGSGVAVTVARYQTPAGVDINKIGVSPDVQLDPEVLPTDLEGVCRVLGSDAAPRLF

>d1k32a4 c.14.1.2 (A:680-762,A:854-1061) Tricorn protease {Archaeon Thermoplasma acidophilum}

SSIHEEFLQMYDEAWKLARDNYWNEAVAKEISERIYEKYRNLVPLCKTRYDLSNVIVEMQGEYRTSHSYEMGGTFTDKDPFRSXDDRFIRYRSWVEANRRYVHERSKGTIGYIHIPDMGMMGLNEFYRLFINESSYQGLIVDVRFNGGGFVSQLIIEKLMNKRIGYDNPRRGTLSPYPTNSVRGKIIAITNEYAGSDGDIFSFSFKKLGLGKLIGTRTWGGVVGITPKRRLIDGTVLTQPEFAFWFRDAGFGVENYGVDPDVEIEYAPHDYLSGKDPQIDYAIDALIEELRN

>d1j7xa\_ c.14.1.2 (A:) Interphotoreceptor retinoid-binding protein IRBP {African clawed frog (Xenopus laevis)}

DPSVTHVLHQLCDILANNYAFSERIPTLLQHLPNLDYSTVISEEDIAAKLNYELQSLTEDPRLVLKSKTDTLVMPGDSIQAENIPEDEAMLQALVNTVFKVSILPGNIGYLRFDQFADVSVIAKLAPFIVNTVWEPITITENLIIDLRYNVGGSSTAVPLLLSYFLDPETKIHLFTLHNRQQNSTDEVYSHPKVLGKPYGSKKGVYVLTSHQTATAAEEFAYLMQSLSRATIIGEITSGNLMHSKVFPFGDTQLSVTVPIINFIDSNGDYWLGGGVVPDAIVLADEALDKAKEIIAFHPPLA

>d1nzya\_ c.14.1.3 (A:) 4-Chlorobenzoyl-CoA dehalogenase {Pseudomonas sp., strain CBS-3}

MYEAIGHRVEDGVAEITIKLPRHRNALSVKAMQEVTDALNRAEEDDSVGAVMITGAEDAFCAGFYLREIPLDKGVAGVRDHFRIAALWWHQMIHKIIRVKRPVLAAINGVAAGGGLGISLASDMAICADSAKFVCAWHTIGIGNDTATSYSLARIVGMRRAMELMLTNRTLYPEEAKDWGLVSRVYPKDEFREVAWKVARELAAAPTHLQVMAKERFHAGWMQPVEECTEFEIQNVIASVTHPHFMPCLTRFLDGHRADRPQVELPAGV

>d1ey3a\_ c.14.1.3 (A:) Enoyl-CoA hydratase (crotonase) {Rat (Rattus norvegicus)}

FQYIITEKKGKNSSVGLIQLNRPKALNALCNGLIEELNQALETFEEDPAVGAIVLTGGEKAFAAGADIKEMQNRTFQDCYSGKFLSHWDHITRIKKPVIAAVNGYALGGGCELAMMCDIIYAGEKAQFGQPEILLGTIPGAGGTQRLTRAVGKSLAMEMVLTGDRISAQDAKQAGLVSKIFPVETLVEEAIQCAEKIANNSKIIVAMAKESVNAAFEMTLTEGNKLEKKLFYSTFATDDRREGMSAFVEKRKANFKDH

>d1dcia\_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Rat (Rattus norvegicus)}

AYESIQVTSAQKHVLHVQLNRPEKRNAMNRAFWRELVECFQKISKDSDCRAVVVSGAGKMFTSGIDLMDMASDILQPPGDDVARIAWYLRDLISRYQKTFTVIEKCPKPVIAAIHGGCIGGGVDLISACDIRYCTQDAFFQVKEVDVGLAADVGTLQRLPKVIGNRSLVNELTFTARKMMADEALDSGLVSRVFPDKDVMLNAAFALAADISSKSPVAVQGSKINLIYSRDHSVDESLDYMATWNMSMLQTQDIIKSVQAAMEKKDSKSITFSKL

>d1hnua\_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Baker's yeast (Saccharomyces cerevisiae)}

NEKISYRIEGPFFIIHLINPDNLNALEGEDYIYLGELLELADRNRDVYFTIIQSSGRFFSSGADFKGIAKAQGDDTNKYPSETSKWVSNFVARNVYVTDAFIKHSKVLICCLNGPAIGLSAALVALCDIVYSINDKVYLLYPFANLGLITEGGTTVSLPLKFGTNTTYECLMFNKPFKYDIMCENGFISKNFNMPSSNAEAFNAKVLEELREKVKGLYLPSCLGMKKLLKSNHIDAFNKANSVEVNESLKYWVDGEPLKRFRQ

>d1hzda\_ c.14.1.3 (A:) AUH protein {Human (Homo sapiens)}

EDELRVRHLEEENRGIVVLGINRAYGKNSLSKNLIKMLSKAVDALKSDKKVRTIIIRSEVPGIFCAGADLKERAKMSSSEVGPFVSKIRAVINDIANLPVPTIAAIDGLALGGGLELALACDIRVAASSAKMGLVETKLAIIPGGGGTQRLPRAIGMSLAKELIFSARVLDGKEAKAVGLISHVLEQNQEGDAAYRKALDLAREFLPQGPVAMRVAKLAINQGMEVDLVTGLAIEEACYAQTIPTKDRLEGLLAFKEKRPPRYKGE

>d1ef8a\_ c.14.1.3 (A:) Methylmalonyl CoA decarboxylase {Escherichia coli}

MSYQYVNVVTINKVAVIEFNYGRKLNALSKVFIDDLMQALSDLNRPEIRCIILRAPSGSKVFSAGHDIHELPSGGRDPLSYDDPLRQITRMIQKFPKPIISMVEGSVWGGAFEMIMSSDLIIAASTSTFSMTPVNLGVPYNLVGIHNLTRDAGFHIVKELIFTASPITAQRALAVGILNHVVEVEELEDFTLQMAHHISEKAPLAIAVIKEELRVLGEAHTMNSDEFERIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVGH

>d1jnxx1 c.15.1.3 (X:1649-1757) Breast cancer associated protein, BRCA1 {Human (Homo sapiens)}

RMSMVVSGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAEFVCERTLKYFLGIAGGKWVVSYFWVTQSIKERKMLNEHDFEVRGDVVNGRNHQGPKRARESQD

>d1jnxx2 c.15.1.3 (X:1758-1859) Breast cancer associated protein, BRCA1 {Human (Homo sapiens)}

RKIFRGLEICCYGPFTNMPTDQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDAWTEDNGFHAIGQMCEAPVVTREWVLDSVALYQCQELDTYLIPQIP

>d1in1a\_ c.15.1.2 (A:) DNA ligase III alpha {Human (Homo sapiens)}

GSADETLCQTKVLLDIFTGVRLYLPPSTPDFSRLRRYFVAFDGDLVQEFDMTSATHVLGSRDKNPAAQQVSPEWIWACIRKRRLVAPC

>d1dgtb3 c.15.1.2 (B:2582-2660) NAD+-dependent DNA ligase, domain 4 {Thermus filiformis}

EEVSDLLSGLTFVLTGELSRPREEVKALLGRLGAKVTDSVSRKTSYLVVGENPGSKLEKARALGVAVLTEEEFWRFLKE

>d1di0a\_ c.16.1.1 (A:) Lumazine synthase {Brucella abortus}

TSFKIAFIQARWHADIVDEARKSFVAELAAKTGGSVEVEIFDVPGAYEIPLHAKTLARTGRYAAIVGAAFVIDGGIYDHDFVATAVINGMMQVQLETEVPVLSVVLTPHHFHESKEHHDFFHAHFKVKGVEAAHAALQIVSERSRIAA

>d1c41a\_ c.16.1.1 (A:) Lumazine synthase {Rice blast fungus (Magnaporthe grisea)}

GPTPQQHDGSALRIGIVHARWNETIIEPLLAGTKAKLLACGVKESNIVVQSVPGSWELPIAVQRLYSASQLQTPSSGPSLSAGDLLGSSTTDLTALPTTTASSTGPFDALIAIGVLIKGETMHFEYIADSVSHGLMRVQLDTGVPVIFGVLTVLTDDQAKARAGVIEGSHNHGEDWGLAAVEMGVRRRDWAAGKT

>d1c2ya\_ c.16.1.1 (A:) Lumazine synthase {Spinach (Spinacia oleracea)}

MNELEGYVTKAQSFRFAIVVARFNEFVTRRLMEGALDTFKKYSVNEDIDVVWVPGAYELGVTAQALGKSGKYHAIVCLGAVVKGDTSHYDAVVNSASSGVLSAGLNSGVPCVFGVLTCDNMDQAINRAGGKAGNKGAESALTAIEMASLFEHHLK

>d1ejba\_ c.16.1.1 (A:) Lumazine synthase {Baker's yeast (Saccharomyces cerevisiae)}

AVKGLGKPDQVYDGSKIRVGIIHARWNRVIIDALVKGAIERMASLGVEENNIIIETVPGSYELPWGTKRFVDRQAKLGKPLDVVIPIGVLIKGSTMHFEYISDSTTHALMNLQEKVDMPVIFGLLTCMTEEQALARAGIDEAHSMHNHGEDWGAAAVEMAVKFGKNAF

>g1ibc.1 c.17.1.1 (A:,B:) Interleukin-1beta converting enzyme (a cysteine protease) {Human (Homo sapiens)}

GNVKLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLLQNLGYSVDVKKNLTASDMTTELEAFAHRPEHKTSDSTFLVFMSHGIREGICGKKHSEQVPDILQLNAIFNMLNTKNCPSLKDKPKVIIIQACRGDSPGVVWFKDXAIKKAHIEKDFIAFCSSTPDNVSWRHPTMGSVFIGRLIEHMQEYACSCDVEEIFRKVRFSFEQPAGRAQMPTTERVTLTRCFYLFPGH

>d1f1ja\_ c.17.1.1 (A:) Caspase-7 {Human (Homo sapiens)}

YQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRSKTLLEKPKLFFIQACRGTELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKDLEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYFS

>d1jxqa\_ c.17.1.1 (A:) Caspase-9 {Human (Homo sapiens)}

MGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS

>d1dmga\_ c.22.1.1 (A:) Ribosomal protein L4 {Thermotoga maritima}

AQVDLLNVKGEKVGTLEISDFVFNIDPNYDVMWRYVDMQLSNRRAGTASTKTRGEVSGGGRKPWPQKHTGRARHGSIRSPIWRHGGVVHGPKPRDWSKKLNKKMKKLALRSALSVKYRENKLLVLDDLKLERPKTKSLKEILQNLQLSDKKTLIVLPWKEEGYMNVKLSGRNLPDVKVIIADNPNNSKNGEKAVRIDGLNVFDMLKYDYLVLTRDMVSKIEEVLG

>d1jj2c\_ c.22.1.1 (C:) Ribosomal protein L4 {Archaeon Haloarcula marismortui}

MQATIYDLDGNTDGEVDLPDVFETPVRSDLIGKAVRAAQANRKQDYGSDEYAGLRTPAESFGSGRGQAHVPKLDGRARRVPQAVKGRSAHPPKTEKDRSLDLNDKERQLAVRSALAATADADLVADRGHEFDRDEVPVVVSDDFEDLVKTQEVVSLLEALDVHADIDRADETKIKAGQGSARGRKYRRPASILFVTSDEPSTAARNLAGADVATASEVNTEDLAPGGAPGRLTVFTESALAEVAER

>d1jbea\_ c.23.1.1 (A:) CheY protein {Escherichia coli}

ADKELKFLVVDDFSTMRRIVRNLLKELGFNNVEEAEDGVDALNKLQAGGYGFVISDWNMPNMDGLELLKTIRADGAMSALPVLMVTAEAKKENIIAAAQAGASGYVVKPFTAATLEEKLNKIFEKLGM

>d1tmy\_\_ c.23.1.1 (-) CheY protein {Thermotoga maritima}

GKRVLIVDDAAFMRMMLKDIITKAGYEVAGEATNGREAVEKYKELKPDIVTMDITMPEMNGIDAIKEIMKIDPNAKIIVCSAMGQQAMVIEAIKAGAKDFIVKPFQPSRVVEALNKVS

>d1a04a2 c.23.1.1 (A:5-142) Nitrate/nitrite response regulator (NARL), receiver domain {Escherichia coli}

EPATILLIDDHPMLRTGVKQLISMAPDITVVGEASNGEQGIELAESLDPDLILLDLNMPGMNGLETLDKLREKSLSGRIVVFSVSNHEEDVVTALKRGADGYLLKDMEPEDLLKALHQAAAGEMVLSEALTPVLAASL

>d1ntr\_\_ c.23.1.1 (-) NTRC receiver domain {Salmonella typhimurium}

MQRGIVWVVDDDSSIRWVLERALAGAGLTCTTFENGNEVLAALASKTPDVLLSDIRMPGMDGLALLKQIKQRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYLPKPFDIDEAVALVERAISHYQE

>d1dbwa\_ c.23.1.1 (A:) Transcriptional regulatory protein FixJ, receiver domain {Rhizobium meliloti}

MQDYTVHIVDDEEPVRKSLAFMLTMNGFAVKMHQSAEAFLAFAPDVRNGVLVTDLRMPDMSGVELLRNLGDLKINIPSIVITGHGDVPMAVEAMKAGAVDFIEKPFEDTVIIEAIERASEHLV

>d1qkka\_ c.23.1.1 (A:) Transcriptional regulatory protein DctD, receiver domain {Sinorhizobium meliloti}

PSVFLIDDDRDLRKAMQQTLELAGFTVSSFASATEALAGLSADFAGIVISDIRMPGMDGLALFRKILALDPDLPMILVTGHGDIPMAVQAIQDGAYDFIAKPFAADRLVQSARRAEEKRRLVMENRSLRRAAEAASEGL

>d1dz3a\_ c.23.1.1 (A:) Sporulation response regulator Spo0A {Bacillus stearothermophilus}

SIKVCIADDNRELVSLLDEYISSQPDMEVIGTAYNGQDCLQMLEEKRPDILLLDIIMPHLDGLAVLERIRAGFEHQPNVIMLTAFGQEDVTKKAVELGASYFILKPFDMENLAHHIRQVYGKT

>d1nat\_\_ c.23.1.1 (-) Sporulation response regulator Spo0F {Bacillus subtilis}

NEKILIVDDQYGIRILLNEVFNKEGYQTFQAANGLQALDIVTKERPDLVLLDMKIPGMDGIEILKRMKVIDENIRVIIMTAYGELDMIQESKELGALTHFAKPFDIDEIRDAVKKYLPL

>d1a2oa1 c.23.1.1 (A:1-140) Methylesterase CheB, N-terminal domain {Salmonella typhimurium}

MSKIRVLSVDDSALMRQIMTEIINSHSDMEMVATAPDPLVARDLIKKFNPDVLTLDVEMPRMDGLDFLEKLMRLRPMPVVMVSSLTGKGSEVTLRALELGAIDFVTKPQLGIREGMLAYSEMIAEKVRTAARARIAAHKP

>d1kgsa2 c.23.1.1 (A:2-123) PhoB receiver domain {Thermotoga maritima}

NVRVLVVEDERDLADLITEALKKEMFTVDVCYDGEEGMYMALNEPFDVVILDIMLPVHDGWEILKSMRESGVNTPVLMLTALSDVEYRVKGLNMGADDYLPKPFDLRELIARVRALIRRKSE

>d1euca2 c.23.4.1 (A:131-306) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Pig (Sus scrofa)}

NCPGVINPGECKIGIMPGHIHKKGRIGIVSRSGTLTYEAVHQTTQVGLGQSLCVGIGGDPFNGTDFTDCLEIFLNDPATEGIILIGEIGGNAEENAAEFLKQHNSGPKSKPVVSFIAGLTAPPGRRMGHAGAIIAGGKGGAKEKITALQSAGVVVSMSPAQLGTTIYKEFEKRKML

>d1jkjb1 c.23.4.1 (B:239-388) Succinyl-CoA synthetase, beta-chain, C-terminal domain {Escherichia coli}

DPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNIFGGIVRCDLIADGIIGAVAEVGVNVPVVVRLEGNNAELGAKKLADSGLNIIAAKGLTDAAQQVVAAVEGK

>d2fcr\_\_ c.23.5.1 (-) Flavodoxin {Chondrus crispus}

KIGIFFSTSTGNTTEVADFIGKTLGAKADAPIDVDDVTDPQALKDYDLLFLGAPTWNTGADTERSGTSWDEFLYDKLPEVDMKDLPVAIFGLGDAEGYPDNFCDAIEEIHDCFAKQGAKPVGFSNPDDYDYEESKSVRDGKFLGLPLDMVNDQIPMEKRVAGWVEAVVSETGV

>d1f4pa\_ c.23.5.1 (A:) Flavodoxin {Desulfovibrio vulgaris}

PKALIVYGSTTGNTEYTAETIARELADAGYEVDSRDAASVEAGGLFEGFDLVLLGCSTWGDDSIELQDDFIPLFDSLEETGAQGRKVACFGCGDSSWEYFCGAVDAIEEKLKNLGAEIVQDGLRIDGDPRAARDDIVGWAHDVRGAI

>d1ag9a\_ c.23.5.1 (A:) Flavodoxin {Escherichia coli}

AITGIFFGSDTGNTENIAKMIQKQLGKDVADVHDIAKSSKEDLEAYDILLLGIPTWYYGEAQCDWDDFFPTLEEIDFNGKLVALFGCGDQEDYAEYFCDALGTIRDIIEPRGATIVGHWPTAGYHFEASKGLADDDHFVGLAIDEDRQPELTAERVEKWVKQISEELHLDEILNA

>d5nul\_\_ c.23.5.1 (-) Flavodoxin {Clostridium beijerinckii}

MKIVYWSGTGNTEKMAELIAKGIIESGKDVNTINVSDVNIDELLNEDILILGCSAMTDEVLEESEFEPFIEEISTKISGKKVALFGSYGWGDGKWMRDFEERMNGYGCVVVETPLIVQNEPDEAEQDCIEFGKKIANI

>d1bvyf\_ c.23.5.1 (F:) FMN-binding domain of the cytochrome P450bm-3 {Bacillus megaterium}

NTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNL

>d1e5da1 c.23.5.1 (A:251-402) Rubredoxin oxygen:oxidoreductase (ROO), C-terminal domain {Desulfovibrio gigas}

PTNKVVIFYDSMWHSTEKMARVLAESFRDEGCTVKLMWCKACHHSQIMSEISDAGAVIVGSPTHNNGILPYVAGTLQYIKGLRPQNKIGGAFGSFGWSGESTKVLAEWLTGMGFDMPATPVKVKNVPTHADYEQLKTMAQTIARALKAKLAA

>d1bmta2 c.23.6.1 (A:741-896) Methionine synthase, C-terminal domain {Escherichia coli}

EQGKTNGKMVIATVKGDVHDIGKNIVGVVLQCNNYEIVDLGVMVPAEKILRTAKEVNADLIGLSGLITPSLDEMVNVAKEMERQGFTIPLLIGGATTSKAHTAVKIEQNYSGPTVYVQNASRTVGVVAALLSDTQRDDFVARTRKEYETVRIQHGR

>d1fmfa\_ c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium tetanomorphum}

MEKKTIVLGVIGSDCHAVGNKILDHSFTNAGFNVVNIGVLSSQEDFINAAIETKADLICVSSLYGQGEIDCKGLREKCDEAGLKGIKLFVGGNIVVGKQNWPDVEQRFKAMGFDRVYPPGTSPETTIADMKEVLGVE

>d7reqa2 c.23.6.1 (A:561-728) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

AQIRTISGVYSKEVKNTPEVEEARELVEEFEQAEGRRPRILLAKMGQDGHDRGQKVIATAYADLGFDVDVGPLFQTPEETARQAVEADVHVVGVSSLAGGHLTLVPALRKELDKLGRPDILITVGGVIPEQDFDELRKDGAVEIYTPGTVIPESAISLVKKLRASLDA

>d7reqb2 c.23.6.1 (B:476-638) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

TKPFPAAPARKGLAWHRDSEVFEQLMDRSTSVSERPKVFLACLGTRRDFGGREGFSSPVWHIAGIDTPQVEGGTTAEIVEAFKKSGAQVADLCSSAKVYAQQGLEVAKALKAAGAKALYLSGAFKEFGDDAAEAEKLIDGRLFMGMDVVDTLSSTLDILGVAK

>d1cex\_\_ c.23.9.1 (-) Cutinase {Fungus (Fusarium solani), subsp. pisi}

RTTRDDLINGNSASCADVIFIYARGSTETGNLGTLGPSIASNLESAFGKDGVWIQGVGGAYRATLGDNALPRGTSSAAIREMLGLFQQANTKCPDATLIAGGYSQGAALAAASIEDLDSAIRDKIAGTVLFGYTKNLQNRGRIPNYPADRTKVFCNTGDLVCTGSLIVAAPHLAYGPDARGPAPEFLIEKVRAVRGS

>d1g66a\_ c.23.9.1 (A:) Acetylxylan esterase {Penicillium purpurogenum}

SCPAIHVFGARETTASPGYGSSSTVVNGVLSAYPGSTAEAINYPACGGQSSCGGASYSSSVAQGIAAVASAVNSFNSQCPSTKIVLVGYSQGGEIMDVALCGGGDPNQGYTNTAVQLSSSAVNMVKAAIFMGDPMFRAGLSYEVGTCAAGGFDQRPAGFSCPSAAKIKSYCDASDPYCCNGSNAATHQGYGSEYGSQALAFVKSKLG

>d2naca2 c.23.12.1 (A:1-147,A:336-374) Formate dehydrogenase {Pseudomonas sp., strain 101}

AKVLCVLYDDPVDGYPKTYARDDLPKIDHYPGGQTLPTPKAIDFTPGQLLGSVSGELGLRKYLESNGHTLVVTSDKDGPDSVFERELVDADVVISQPFWPAYLTPERIAKAKNLKLALTAGIGSDHVDLQSAIDRNVTVAEVTYCNSXTTLTAQARYAAGTREILECFFEGRPIRDEYLIVQGGALA

>d1qp8a2 c.23.12.1 (A:1-82,A:264-302) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}

MELYVNFELPPEAEEELRKYFKIVRGGDLGNVEAALVSRITAEELAKMPRLKFIQVVTAGLDHLPWESIPPHVTVAGNAGSNXGYGNERVWRQMVMEAVRNLITYATGGRPRNIAKREDYIG

>d1dxy\_2 c.23.12.1 (1-100,300-330) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}

MKIIAYGARVDEIQYFKQWAKDTGNTLEYHTEFLDENTVEWAKGFDGINSLQTTPYAAGVFEKMHAYGIKFLTIRNVGTDNIDMTAMKQYGIRLSNVPAYXTETAVHNMVYFSLQHLVDFLTKGETSTEVTG

>d1gdha2 c.23.12.1 (A:2-100,A:292-321) D-glycerate dehydrogenase {Hyphomicrobium methylovorum}

KKKILITWPLPEAAMARARESYDVIAHGDDPKITIDEMIETAKSVDALLITLNEKCRKEVIDRIPENIKCISTYSIGFDHIDLDACKARGIKVGNAPHGXATQAREDMAHQANDLIDALFGGADMSYALA

>d1psda2 c.23.12.1 (A:7-107,A:296-326) Phosphoglycerate dehydrogenase {Escherichia coli}

EKDKIKFLLVEGVHQKALESLRAAGYTNIEFHKGALDDEQLKESIRDAHFIGLRSRTHLTEDVINAAEKLVAIGCFCIGTNQVDLDAAAKRGIPVFNAPFSXSTQEAQENIGLEVAGKLIKYSDNGSTLSAVN

>d2dlda2 c.23.12.1 (A:1-103,A:301-337) D-lactate dehydrogenase {Lactobacillus helveticus}

MTKVFAYAIRKDEEPFLNEWKEAHKDIDVDYTDKLLTPETAKLAKGADGVVVYQQLDYTADTLQALADAGVTKMSLRNVGVDNIDMDKAKELGFQITNVPVYSXYTTHAVRNMVVKAFNNNLKLINGEKPDSPVALNKNKF

>d1pjca2 c.23.12.2 (A:1-135,A:304-361) L-alanine dehydrogenase {Phormidium lapideum}

MEIGVPKEIKNQEFRVGLSPSSVRTLVEAGHTVFIETQAGIGAGFADQDYVQAGAQVVPSAKDAWSREMVVKVKEPLPAEYDLMQKDQLLFTYLHLAAARELTEQLMRVGLTAIAYETVELPNRSLPLLTPMSIIXVPWTATQALNNSTLPYVVKLANQGLKALETDDALAKGLNVQAHRLVHPAVQQVFPDLA

>d1f8ga2 c.23.12.2 (A:1-143,A:327-384) Nicotinamide nucleotide transhydrogenase dI component {Rhodospirillum rubrum}

MKIAIPKERRPGEDRVAISPEVVKKLVGLGFEVIVEQGAGVGASITDDALTAAGATIASTAAQALSQADVVWKVQRPMTAEEGTDEVALIKEGAVLMCHLGALTNRPVVEALTKRKITAYAMELMPRISRAQSMDILSSQSNLXVAADASPLFAKNLLNFLTPHVDKDTKTLVMKLEDETVSGTCVTRDGAIVHPALTGQGA

>d1gpma2 c.23.16.1 (A:3-207) GMP synthetase {Escherichia coli}

ENIHKHRILILDFGSQYTQLVARRVRELGVYCELWAWDVTEAQIRDFNPSGIILSGGPESTTEENSPRAPQYVFEAGVPVFGVCYGMQTMAMQLGGHVEASNEREFGYAQVEVVNDSALVRGIEDALTADGKPLLDVWMSHGDKVTAIPSDFITVASTESCPFAIMANEEKRFYGVQFHPEVTHTRQGMRMLERFVRDICQCEAL

>d1a9xb2 c.23.16.1 (B:1653-1880) Carbamoyl phosphate synthetase, small subunit C-terminal domain {Escherichia coli}

LNGMDLAKEVTTAEAYSWTQGSWTLTGGLPQAKKEDELPFHVVAYDFGAKRNILRMLVDRGCRLTIVPAQTSAEDVLKMNPDGIFLSNGPGDPAPCDYAITAIQKFLETDIPVFGICLGHQLLALASGAKTVKMKFGHHGGNHPVKDVEKNVVMITAQNHGFAVDEATLPANLRVTHKSLFDGTLQGIHRTDKPAFSFQGNPEASPGPHDAAPLFDHFIELIEQYRKT

>d1qdlb\_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Archaeon Sulfolobus solfataricus}

MDLTLIIDNYDSFVYNIAQIVGELGSYPIVIRNDEISIKGIERIDPDRLIISPGPGTPEKREDIGVSLDVIKYLGKRTPILGVCLGHQAIGYAFGAKIRRARKVFHGKISNIILVNNSPLSLYYGIAKEFKATRYHSLVVDEVHRPLIVDAISAEDNEIMAIHHEEYPIYGVQFHPESVGTSLGYKILYNFLNRV

>d1i1qb\_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Salmonella typhimurium}

ADILLLDNIDSFTWNLADQLRTNGHNVVIYRNHIPAQTLIDRLATMKNPVLMLSPGPGVPSEAGCMPELLTRLRGKLPIIGICLGHQAIVEAYGGYVGQAGEILHGKATSIEHDGQAMFAGLANPLPVARYHSLVGSNVPAGLTINAHFNGMVMAVRHDADRVCGFQFHPESILTTQGARLLEQTLAWAQQK

>d1k9vf\_ c.23.16.1 (F:) GAT subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}

MRIGIISVGPGNIMNLYRGVKRASENFEDVSIELVESPRNDLYDLLFIPGVGHFGEGMRRLRENDLIDFVRKHVEDERYVVGVCLGMQLLFEESEEAPGVKGLSLIEGNVVKLRSRRLPHMGWNEVIFKDTFPNGYYYFVHTYRAVCEEEHVLGTTEYDGEIFPSAVRKGRILGFQFHPEKSSKIGRKLLEKVIECSLSR

>d1jvna2 c.23.16.1 (A:-3-229) GAT subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}

GSHMPVVHVIDVESGNLQSLTNAIEHLGYEVQLVKSPKDFNISGTSRLILPGVGNYGHFVDNLFNRGFEKPIREYIESGKPIMGICVGLQALFAGSVESPKSTGLNYIDFKLSRFDDSEKPVPEIGWNSCIPSENLFFGLDPYKRYYFVHSFAAILNSEKKKNLENDGWKIAKAKYGSEEFIAAVNKNNIFATQFHPEKSGKAGLNVIENFLKQQSPPIPNYSAEEKELLMN

>d1que\_2 c.25.1.1 (142-303) Ferredoxin reductase (flavodoxin reductase) {Cyanobacterium (Anabaena sp.), pcc 7119}

LPDDPEANVIMLATGTGIAPMRTYLWRMFKDAERAANPEYQFKGFSWLVFGVPTTPNILYKEELEEIQQKYPDNFRLTYAISREQKNPQGGRMYIQDRVAEHADQLWQLIKNQKTHTYICGLRGMEEGIDAALSAAAAKEGVTWSDYQKDLKKAGRWHVETY

>d1fdr\_2 c.25.1.1 (101-248) Ferredoxin reductase (flavodoxin reductase) {Escherichia coli}

DEVPHCETLWMLATGTAIGPYLSILRLGKDLDRFKNLVLVHAARYAADLSYLPLMQELEKRYEGKLRIQTVVSRETAAGSLTGRIPALIESGELESTIGLPMNKETSHVMLCGNPQMVRDTQQLLKETRQMTKHLRRRPGHMTAEHYW

>d1a8p\_2 c.25.1.1 (101-258) Ferredoxin reductase (flavodoxin reductase) {Azotobacter vinelandii}

TSDLLPGKHLYMLSTGTGLAPFMSLIQDPEVYERFEKVVLIHGVRQVNELAYQQFITEHLPQSEYFGEAVKEKLIYYPTVTRESFHNQGRLTDLMRSGKLFEDIGLPPINPQDDRAMICGSPSMLDESCEVLDGFGLKISPRMGEPGDYLIERAFVEK

>d1qfja2 c.25.1.1 (A:98-232) NAD(P)H:flavin oxidoreductase {Escherichia coli}

RDDEERPMILIAGGTGFSYARSILLTALARNPNRDITIYWGGREEQHLYDLCELEALSLKHPGLQVVPVVEQPEAGWRGRTGTVLTAVLQDHGTLAEHDIYIAGRFEMAKIARDLFCSERNAREDRLFGDAFAFI

>d1ndh\_2 c.25.1.1 (126-272) cytochrome b5 reductase {Pig (Sus scrofa), liver}

GKFAIRPDKKSSPVIKTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPELEELRNEHSARFKLWYTVDRAPEAWDYSQGFVNEEMIRDHLPPPEEEPLVLMCGPPPMIQYACLPNLERVGHPKERCFAF

>d1ja1a3 c.25.1.4 (A:519-678) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}

RLPFKSTTPVIMVGPGTGIAPFMGFIQERAWLREQGKEVGETLLYYGCRRSDEDYLYREELARFHKDGALTQLNVAFSREQAHKVYVQHLLKRDREHLWKLIHEGGAHIYVAGDARNMAKDVQNTFYDIVAEFGPMEHTQAVDYVKKLMTKGRYSLNVWS

>d1f20a2 c.25.1.4 (A:1233-1397) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}

SFHLPRNPQVPCILVGPGTGIAPFRSFWQQRQFDIQHKGMNPCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYTAYSREPDRPKKYVQDVLQEQLAESVYRALKEQGGHIYVCGDVTMAADVLKAIQRIMTQQGKLSEEDAGVFISRLRDDNRYHEDIFGV

>d1jila\_ c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Staphylococcus aureus}

TNVLIEDLKWRGLIYQQTDEQGIEDLLNKEQVTLYCGADPTADSLHIGHLLPFLTLRRFQEHGHRPIVLIGGGTGMIGDPSGKSEERVLQTEEQVDKNIEGISKQMHNIFEFGTDHGAVLVNNRDWLGQISLISFLRDYGKHVGVNYMLGKDSIQSRLEHGISYTEFTYTILQAIDFGHLNRELNCKIQVGGSDQWGNITSGIELMRRMYGQTDAYGLTIPLVTKSDGKKFGKSESGAVWLDAEKTSPYEFYQFWINQSDEDVIKFLKYFTFLGKEEIDRLEQSKNEAPHLREAQKTLAEEVTKFIHGEDALNDAIRISQALF

>d1i6la\_ c.26.1.1 (A:) Tryptophanyl-tRNA synthetase (TrpRS) {Bacillus stearothermophilus}

MKTIFSGIQPSGVITIGNYIGALRQFVELQHEYNCYFCIVDQHAITVWQDPHELRQNIRRLAALYLAVGIDPTQATLFIQSEVPAHAQAAWMLQCIVYIGELERMTQFKEKSAGKEAVSAGLLTYPPLMAADILLYNTDIVPVGEDQKQHIELTRDLAERFNKRYGELFTIPEARIPKVGARIMSLVDPTKKMSKSDPNPKAYITLLDDAKTIEKKIKSAVTDSEGTIRYDKEAKPGISNLLNIYSTLSGQSIEELERQYEGKGYGVFKADLAQVVIETLRPIQERYHHWMESEELDRVLDEGAEKANRVASEMVRKMEQAMGLGR

>d1gtra2 c.26.1.1 (A:8-338) Glutaminyl-tRNA synthetase (GlnRS) {Escherichia coli}

TNFIRQIIDEDLASGKHTTVHTRFPPEPNGYLHIGHAKSICLNFGIAQDYKGQCNLRFDDTNPVKEDIEYVESIKNDVEWLGFHWSGNVRYSSDYFDQLHAYAIELINKGLAYVDELTPEQIREYRGTLTQPGKNSPYRDRSVEENLALFEKMRAGGFEEGKACLRAKIDMASPFIVMRDPVLYRIKFAEHHQTGNKWCIYPMYDFTHCISDALEGITHSLCTLEFQDNRRLYDWVLDNITIPVHPRQYEFSRLNLEYTVMSKRKLNLLVTDKHVEGWDDPRMPTISGLRRRGYTAASIREFCKRIGVTKQDNTIEMASLESCIREDLNEN

>d1gln\_2 c.26.1.1 (1-305) Glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}

MVVTRIAPSPTGDPHVGTAYIALFNYAWARRNGGRFIVRIEDTDRARYVPGAEERILAALKWLGLSYDEGPDVAAPTGPYRQSERLPLYQKYAEELLKRGWAYRAFETPEELEQIRKEKGGYDGRARNIPPEEAEERARRGEPHVIRLKVPRPGTTEVKDELRGVVVYDNQEIPDVVLLKSDGYPTYHLANVVDDHLMGVTDVIRAEEWLVSTPIHVLLYRAFGWEAPRFYHMPLLRNPDKTKISKRKSHTSLDWYKAEGFLPEALRNYLCLMGFSMPDGREIFTLEEFIQAFTWERVSLGGPVF

>d1a8h\_2 c.26.1.1 (1-348) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}

MEKVFYVTTPIYYVNAEPHLGHAYTTVVADFLARWHRLDGYRTFFLTGTDEHGETVYRAAQAAGEDPKAFVDRVSGRFKRAWDLLGIAYDDFIRTTEERHKKVVQLVLKKVYEAGDIYYGEYEGLYCVSCERFYTEKELVEGLCPIHGRPVERRKEGNYFFRMEKYRPWLQEYIQENPDLIRPEGYRNEVLAMLAEPIGDLSISRPKSRVPWGIPLPWDENHVTYVWFDALLNYVSALDYPEGEAYRTFWPHAWHLIGKDILKPHAVFWPTMLKAAGIPMYRHLNVGGFLLGPDGRKMSKTLGNVVDPFALLEKYGRDALRYYLLREIPYGQDTPVSEEALRTRYEAD

>d1f4la2 c.26.1.1 (A:4-140,A:176-388) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}

AKKILVTCALPYANGSIHLGHMLEHIQADVWVRYQRMRGHEVNFICADDAHGTPIMLKAQQLGITPEQMIGEMSQEHQTDFAGFNISYDNYHSTHSEENRQLSELIYSRLKENGFIKNRTISQLYDPEKGMFLPDRFXVVSGATPVMRDSEHFFFDLPSFSEMLQAWTRSGALQEQVANKMQEWFESGLQQWDISRDAPYFGFEIPNAPGKYFYVWLDAPIGYMGSFKNLCDKRGDSVSFDEYWKKDSTAELYHFIGKDIVYFHSLFWPAMLEGSNFRKPSNLFVHGYVTVNGAKMSKSRGTFIKASTWLNHFDADSLRYYYTAKLSSRIDDIDLNLEDFVQRVNADIVNK

>d1ile\_3 c.26.1.1 (1-197,387-641) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

MFKEVGEPNFPKLEEEVLAFWKREKIFQKSVENRKGGPRYTVYEGPPTANGLPHVGHAQARSYKDLFPRYKTMRGYYAPRRAGWDTHGLPVELEVEKKLGLKSKREIEAYGIERFNQACRESVFTYEKEWEAFTERIAYWVDLEDAYATLEPTYIESIWWSLKNLFDRGLLYRDHKVVPYCPRCGTPLSSHEVALGYXPHCWRCSTPLMYYATESWFIKNTLFKDELIRNNQEIHWVPPHIKEGRYGEWLKNLVDWALSRNRYWGTPLPIWVCQACGKEEAIGSFQELKARATKPLPEPFDPHRPYVDQVELACACGGTMRRVPYVIDVWYDSGAMPFASLHYPFEHEEVFRESFPADFIAEGIDQTRGWFNSLHQLGVMLFGSIAFKNVICHGLILDEKGQKMSKSKGNVVDPWDIIRKFGADALRWYIYVSAPPEADRRFGPNLVRETVRD

>d1ffya3 c.26.1.1 (A:1-200,A:395-644) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

MDYEKTLLMPKTDFPMRGGLPNKEPQIQEKWDAEDQYHKALEKNKGNETFILHDGPPYANGNLHMGHALNKILKDFIVRYKTMQGFYAPYVPGWDTHGLPIEQALTKKGVDRKKMSTAEFREKCKEFALEQIELQKKDFRRLGVRGDFNDPYITLKPEYEAAQIRIFGEMADKGLIYKGKKPVYWSPSSESSLAEAEIEYXPHDWRTKKPVIFRATPQWFASISKVRQDILDAIENTNFKVNWGKTRIYNMVRDRGEWVISRQRVWGVPLPVFYAENGEIIMTKETVNHVADLFAEHGSNIWFEREAKDLLPEGFTHPGSPNGTFTKETDIMDVWFDSGSSHRGVLETRPELSFPADMYLEGSDQYRGWFNSSITTSVATRGVSPYKFLLSHGFVMDGEGKKMSKSLGNVIVPDQVVKQKGADIARLWVSSTDYLADVRISDEILKQTSDD

>d1gaxa3 c.26.1.1 (A:1-189,A:343-578) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

MDLPKAYDPKSVEPKWAEKWAKNPFVANPKSGKPPFVIFMPPPNVTGSLHMGHALDNSLQDALIRYKRMRGFEAVWLPGTDHAGIATQVVVERLLLKEGKTRHDLGREKFLERVWQWKEESGGTILKQLKRLGASADWSREAFTMDEKRSRAVRYAFSRYYHEGLAYRAPRLVNWCPRCETTLSDLEVEXTCSRCGTPIEYAIFPQWWLRMRPLAEEVLKGLRRGDIAFVPERWKKVNMDWLENVKDWNISRQLWWGHQIPAWYCEDCQAVNVPRPERYLEDPTSCEACGSPRLKRDEDVFDTWFSSALWPLSTLGWPEETEDLKAFYPGDVLVTGYDILFLWVSRMEVSGYHFMGERPFKTVLLHGLVLDEKGQKMSKSKGNVIDPLEMVERYGADALRFALIYLATGGQDIRLDLRWLEMARNF

>d1f7ua2 c.26.1.1 (A:136-483) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (Saccharomyces cerevisiae)}

SCKLVENKKVIIEFSSPNIAKPFHAGHLRSTIIGGFLANLYEKLGWEVIRMNYLGDWGKQFGLLAVGFERYGNEEALVKDPIHHLFDVYVRINKDIEEEGDSIPLEQSTNGKAREYFKRMEDGDEEALKIWKRFREFSIEKYIDTYARLNIKYDVYSGESQVSKESMLKAIDLFKEKGLTHEDKGAVLIDLTKFNKKLGKAIVQKSDGTTLYLTRDVGAAMDRYEKYHFDKMIYVIASQQDLHAAQFFEILKQMGFEWAKDLQHVNFGMVQGMSTRKGTVVFLDNILEETKEKMHEVMKKNENKYAQIEHPEEVADLVGISAVMIQDMQGKRINNYEFKWERMLSFEG

>d1iq0a2 c.26.1.1 (A:97-466) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}

PFPRRPGVVLVEHTSVNPNKELHVGHLRNIALGDAIARILAYAGREVLVLNYIDDTGRQAAETLFALRHYGLTWDGKEKYDHFAGRAYVRLHQDPEYERLQPAIEEVLHALERGELREEVNRILLAQMATMHALNARYDLLVWESDIVRAGLLQKALALLEQSPHVFRPREGKYAGALVMDASPVIPGLEDPFFVLLRSNGTATYYAKDIAFQFWKMGILEGLRFRPYENPYYPGLRTSAPEGEAYTPKAEETINVVDVRQSHPQALVRAALALAGYPALAEKAHHLAYETVLLEGRQMSGRKGLAVSVDEVLEEATRRARAIVEEKNPDHPDKEEAARMVALGAIRFSMVKTEPKKQIDFRYQEALSFE

>d1qjca\_ c.26.1.3 (A:) Phosphopantetheine adenylyltransferase {Escherichia coli}

KRAIYPGTFDPITNGHIDIVTRATQMFDHVILAIAASPSKKPMFTLEERVALAQQATAHLGNVEVVGFSDLMANFARNQHATVLIRGLRAVADFEYEMQLAHMNRHLMPELESVFLMPSKEWSFISSSLVKEVARHQGDVTHFLPENVHQALMAKLA

>d1ej2a\_ c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon Methanobacterium thermoautotrophicum}

MRGLLVGRMQPFHRGHLQVIKSILEEVDELIICIGSAQLSHSIRDPFTAGERVMMLTKALSENGIPASRYYIIPVQDIECNALWVGHIKMLTPPFDRVYSGNPLVQRLFSEDGYEVTAPPLFYRDRYSGTEVRRRMLDDGDWRSLLPESVVEVIDEINGVERIKHLA

>d1g8fa2 c.26.1.5 (A:169-389) ATP sulfurylase central domain {Baker's yeast (Saccharomyces cerevisiae)}

YPGLRKTPAQLRLEFQSRQWDRVVAFQTRNPMHRAHRELTVRAAREANAKVLIHPVVGLTKPGDIDHHTRVRVYQEIIKRYPNGIAFLSLLPLAMRMSGDREAVWHAIIRKNYGASHFIVGRDHAGPGKNSKGVDFYGPYDAQELVESYKHELDIEVVPFRMVTYLPDEDRYAPIDQIDTTKTRTLNISGTELRRRLRVGGEIPEWFSYPEVVKILRESNP

>d1jhda2 c.26.1.5 (A:174-396) ATP sulfurylase central domain {unnamed symbiont of Riftia pachyptila}

PDTFRTAVEIRNEIKEHGWSKVVAFQTRNPMHRAHEELCRMAMESLDADGVVVHMLLGKLKKGDIPAPVRDAAIRTMAEVYFPPNTVMVTGYGFDMLYAGPREAVLHAYFRQNMGATHFIIGRDHAGVGDYYGAFDAQTIFDDEVPEGAMEIEIFRADHTAYSKKLNKIVMMRDVPDHTKEDFVLLSGTKVREMLGQGIAPPPEFSRPEVAKILMDYYQSINS

>d1gpma1 c.26.2.1 (A:208-404) GMP synthetase, central domain {Escherichia coli}

WTPAKIIDDAVARIREQVGDDKVILGLSGGVDSSVTAMLLHRAIGKNLTCVFVDNGLLRLNEAEQVLDMFGDHFGLNIVHVPAEDRFLSALAGENDPEAKRKIIGRVFVEVFDEEALKLEDVKWLAQGTIYPDVIESAASATGKAHVIKSHHNVGGLPKEMKMGLVEPLKELFKDEVRKIGLELGLPYDMLYRHPFP

>d1ih8a\_ c.26.2.1 (A:) NH3-dependent NAD+-synthetase {Bacillus subtilis}

SMQEKIMRELHVKPSIDPKQEIEDRVNFLKQYVKKTGAKGFVLGISGGQDSTLAGRLAQLAVESIREEGGDAQFIAVRLPHGTQQDEDDAQLALKFIKPDKSWKFDIKSTVSAFSDQYQQETGDQLTDFNKGNVKARTRMIAQYAIGGQEGLLVLGTDHAAEAVTGFFTKYGDGGADLLPLTGLTKRQGRTLLKELGAPERLYLKEPTADLLDEKPQQSDETELGISYDEIDDYLEGKEVSAKVSEALEKRYSMTEHKRQVPASMFDDWWK

>d1ct9a1 c.26.2.1 (A:193-516) Asparagine synthetase B, C-terminal domain {Escherichia coli}

RDWFDYDAVKDNVTDKNELRQALEDSVKSHLMSDVPYGVLLSGGLDSSIISAITKKYAARRVEDQERSEAWWPQLHSFAVGLPGSPDLKAAQEVANHLGTVHHEIHFTVQEGLDAIRDVIYHIETYDVTTIRASTPMYLMSRKIKAMGIKMVLSGEGSDEVFGGYLYFHKAPNAKELHEETVRKLLALHMYDCARANKAMSAWGVEARVPFLDKKFLDVAMRINPQDKMCGNGKMEKHILRECFEAYLPASVAWRQKEQFSDGVGYSWIDTLKEVAAQQVSDQQLETARFRFPYNTPTSKEAYLYREIFEELFPLPSAAECVPG

>d1jgta1 c.26.2.1 (A:210-508) beta-Lactam synthetase {Streptomyces clavuligerus}

PGLSRRILPEGEAVAAVRAALEKAVAQRVTPGDTPLVVLSGGIDSSGVAACAHRAAGELDTVSMGTDTSNEFREARAVVDHLRTRHREITIPTTELLAQLPYAVWASESVDPDIIEYLLPLTALYRALDGPERRILTGYGADIPLGGMHREDRLPALDTVLAHDMATFDGLNEMSPVLSTLAGHWTTHPYWDREVLDLLVSLEAGLKRRHGRDKWVLRAAMADALPAETVNRPKLGVHEGSGTTSSFSRLLLDHGVAEDRVHEAKRQVVRELFDLTVGGGRHPSEVDTDDVVRSVADRT

>d1k92a1 c.26.2.1 (A:1-188) Argininosuccinate synthetase, N-terminal domain {Escherichia coli}

TTILKHLPVGQRIGIAFSGGLDTSAALLWMRQKGAVPYAYTANLGQPDEEDYDAIPRRAMEYGAENARLIDCRKQLVAEGIAAIQCGAFHNTTGGLTYFNTTPLGRAVTGTMLVAAMKEDGVNIWGDGSTYKGNDIERFYRYGLLTNAELQIYKPWLDTDFIDELGGRHEMSEFMIACGFDYKMSVEK

>d1dnpa2 c.28.1.1 (A:1-200) N-terminal domain of DNA photolyase {Escherichia coli}

TTHLVWFRQDLRLHDNLALAAACRNSSARVLALYIATPRQWATHNMSPRQAELINAQLNGLQIALAEKGIPLLFREVDDFVASVEIVKQVCAENSVTHLFYNYQYEVNERARDVEVERALRNVVCEGFDDSVILPPGAVMTGNHEMYKVFTPFKNAWLKRLREGMPECVAAPKVRSSGSIEPSPSITLNYPRQSFDTAHF

>d1iqra2 c.28.1.1 (A:2-171) N-terminal domain of DNA photolyase {Thermus thermophilus}

GPLLVWHRGDLRLHDHPALLEALARGPVVGLVVLDPNNLKTTPRRRAWFLENVRALREAYRARGGALWVLEGLPWEKVPEAARRLKAKAVYALTSHTPYGRYRDGRVREALPVPLHLLPAPHLLPPDLPRAYRVYTPFSRLYRGAAPPLPPPEALPKGPEEGEIPREDPG

>d1qnf\_2 c.28.1.1 (1-204) N-terminal domain of DNA photolyase {Anacystis nidulans}

MAAPILFWHRRDLRLSDNIGLAAARAQSAQLIGLFCLDPQILQSADMAPARVAYLQGCLQELQQRYQQAGSRLLLLQGDPQHLIPQLAQQLQAEAVYWNQDIEPYGRDRDGQVAAALKTAGIRAVQLWDQLLHSPDQILSGSGNPYSVYGPFWKNWQAQPKPTPVATPTELVDLSPEQLTAIAPLLLSELPTLKQLGFDWDGGF

>d1efva1 c.29.1.1 (A:20-207) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}

QSTLVIAEHANDSLAPITLNTITAATRLGGEVSCLVAGTKCDKVAQDLCKVAGIAKVLVAQHDVYKGLLPEELTPLILATQKQFNYTHICAGASAFGKNLLPRVAAKLEVAPISDIIAIKSPDTFVRTIYAGNALCTVKCDEKVKVFSVRGTSFDAAATSGGSASSEKASSTSPVEISEWLDQKLTKS

>d1efvb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}

LRVLVAVKRVIDYAVKIRVKPDRTGVVTDGVKHSMNPFCEIAVEEAVRLKEKKLVKEVIAVSCGPAQCQETIRTALAMGADRGIHVEVPPAEAERLGPLQVARVLAKLAEKEKVDLVLLGKQAIDDDCNQTGQMTAGFLDWPQGTFASQVTLEGDKLKVEREIDGGLETLRLKLPAVVTADLRLNEPRYATLPNIMKAKKKKIEVIKPGDLGVDLTSKLSVISVEDPPQRTAGVKVETTEDLVAKLKEIGRI

>d1efpa1 c.29.1.1 (A:2-184) Electron transfer flavoprotein, ETFP {Paracoccus denitrificans}

AVLLLGEVTNGALNRDATAKAVAAVKALGDVTVLCAGASAKAAAEEAAKIAGVAKVLVAEDALYGHRLAEPTAALIVGLAGDYSHIAAPATTDAKNVMPRVAALLDVMVLSDVSAILDADTFERPIYAGNAIQVVKSKDAKKVFTIRTASFDAAGEGGTAPVTETAAAADPGLSSWVADEVAE

>d1mjha\_ c.29.1.2 (A:) "Hypothetical" protein MJ0577 {Archaeon Methanococcus jannaschii}

VMYKKILYPTDFSETAEIALKHVKAFKTLKAEEVILLHVIDEREIKKRDIFSLLLGVAGLNKSVEEFENELKNKLTEEAKNKMENIKKELEDVGFKVKDIIVVGIPHEEIVKIAEDEGVDIIIMGSHGKTNLKEILLGSVTENVIKKSNKPVLVVKRKNS

>d1jmva\_ c.29.1.2 (A:) Universal stress protein A, UspA {Haemophilus influenzae}

MYKHILVAVDLSEESPILLKKAVGIAKRHDAKLSIIHVDVNFSDLYTGLIDVNMSSMQDRISTETQKALLDLAESVDYPISEKLSGSGDLGQVLSDAIEQYDVDLLVTGHHQDFWSKLMSSTRQVMNTIKIDMLVVPLRD

>d1dv1a2 c.30.1.1 (A:1-114) Biotin carboxylase (BC) subunit of acetyl-CoA carboxylase {Escherichia coli}

MLDKIVIANRGEIALRILRACKELGIKTVAVHSSADRDLKHVLLADETVCIGPAPSVKSYLNIPAIISAAEITGAVAIHPGYGFLSENANFAEQVERSGFIFIGPKAETIRLMG

>d1gsoa2 c.30.1.1 (A:-2-103) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}

EFMKVLVIGNGGREHALAWKAAQSPLVETVFVAPGNAGTALEPALQNVAIGVTDIPALLDFAQNEKIDLTIVGPEAPLVKGVVDTFRAAGLKIFGPTAGAAQLEG

>d1b6ra2 c.30.1.1 (A:1-78) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

MKQVCVLGNGQLGRMLRQAGEPLGIAVWPVGLDAEPAAVPFQQSVITAEIERWPETALTRQLARHPAFVNRDVFPIIA

>d1eyza2 c.30.1.1 (A:2-112) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

TLLGTALRPAATRVMLLGSGELGKEVAIECQRLGVEVIAVDRYADAPAMHVAHRSHVINMLDGDALRRVVELEKPHYIVPEIEAIATDMLIQLEEEGLNVVPCARATKLTM

>d1a9xa3 c.30.1.1 (A:1-127) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

MPKRTDIKSILILGAGPIVIGQACEFDYSGAQACKALREEGYRVINVNSNPATIMTDPEMADATYIEPIHWEVVRKIIEKERPDAVLPTMGGQTALNCALELERQGVLEEFGVTMIGATADAIDKAE

>d1iow\_1 c.30.1.2 (1-96) D-Ala-D-Ala ligase {Escherichia coli, gene ddlB}

MTDKIAVLLGGTSAEREVSLNSGAAVLAGLREGGIDAYPVDPKEVDVTQLKSMGFQKVFIALHGRGGEDGTLQGMLELMGLPYTGSGVMASALSMD

>d1ehia1 c.30.1.2 (A:3-134) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}

KKRVALIFGGNSSEHDVSKRSAQNFYNAIEATGKYEIIVFAIAQNGFFLDTESSKKILALEDEQPIVDAFMKTVDASDPLARIHALKSAGDFDIFFPVVHGNLGEDGTLQGLFKLLDKPYVGAPLRGHAVSF

>d1e4ea1 c.30.1.2 (A:2-131) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}

NRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGITKSGVWKMCEKPCAEWENENCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKSGEDGSIQGLFELSGIPFVGCDIQSSAICM

>d1poxa1 c.31.1.3 (A:183-365) Pyruvate oxidase {Lactobacillus plantarum}

YASANNYQTPLLPEPDVQAVTRLTQTLLAAERPLIYYGIGARKAGKELEQLSKTLKIPLMSTYPAKGIVADRYPAYLGSANRVAQKPANEALAQADVVLFVGNNYPFAEVSKAFKNTRYFLQIDIDPAKLGKRHKTDIAVLADAQKTLAAILAQVSERESTPWWQANLANVKNWRAYLASLED

>d1qpba1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QTPIDMSLKPNDAESEKEVIDTILVLIKDAKNPVILADACCSRHDVKAETKKLIDLTQFPAFVTPMGKGSIDEQHPRYGGVYVGTLSKPEVKEAVESADLILSVGALLSDFNTGSFSYSYKTKNIVEFHSDHMKIRNATFPGVQMKFVLQKLLTAIADAAKGYKPVAVPARTPANAAVP

>d1zpda1 c.31.1.3 (A:188-362) Pyruvate decarboxylase {Zymomonas mobilis}

EASDEASLNAAVDETLKFIANRDKVAVLVGSKLRAAGAEEAAVKFTDALGGAVATMAAAKSFFPEENALYIGTSWGEVSYPGVEKTMKEADAVIALAPVFNDYSTTGWTDIPDPKKLVLAEPRSVVVNGIRFPSVHLKDYLTRLAQKVSKKTGSLDFFKSLNAGELKKAAPADPS

>d1bfd\_1 c.31.1.3 (182-341) Benzoylformate decarboxylase {Pseudomonas putida}

SVRLNDQDLDILVKALNSASNPAIVLGPDVDAANANADCVMLAERLKAPVWVAPSAPRCPFPTRHPCFRGLMPAGIAAISQLLEGHDVVLVIGAPVFRYHQYDPGQYLKPGTRLISVTCDPLEAARAPMGDAIVADIGAMASALANLVEESSRQLPTAAP

>d1jsca1 c.31.1.3 (A:280-460) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

AQDEFVMQSINKAADLINLAKKPVLYVGAGILNHADGPRLLKELSDRAQIPVTTTLQGLGSFDQEDPKSLDMLGMHGCATANLAVQNADLIIAVGARFDDRVTGNISKFAPEARRAAAEGRGGIIHFEVSPKNINKVVQTQIAVEGDATTNLGKMMSKIFPVKERSEWFAQINKWKKEYPY

>d1icia\_ c.31.1.5 (A:) AF1676 sir2 homolog {Archaeon Archaeoglobus fulgidus}

GSHHHHHHGSHMDEKLLKTIAESKYLVALTGAGVSAESGIPTFRGKDGLWNRYRPEELANPQAFAKDPEKVWKWYAWRMEKVFNAQPNKAHQAFAELERLGVLKCLITQNVDDLHERAGSRNVIHLHGSLRVVRCTSCNNSFEVESAPKIPPLPKCDKCGSLLRPGVVWFGEMLPPDVLDRAMREVERADVIIVAGTSAVVQPAASLPLIVKQRGGAIIEINPDETPLTPIADYSLRGKAGEVMDELVRHVRKALS

>d1j8fa\_ c.31.1.5 (A:) Sirt2 histone deacetylase {Human (Homo sapiens)}

GEADMDFLRNLFSQTLSLGSQKERLLDELTLEGVARYMQSERCRRVICLVGAGISTSAGIPDFRSPSTGLYDNLEKYHLPYPEAIFEISYFKKHPEPFFALAKELYPGQFKPTICHYFMRLLKDKGLLLRCYTQNIDTLERIAGLEQEDLVEAHGTFYTSHCVSASCRHEYPLSWMKEKIFSEVTPKCEDCQSLVKPDIVFFGESLPARFFSCMQSDFLKVDLLLVMGTSLQVQPFASLISKAPLSTPRLLINKEKAGQSDPFLGMIMGLGGGMDFDSKKAYRDVAWLGECDQGCLALAELLGWKKELEDLVRREHASIDAQS

>d1fsz\_1 c.32.1.1 (23-231) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}

SPEDKELLEYLQQTKAKITVVGCGGAGNNTITRLKMEGIEGAKTVAINTDAQQLIRTKADKKILIGKKLTRGLGAGGNPKIGEEAAKESAEEIKAAIQDSDMVFITCGLGGGTGTGSAPVVAEISKKIGALTVAVVTLPFVMEGKVRMKNAMEGLERLKQHTDTLVVIPNEKLFEIVPNMPLKLAFKVADEVLINAVKGLVELITKDGL

>d1tuba1 c.32.1.1 (A:1-245) Tubulin alpha-subunit {Pig (Sus scrofa)}

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIRKLADQCTGLQGFSVFHSFGGGTGSGFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLIGQIVSSITASLRFD

>d1im5a\_ c.33.1.2 (A:) Pyrazinamidase/nicotinamidase {Archaeon Pyrococcus horikoshii}

PEEALIVVDMQRDFMPGGALPVPEGDKIIPKVNEYIRKFKEKGALIVATRDWHPENHISFRERGGPWPRHCVQNTPGAEFVVDLPEDAVIISKATEPDKEAYSGFEGTDLAKILRGNGVKRVYICGVATEYCVRATALDALKHGFEVYLLRDAVKGIKPEDEERALEEMKSRGIKIVQF

>d1yaca\_ c.33.1.2 (A:) YcaC {Escherichia coli}

TKPYVRLDKNDAAVLLVDHQAGLLSLVRDIEPDKFKNNVLALGDLAKYFNLPTILTTSAETGPNGPLVPELKAQFPDAPYIARPGNINAWDNEDFVKAVKATGKKQLIIAGVVTEVCVAFPALSAIEEGFDVFVVTDASGTFNEITRHSAWDRMSQAGAQLMTWFGVACELHRDWRNDIAGLATLFSNHIPDYRNLMTSYDTLT

>d1e20a\_ c.34.1.1 (A:) Halotolerance protein Hal3 {Mouse-ear cress (Arabidopsis thaliana)}

RKPRVLLAASGSVAAIKFGNLCHCFTEWAEVRAVVTKSSLHFLDKLSLPQEVTLYTDEDEWSSWNKIGDPVLHIELRRWADVLVIAPLSANTLGKIAGGLCDNLLTCIIRAWDYTKPLFVAPAMNTLMWNNPFTERHLLSLDELGITLIPPIKKRLACGDYGNGAMAEPSLIYSTVRLFWESQAH

>d1g5qa\_ c.34.1.1 (A:) Epidermin modifying enzyme (peptidyl-cysteine decarboxylase) EpiD {Staphylococcus epidermidis}

MYGKLLICATASINVININHYIVELKQHFDEVNILFSPSSKNFINTDVLKLFCDNLYDEIKDPLLNNINIVENHEYILVLPASANTINKIANGICDNLLTTVCLTGYQKLFIFPNMNIRMWGNPFLQKNIDLLKNNDVKVYSPDMNKSFEISSGRYKNNITMPNIENVLNFVLN

>d1ig3a2 c.100.1.1 (A:10-178) Thiamin pyrophosphokinase, catalytic domain {Mouse (Mus musculus)}

HSSGLVPRGSHMEHAFTPLEPLLPTGNLKYCLVVLNQPLDARFRHLWKKALLRACADGGANHLYDLTEGERESFLPEFVSGDFDSIRPEVKEYYTKKGCDLISTPDQDHTDFTKCLQVLQRKIEEKELQVDVIVTLGGLGGRFDQIMASVNTLFQATHITPVPIIIIQK

>d1ig0a2 c.100.1.1 (A:3-223) Thiamin pyrophosphokinase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

EECIENPERIKIGTDLINIRNKMNLKELIHPNEDENSTLLILNQKIDIPRPLFYKIWKLHDLKVCADGAANRLYDYLDDDETLRIKYLPNYIIGDLDSLSEKVYKYYRKNKVTIIKQTTQYSTDFTKCVNLISLHFNSPEFRSLISNKDNLQSNHGIELEKGIHTLYNTMTESLVFSKVTPISLLALGGIGGRFDQTVHSITQLYTLSENASYFKLCYMTP

>d1f75a\_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Micrococcus luteus}

NINAAQIPKHIAIIMDGNGRWAKQKKMPRIKGHYEGMQTVRKITRYASDLGVKYLTLYAFSTENWSRPKDEVNYLMKLPGDFLNTFLPELIEKNVKVETIGFIDDLPDHTKKAVLEAKEKTKHNTGLTLVFALNYGGRKEIISAVQLIAERYKSGEISLDEISETHFNEYLFTANMPDPELLIRTSGEERLSNFLIWQCSYSEFVFIDEFWPDFNEESLAQCISIYQNR

>d1jp3a\_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Escherichia coli}

LPAHGCRHVAIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALTLYAFSSENWNRPAQEVSALMELFVWALDSEVKSLHRHNVRLRIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVQGVRQLAEKVQQGNLQPDQIDEEMLNQHVCMHELAPVDLVIRTGGEHRISNFLLWQIAYAELYFTDVLWPDFDEQDFEGALNAFANRE

>d1pvda2 c.36.1.1 (A:2-181) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

SEITLGKYLFERLKQVNVNTVFGLPGDFNLSLLDKIYEVEGMRWAGNANELNAAYAADGYARIKGMSCIITTFGVGELSALNGIAGSYAEHVGVLHVVGVPSISHHTLGNGDFTVFHRMSANISETTAMITDIATAPAEIDRCIRTTYVTQRPVYLGLPANLVDLNVPAKLL

>d1pvda3 c.36.1.1 (A:361-556) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

ASTPLKQEWMWNQLGNFLQEGDVVIAETGTSAFGINQTTFPNNTYGISQVLWGSIGFTTGATLGAAFAAEEIDPKKRVILFIGDGSLQLTVQEISTMIRWGLKPYLFVLNNDGYTIEKLIHGPKAQYNEIQGWDHLSLLPTFGAKDYETHRVATTGEWDKLTQDKSFNDNSKIRMIEIMLPVFDAPQNLVKQAKLT

>d1zpda2 c.36.1.1 (A:2-187) Pyruvate decarboxylase {Zymomonas mobilis}

SYTVGTYLAERLVQIGLKHHFAVAGDYNLVLLDNLLLNKNMEQVYCCNELNCGFSAEGYARAKGAAAAVVTYSVGALSAFDAIGGAYAENLPVILISGAPNNNDHAAGHVLHHALGKTDYHYQLEMAKNITAAAEAIYTPEEAPAKIDHVIKTALREKKPVYLEIACNIASMPCAAPGPASALFND

>d1zpda3 c.36.1.1 (A:363-566) Pyruvate decarboxylase {Zymomonas mobilis}

APLVNAEIARQVEALLTPNTTVIAETGDSWFNAQRMKLPNGARVEYEMQWGHIGWSVPAAFGYAVGAPERRNILMVGDGSFQLTAQEVAQMVRLKLPVIIFLINNYGYTIEVMIHDGPYNNIKNWDYAGLMEVFNGNGGYDSGAAKGLKAKTGGELAEAIKVALANTDGPTLIECFIGREDCTEELVKWGKRVAAANSRKPVNK

>d1poxa2 c.36.1.1 (A:9-182) Pyruvate oxidase {Lactobacillus plantarum}

TNILAGAAVIKVLEAWGVDHLYGIPGGSINSIMDALSAERDRIHYIQVRHEEVGAMAAAADAKLTGKIGVCFGSAGPGGTHLMNGLYDAREDHVPVLALIGQFGTTGMNMDTFQEMNENPIYADVADYNVTAVNAATLPHVIDEAIRRAYAHQGVAVVQIPVDLPWQQISAEDW

>d1poxa3 c.36.1.1 (A:366-593) Pyruvate oxidase {Lactobacillus plantarum}

KQEGPLQAYQVLRAVNKIAEPDAIYSIDVGDINLNANRHLKLTPSNRHITSNLFATMGVGIPGAIAAKLNYPERQVFNLAGDGGASMTMQDLVTQVQYHLPVINVVFTNCQYGFIKDEQEDTNQNDFIGVEFNDIDFSKIADGVHMQAFRVNKIEQLPDVFEQAKAIAQHEPVLIDAVITGDRPLPAEKLRLDSAMSSAADIEAFKQRYEAQDLQPLSTYLKQFGLDD

>d1bfd\_2 c.36.1.1 (2-181) Benzoylformate decarboxylase {Pseudomonas putida}

ASVHGTTYELLRRQGIDTVFGNPGSNELPFLKDFPEDFRYILALQEACVVGIADGYAQASRKPAFINLHSAAGTGNAMGALSNAWNSHSPLIVTAGQQTRAMIGVEALLTNVDAANLPRPLVKWSYEPASAAEVPHAMSRAIHMASMAPQGPVYLSVPYDDWDKDADPQSHHLFDRHVSS

>d1bfd\_3 c.36.1.1 (342-524) Benzoylformate decarboxylase {Pseudomonas putida}

EPAKVDQDAGRLHPETVFDTLNDMAPENAIYLNESTSTTAQMWQRLNMRNPGSYYFCAAGGLGFALPAAIGVQLAEPERQVIAVIGDGSANYSISALWTAAQYNIPTIFVIMNNGTYGALRWFAGVLEAENVPGLDVPGIDFRALAKGYGVQALKADNLEQLKGSLQEALSAKGPVLIEVSTV

>d1jsca2 c.36.1.1 (A:83-270) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

PDMDTSFVGLTGGQIFNEMMSRQNVDTVFGYPGGAILPVYDAIHNSDKFNFVLPKHEQGAGHMAEGYARASGKPGVVLVTSGPGATNVVTPMADAFADGIPMVVFTGQVPTSAIGTDAFQEADVVGISRSCTKWNVMVKSVEELPLRINEAFEIATSGRPGPVLVDLPKDVTAAILRNPIPTKTTLPS

>d1jsca3 c.36.1.1 (A:461-648) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

AYMEETPGSKIKPQTVIKKLSKVANDTGRHVIVTTGVGQHQMWAAQHWTWRNPHTFITSGGLGTMGYGLPAAIGAQVAKPESLVIDIDGDASFNMTLTELSSAVQAGTPVKILILNNEEQGMVTQWQSLFYEHRYSHTHQLNPDFIKLAEAMGLKGLRVKKQEELDAKLKEFVSTKGPVLLEVEVDKK

>d1gpua1 c.36.1.2 (A:3-337) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}

QFTDIDKLAVSTIRILAVDTVSKANSGHPGAPLGMAPAAHVLWSQMRMNPTNPDWINRDRFVLSNGHAVALLYSMLHLTGYDLSIEDLKQFRQLGSRTPGHPEFELPGVEVTTGPLGQGISNAVGMAMAQANLAATYNKPGFTLSDNYTYVFLGDGCLQEGISSEASSLAGHLKLGNLIAIYDDNKITIDGATSISFDEDVAKRYEAYGWEVLYVENGNEDLAGIAKAIAQAKLSKDKPTLIKMTTTIGYGSLHAGSHSVHGAPLKADDVKQLKSKFGFNPDKSFVVPQEVYDHYQKTILKPGVEANNKWNKLFSEYQKKFPELGAELARRLSGQ

>d1gpua2 c.36.1.2 (A:338-534) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}

LPANWESKLPTYTAKDSAVATRKLSETVLEDVYNQLPELIGGSADLTPSNLTRWKEALDFQPPSSGSGNYSGRYIRYGIREHAMGAIMNGISAFGANYKPYGGTFLNFVSYAAGAVRLSALSGHPVIWVATHDSIGVGEDGPTHQPIETLAHFRSLPNIQVWRPADGNEVSAAYKNSLESKHTPSIIALSRQNLPQL

>d1dtwa1 c.36.1.3 (A:) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}

PQFPGASAEFIDKLEFIQPNVISGIPIYRVMDRQGQIINPSEDPHLPKEKVLKLYKSMTLLNTMDRILYESQRQGRISFYMTNYGEEGTHVGSAAALDNTDLVFGQYREAGVLMYRDYPLELFMAQCYGNISDLGKGRQMPVHYGCKERHFVTISSPLATQIPQAVGAAYAAKRANANRVVICYFGEGAASEGDAHAGFNFAATLECPIIFFCRNNGYAISTPTSEQYRGDGIAARGPGYGIMSIRVDGNDVFAVYNATKEARRRAVAENQPFLIEAMTYRIGHHSTSDDSSAYRSVDEVNYWDKQDHPISRLRHYLLSQGWWDEEQEKAWRKQSRRKVMEAFEQAERKPKPNPNLLFSDVYQEMPAQLRKQQESLARHLQTYGEHYPLDHFDK

>d1qs0a1 c.36.1.3 (A:) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

NEYAPLRLHVPEPTGRPGCQTDFSYLRLNDAGQARKPPVDVDAADTADLSYSLVRVLDEQGDAQGPWAEDIDPQILRQGMRAMLKTRIFDSRMVVAQRQKKMSFYMQSLGEEAIGSGQALALNRTDMCFPTYRQQSILMARDVSLVEMICQLLSNERDPLKGRQLPIMYSVREAGFFTISGNLATQFVQAVGWAMASAIKGDTKIASAWIGDGATAESDFHTALTFAHVYRAPVILNVVNNQWAISTFQAIAGGESTTFAGRGVGCGIASLRVDGNDFVAVYAASRWAAERARRGLGPSLIEWVTYRAGPHSTSDDPSKYRPADDWSHFPLGDPIARLKQHLIKIGHWSEEEHQATTAEFEAAVIAAQKEAEQYGTLANGHIPSAASMFEDVYKEMPDHLRRQRQEL

>d1qs0b1 c.36.1.3 (B:2-205) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

ATTTMTMIQALRSAMDVMLERDDNVVVYGQDVGYFGGVFRCTEGLQTKYGKSRVFDAPISESGIVGTAVGMGAYGLRPVVEIQFADYFYPASDQIVSEMARLRYRSAGEFIAPLTLRMPCGGGIYGGQTHSQSPEAMFTQVCGLRTVMPSNPYDAKGLLIASIECDDPVIFLEPKRLYNGPFDGHHDRPVTPWSKHPHSAVPDG

>d1keka1 c.36.1.4 (A:2-258) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

GKKMMTTDGNTATAHVAYAMSEVAAIYPITPSSTMGEEADDWAAQGRKNIFGQTLTIREMQSEAGAAGAVHGALAAGALTTTFTASQGLLLMIPNMYKISGELLPGVFHVTARAIAAHALSIFGDHQDIYAARQTGFAMLASSSVQEAHDMALVAHLAAIESNVPFMHFFDGFRTSHEIQKIEVLDYADMASLVNQKALAEFRAKSMNPEHPHVRGTAQNPDIYFQGREAANPYYLKVPGIVAEYMQKVASLTGRSY

>d1keka2 c.36.1.4 (A:786-1232) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

VKSEVLPRDSLKGSQFQEPLMEFSGACSGCGETPYVRVITQLFGERMFIANATGCSSIWGASAPSMPYKTNRLGQGPAWGNSLFEDAAEYGFGMNMSMFARRTHLADLAAKALESDASGDVKEALQGWLAGKNDPIKSKEYGDKLKKLLAGQKDGLLGQIAAMSDLYTKKSVWIFGGDGWAYDIGYGGLDHVLASGEDVNVFVMDTEVYSNTGGQSSKATPTGAVAKFAAAGKRTGKKDLARMVMTYGYVYVATVSMGYSKQQFLKVLKEAESFPGPSLVIAYATCINQGLRKGMGKSQDVMNTAVKSGYWPLFRYDPRLAAQGKNPFQLDSKAPDGSVEEFLMAQNRFAVLDRSFPEDAKRLRAQVAHELDVRFKELEHMAATNIFESFAPAGGKADGSVDFGEGAEFCTRDDTPMMARPDSGEACDQNRAGTSEQQGDLSKRTKK

>d1gky\_\_ c.37.1.1 (-) Guanylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SRPIVISGPSGTGKSTLLKKLFAEYPDSFGFSVSSTTRTPRAGEVNGKDYNFVSVDEFKSMIKNNEFIEWAQFSGNYYGSTVASVKQVSKSGKTCILDIDMQGVKSVKAIPELNARFLFIAPPSVEDLKKRLEGRGTETEESINKRLSAAQAELAYAETGAHDKVIVNDDLDKAYKELKDFIFAEK

>d1kgda\_ c.37.1.1 (A:) Guanylate kinase-like domain of Cask {Human (Homo sapiens)}

HMRKTLVLLGAHGVGRRHIKNTLITKHPDRFAYPIPHTTRPPKKDEENGKNYYFVSHDQMMQDISNNEYLEYGSHEDAMYGTKLETIRKIHEQGLIAILDVEPQALKVLRTAEFAPFVVFIAAPTITPGLNEDESLQRLQKESDILQRTYAHYFDLTIINNEIDETIRHLEEAVELVC

>d1kjwa2 c.37.1.1 (A:526-724) Guanylate kinase-like domain of Psd-95 {Rat (Rattus norvegicus)}

VTQMEVHYARPIIILGPTKDRANDDLLSEFPDKFGSCVPHTTRPKREYEIDGRDYHFVSSREKMEKDIQAHKFIEAGQYNSHLYGTSVQSVREVAEQGKHCILDVSANAVRRLQAAHLHPIAIFIRPRSLENVLEINKRITEEQARKAFDRATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWVPARERL

>d1ukz\_\_ c.37.1.1 (-) Uridylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

PAFSPDQVSVIFVLGGPGAGKGTQCEKLVKDYSFVHLSAGDLLRAEQGRAGSQYGELIKNCIKEGQIVPQEITLALLRNAISDNVKANKHKFLIDGFPRKMDQAISFERDIVESKFILFFDCPEDIMLERLLERGKTSGRSDDNIESIKKRFNTFKETSMPVIEYFETKSKVVRVRCDRSVEDVYKDVQDAIRDSL

>d1deka\_ c.37.1.1 (A:) Deoxynucleoside monophosphate kinase {Bacteriophage T4}

MKLIFLSGVKRSGKDTTADFIMSNYSAVKYQLAGPIKDALAYAWGVFAANTDYPCLTRKEFEGIDYDRETNLNLTKLEVITIMEQAFCYLNGKSPIKGVFVFDDEGKESVNFVAFNKITDVINNIEDQWSVRRLMQALGTDLIVNNFDRMYWVKLFALDYLDKFNSGYDYYIVPDTRQDHEMDAARAMGATVIHVVRPGQKSNDTHITEAGLPIRDGDLVITNDGSLEELFSKIKNTLKVL

>d1j90a\_ c.37.1.1 (A:) Deoxyribonucleoside kinase {Fruit fly (Drosophila melanogaster)}

TQPFTVLIEGNIGSGKTTYLNHFEKYKNDICLLTEPVEKWRNVNGVNLLELMYKDPKKWAMPFQSYVTLTMLQSHTAPTNKKLKIMERSIFSARYCFVENMRRNGSLEQGMYNTLEEWYKFIEESIHVQADLIIYLRTSPEVAYERIRQRARSEESCVPLKYLQELHELHEDWLIHQRRPQSCKVLVLDADLNLE

>d1jaga\_ c.37.1.1 (A:) Deoxyguanosine kinase {Human (Homo sapiens)}

GPRRLSIEGNIAVGKSTFVKLLTKTYPEWHVATEPVATWQNIQAAGNQKACTAQSLGNLLDMMYREPARWSYTFQTFSFLSRLKVQLEPFPEKLLQARKPVQIFERSVYSDRYIFAKNLFENGSLSDIEWHIYQDWHSFLLWEFASRITLHGFIYLQASPQVCLKRLYQRAREEEKGIELAYLEQLHGQHEAWLIHKTTKLHFEALMNIPVLVLDVNDDFSEEVTKQEDLMREVNTFVKNL

>d1ckea\_ c.37.1.1 (A:) CMP kinase {Escherichia coli}

AIAPVITIDGPSGAGKGTLCKAMAEALQWHLLDSGAIYRVLALAALHHHVDVASEDALVPLASHLDVRFVSTNGNLEVILEGEDVSGEIRTQEVANAASQVAAFPRVREALLRRQRAFRELPGLIADGRDMGTVVFPDAPVKIFLDASSEERAHRRMLQLQVKGFSVNFERLLAEIKERDDRDRNRAVAPLVPAADALVLDSTTLSIEQVIEKALQYARQKLALA

>d1e2ka\_ c.37.1.1 (A:) Thymidine kinase {Herpes simplex virus type 1, different strains}

MPTLLRVYIDGPHGMGKTTTTQLLVALGSRDDIVYVPEPMTYWRVLGASETIANIYTTQHRLDQGEISAGDAAVVMTSAQITMGMPYAVTDAVLAPHIGGEAGSSHAPPPALTLIFDRHPIAALLCYPAARYLMGSMTPQAVLAFVALIPPTLPGTNIVLGALPEDRHIDRLAKRQRPGERLDLAMLAAIRRVYGLLANTVRYLQCGGSWREDWGQLSGTAVPPQGAEPQSNAGPRPHIGDTLFTLFRAPELLAPNGDLYNVFAWALDVLAKRLRSMHVFILDYDQSPAGCRDALLQLTSGMVQTHVTTPGSIPTICDLARTFAREMGE

>d1nksa\_ c.37.1.1 (A:) Adenylate kinase {Archaeon Sulfolobus acidocaldarius}

MKIGIVTGIPGVGKSTVLAKVKEILDNQGINNKIINYGDFMLATALKLGYAKDRDEMRKLSVEKQKKLQIDAAKGIAEEARAGGEGYLFIDTHAVIRTPSGYLPGLPSYVITEINPSVIFLLEADPKIILSRQKRDTTRNRNDYSDESVILETINFARYAATASAVLAGSTVKVIVNVEGDPSIAANEIIRSMK

>d2ak3a1 c.37.1.1 (A:0-124,A:162-225) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-3}

GASARLLRAAIMGAPGSGKGTVSSRITKHFELKHLSSGDLLRDNMLRGTEIGVLAKTFIDQGKLIPDDVMTRLVLHELKNLTQYNWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRLTXDRPETVVKRLKAYEAQTEPVLEYYRKKGVLETFSGTETNKIWPHVYAFLQTKLPQRSQETSVTP

>d1ak2\_1 c.37.1.1 (14-146,177-233) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-2}

PKGVRAVLLGPPGAGKGTQAPKLAKNFCVCHLATGDMLRAMVASGSELGKKLKATMDAGKLVSDEMVLELIEKNLETPPCKNGFLLDGFPRTVRQAEMLDDLMEKRKEKLDSVIEFSIPDSLLIRRITGRLIHXSDDNKKALKIRLEAYHTQTTPLVEYYSKRGIHSAIDASQTPDVVFASILAAFSKATS

>d1zaka1 c.37.1.1 (A:3-127,A:159-222) Adenylate kinase {Maize (Zea mays)}

ADPLKVMISGAPASGKGTQCELIKTKYQLAHISAGDLLRAEIAAGSENGKRAKEFMEKGQLVPDEIVVNMVKERLRQPDAQENGWLLDGYPRSYSQAMALETLEIRPDTFILLDVPDELLVERVVXFDDTEEKVKLRLETYYQNIESLLSTYENIIVKVQGDATVDAVFAKIDELLGSILEKKNEMVSST

>d1tmka\_ c.37.1.1 (A:) Thymidylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

GRGKLILIEGLDRTGKTTQCNILYKKLQPNCKLLKFPERSTRIGGLINEYLTDDSFQLSDQAIHLLFSANRWEIVDKIKKDLLEGKNIVMDRYVYSGVAYSAAKGTNGMDLDWCLQPDVGLLKPDLTLFLSTQDVDNNAEKSGFGDERYETVKFQEKVKQTFMKLLDKEIRKGDESITIVDVTNKGIQEVEALIWQIVEPVLSTHIDHDKFSFF

>d4tmka\_ c.37.1.1 (A:) Thymidylate kinase {Escherichia coli}

RSKYIVIEGLEGAGKTTARNVVVETLEQLGIRDMVFTREPGGTQLAEKLRSLLLDIKSVGDEVITDKAEVLMFYAARVQLVETVIKPALANGTWVIGDRHDLSTQAYQGGGRGIDQHMLATLRDAVLGDFRPDLTLYLDVTPEVGLKRARARGELDRIEQESFDFFNRTRARYLELAAQDKSIHTIDATQPLEAVMDAIRTTVTHWVKEL

>d1g3ua\_ c.37.1.1 (A:) Thymidylate kinase {Mycobacterium tuberculosis}

MLIAIEGVDGAGKRTLVEKLSGAFRAAGRSVATLAFPRYGQSVAADIAAEALHGEHGDLASSVYAMATLFALDRAGAVHTIQGLCRGYDVVILDRYVASNAAYSAARLHENAAGKAAAWVQRIEFARLGLPKPDWQVLLAVSAELAGERSRGRAQRDPGRARDNYERDAELQQRTGAVYAELAAQGWGGRWLVVGADVDPGRLAATLA

>d1g8fa3 c.37.1.15 (A:390-511) ATP sulfurylase C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

PRPKQGFSIVLGNSLTVSREQLSIALLSTFLQFGGGRYYKIFEHNNKTELLSLIQDFIGSGSGLIIPDQWEDDKDSVVGKQNVYLLDTSSSADIQLESADEPISHIVQKVVLFLEDNGFFVF

>d1i2da3 c.37.1.15 (A:391-573) ATP sulfurylase C-terminal domain {Fungus (Penicillium chrysogenum)}

PRATQGFTIFLTGYMNSGKDAIARALQVTLNQQGGRSVSLLLGDTVRHELSSELGFTREDRHTNIQRIAFVATELTRAGAAVIAAPIAPYEESRKFARDAVSQAGSFFLVHVATPLEHCEQSDKRGIYAAARRGEIKGFTGVDDPYETPEKADLVVDFSKQSVRSIVHEIILVLESQGFLERQ

>d1aqua\_ c.37.1.5 (A:) Estrogen sulfotransferase {Mouse (Mus musculus)}

EYYEVFGEFRGVLMDKRFTKYWEDVEMFLARPDDLVIATYPKSGTTWISEVVYMIYKEGDVEKCKEDAIFNRIPYLECRNEDLINGIKQLKEKESPRIVKTHLPPKLLPASFWEKNCKMIYLCRNAKDVAVSYYYFLLMITSYPNPKSFSEFVEKFMQGQVPYGSWYDHVKAWWEKSKNSRVLFMFYEDMKEDIRREVVKLIEFLERKPSAELVDRIIQHTSFQEMKNNPSTNYTMMPEEMMNQKVSPFMRKGIIGDWKNHFPEALRERFDEHYKQQMKDCTVKFRME

>d1efha\_ c.37.1.5 (A:) Hydroxysteroid sulfotransferase {Human (Homo sapiens)}

DFLWFEGIAFPTMGFRSETLRKVRDEFVIRDEDVIILTYPKSGTNWLAEILCLMHSKGDAKWIQSVPIWERSPWVESEIGYTALSETESPRLFSSHLPIQLFPKSFFSSKAKVIYLMRNPRDVLVSGYFFWKNMKFIKKPKSWEEYFEWFCQGTVLYGSWFDHIHGWMPMREEKNFLLLSYEELKQDTGRTIEKICQFLGKTLEPEELNLILKNSSFQSMKENKMSNYSLLSVDYVVDKAQLLRKGVSGDWKNHFTVAQAEDFDKLFQEKMADLPRKLAAALE

>d1nsta\_ c.37.1.5 (A:) Heparan sulfate N-deacetylase/N-sulfotransferase domain {Human (Homo sapiens)}

DPLWQDPCEDKRHKDIWSKEKTCDRFPKLLIIGPQKTGTTALYLFLGMHPDLSSNYPSSETFEEIQFFNGHNYHKGIDWYMEFFPIPSNTTSDFYFEKSANYFDSEVAPRRAAALLPKAKVLTILINPADRAYSWYQHQRAHDDPVALKYTFHEVITAGSDASSKLRALQNRCLVPGWYATHIERWLSAYHANQILVLDGKLLRTEPAKVMDMVQKFLGVTNTIDYHKTLAFDPKKGFWCQLLEGGKTKCLGKSKGRKYPEMDLDSRAFLKDYYRDHNIELSKLLYKMGQTLPTWLREDLQ

>d1fmja\_ c.37.1.5 (A:) Retinol dehydratase {Fall armyworm (Spodoptera frugiperda)}

PFPYEFRELNPEEDKLVKANLGAFPTTYVKLGPKGYMVYRPYLKDAANIYNMPLRPTDVFVASYQRSGTTMTQELVWLIENDLNFEAAKTYMSLRYIYLDGFMIYDPEKQEEYNDILPNPENLDMERYLGLLEYSSRPGSSLLAAVPPTEKRFVKTHLPLSLMPPNMLDTVKMVYLARDPRDVAVSSFHHARLLYLLNKQSNFKDFWEMFHRGLYTLTPYFEHVKEAWAKRHDPNMLFLFYEDYLKDLPGCIARIADFLGKKLSEEQIQRLCEHLNFEKFKNNGAVNMEDYREIGILADGEHFIRKGKAGCWRDYFDEEMTKQAEKWIKDNLKDTDLRYPNM

>d1a7j\_\_ c.37.1.6 (-) Phosphoribulokinase {Rhodobacter sphaeroides}

SKKHPIISVTGSSGAGTSTVKHTFDQIFRREGVKAVSIEGDAFHRFNRADMKAELDRRYAAGDATFSHFSYEANELKELERVFREYGETGQGRTRTYVHDDAEAARTGVAPGNFTDWRDFDSDSHLLFYEGLHGAVVNSEVNIAGLADLKIGVVPVINLEWIQKIHRDRATRGYTTEAVTDVILRRMHAYVHCIVPQFSQTDINFQRVPVVDTSNPFIARWIPTADESVVVIRFRNPRGIDFPYLTSMIHGSWMSRANSIVVPGNKLDLAMQLILTPLIDRVVRESKV

>d1esma\_ c.37.1.6 (A:) Pantothenate kinase PanK {Escherichia coli}

QTLMTPYLQFDRNQWAALRDSVPMTLSEDEIARLKGINEDLSLEEVAEIYLPLSRLLNFYISSNLRRQAVLEQFLGTNGQRIPYIISIAGSVAVGKSTTARVLQALLSRWPEHRRVELITTDGFLHPNQVLKERGLMKKKGFPESYDMHRLVKFVSDLKSGVPNVTAPVYSHLIYDVIPDGDKTVVQPDILILEGLNVLQSGMDYPHDPHHVFVSDFVDFSIYVDAPEDLLQTWYINRFLKFREGAFTDPDSYFHNYAKLTKEEAIKTAMTLWKEINWLNLKQNILPTRERASLILTKSANHAVEEVRLRK

>d1c1ya\_ c.37.1.8 (A:) Rap1A {Human (Homo sapiens)}

MREYKLVVLGSGGVGKSALTVQFVQGIFVEKYDPTIEDSYRKQVEVDCQQCMLEILDTAGTEQFTAMRDLYMKNGQGFALVYSITAQSTFNDLQDLREQILRVKDTEDVPMILVGNKCDLEDERVVGKEQGQNLARQWCNCAFLESSAKSKINVNEIFYDLVRQINR

>d3raba\_ c.37.1.8 (A:) Rab3a {Rat (Rattus norvegicus)}

NFDYMFKILIIGNSSVGKTSFLFRYADDSFTPAFVSTVGIDFKVKTIYRNDKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITNEESFNAVQDWSTQIKTYSWDNAQVLLVGNKCDMEDERVVSSERGRQLADHLGFEFFEASAKDNINVKQTFERLVDVICEK

>d1byua\_ c.37.1.8 (A:) Ran {Dog (Canis familiaris)}

EPQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYVPTLGVEVHPLVFHTNRGPIKFNVWDTAGQEKFGGLRDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFVAMPALAPPEVVMDPALAAQYEHDLEVAQTT

>d1hura\_ c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF1}

GNIFANLFKGLFGKKEMRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRERVNEAREELMRMLAEDELRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRHRNWYIQATCATSGDGLYEGLDWLSNQLRNQK

>d1f6ba\_ c.37.1.8 (A:) SAR1 {Chinese hamster (Cricetulus griseus)}

SSVLQFLGLYKKTGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPTSEELTIAGMTFTTFDLGGHIQARRVWKNYLPAINGIVFLVDCADHERLLESKEELDSLMTDETIANVPILILGNKIDRPEAISEERLREMFGLYGQTTGKGSVSLKELNARPLEVFMCSVLKRQGYGEGFRWMAQYID

>d2ngra\_ c.37.1.8 (A:) CDC42 {Human (Homo sapiens)}

MQTIKCVVVGDGAVGKTCLLISYTTNKFPSEYVPTVFDNYAVTVMIGGEPYTLGLFDTAGQEDYDRLRPLSYPQTDVFLVCFSVVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPITPETAEKLARDLKAVKYVECSALTQKGLKNVFDEAILAALEPPEPKKSRRCVLL

>d1ek0a\_ c.37.1.8 (A:) Ypt51 {Baker's yeast (Saccharomyces cerevisiae)}

VTSIKLVLLGEAAVGKSSIVLRFVSNDFAENKEPTIGAAFLTQRVTINEHTVKFEIWDTAGQERFASLAPMYYRNAQAALVVYDVTKPQSFIKARHWVKELHEQASKDIIIALVGNKIDMLQEGGERKVAREEGEKLAEEKGLLFFETSAKTGENVNDVFLGIGEKIPLK

>d1h65a\_ c.37.1.8 (A:) Chloroplast protein translocon GTPase Toc34 {Garden pea (Pisum sativum)}

VREWSGINTFAPATQTKLLELLGNLKQEDVNSLTILVMGKGGVGKSSTVNSIIGERVVSISPFQSEGPRPVMVSRSRAGFTLNIIDTPGLIEGGYINDMALNIIKSFLLDKTIDVLLYVDRLDAYRVDNLDKLVAKAITDSFGKGIWNKAIVALTHAQFSPPDGLPYDEFFSKRSEALLQVVRSGASLKKDAQASDIPVVLIENSGRCNKNDSDEKVLPNGIAWIPHLVQTITEVALNKSESIFVDKNLIDKLAAAD

>d1bof\_2 c.37.1.8 (10-60,182-354) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

KAAVERSKMIDRNLREDGEKAAREVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDLHFKMFDVGGQRSERKKWIHCFEGVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAAAYIQCQFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDAVTDVIIKNNLKDCGLF

>d1exma3 c.37.1.8 (A:3-212) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Thermus thermophilus}

GEFIRTKPHVNVGTIGHVDHGKTTLTAALTFVTAAENPNVEVKDYGDIDKAPEERARGITINTAHVEYETAKRHYSHVDCPGHADYIKNMITGAAQMDGAILVVSAADGPMPQTREHILLARQVGVPYIVVFMNKVDMVDDPELLDLVEMEVRDLLNQYEFPGDEVPVIRGSALLALEQMHRNPKTRRGENEWVDKIWELLDAIDEYIPT

>d1f60a3 c.37.1.8 (A:2-240) Elongation factor eEF-1alpha, N-terminal (G) domain {Baker's yeast (Saccharomyces cerevisiae)}

GKEKSHINVVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVLDKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGVGEFEAGISKDGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNFIKKVGYNPKTVPFVPISGWNGDNMIEATTNAPWYKGWEKETKAGVVKGKTLLEAIDAIEQPSRPT

>d1dar\_2 c.37.1.8 (1-282) Elongation factor G (EF-G), N-terminal (G) domain {Thermus thermophilus}

MAVKVEYDLKRLRNIGIAAHIDAGKTTTTERILYYTGRIHKIGEVHEGAATMDFMEQERERGITITAAVTTCFWKDHRINIIDTPGHVDFTIEVERSMRVLDGAIVVFDSSQGVEPQSETVWRQAEKYKVPRIAFANKMDKTGADLWLVIRTMQERLGARPVVMQLPIGREDTFSGIIDVLRMKAYTYGNDLGTDIREIPIPEEYLDQAREYHEKLVEVAADFDENIMLKYLEGEEPTEEELVAAIRKGTIDLKITPVFLGSALKNKGVQLLLDAVVDYLPS

>d1g7sa4 c.37.1.8 (A:1-227) Initiation factor IF2/eIF5b, N-terminal (G) domain {Archaeon Methanobacterium thermoautotrophicum}

MKIRSPIVSVLGHVDHGKTTLLDHIRGSAVASREAGGITQHIGATEIPMDVIEGICGDFLKKFSIRETLPGLFFIDTPGHEAFTTLRKRGGALADLAILIVDINEGFKPQTQEALNILRMYRTPFVVAANKIDRIHGWRVHEGRPFMETFSKQDIQVQQKLDTKVYELVGKLHEEGFESERFDRVTDFASQVSIIPISAITGEGIPELLTMLMGLAQQYLREQLKIE

>d1egaa1 c.37.1.8 (A:4-182) GTPase Era, N-terminal domain {Escherichia coli}

DKSYCGFIAIVGRPNVGKSTLLNKLLGQKISITSRKAQTTRHRIVGIHTEGAYQAIYVDTPGLHMEEKRAINRLMNKAASSSIGDVELVIFVVEGTRWTPDDEMVLNKLREGKAPVILAVNKVDNVQEKADLLPHLQFLASQMNFLDIVPISAETGLNVDTIAAIVRKHLPEATHHFPE

>d1f5na2 c.37.1.8 (A:7-283) Interferon-induced guanylate-binding protein 1 (GBP1), N-terminal domain {Human (Homo sapiens)}

MTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLAGKKKGFSLGSTVQSHTKGIWMWCVPHPKKPGHILVLLDTEGLGDVEKGDNQNDSWIFALAVLLSSTFVYNSIGTINQQAMDQLYYVTELTHRIRSKSSPDENENEVEDSADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLTYSLKLKKGTSQKDETFNLPRLCIRKFFPKKKCFVFDRPVHRRKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLS

>d1jwyb\_ c.37.1.8 (B:) Dynamin G domain {Slime mold (Dictyostelium discoideum)}

DQLIPVINKLQDVFNTLGSDPLDLPQIVVVGSQSSGKSSVLENIVGRDFLPRGSGIVTRRPLILQLTHLPIADDGSQTQEWGEFLHKPNDMFYDFSEIREEIIRDTDRMTGKNKGISAQPINLKIYSPHVVNLTLVDLPGITKVPVGDQPTDIEQQIRRMVMAYIKKQNAIIVAVTPANTDLANSDALQLAKEVDPEGKRTIGVITKLDLMDKGTDAMEVLTGRVIPLTLGFIGVINRSQEDIIAKKSIRESLKSEILYFKNHPIYKSIANRSGTAYLSKTLNKLLMFHIRDTLPDLKVKVSKMLS

>d2mysa2 c.37.1.9 (A:4-33,A:80-843) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral muscle}

DAEMAAFGEAAPYLRKSEKERIEAQNKPFDXMNPPKYDKIEDMAMMTHLHEPAVLYNLKERYAAWMIYTYSGLFCVTVNPYKWLPVYNPKVVLAYRGKKRQEAPPHIFSISDNAYQFMLTDRENQSILITGESGAGKTVNTKRVIQYFATIAASGEKKKEEQSGKMQGTLEDQIISANPLLEAFGNAKTVRNDNSSRFGKFIRIHFGATGKLASADIETYLLEKSRVTFQLPAERSYHIFYQIMSNKKPELIDMLLITTNPYDYHYVSEGEITVPSIDDQEELMATDSAIDILGFSADEKTAIYKLTGAVMHYGNLKFKQKQREEQAEPDGTEVADKAAYLMGLNSAELLKALCYPRVGVGNEAVTKGETVSEVHNSVGALAKAVYEKMFLWMVIRINQQLDTKQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKLQQFFNHHMFVLEQEEYKKEGIEWEFIDFGMDLAACIELIEKPMGIFSILEEECMFPKATDTSFKNKLYDEHLGKSNNFQKPKPAKGKAEAHFSLVHYAGTVDYNISGWLEKNKDPLNETVIGLYQKSSVKTLALLFATYGGEAEGGGGKKGGKKKGSSFQTVSALFRENLNKLMANLRSTHPHFVRCIIPNETKTPGAMEHELVLHQLRCNGVLEGIRICRKGFPSRVLYADFKQRYRVLNASAIPEGQFMDSKKASEKLLGGGDVDHTQYAFGHTKVFFKAGLLGLLEEMRDDKLAEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNVKHWPWMKLFFKIKPLLK

>g2kin.1 c.37.1.9 (A:,B:) Kinesin {Rat (Rattus norvegicus)}

ADPAECSIKVMCRFRPLNEAEILRGDKFIPKFKGEETVVIGQGKPYVFDRVLPPNTTQEQVYNACAKQIVKDVLEGYNGTIFAYGQTSSGKTHTMEGKLHDPQLMGIIPRIAHDIFDHIYSMDENLEFHIKVSYFEIYLDKIRDLLDVSKTNLAVHEDKNRVPYVKGCTERFVSSPEEVMDVIDEGKANRHVAVTNMNEHSSRSHSIFLINIKQENVETEKKLSGKLYLVDLAGSEKVXAKNINKSLSALGNVISALAEGTKTHVPYRDSKMTRILQDSLDGNCRTTIVICCSPSVFNEAETKSTLMFGQRAKTIKNTVSVNLELTAEEWKKKYEKEKE

>d1i6ia\_ c.37.1.9 (A:) Kinesin {Mouse (Mus musculus), kif1a}

GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDLFSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVREHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQIRNTVSVNHHHHH

>d1ii6a\_ c.37.1.9 (A:) Kinesin {Human (Homo sapiens), mitotic kinesin eg5}

GKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRKTYTFDMVFGASTKQIDVYRSVVCPILDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEDPLAGIIPRTLHQIFEKLTDNGTEFSVKVSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFSVTIHMKETTIDGEELVKIGKLNLVDLAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVERTPHVPYRESKLTRILQDSLGGRTRTSIIATISPASLNLEETLSTLEYAHRAKNILNKPEV

>d2ncda\_ c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional) {Fruit fly (Drosophila melanogaster)}

LRQRTEELLRCNEQQAAELETCKEQLFQSNMERKELHNTVMDLRGNIRVFCRIRPPLESEENRMCCTWTYHDESTVELQSIDAQAKSKMGQQIFSFDQVFHPLSSQSDIFEMVSPLIQSALDGYNICIFAYGQTGSGKTYTMDGVPESVGVIPRTVDLLFDSIRGYRNLGWEYEIKATFLEIYNEVLYDLLSNEQKDMEIRMAKNNKNDIYVSNITEETVLDPNHLRHLMHTAKMNRATASTAGNERSSRSHAVTKLELIGRHAEKQEISVGSINLVDLAGSESPKTSTRMTETKNINRSLSELTNVILALLQKQDHIPYRNSKLTHLLMPSLGGNSKTLMFINVSPFQDCFQESVKSLRFAASVNSC

>d1byi\_\_ c.37.1.10 (-) Dethiobiotin synthetase {Escherichia coli}

SKRYFVTGTDTEVGKTVASCALLQAAKAAGYRTAGYKPVASGSEKTPEGLRNSDALALQRNSSLQLDYATVNPYTFAEPTSPHIISAQEGRPIESLVMSAGLRALEQQADWVLVEGAGGWFTPLSDTFTFADWVTQEQLPVILVVGVKLGCINHAMLTAQVIQHAGLTLAGWVANDVTPPGKRHAEYMTTLTRMIPAPLLGEIPWLAENPENAATGKYINLALL

>d1dj3a\_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Bread wheat (Triticum aestivum)}

ADRVSSLSNVSGVLGSQWGDEGKGKLVDVLAPRFDIVARCQGGANAGHTIYNSEGKKFALHLVPSGILHEGTLCVVGNGAVIHVPGFFGEIDGLQSNGVSCDGRILVSDRAHLLFDLHQTVDGLREAELANSFIGTTKRGIGPCYSSKVTRNGLRVCDLRHMDTFGDKLDVLFEDAAARFEGFKYSKGMLKEEVERYKKFAERLEPFIADTVHVLNESIRQKKKILVEGGQATMLDIDFGTYPFVTSSSPSAGGICTGLGIAPRVIGDLIGVVKAYTTRVGSGPFPTELLGEEGDVLRKAGMEFGTTTGRPRRCGWLDIVALKYCCDINGFSSLNLTKLDVLSGLPEIKLGVSYNQMDGEKLQSFPGDLDTLEQVQVNYEVLPGWDSDISSVRSYSELPQAARRYVERIEELAGVPVHYIGVGPGRDALIYK

>d1eg7a\_ c.37.1.10 (A:) Formyltetrahydrofolate synthetase {Moorella thermoacetica}

DIEIAQAAKMKPVMELARGLGIQEDEVELYGKYKAKISLDVYRRLKDKPDGKLILVTAITPTPAGEGKTTTSVGLTDALARLGKRVMVCLREPSLGPSFGIKGGAAGGGYAQVVPMEDINLHFTGDIHAVTYAHNLLAAMVDNHLQQGNVLNIDPRTITWRRVIDLNERALRNIVIGLGGKANGVPRETGFDISVASEVMACLCLASDLMDLKERFSRKVVGYTYDGKPVTAGDLEAQGSMALLMKDAIKPNLVQTLENTPAFIHGGPFANIAHGCNSIIATKTALKLADYVVTEAGFGADLGAEKFYDVKCRYAGFKPDATVIVATVRALKMHGGVPKSDLATENLEALREGFANLEKHIENIGKFGVPAVVAINAFPTDTEAELNLLYELCAKAGAEVALSWAKGGEGGLELARKVLQTLESRPSNFHVLYNLDLSIKDKIAKIATEIYGADGVNYTAEADKAIQRYESLGYGNLPVVMAKTQYSFSDDMTKLGRPRNFTITVREVRLSAGGRLIVPITGAIMTMPGLPKRPAACNIDIDADGVITG

>d1fp6a\_ c.37.1.10 (A:) Nitrogenase iron protein {Azotobacter vinelandii}

AMRQCAIYGKGGIGKSTTTQNLVAALAEMGKKVMIVGCDPKADSTRLILHSKAQNTIMEMAAEAGTVEDLELEDVLKAGYGGVKCVESGGPEPGVGCAGRGVITAINFLEEEGAYEDDLDFVFYDVLGDVVCGGFAMPIRENKAQEIYIVCSGEMMAMYAANNISKGIVKYANSGSVRLGGLICNSRNTDREDELIIALANKLGTQMIHFVPRDNVVQRAEIRRMTVIEYDPKAKQADEYRALARKVVDNKLLVIPNPITMDELEELLMEFGIMEVEDESIVGKTAEEV

>d1iona\_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus horikoshii}

MTRIISIVSGKGGTGKTTVTANLSVALGEMGRKVLAVDGDLTMANLSLVLGVDDVNITLHDVLAGDAKLEDAIYMTQFENVYILPGAVDWEHVIKADPRKLPEVIKSLKGKYDFILIDCPAGLQLRAMSAMLSGEEAILVTNPEISCLTDTMKVGMVLKKAGLAILGFILNRYGRSERDIPPEAAQDVMDVPLLAVIPEDPVIREGTLEGIPAVKYKPESKGAQAFIKLAEEVDKLAGIKAKI

>d1j8mf2 c.37.1.10 (F:87-297) GTPase domain of the signal sequence recognition protein Ffh {Archaeon Acidianus ambivalens}

DKEPKVIPDKIPYVIMLVGVQGTGKTTTAGKLAYFYKKKGFKVGLVGADVYRPAALEQLQQLGQQIGVPVYGEPGEKDVVGIAKRGVEKFLSEKMEIIIVDTAGRHGYGEEAALLEEMKNIYEAIKPDEVTLVIDASIGQKAYDLASKFNQASKIGTIIITKMDGTAKGGGALSAVAATGATIKFIGTGEKIDELEVFNPRRFVARLHHHH

>d1fts\_2 c.37.1.10 (285-495) GTPase domain of the signal recognition particle receptor FtsY {Escherichia coli}

PLNVEGKAPFVILMVGVNGVGKTTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQLQVWGQRNNIPVIAQHTGADSASVIFDAIQAAKARNIDVLIADTAGRLQNKSHLMEELKKIVRVMKKLDVEAPHEVMLTIDASTGQNAVSQAKLFHEAVGLTGITLTKLDGTAKGGVIFSVADQFGIPIRYIGVGERIEDLRPFKADDFIEALFAR

>d1ihua1 c.37.1.10 (A:1-296) Arsenite-translocating ATPase ArsA {Escherichia coli}

MQFLQNIPPYLFFTGKGGVGKTSISCATAIRLAEQGKRVLLVSTDPASNVGQVFSQTIGNTIQAIASVPGLSALEIDPQAAAQQYRARIVDPIKGVLPDDVVSSINEQLSGACTTEIAAFDEFTGLLTDASLLTRFDHIIFDTAPTGHTIRLLQLPGAWSSFIDSNPEGASCLGPMAGLEKQREQYAYAVEALSDPKRTRLVLVARLQKSTLQEVARTHLELAAIGLKNQYLVINGVLPKTEAANDTLAAAIWEREQEALANLPADLAGLPTDTLFLQPVNMVGVSALSRLLSTQP

>d1ihua2 c.37.1.10 (A:308-586) Arsenite-translocating ATPase ArsA {Escherichia coli}

QRPDIPSLSALVDDIARNEHGLIMLMGKGGVGKTTMAAAIAVRLADMGFDVHLTTSDPAAHLSMTLNGSLNNLQVSRIDPHEETERYRQHVLETKGKELDEAGKRLLEEDLRSPCTEEIAVFQAFSRVIREAGKRFVVMDTAPTGHTLLLLDATGAYHREIAKKMGEKGHFTTPMMLLQDPERTKVLLVTLPETTPVLEAANLQADLERAGIHPWGWIINNSLSIADTRSPLLRMRAQQELPQIESVKRQHASRVALVPVLASEPTGIDKLKQLAGHHH

>d1g19a1 c.37.1.11 (A:1-269) RecA protein, ATPase-domain {Mycobacterium tuberculosis}

MTQTPDREKALELAVAQIEKSYGKGSVMRLGDEARQPISVIPTGSIALDVALGIGGLPRGRVIEIYGPESSGKTTVALHAVANAQAAGGVAAFIDAEHALDPDYAKKLGVDTDSLLVSQPDTGEQALEIADMLIRSGALDIVVIDSVAALVPRAELEGEMGDSHVGLQARLMSQALRKMTGALNNSGTTAIFINQLRDKIGVMFGSPETTTGGKALKFYASVRMDVRRVETLKDGTNAVGNRTRVKVVKNKCLAPFKQAEFDILYGKGI

>d1cr1a\_ c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase domain {Bacteriophage T7}

MRERIREHLSSEESVGLLFSGCTGINDKTLGARGGEVIMVTSGSGMGKSTFVRQQALQWGTAMGKKVGLAMLEESVEETAEDLIGLHNRVRLRQSDSLKREIIENGKFDQWFDELFGNDTFHLYDSFAEAETDRLLAKLAYMRSGLGCDVIILDHISIVVSASGESDERKMIDNLMTKLKGFAKSTGVVLVVICHLKNPDKGKAHEEGRPVSITDLRGSGALRQLSDTIIALERNQQGDMPNLVLVRILKCRFTGDTGIAGYMEYNKETGWLEPSSY

>d1g8ya\_ c.37.1.11 (A:) Hexameric replicative helicase repA {Escherichia coli, plasmid rsf1010}

ATHKPINILEAFAAAPPPLDYVLPNMVAGTVGALVSPGGAGKSMLALQLAAQIAGGPDLLEVGELPTGPVIYLPAEDPPTAIHHRLHALGAHLSAEERQAVADGLLIQPLIGSLPNIMAPEWFDGLKRAAEGRRLMVLDTLRRFHIEEENASGPMAQVIGRMEAIAADTGCSIVFLHHASKGAAMMGAGDQQQASRGSSVLVDNIRWQSYLSSMTSAEAEEWGVDDDQRRFFVRFGVSKANYGAPFADRWFRRHDGGVLKPA

>d1e9ra\_ c.37.1.11 (A:) Bacterial conjugative coupling protein TrwB {Escherichia coli}

VGQGEFGGAPFKRFLRGTRIVSGGKLKRMTREKAKQVTVAGVPMPRDAEPRHLLVNGATGTGKSVLLRELAYTGLLRGDRMVIVDPNGDMLSKFGRDKDIILNPYDQRTKGWSFFNEIRNDYDWQRYALSVVPRGKTDEAEEWASYGRLLLRETAKKLALIGTPSMRELFHWTTIATFDDLRGFLEGTLAESLFAGSNEASKALTSARFVLSDKLPEHVTMPDGDFSIRSWLEDPNGGNLFITWREDMGPALRPLISAWVDVVCTSILSLPEEPKRRLWLFIDELASLEKLASLADALTKGRKAGLRVVAGLQSTSQLDDVYGVKEAQTLRASFRSLVVLGGSRTDPKTNEDMSLSLGEHEVERDRYSKNTGKHHSTGRALERVRERVVMPAEIANLPDLTAYVGFAGNRPIAKVPLEIKQFANRQPAFVEGT

>d1e79a3 c.37.1.11 (A:95-379) Central domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

VDVPVGEELLGRVVDALGNAIDGKGPIGSKARRRVGLKAPGIIPRISVREPMQTGIKAVDSLVPIGRGQRELIIGDRQTGKTSIAIDTIINQKRFNDGTDEKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYTIVVSATASDAAPLQYLAPYSGCSMGEYFRDNGKHALIIYDDLSKQAVAYRQMSLLLRRPPGREAYPGDVFYLHSRLLERAAKMNDAFGGGSLTALPVIETQAGDVSAYIPTNVISITDGQIFLETELFYKGIRPAINVGLSVSRVGSAAQ

>d1fx0b3 c.37.1.11 (B:98-377) Central domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

LSVPVGGPTLGRIFNVLGEPVDNLRPVDTRTTSPIHRSAPAFTQLDTKLSIFETGIKVVNLLAPYRRGGKIGLFGGAGVGKTVLIMELINNIAKAHGGVSVFGGVGERTREGNDLYMEMKESGVINEQNIAESKVALVYGQMNEPPGARMRVGLTALTMAEYFRDVNEQDVLLFIDNIFRFVQAGSEVSALLGRMPSAVGYQPTLSTEMGSLQERITSTKEGSITSIQAVYVPADDLTDPAPATTFAHLDATTVLSRGLAAKGIYPAVDPLDSTSTMLQP

>d1cbua\_ c.37.1.11 (A:) Adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase CobU {Salmonella typhimurium}

MILVTGGARSGKSRHAEALIGDAPQVLYIATSQILDDEMAARIQHHKDGRPAHWRTAECWRHLDTLITADLAPDDAILLECITTMVTNLLFALGGENDPEQWDYAAMERAIDDEIQILIAACQRCPAKVVLVTNEVGMGIVPENRLARHFRDIAGRVNQRLAAAADEVWLVVSGIGVKIK

>d1g64b\_ c.37.1.11 (B:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}

QQRQQKVKDRVDARVAQAQEERGIIIVFTGNGKGKTTAAFGTAARAVGHGKNVGVVQFIKGTWPNGERNLLEPHGVEFQVMATGFTWETQNREADTAACMAVWQHGKRMLADPLLDMVVLDELTYMVAYDYLPLEEVISALNARPGHQTVIITGRGCHRDILDLADTVSELRPVKHAFDAGVKAQMGIDY

>d1b0ua\_ c.37.1.12 (A:) ATP-binding subunit of the histidine permease {Salmonella typhimurium}

NKLHVIDLHKRYGGHEVLKGVSLQARAGDVISIIGSSGSGKSTFLRCINFLEKPSEGAIIVNGQNINLVRDKDGQLKVADKNQLRLLRTRLTMVFQHFNLWSHMTVLENVMEAPIQVLGLSKHDARERALKYLAKVGIDERAQGKYPVHLSGGQQQRVSIARALAMEPDVLLFDEPTSALDPELVGEVLRIMQQLAEEGKTMVVVTHEMGFARHVSSHVIFLHQGKIEEEGDPEQVFGNPQSPRLQQFLKGSLKKLEH

>d1g6ha\_ c.37.1.12 (A:) MJ1267 {Archaeon Methanococcus jannaschii}

TMEILRTENIVKYFGEFKALDGVSISVNKGDVTLIIGPNGSGKSTLINVITGFLKADEGRVYFENKDITNKEPAELYHYGIVRTFQTPQPLKEMTVLENLLIGEICPGESPLNSLFYKKWIPKEEEMVEKAFKILEFLKLSHLYDRKAGELSGGQMKLVEIGRALMTNPKMIVMDEPIAGVAPGLAHDIFNHVLELKAKGITFLIIEHRLDIVLNYIDHLYVMFNGQIIAEGRGEEEIKNVLSDPKVVEIYIGE

>d1jj7a\_ c.37.1.12 (A:) Peptide transporter Tap1, C-terminal ABC domain {Human (Homo sapiens)}

GLLTPLHLEGLVQFQDVSFAYPNRPDVLVLQGLTFTLRPGEVTALVGPNGSGKSTVAALLQNLYQPTGGQLLLDGKPLPQYEHRYLHRQVAAVGQEPQVFGRSLQENIAYGLTQKPTMEEITAAAVKSGAHSFISGLPQGYDTEVDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSALDANSQLQVEQLLYESPERYSRSVLLITQHLSLVEQADHILFLEGGAIREGGTHQQLMEKKGCYWAMVQA

>d1g2912 c.37.1.12 (1:1-240) Maltose transport protein MalK, N-terminal domain {Archaeon Thermococcus litoralis}

MAGVRLVDVWKVFGEVTAVREMSLEVKDGEFMILLGPSGCGKTTTLRMIAGLEEPSRGQIYIGDKLVADPEKGIFVPPKDRDIAMVFQSYALYPHMTVYDNIAFPLKLRKVPRQEIDQRVREVAELLGLTELLNRKPRELSGGQRQRVALGRAIVRKPQVFLMDEPLSNLDAKLRVRMRAELKKLQRQLGVTTIYVTHDQVEAMTMGDRIAVMNRGVLQQVGSPDEVYDKPANTFVAGFI

>g1ii8.1 c.37.1.12 (A:,B:) Rad50 {Archaeon Pyrococcus furiosus}

MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVGARDTYIDLIFEKDGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTEPSSKAISAFMEKLIPYNIFLNAIYIRQGQIDAILESDEAREKVVREVLNLDKFETAYKKLSELKKTINNRIKEYRDILARTEXRERVKKEIKDLEKAKDFTEELIEKVKKYKALAREAALSKIGELASEIFAEFTEGKYSEVVVRAEENKVRLFVVWEGKERPLTFLSGGERIALGLAFRLAMSLYLAGEISLLILDEPTPYLDEERRRKLITIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS

>d1e69a\_ c.37.1.12 (A:) Smc head domain {Thermotoga maritima}

MRLKKLYLKGFKSFGRPSLIGFSDRVTAIVGPNGSGKSNIIDAIKWVFGEQSKKELRASEKFDMIFAGSENLPPAGSAYVELVFEENGEEITVARELKRTGENTYYLNGSPVRLKDIRDRFAGTGLGVDFYSIVGQGQIDRIVNASPEELRLESSKHPTSLVPRGSYQRVNESFNRFISLLFFGGEGRLNIVSEAKSILDAGFEISIRKPGRRDQKLSLLSGGEKALVGLALLFALMEIKPSPFYVLDEVDSPLDDYNAERFKRLLKENSKHTQFIVITHNKIVMEAADLLHGVTMVNGVSAIVPVEV

>d1qhla\_ c.37.1.12 (A:) Cell division protein MukB {Escherichia coli}

RGKFRSLTLINWNGFFARTFDLDELVTTLSGGNGAGKSTTMAAFVTALIPDLTLLHFRNTTEAGATSGSRDKGLHGKLKAGVCYSMLDTINSRHQRVVVGVRLQQVAGRDRKVDIKPFAIQGLPMSVQPTQLVTETLNERQARVLPLNELKDKLEAMEGVQFKQFNSITDYHSLMFDLGIIARRLRSASDRSKFYRLIEASLYGGISSAITRSLRDYLLPEN

>d1e3ma2 c.37.1.12 (A:567-800) DNA repair protein MutS, the C-terminal domain {Escherichia coli}

YTCPTFIDKPGIRITEGRHPVVEQVLNEPFIANPLNLSPQRRMLIITGPNMGGKSTYMRQTALIALMAYIGSYVPAQKVEIGPIDRIFTRVGAADDLASGRSTFMVEMTETANILHNATEYSLVLMDEIGRGTSTYDGLSLAWACAENLANKIKALTLFATHYFELTQLPEKMEGVANVHLDALEHGDTIAFMHSVQDGAASKSYGLAVAALAGVPKEVIKRARQKLRELESIS

>g1qhh.1 c.37.1.13 (A:,B:,C:,D:) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}

MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTNKAAREMRERVQSLLGGAAEDVWISTFHSMCVRILRRDIDRIGINRNFSILDPTDQLSVMKTILKEKNIDPKKFEPRTILGTISAAKNELLPPEQFAKRXYYEKVVSDVYQEYQQRLLRNHSLDFDDLIMTTIQLFDRVPDVLHYYQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWRGADIQNILSFERDYPNAKVILLEQNYRSTKRILQAANEVIEHNVNRKPKRIWTENPEGKPILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANIPYQIVGGLKFYDRKEIKDILAYLRVIANPDDDLSLLRIINVPKRGIGASTIDXLFEALGELEMIGLGAKAAGALAAFRSQLEQWTQLQEYVSVTELVEEVLDKSGYREMLKAERTIEAQSRLENLDEFLSVTKHFENVSDDKSLIAFLTDLALISXGDAVMLMTLHAAKGLEFPVVFLIGMEEGIFPHNRSLEDDDEMEEERRLAYVGITRAEEELVLTSAQMRTLFGNIQMDPPSRFLNEIPAHLLETASR

>d1uaaa2 c.37.1.13 (A:308-640) DEXX box DNA helicase {Escherichia coli, RepD}

YGAELKVLSANNEEHEAERVTGELIAHHFVNKTQYKDYAILYRGNHQSRVFEKFLMQNRIPYKISGGTSFFSRPEIKDLLAYLRVLTNPDDDSAFLRIVNTPKREIGPATLKKLGEWAMTRNKSMFTASFDMGLSQTLSGRGYEALTRFTHWLAEIQRLAEREPIAAVRDLIHGMDYESWLYETSPSPKAAEMRMKNVNQLFSWMTEMLEGSELDEPMTLTQVVTRFTLRDMMERGESEEELDQVQLMTLHASKGLEFPYVYMVGMEEGFLPHQSSIDEDNIDEERRLAYVGITRAQKELTFTLCKERRQYGELVRPEPSRFLLELPQDDLIW

>d1hv8a1 c.37.1.13 (A:3-210) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}

VEYMNFNELNLSDNILNAIRNKGFEKPTDIQMKVIPLFLNDEYNIVAQARTGSGKTASFAIPLIELVNENNGIEAIILTPTRELAIQVADEIESLKGNKNLKIAKIYGGKAIYPQIKALKNANIVVGTPGRILDHINRGTLNLKNVKYFILDEADEMLNMGFIKDVEKILNACNKDKRILLFSATMPREILNLAKKYMGDYSFIKAKI

>d1gm5a3 c.37.1.13 (A:286-549) RecG helicase domain {Thermotoga maritima}

ETLPERILEKRKLLGVKDAYYGMHFPKTFYHLEKARERLAYEELFVLQLAFQKIRKEREKHGGIPKKIEGKLAEEFIKSLPFKLTNAQKRAHQEIRNDMISEKPMNRLLQGDVGSGKTVVAQLAILDNYEAGFQTAFMVPTSILAIQHYRRTVESFSKFNIHVALLIGATTPSEKEKIKSGLRNGQIDVVIGTHALIQEDVHFKNLGLVIIDEQHRFGVKQREALMNKGKMVDTLVMSATPIPRSMALAFYGDLDVTVIDEMPP

>d1gm5a4 c.37.1.13 (A:550-755) RecG helicase domain {Thermotoga maritima}

GRKEVQTMLVPMDRVNEVYEFVRQEVMRGGQAFIVYPLIEESDKLNVKSAVEMYEYLSKEVFPEFKLGLMHGRLSQEEKDRVMLEFAEGRYDILVSTTVIEVGIDVPRANVMVIENPERFGLAQLHQLRGRVGRGGQEAYCFLVVGDVGEEAMERLRFFTLNTDGFKIAEYDLKTRGPGEFFGVKQHGLSGFKVADLYRDLKLLEW

>d1fuka\_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IKQFYVNVEEEEYKYECLTDLYDSISVTQAVIFCNTRRKVEELTTKLRNDKFTVSAIYSDLPQQERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLPANKENYIHRIGRGGRFGRKGVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

>d1qdea\_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IQTNYDKVVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIIEGHDVLAQAQSGTGKTGTFSIAALQRIDTSVKAPQALMLAPTRELALQIQKVVMALAFHMDIKVHACIGGTSFVEDAEGLRDAQIVVGTPGRVFDNIQRRRFRTDKIKMFILDEADEMLSSGFKEQIYQIFTLLPPTTQVVLLSATMPNDVLEVTTKFMRNPVRILV

>d1d9xa1 c.37.1.13 (A:2-414) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}

EGRFQLVAPYEPQGDQPQAIAKLVDGLRRGVKHQTLLGATGTGKTFTISNVIAQVNKPTLVIAHNKTLAGQLYSELKEFFPHNAVEYFVSYYDYYQPEAYVPQTDTYIEKDAKINDEIDKLRHSATSALFERRDVIIVASVSCIYGLGSPEEYRELVVSLRVGMEIERNALLRRLVDIQYDRNDIDFRGTFRVRGDVVEIFPASRDEHCIRVEFFGDEIERIRAEVDALTGKVLGEREHVAIFPASHFVTREEKMRLAIQNIEQELEERLAELRAQGKLLEAQRLEQRTRYDLEMMREMGFCSGIENYSRHLALRPPGSTPYTLLDYFPDDFLIIVDESHVTLPQLRGMYNGDRARKQVLVDHGFRLPSALDNRPLTFEEFEQKINQIIYVSATPGPYELEHSPGVVEQIIRP

>d1d9xa2 c.37.1.13 (A:415-595) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}

TGLLDPTIDVRPTKGQIDDLIGEIRERVERNERTLVTTLTKKMAEDLTDYLKEAGIKVAYLHSEIKTLERIEIIRDLRLGKYDVLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARNANGHVIMYADTITKSMEIAIQETKRRRAIQEEYNRKHGIVPRTVKKEIRDV

>d1jr3a2 c.37.1.13 (A:3-242) gamma subunit of DNA polymerase III, N-domain {Escherichia coli}

YQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAKGLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRFKVYLIDEVHMLSRHSFNALLKTLEEPPEHVKFLLATTDPQKLPVTILSRCLQFHLKALDVEQIRHQLEHILNEEHIAHEPRALQLLARAAEGSLRDALSLTDQAIASGDGQVSTQAVSAMLG

>d1a5t\_2 c.37.1.13 (1-207) delta prime subunit of DNA polymerase III, N-domain {Escherichia coli}

MRWYPWLRPDFEKLVASYQAGRGHHALLIQALPGMGDDALIYALSRYLLCQQPQGHKSCGHCRGCQLMQAGTHPDYYTLAPEKGKNTLGVDAVREVTEKLNEHARLGGAKVVWVTDAALLTDAAANALLKTLEEPPAETWFFLATREPERLLATLRSRCRLHYLAPPPEQYAVTWLSREVTMSQDALLAALRLSAGSPGAALALFQG

>d1jr3d2 c.37.1.13 (D:1-211) delta subunit of DNA polymerase III, N-domain {Escherichia coli}

MIRLYPEQLRAQLNEGLRAAYLLLGNDPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAIFSLCQAMSLFASRQTLLLLLPENGPNAAINEQLLTLTGLLHDDLLLIVRGNKLSKAQENAAWFTALANRSVQVTCQTPEQAQLPRWVAARAKQLNLELDDAANQVLCYCYEGNLLALAQALERLSLLWPDGKLTLPRVEQAVNDAAH

>d1iqpa2 c.37.1.13 (A:2-232) Replication factor C {Archaeon Pyrococcus furiosus}

SEEIREVKVLEKPWVEKYRPQRLDDIVGQEHIVKRLKHYVKTGSMPHLLFAGPPGVGKTTAALALARELFGENWRHNFLELNASDERGINVIREKVKEFARTKPIGGASFKIIFLDEADALTQDAQQALRRTMEMFSSNVRFILSCNYSSKIIEPIQSRCAIFRFRPLRDEDIAKRLRYIAENEGLELTEEGLQAILYIAEGDMRRAINILQAAAALDKKITDENVFMVAS

>d1hqca2 c.37.1.13 (A:5-242) Holliday junction helicase RuvB {Thermus thermophilus}

ALRPKTLDEYIGQERLKQKLRVYLEAAKARKEPLEHLLLFGPPGLGKTTLAHVIAHELGVNLRVTSGPAIEKPGDLAAILANSLEEGDILFIDEIHRLSRQAEEHLYPAMEDFVMDIVIGQGPAARTIRLELPRFTLIGATTRPGLITAPLLSRFGIVEHLEYYTPEELAQGVMRDARLLGVRITEEAALEIGRRSRGTMRVAKRLFRRVRDFAQVAGEEVITRERALEALAALGLDE

>d1fnna2 c.37.1.13 (A:1-276) CDC6, N-domain {Archaeon Pyrobaculum aerophilum}

AIVVDDSVFSPSYVPKRLPHREQQLQQLDILLGNWLRNPGHHYPRATLLGRPGTGKTVTLRKLWELYKDKTTARFVYINGFIYRNFTAIIGEIARSLNIPFPRRGLSRDEFLALLVEHLRERDLYMFLVLDDAFNLAPDILSTFIRLGQEADKLGAFRIALVIVGHNDAVLNNLDPSTRGIMGKYVIRFSPYTKDQIFDILLDRAKAGLAEGSYSEDILQMIADITGAQTPLDTNRGDARLAIDILYRSAYAAQQNGRKHIAPEDVRKSSKEVLFG

>d1d2na\_ c.37.1.13 (A:) Hexamerization domain of N-ethylmalemide-sensitive fusion (NSF) protein {Chinese hamster (Cricetulus griseus)}

EDYASYIMNGIIKWGDPVTRVLDDGELLVQQTKNSDRTPLVSVLLEGPPHSGKTALAAKIAEESNFPFIKICSPDKMIGFSETAKCQAMKKIFDDAYKSQLSCVVVDDIERLLDYVPIGPRFSNLVLQALLVLLKKAPPQGRKLLIIGTTSRKDVLQEMEMLNAFSTTIHVPNIATGEQLLEALELLGNFKDKERTTIAQQVKGKKVWIGIKKLLMLIEMSLQMDPEYRVRKFLALLREEGASPLD

>d1e32a2 c.37.1.13 (A:201-458) Membrane fusion atpase p97, D1 domain {Mouse (Mus musculus)}

VGYDDVGGCRKQLAQIKEMVELPLRHPALFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLRKAFEEAEKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGLKQRAHVIVMAATNRPNSIDPALRRFGRFDREVDIGIPDATGRLEILQIHTKNMKLADDVDLEQVANETHGHVGADLAALCSEAALQAIRKKMDLIDLEDETIDAEVMNSLAVTMDDFRWALSQ

>d1g6oa\_ c.37.1.13 (A:) Hexameric traffic ATPase, HP0525 {Helicobacter pylori}

LSAEDKKFLEVERALKEAALNPLRHATEELFGDFLKMENITEICYNGNKVVWVLKNNGEWQPFDVRDRKAFSLSRLMHFARCCASFKKKTIDNYENPILSSNLANGERVQIVLSPVTVNDETISISIRIPSKTTYPHSFFEEQGFYNLLDNKEQAISAIKDGIAIGKNVIVCGGTGSGKTTYIKSIMEFIPKEERIISIEDTEEIVFKHHKNYTQLFFGGNITSADCLKSCLRMRPDRIILGELRSSEAYDFYNVLCSGHKGTLTTLHAGSSEEAFIRLANMSSSNSAARNIKFESLIEGFKDLIDMIVHINHHKQCDEFYIK

>d1ht1e\_ c.37.1.13 (E:) HslU {Escherichia coli}

HSEMTPREIVSELDKHIIGQDNAKRSVAIALRNRWRRMQLNEELRHEVTPKNILMIGPTGVGKTEIARRLAKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDAAVKMVRVQAIEKNRYRAEELAEERILDVLIPPAKNNWGQTEQQQEPSAARQAFRKKLREGQLDDKEIEIDLAAAPMGVEIMAPPGMEEMTSQLQSMFQNLGGQKQKARKLKIKDAMKLLIEEEAAKLVNPEELKQDAIDAVEQHGIVFIDEIDKICKRGESSGPDVSREGVQRDLLPLVEGCTVSTKHGMVKTDHILFIASGAFQIAKPSDLIPELQGRLPIRVELQALTTSDFERILTEPNASITVQYKALMATEGVNIEFTDSGIKRIAEAAWQVNESTENIGARRLHTVLERLMEEISYDASDLSGQNITIDADYVSKHLDALVADEDLSRFIL

>d1g8pa\_ c.37.1.13 (A:) ATPase subunit of magnesium chelatase, BchI {Rhodobacter capsulatus}

RPVFPFSAIVGQEDMKLALLLTAVDPGIGGVLVFGDRGTGKSTAVRALAALLPEIEAVEGCPVSSPNVEMIPDWATVLSTNVIRKPTPVVDLPLGVSEDRVVGALDIERAISKGEKAFEPGLLARANRGYLYIDECNLLEDHIVDLLLDVAQSGENVVERDGLSIRHPARFVLVGSGNPEEGDLRPQLLDRFGLSVEVLSPRDVETRVEVIRRRDTYDADPKAFLEEWRPKDMDIRNQILEARERLPKVEAPNTALYDCAALCIALGSDGLRGELTLLRSARALAALEGATAVGRDHLKRVATMALSHRLRRDPLDEAGSTARVARTVEETLP

>d1a1va1 c.37.1.14 (A:190-325) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}

PPAVPQSFQVAHLHAPTGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGVDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATATP

>d1cu1a3 c.37.1.14 (A:326-631) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}

PGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIRGGRHLIFCHSKKKCDELAAKLSGLGINAVAYYRGLDVSVIPTIGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGERPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVCQDHLEFWESVFTGLTHIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEVTLTHPITKYIMACMSADLEVVT

>d1gkub1 c.37.1.16 (B:1-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAASLCLFPEDFLLKEFVEFFRKCVGEPRAIQKMWAKRILRKESFAATAPTGVGKTSFGLAMSLFLALKGKRCYVIFPTSLLVIQAAETIRKYAEKAGVGTENLIGYYHGRIPKREKENFMQNLRNFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDKLLHLLGFHYDLKTKSWVGEARGCLMVSTATAKKGKKAELFRQLLNFDIGSSRIT

>d1gkub2 c.37.1.16 (B:251-498) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

VRNVEDVAVNDESISTLSSILEKLGTGGIIYARTGEEAEEIYESLKNKFRIGIVTATKKGDYEKFVEGEIDHLIGTAHYYGTLVRGLDLPERIRFAVFVGCPSFRVTIEDIDSLSPQMVKLLAYLYRNVDEIERLLPAVERHIDEVREILKKVMGKERPQAKDVVVREGEVIFPDLRTYIQGSGRTSRLFAGGLTKGASFLLEDDSELLSAFIERAKLYDIEFKSIDEVDFEKLSRELDESRDRYRRR

>d1dbia\_ c.41.1.1 (A:) Thermostable serine protease {Bacillus sp., AK.1}

WTPNDTYYQGYQYGPQNTYTDYAWDVTKGSSGQEIAVIDTGVDYTHPDLDGKVIKGYDFVDNDYDPMDLNNHGTHVAGIAAAETNNATGIAGMAPNTRILAVRALDRNGSGTLSDIADAIIYAADSGAEVINLSLGCDCHTTTLENAVNYAWNKGSVVVAAAGNNGSSTTFEPASYENVIAVGAVDQYDRLASFSNYGTWVDVVAPGVDIVSTITGNRYAYMSGTSMASPHVAGLAALLASQGRNNIEIRQAIEQTADKISGTGTYFKYGRINSYNAVTY

>d1ic6a\_ c.41.1.1 (A:) Proteinase K {Fungus (Tritirachium album), strain limber}

AAQTNAPWGLARISSTSPGTSTYYYDESAGQGSCVYVIDTGIEASHPEFEGRAQMVKTYYYSSRDGNGHGTHCAGTVGSRTYGVAKKTQLFGVKVLDDNGSGQYSTIIAGMDFVASDKNNRNCPKGVVASLSLGGGYSSSVNSAAARLQSSGVMVAVAAGNNNADARNYSPASEPSVCTVGASDRYDRRSSFSNYGSVLDIFGPGTDILSTWIGGSTRSISGTSMATPHVAGLAAYLMTLGKTTAASACRYIADTANKGDLSNIPFGTVNLLAYNNYQA

>d1nocb\_ c.43.1.1 (B:) Chloramphenicol acetyltransferase {Escherichia coli}

ITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAFLKTVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQG

>d1eaf\_\_ c.43.1.1 (-) Dihydrolipoamide acetyltransferase {Azotobacter vinelandii}

IPPIPPVDFAKYGEIEEVPMTRLMQIGATNLHRSWLNVPHVTQFESADITELEAFRVAQKAVAKKAGVKLTVLPLLLKACAYLLKELPDFNSSLAPSGQALIRKKYVHIGFAVDTPDGLLVPVIRNVDQKSLLQLAAEAAELAEKARSKKLGADAMQGACFTISSLGHIGGTAFTPIVNAPEVAILGVSKASMQPVWDGKAFQPRLMLPLSLSYDHRVINGAAAARFTKRLGDLLADIRAILL

>d1e2o\_\_ c.43.1.1 (-) Dihydrolipoamide succinyltransferase {Escherichia coli}

ARSEKRVPMTRLRKRVAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRLGFMSFYVKAVVEALKRYPEVNASIDGDDVVYHNYFDVSMAVSTPRGLVTPVLRDVDTLGMADIEKKIKELAVKGRDGKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAVNGQVEILPMMYLALSYDHRLIDGRESVGFLVTIKELLEDPTRLLLDV

>d1d1qa\_ c.44.1.1 (A:) Tyrosine phosphatase {Baker's yeast (Saccharomyces cerevisiae)}

IEKPKISVAFIALGNFCRSPMAEAIFKHEVEKANLENRFNKIDSFGTSNYHVGESPDHRTVSICKQHGVKINHKGKQIKTKHFDEYDYIIGMDESNINNLKKIQPEGSKAKVCLFGDWNTNDGTVQTIIEDPWYGDIQDFEYNFKQITYFSKQFLKKEL

>d1jl3a\_ c.44.1.1 (A:) Arsenate reductase ArsC {Bacillus subtilis}

NKIIYFLCTGNSCRSQMAEGWAKQYLGDEWKVYSAGIEAHGLNPNAVKAMKEVGIDISNQTSDIIDSDILNNADLVVTLCGDAADKCPMTPPHVKREHWGFDDPARAQGTEEEKWAFFQRVRDEIGNRLKEFAETGK

>d1vhra\_ c.45.1.1 (A:) VH1-related dual-specificity phosphatase, VHR {Human (Homo sapiens)}

SVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRVLVHCREGYSRSPTLVIAYLMMRQKMDVKSALSIVRQNREIGPNDGFLAQLCQLNDRLAKEGKLKP

>d1mkp\_\_ c.45.1.1 (-) Mapk phosphatase Pyst1 (mkp3) {Human (Homo sapiens)}

ASFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTPNLPNLFENAGEFKYKQIPISDHWSQNLSQFFPEAISFIDEARGKNCGVLVHSLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPNFNFMGQLLDFERTL

>d1d5ra2 c.45.1.1 (A:14-187) Phoshphoinositide phosphatase Pten (Pten tumor suppressor), N-terminal domain {Human (Homo sapiens)}

RRYQEDGFDLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCEDLDQWLSEDDNHVAAIHCKAGKGRTGVMICAYLLHRGKFLKAQEALDFYGEVRTRDKKGVTIPSQRRYVYYYSYLLKNHLD

>d1i9sa\_ c.45.1.1 (A:) mRNA capping enzyme, triphosphatase domain {Mouse (Mus musculus)}

KIPPRWLNCPRRGQPVAGRFLPLKTMLGPRYDSQVAEENRFHPSMLSNYLKSLKVKMSLLVDLTNTSRFYDRNDIEKEGIKYIKLQCKGHGECPTTENTETFIRLCERFNERSPPELIGVHCTHGFNRTGFLICAFLVEKMDWSIEAAVATFAQARPPGIYKGDYLKELFRRYGDIEEAPPPPVLPDWCFEDED

>d1fpza\_ c.45.1.1 (A:) Kinase associated phosphatase (kap) {Human (Homo sapiens)}

TPIHISWLSLSRVNCSQFLGLCALPGCKFKDVRRNVQKDTEELKSCGIQDIFVFCTRGELSKYRVPNLLDLYQQCGIITHHHPIADGGTPDIASCCEIMEELTTCLKNYRKTLIHSYGGLGRSCLVAACLLLYLSDTISPEQAIDSLRDLRGSGAIQTIKQYNYLHEFRDKLAAHL

>d1eeoa\_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), 1B}

EMEKEFEQIDKSGSWAAIYQDIRHEASDFPCRVAKLPKNKNRNRYRDVSPFDHSRIKLHQEDNDYINASLIKMEEAQRSYILTQGPLPNTCGHFWEMVWEQKSRGVVMLNRVMEKGSLKCAQYWPQKEEKEMIFEDTNLKLTLISEDIKSYYTVRQLELENLTTQETREILHFHYTTWPDFGVPESPASFLNFLFKVRESGSLSPEHGPVVVHSSAGIGRSGTFCLADTCLLLMDKRKDPSSVDIKKVLLEMRKFRMGLIQTADQLRFSYLAVIEGAKFIMGDSSVQDQWKELSHED

>d2shpa1 c.45.1.2 (A:219-525) Tyrosine phosphatase {Human (Homo sapiens), shp-2}

TRINAAEIESRVRELSKLAETTDKVKQGFWEEFETLQQQECKLLYSRKEGQRQENKNKNRYKNILPFDHTRVVLHDGDPNEPVSDYINANIIMPEFETKCNNSKPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKVGQGNTERTVWQYHFRTWPDHGVPSDPGGVLDFLEEVHHKQESIMDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRSIYMAVQHYIETL

>d1jlna\_ c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus), ptp-sl/br7}

GSPREKVAMEYLQSASRVLTRSQLRDVVASSHLLQSEFMEIPMNFVDPKEIDIPRHGTKNRYKTILPNPLSRVCLRPKNITDSLSTYINANYIRGYSGKEKAFIATQGPMINTVNDFWQMVWQEDSPVIVMITKLKEKNEKCVLYWPEKRGIYGKVEVLVTGVTECDNYTIRNLVLKQGSHTQHVKHYWYTSWPDHKTPDSAQPLLQLMLDVEEDRLASEGRGPVVVHCSAGIGRTGCFIATSIGCQQLKEEGVVDALSIVCQLRVDRGGMVQTSEQYEFVHHALCLFESRLSPETV

>d1ypta\_ c.45.1.2 (A:) Tyrosine phosphatase {Yersinia enterocolitica}

PEARAELSSRLTTLRNTLAPATNDPRYLQACGGEKLNRFRDIQCRRQTAVRADLNANYIQVGNTRTIACQYPLQSQLESHFRMLAENRTPVLAVLASSSEIANQRFGMPDYFRQSGTYGSITVESKMTQQVGLGDGIMADMYTLTIREAGQKTISVPVVHVGNWPDQTAVSSEVTKALASLVDQTAETKRNMYESKGSSAVADDSKLRPVIHCRAGVGRTAQLIGAMCMNDSRNSQLSVEDMVSQMRVQRNGIMVQKDEQLDVLIKLAEGQGRPLLNS

>d1g4us2 c.45.1.2 (S:297-539) SptP tyrosine phosphatase, catalytic domain {Salmonella typhimurium}

PQTMSGPTLGLARFAVSSIPINQQTQVKLSDGMPVPVNTLTFDGKPVALAGSYPKNTPDALEAHMKMLLEKECSCLVVLTSEDQMQAKQLPPYFRGSYTFGEVHTNSQKVSSASQGEAIDQYNMQLSCGEKRYTIPVLHVKNWPDHQPLPSTDQLEYLADRVKNSNQNGAPGRSSSDKHLPMIHCLGGVGRTGTMAAALVLKDNPHSNLEQVRADFRDSRNNRMLEDASQFVQLKAMQAQLLM

>d1lara1 c.45.1.2 (A:1307-1623) RPTP Lar {Human (Homo sapiens)}

MITDLADNIERLKANDGLKFSQEYESIDPGQQFTWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQNAYIATQGPLPETMGDFWRMVWEQRTATVVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLLDTVELATYTVRTFALHKSGSSEKRELRQFQFMAWPDHGVPEYPTPILAFLRRVKACNPLDAGPMVVHCSAGVGRTGCFIVIDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASS

>d1qb0a\_ c.46.1.1 (A:) CDC25b {Human (Homo sapiens)}

DHRELIGDYSKAFLLQTVDGKHQDLKYISPETMVALLTGKFSNIVDKFVIVDCRYPYEYEGGHIKTAVNLPLERDAESFLLKSPIAPCSLDKRVILIFHCEFSSERGPRMCRFIRERDRAVNDYPSLYYPEMYILKGGYKEFFPQHPNFCEPQDYRPMNHEAFKDELKTFRLKTRSWA

>d1hzma\_ c.46.1.1 (A:) Erk2 binding domain of Mapk phosphatase mkp-3 {Human (Homo sapiens)}

MIDTLRPVPFASEMAISKTVAWLNEQLELGNERLLLMDCRPQELYESSHIESAINVAIPGIMLRRLQKGNLPVRALFTRGEDRDRFTRRCGTDTVVLYDESSSDWNENTGGESLLGLLLKKLKDEGCRAFYLEGGFSKFQAEFSLHCETNLDGS

>d1rhs\_1 c.46.1.2 (1-149) Rhodanese {Cow (Bos taurus)}

VHQVLYRALVSTKWLAESVRAGKVGPGLRVLDASWYSPGTREARKEYLERHVPGASFFDIEECRDKASPYEVMLPSEAGFADYVGSLGISNDTHVVVYDGDDLGSFYAPRVWWMFRVFGHRTVSVLNGGFRNWLKEGHPVTSEPSRPEP

>d1rhs\_2 c.46.1.2 (150-293) Rhodanese {Cow (Bos taurus)}

AIFKATLNRSLLKTYEQVLENLESKRFQLVDSRAQGRYLGTQPEPDAVGLDSGHIRGSVNMPFMNFLTEDGFEKSPEELRAMFEAKKVDLTKPLIATCRKGVTACHIALAAYLCGKPDVAIYDGSWFEWFHRAPPETWVSQGKG

>d1e0ca1 c.46.1.2 (A:1-135) Sulfurtransferase {Azotobacter vinelandii}

MDDFASLPLVIEPADLQARLSAPELILVDLTSAARYAEGHIPGARFVDPKRTQLGQPPAPGLQPPREQLESLFGELGHRPEAVYVVYDDEGGGWAGRFIWLLDVIGQQRYHYLNGGLTAWLAEDRPLSRELPAPA

>d1e0ca2 c.46.1.2 (A:136-271) Sulfurtransferase {Azotobacter vinelandii}

GGPVALSLHDEPTASRDYLLGRLGAADLAIWDARSPQEYRGEKVLAAKGGHIPGAVNFEWTAAMDPSRALRIRTDIAGRLEELGITPDKEIVTHCQTHHRSGLTYLIAKALGYPRVKGYAGSWGEWGNHPDTPVEL

>d2trxa\_ c.47.1.1 (A:) Thioredoxin {Escherichia coli}

SDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

>d1ep7a\_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}

GGSVIVIDSKAAWDAQLAKGKEEHKPIVVDFTATWCGPCKMIAPLFETLSNDYAGKVIFLKVDVDAVAAVAEAAGITAMPTFHVYKDGVKADDLVGASQDKLKALVAKHAAA

>d1f9ma\_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin F}

MEAIVGKVTEVNKDTFWPIVKAAGDKPVVLDMFTQWCGPCKAMAPKYEKLAEEYLDVIFLKLDCNQENKTLAKELGIRVVPTFKILKENSVVGEVTGAKYDKLLEAIQAARS

>d1aba\_\_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Bacteriophage T4}

MFKVYGYDSNIHKCGPCDNAKRLLTVKKQPFEFINIMPEKGVFDDEKIAELLTKLGRDTQIGLTMPQVFAPDGSHIGGFDQLREYFK

>d1qfna\_ c.47.1.1 (A:) Glutaredoxin (Thioltransferase) {Escherichia coli}

MQTVIFGRSGCPYSVRAKDLAEKLSNERDDFQYQYVDIRAEGITKEDLQQKAGKPVETVPQIFVDQQHIGGYTDFAAWVKENLDA

>d1kte\_\_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Pig (Sus scrofa)}

AQAFVNSKIQPGKVVVFIKPTCPFCRKTQELLSQLPFKEGLLEFVDITATSDTNEIQDYLQQLTGARTVPRVFIGKECIGGCTDLESMHKRGELLTRLQQVGAVK

>d1h75a\_ c.47.1.1 (A:) Glutaredoxin-like NRDH-redoxin {Escherichia coli}

MRITIYTRNDCVQCHATKRAMENRGFDFEMINVDRVPEAAEALRAQGFRQLPVVIAGDLSWSGFRPDMINRLHPAP

>d1fo5a\_ c.47.1.1 (A:) MJ0307, thioredoxin/glutaredoxin-like protein {Archaeon Methanococcus jannaschii}

MSKVKIELFTSPMCPHCPAAKRVVEEVANEMPDAVEVEYINVMENPQKAMEYGIMAVPTIVINGDVEFIGAPTKEALVEAIKKRL

>d1iloa\_ c.47.1.1 (A:) MTH985, a thioredoxin {Archaeon Methanobacterium thermoautotrophicum}

MMKIQIYGTGCANCQMLEKNAREAVKELGIDAEFEKIKEMDQILEAGLTALPGLAVDGELKIMGRVASKEEIKKILS

>d1gh2a\_ c.47.1.1 (A:) Thioredoxin-like protein, N-terminal domain {Human (Homo sapiens)}

VGVKPVGSDPDFQPELSGAGSRLAVVKFTMRGCGPCLRIAPAFSSMSNKYPQAVFLEVDVHQCQGTAATNNISATPTFQFFRNKVRIDQYQGADAVGLEEKIKQHLE

>d1bjx\_\_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}

AATTLPDGAAAESLVESSEVAVIGFFKDVESDSAKQFLQAAEAIDDIPFGITSNSDVFSKYQLDKDGVVLFKKFDEGRNNFEGEVTKENLLDFIKHNQLPLVIEFTEQTA

>d1mek\_\_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}

DAPEEEDHVLVLRKSNFAEALAAHKYLLVEFYAPWCGHCKALAPEYAKAAGKLKAEGSEIRLAKVDATEESDLAQQYGVRGYPTIKFFRNGDTASPKEYTAGREADDIVNWLKKRTGPAA

>d1a8l\_1 c.47.1.2 (1-119) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}

MGLISDADKKVIKEEFFSKMVNPVKLIVFVRKDHCQYCDQLKQLVQELSELTDKLSYEIVDFDTPEGKELAKRYRIDRAPATTITQDGKDFGVRYFGLPAGHEFAAFLEDIVDVSREET

>d1a8l\_2 c.47.1.2 (120-226) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}

NLMDETKQAIRNIDQDVRILVFVTPTCPYCPLAVRMAHKFAIENTKAGKGKILGDMVEAIEYPEWADQYNVMAVPKIVIQVNGEDRVEFEGAYPEKMFLEKLLSALS

>d1hyua3 c.47.1.2 (A:1-102) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}

MLDTNMKTQLRAYLEKLTKPVELIATLDDSAKSAEIKELLAEIAELSDKVTFKEDNTLPVRKPSFLITNPGSQQGPRFAGSPLGHEFTSLVLALLWTGGHPS

>d1hyua4 c.47.1.2 (A:103-198) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}

KEAQSLLEQIRDIDGDFEFETYYSLSCHNCPDVVQALNLMAVLNPRIKHTAIDGGTFQNEITERNVMGVPAVFVNGKEFGQGRMTLTEIVAKVDTG

>d1a8y\_1 c.47.1.3 (3-126) Calsequestrin {Rabbit (Oryctolagus cuniculus)}

GLDFPEYDGVDRVINVNAKNYKNVFKKYEVLALLYHEPPEDDKASQRQFEMEELILELAAQVLEDKGVGFGLVDSEKDAAVAKKLGLTEEDSIYVFKEDEVIEYDGEFSADTLVEFLLDVLEDP

>d1a8y\_2 c.47.1.3 (127-228) Calsequestrin {Rabbit (Oryctolagus cuniculus)}

VELIEGERELQAFENIEDEIKLIGYFKNKDSEHYKAFKEAAEEFHPYIPFFATFDSKVAKKLTLKLNEIDFYEAFMEEPVTIPDKPNSEEEIVNFVEEHRRS

>d1a8y\_3 c.47.1.3 (229-347) Calsequestrin {Rabbit (Oryctolagus cuniculus)}

TLRKLKPESMYETWEDDMDGIHIVAFAEEADPDGYEFLEILKSVAQDNTDNPDLSIIWIDPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADSVWMEMDDEEDLPSAEELEDWLEDVL

>d1glqa2 c.47.1.5 (A:1-78) Glutathione S-transferase {Mouse (Mus musculus), class pi}

PPYTIVYFPVRGRCEAMRMLLADQGQSWKEEVVTIDTWMQGLLKPTCLYGQLPKFEDGDLTLYQSNAILRHLGRSLGL

>d1gtua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}

PMILGYWDIRGLAHAIRLLLEYTDSSYEEKKYTMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDGAHKITQSNAILCYIARKHN

>d1gsea2 c.47.1.5 (A:2-80) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}

AEKPKLHYFNARGKMESTRWLLAAAGVEFEEKFIKSAEDLDKLRNDGYLMFQQVPMVEIDGMKLVQTRAILNYIASKYN

>d1ljra2 c.47.1.5 (A:1-79) Glutathione S-transferase {Human (Homo sapiens), class theta}

MGLELFLDLVSQPSRAVYIFAKKNGIPLELRTVDLVKGQHKSKEFLQINSLGKLPTLKDGDFILTESSAILIYLSCKYQ

>d1pd212 c.47.1.5 (1:1-75) Glutathione S-transferase {Rat (Rattus norvegicus), class sigma}

MPNYKLLYFNMRGRAEIIRYIFAYLDIKYEDHRIEQADWPKIKPTLPFGKIPVLEVEGLTLHQSLAIARYLTKNT

>d2gsq\_2 c.47.1.5 (1-75) Glutathione S-transferase {Squid (Ommastrephes sloani pacificus), class sigma}

PKYTLHYFPLMGRAELCRFVLAAHGEEFTDRVVEMADWPNLKATMYSNAMPVLDIDGTKMSQSMCIARHLAREFG

>d1eema2 c.47.1.5 (A:5-102) Glutathione S-transferase {Human (Homo sapiens), class omega}

SARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRLVLKAKGIRHEVININLKNKPEWFFKKNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKKL

>d1fw1a2 c.47.1.5 (A:5-87) Glutathione S-transferase {Human (Homo sapiens), class zeta}

KPILYSYFRSSCSWRVRIALALKGIDYKTVPINLIKDGGQQFSKDFQALNPMKQVPTLKIDGITIHQSLAIIEYLEETRPTPR

>d1gnwa2 c.47.1.5 (A:2-85) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}

GIKVFGHPASIATRRVLIALHEKNLDFELVHVELKDGEHKKEPFLSRNPFGQVPAFEDGDLKLFESRAITQYIAHRYENQGTNL

>d1a0fa2 c.47.1.5 (A:1-80) Glutathione S-transferase {Escherichia coli}

MKLFYKPGACSLASHITLRESGKDFTLVSVDLMKKRLENGDDYFAVNPKGQVPALLLDDGTLLTEGVAIMQYLADSVPDR

>d1g7oa2 c.47.1.5 (A:1-75) Glutaredoxin 2 {Escherichia coli}

MKLYIYDHCPYCLKARMIFGLKNIPVELHVLLNDDAETPTRMVGQKQVPILQKDDSRYMPESMDIVHYVDKLDGK

>d1k0dd2 c.47.1.5 (D:99-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}

YSRITKFFQEQPLEGYTLFSHRSAPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVNPNARVPALIDHGMDNLSIWESGAILLHLVNKYYKETGNPL

>d1k0ma2 c.47.1.5 (A:6-91) Chloride intracellular channel 1 (clic1) {Human (Homo sapiens)}

PQVELFVKAGSDGAKIGNCPFSQRLFMVLWLKGVTFNVTTVDTKRRTETVQKLCPGGELPFLLYGTEVHTDTNKIEEFLEAVLCPP

>d1gp1a\_ c.47.1.10 (A:) Glutathione peroxidase {Cow (Bos taurus)}

RTVYAFSARPLAGGEPFNLSSLRGKVLLIENVASLXGTTVRDYTQMNDLQRRLGPRGLVVLGFPCNQFGHQENAKNEEILNCLKYVRPGGGFEPNFMLFEKCEVNGEKAHPLFAFLREVLPTPSDDATALMTDPKFITWSPVCRNDVSWNFEKFLVGPDGVPVRRYSRRFLTIDIEPDIETLLSQ

>d1i5ga\_ c.47.1.10 (A:) Tryparedoxin II {Crithidia fasciculata}

SGLKKFFPYSTNVLKGAAADIALPSLAGKTVFFYFSASWCPPSRAFTPQLIDFYKAHAEKKNFEVMLISWDESAEDFKDYYAKMPWLALPFEDRKGMEFLTTGFDVKSIPTLVGVEADSGNIITTQARTMVVKDPEAKDFPWPN

>d1qmva\_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys peroxiredoxin) {Human (Homo sapiens)}

SGNARIGKPAPDFKATAVVDGAFKEVKLSDYKGKYVVLFFYPLDFTFVAPTEIIAFSNRAEDFRKLGCEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEDYGVLKTDEGIAYRGLFIIDGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYFSKHN

>d1hd2a\_ c.47.1.10 (A:) Peroxiredoxin 5 {Human (Homo sapiens)}

APIKVGDAIPAVEVFEGEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSKTHLPGFVEQAEALKAKGVQVVACLSVNDAFVTGEWGRAHKAEGKVRLLADPTGAFGKETDLLLDDSLVSIFGNRRLKRFSMVVQDGIVKALNVEPDGTGLTCSLAPNIISQL

>d1prxa\_ c.47.1.10 (A:) HorF6 peroxidase {Human (Homo sapiens)}

LLLGDVAPNFEANTTVGRIRFHDFLGDSWGILFSHPRDFTPVCTTELGRAAKLAPEFAKRNVKLIALSIDSVEDHLAWSKDINAYNSEEPTEKLPFPIIDDRNRELAILLGMLDPAEKDEKGMPVTARVVFVFGPDKKLKLSILYPATTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVMVLPTIPEEEAKKLFPKGVFTKELPSGKKYLRYTPQP

>d1kyga\_ c.47.1.10 (A:) Alkyl hydroperoxide reductase AhpC {Salmonella typhimurium}

SLINTKIKPFKNQAFKNGEFIEVTEKDTEGRWSVFFFYPADFTFVCPTELGDVADHYEELQKLGVDVYSVSTDTHFTHKAWHSSSETIAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVVDPQGIIQAIEVTAEGIGRDASDLLRKIKAAQYVAAHPGEVCP

>d1jfua\_ c.47.1.10 (A:) Membrane-anchored thioredoxin-like protein TlpA, soluble domain {Bradyrhizobium japonicum}

TGDPACRAAVATAQKIAPLAHGEVAALTMASAPLKLPDLAFEDADGKPKKLSDFRGKTLLVNLWATWCVPCRKEMPALDELQGKLSGPNFEVVAINIDTRDPEKPKTFLKEANLTRLGYFNDQKAKVFQDLKAIGRALGMPTSVLVDPQGCEIATIAGPAEWASEDALKLIRAATG

>d1foha3 c.47.1.10 (A:462-662) Phenol hydroxylase, C-terminal domain {Soil-living yeast (Trichosporon cutaneum)}

NLVTDKKSSKQELAKNCVVGTRFKSQPVVRHSEGLWMHFGDRLVTDGRFRIIVFAGKATDATQMSRIKKFSAYLDSENSVISLYTPKVSDRNSRIDVITIHSCHRDDIEMHDFPAPALHPKWQYDFIYADCDSWHHPHPKSYQAWGVDETKGAVVVVRPDGYTSLVTDLEGTAEIDRYFSGILVEPKEKSGAQTEADWTKS

>d1a49a3 c.49.1.1 (A:396-530) Pyruvate kinase, C-terminal domain {Rabbit (Oryctolagus cuniculus)}

ELARSSSHSTDLMEAMAMGSVEASYKCLAAALIVLTESGRSAHQVARYRPRAPIIAVTRNHQTARQAHLYRGIFPVVCKDPVQEAWAEDVDLRVNLAMNVGKARGFFKKGDVVIVLTGWRPGSGFTNTMRVVPVP

>d1pkla3 c.49.1.1 (A:358-498) Pyruvate kinase, C-terminal domain {Leishmania mexicana}

NEYVFFNSIKKLQHIPMSADEAVCSSAVNSVYETKAKAMVVLSNTGRSARLVAKYRPNCPIVCVTTRLQTCRQLNITQGVESVFFDADKLGHDEGKEHRVAAGVEFAKSKGYVQTGDYCVVIHADHKVKGYANQTRILLVE

>d1a3wa3 c.49.1.1 (A:367-500) Pyruvate kinase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

DMRNCTPKPTSTTETVAASAVAAVFEQKAKAIIVLSTSGTTPRLVSKYRPNCPIILVTRCPRAARFSHLYRGVFPFVFEKEPVSDWTDDVEARINFGIEKAKEFGILKKGDTYVSIQGFKAGAGHSNTLQVSTV

>d1e0ta3 c.49.1.1 (A:354-470) Pyruvate kinase, C-terminal domain {Escherichia coli}

ITEAVCRGAVETAEKLDAPLIVVATQGGKSARAVRKYFPDATILALTTNEKTAHQLVLSKGVVPQLVKEITSTDDFYRLGKELALQSGLAHKGDVVVMVSGALVPSGTTNTASVHVL

>d1e79g\_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Cow (Bos taurus)}

ATLKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGVGSLALYEKADIKTPEDKKKHLIIGVSSDRGLCGAIHSSVAKQMKSEAANLAAAGKEVKIIGVGDKIRSILHRTHSDQFLVTFKEVGRRPPTFGDASVIALELLNSGYEFDEGSIIFNRFRSVISYKTEEKPIFSLDTISSAESMSIYDDIDADVLRNYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFNRTRQAVITKELIEIISGAAAL

>d1fs0g\_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Escherichia coli}

KITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGNLEYKHPYLEDRDVKRVGYLVVSTDRGLCGGLNINLFKKLLAEMKTWTDKGVQCDLAMIGSKGVSFFNSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVSNKFINTMSQVPTISQLLPLPASDDDDLKHKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLASEQAARMVAMK

>d1kmma1 c.51.1.1 (A:326-424) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Escherichia coli}

DPVVDIYLVASGADTQSAAMALAERLRDELPGVKLMTNHGGGNFKKQFARADKWGARVAVVLGESEVANGTAVVKDLRSGEQTAVAQDSVAAHLRTLLG

>d1qe0a1 c.51.1.1 (A:326-420) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Staphylococcus aureus}

IEENLDLFIVTMGDQADRYAVKLLNHLRHNGIKADKDYLQRKIKGQMKQADRLGAKFTIVIGDQELENNKIDVKNMTTGESETIELDALVEYFKK

>d1h4vb1 c.51.1.1 (B:326-421) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Thermus thermophilus}

EKGPDLYLIPLTEEAVAEAFYLAEALRPRLRAEYALAPRKPAKGLEEALKRGAAFAGFLGEDELRAGEVTLKRLATGEQVRLSREEVPGYLLQALG

>d1atia1 c.51.1.1 (A:395-505) Glycyl-tRNA synthetase (GlyRS), C-terminal domain {Thermus thermophilus}

QLAPIKVAVIPLVKNRPEITEYAKRLKARLLALGLGRVLYEDTGNIGKAYRRHDEVGTPFAVTVDYDTIGQSKDGTTRLKDTVTVRDRDTMEQIRLHVDELEGFLRERLRW

>d1qf6a1 c.51.1.1 (A:533-642) Threonyl-tRNA synthetase (ThrRS), C-terminal domain {Escherichia coli}

FPTWLAPVQVVIMNITDSQSEYVNELTQKLSNAGIRVKADLRNEKIGFKIREHTLRRVPYMLVCGDKEVESGKVAVRTRRGKDLGSMDVNEVIEKLQQEIRSRSLKQLEE

>d1hc7a1 c.51.1.1 (A:277-403) C-terminal domain of ProRS {Thermus thermophilus}

RGLVLPPRLAPIQVVIVPIYKDESRERVLEAAQGLRQALLAQGLRVHLDDRDQHTPGYKFHEWELKGVPFRVELGPKDLEGGQAVLASRLGGKETLPLAALPEALPGKLDAFHEELYRRALAFREDH

>d1g5ha1 c.51.1.1 (A:343-469) The aaRS-like accessory subunit of mitochondrial polymerase gamma, C-terminal domain {Mouse (Mus musculus)}

RKVLKLHPCLAPIKVALDVGKGPTVELRQVCQGLLNELLENGISVWPGYSETVHSSLEQLHSKYDEMSVLFSVLVTETTLENGLIQLRSRDTTMKEMMHISKLRDFLVKYLASASNVAAALDHHHHH

>d1cfr\_\_ c.52.1.7 (-) Restriction endonuclease Cfr10I {Citrobacter freundii}

MDIISKSGEGNKYTINSAIAFVAYASHIDINTTEFSKVLSGLRDFINDEAIRLGGKISDGSFNKCNGDWYEWLIGIRAIEFFLESETNFIVVKMPNATSFDVMSIYKSCLSEFIYDLRSKLSLNNVNLITSNPDFSIIDIRGRREELKSMLKDISFSNISLSTISEIDNLYKNFIDYAELEHIKSFLSVKTTFRPDRRLQLAHEGSLMKALYTHLQTRTWTINPTGIRYYAAATSIGNADVIGLKTVATHSITDVKSLPQSAVDEIFKINSVLDVDSCLSHIL

>d1knva\_ c.52.1.7 (A:) Restriction endonuclease Bse634I {Bacillus stearothermophilus}

NLTNSNCVEEYKENGKTKIRIKPFNALIELYHHQTPTGSIKENLDKLENYVKDVVKAKGLAIPTSGAFSNTRGTWFEVMIAIQSWNYRVKRELNDYLIIKMPNVKTFDFRKIFDNETREKLHQLEKSLLTHKQQVRLITSNPDLLIIRQKDLIKSEYNLPINKLTHENIDVALTLFKDIEGKCKWDSLVAGVGLKTSLRPDRRLQLVHEGNILKSLFAHLKMRYWNPKAEFKYYGASSEPVSKADDDALQTAATHTIVNVNSTPERAVDDIFSLTSFEDIDKMLDQIIKK

>d1gefa\_ c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Pyrococcus furiosus}

MYRKGAQAERELIKLLEKHGFAVVRSAGSKKVDLVAGNGKKYLCIEVKVTKKDHLYVGKRDMGRLIEFSRRFGGIPVLAVKFLNVGWRFIEVSPKIEKFVFTPSSGVSLEVLLGIQKTLE

>d1hh1a\_ c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Sulfolobus solfataricus}

SAVERNIVSRLRDKGFAVVRAPASGSKRKDPIPDIIALKNGVIILIEMKSRKDIEGKIYVRREQAEGIIEFARKSGGSLFLGVKKPGVLKFIPFEKLRRTETGNYVADSEIEGLDLEDLVRLVEAKISRTLD

>d1tfr\_2 c.53.1.2 (12-180) T4 RNase H {Bacteriophage T4}

KEGICLIDFSQIALSTALVNFPDKEKINLSMVRHLILNSIKFNVKKAKTLGYTKIVLCIDNAKSGYWRRDFAYYYKKNRGKAREESTWDWEGYFESSHKVIDELKAYMPYIVMDIDKYEADDHIAVLVKKFSLEGHKILIISSDGDFTQLHKYPNVKQWSPMHKKWVKI

>d1bgxt2 c.53.1.2 (T:1-173) 5' to 3' exonuclease domain of DNA polymerase {Thermus aquaticus}

MRGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGEPVQAVYGFAKSLLKALKEDGDAVIVVFDAKAPSFRHEAYGGYKAGRAPTPEDFPRQLALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSDRIHVLHPEGYLITPAWLWEKYG

>d1xo1a2 c.53.1.2 (A:19-185) T5 5'-exonuclease {Bacteriophage T5}

RRNLMIVDGTNLGFRFKHNNSKKPFASSYVSTIQSLAKSYSARTTIVLGDKGKSVFRLEHLPEYAGNRDEKYAQRTEEEKALDEQFFEYLKDAFELCKTTFPTFTIRGVEADDMAAYIVKLIGHLYDHVWLISTDGDWDTLLTDKVSRFSFTTRREYHLRDMYEHHN

>d1b43a2 c.53.1.2 (A:1-219) Fen-1 nuclease {Archaeon Pyrococcus furiosus}

GVPIGEIIPRKEIELENLYGKKIAIDALNAIYQFLSTIRQKDGTPLMDSKGRITSHLSGLFYRTINLMEAGIKPVYVFDGEPPEFKKKELEKRREAREEAEEKWREALEKGEIEEARKYAQRATRVNEMLIEDAKKLLELMGIPIVQAPSEGEAQAAYMAAKGSVYASASQDYDSLLFGAPRLVRNLTITGKRKLPGKNVYVEIKPELIILEEVLKELK

>d1ekja\_ c.53.2.1 (A:) beta-carbonic anhydrase {Pea (Pisum sativum)}

EASERIKTGFLHFKKEKYDKNPALYGELAKGQSPPFMVFACSDSRVCPSHVLDFQPGEAFVVRNVANLVPPYDQAKYAGTGAAIEYAVLHLKVSNIVVIGHSACGGIKGLLSFPFDGTYSTDFIEEWVKIGLPAKAKVKAQHGDAPFAELCTHCEKEAVNASLGNLLTYPFVREGLVNKTLALKGGYYDFVKGSFELWGLEFGLSSTFSV

>d1g5ca\_ c.53.2.1 (A:) beta-carbonic anhydrase {Archaeon Methanobacterium thermoautotrophicum}

IIKDILRENQDFRFRDLSDLKHSPKLCIITCMDSRLIDLLERALGIGRGDAKVIKNAGNIVDDGVIRSAAVAIYALGDNEIIIVGHTDCGMARLDEDLIVSRMRELGVEEEVIENFSIDVLNPVGDEEENVIEGVKRLKSSPLIPESIGVHGLIIDINTGRLKPLYLDE

>d1ddza1 c.53.2.1 (A:84-325) beta-carbonic anhydrase {Red alga (Porphyridium purpureum)}

VMSDLEKKFIELEAKLVAQPAGQAMPGKSNIFANNEAWRQEMLKQDPEFFNRLANGQSPEYLWIGCADSRVPANQLLDLPAGEVFVHRNIANQCIHSDISFLSVLQYAVQYLKVKHILVCGHYGCGGAKAALGDSRLGLIDNWLRHIRDVRRMNAKYLDKCKDGDEELNRLIELNVLEQVHNVCATSIVQDAWDAGQELTVQGVVYGVGDGKLRDLGVVVNSSDDISKFYRTKSDSGALKAG

>d1hjoa1 c.55.1.1 (A:3-188) Heat shock protein 70kDa, ATPase fragment {Human (Homo sapiens)}

KAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRT

>d1dkgd2 c.55.1.1 (D:186-383) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}

GNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATNGDTHLGGEDFDSRLINYLVEEFKKDQGIDLRNDPLAMQRLKEAAEKAKIELSSAQQTDVNLPYITADATGPKHMNIKVTRAKLESLVEDLVNRSIELLKVALQDAGLSVSDIDDVILVGGQTRMPMVQKKVAEFFGKEPRKDVNPDEAVAIGAAVQGGVLT

>d1d4xa2 c.55.1.1 (A:147-375) Actin {Nematode (Caenorhabditis elegans)}

RTTGVVLDSGDGVTHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITVGNERFRCPEAMFQPSFLGMESAGIHETSYNSIMKCDIDIRKDLYANTVLSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCF

>d1jcfa1 c.55.1.1 (A:1-140) Prokaryotic actin homolog MreB {Thermotoga maritima}

MLRKDIGIDLGTANTLVFLRGKGIVVNEPSVIAIDSTTGEILKVGLEAKNMIGKTPATIKAIRPMRDGVIADYTVALVMLRYFINKAKGGMNLFKPRVVIGVPIGITDVERRAILDAGLEAGASKVFLIEEPMAAAIGSN

>d1jcfa2 c.55.1.1 (A:141-336) Prokaryotic actin homolog MreB {Thermotoga maritima}

LNVEEPSGNMVVDIGGGTTEVAVISLGSIVTWESIRIAGDEMDEAIVQYVRETYRVAIGERTAERVKIEIGNVFPSKENDELETTVSGIDLSTGLPRKLTLKGGEVREALRSVVVAIVESVRTTLEKTPPELVSDIIERGIFLTGGGSLLRGLDTLLQKETGISVIRSEEPLTAVAKGAGMVLDKVNILKKLQGAG

>d1k8ka1 c.55.1.1 (A:3-160) Actin-related protein 3, Arp3 {Cow (Bos taurus)}

GRLPACVVDCGTGYTKLGYAGNTEPQFIIPSCIAIKESAKVGDQAQRRVMKGVDDLDFFIGDEAIEKPTYATKWPIRHGIVEDWDLMERFMEQVIFKYLRAEPEDHYFLLTEPPLNTPENREYTAEIMFESFNVPGLYIAVQAVLALAASWTSRQVGE

>d1k8ka2 c.55.1.1 (A:161-418) Actin-related protein 3, Arp3 {Cow (Bos taurus)}

RTLTGTVIDSGDGVTHVIPVAEGYVIGSCIKHIPIAGRDITYFIQQLLRDREVGIPPEQSLETAKAVKERYSYVCPDLVKEFNKYDTDGSKWIKQYTGINAISKKEFSIDVGYERFLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVRRPLYKNIVLSGGSTMFRDFGRRLQRDLKRTVDARLKLSEELSGGRLKPKPIDVQVITHHMQRYAVWFGGSMLASTPEFYQVCHTKKDYEEIGPSICRHNPVFGVMS

>d1e4ft1 c.55.1.1 (T:7-199) Cell division protein FtsA {Thermotoga maritima}

TVFYTSIDIGSRYIKGLVLGKRDQEWEALAFSSVKSRGLDEGEIKDAIAFKESVNTLLKELEEQLQKSLRSDFVISFSSVSFEREDTVIERDFGEEKRSITLDILSEMQSEALEKLKENGKTPLHIFSKRYLLDDERIVFNPLDMKASKIAIEYTSIVVPLKVYEMFYNFLQDTVKSPFQLKSSLVSTAEGVL

>d1e4ft2 c.55.1.1 (T:200-390) Cell division protein FtsA {Thermotoga maritima}

TTPEKDRGVVVVNLGYNFTGLIAYKNGVPIKISYVPVGMKHVIKDVSAVLDTSFEESERLIITHGNAVYNDLKEEEIQYRGLDGNTIKTTTAKKLSVIIHARLREIMSKSKKFFREVEAKIVEEGEIGIPGGVVLTGGGAKIPRINELATEVFKSPVRTGCYANSDRPSIINADEVANDPSFAAAFGNVFA

>d1g99a1 c.55.1.2 (A:1-156) Acetate kinase {Archaeon Methanosarcina thermophila}

MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKKLEKLTDLPTHKDALEEVVKALTDDEFGVIKDMGEINAVGHRVVHGGEKFTTSALYDEGVEKAIKDCFELAPLHNPPNMMGISACAEIMPGTPMVIVFDTAFHQTMP

>d1g99a2 c.55.1.2 (A:157-398) Acetate kinase {Archaeon Methanosarcina thermophila}

PYAYMYALPYDLYEKHGVRKYGFHGTSHKYVAERAALMLGKPAEETKIITCHLGNGSSITAVEGGKSVETSMGFTPLEGLAMGTRCGSIDPAIVPFLMEKEGLTTREIDTLMNKKSGVLGVSGLSNDFRDLDEAASKGNRKAELALEIFAYKVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIGIKIDDEKNKIRGQEIDISTPDAKVRVFVIPTNEELAIARETKEIVET

>d1ig8a1 c.55.1.3 (A:18-224) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}

DVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKKGGNIPMIPGWVMDFPTGKESGDFLAIDLGGTNLRVVLVKLGGDRTFDTTQSKYRLPDAMRTTQNPDELWEFIADSLKAFIDEQFPQGISEPIPLGFTFSFPASQNKINEGILQRWTKGFDIPNIENHDVVPMLQKQITKRNIPIEVVALINDTTGTLVASYYTDP

>d1ig8a2 c.55.1.3 (A:225-486) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}

ETKMGVIFGTGVNGAYYDVCSDIEKLQGKLSDDIPPSAPMAINCEYGSFDNEHVVLPRTKYDITIDEESPRPGQQTFEKMSSGYYLGEILRLALMDMYKQGFIFKNQDLSKFDKPFVMDTSYPARIEEDPFENLEDTDDLFQNEFGINTTVQERKLIRRLSELIGARAARLSVCGIAAICQKRGYKTGHIAADGSVYNRYPGFKEKAANALKDIYGWTQTSLDDYPIKIVPAEDGSGAGAAVIAALAQKRIAEGKSVGIIGA

>d1czan2 c.55.1.3 (N:223-465) Mammalian type I hexokinase {Human (Homo sapiens)}

HCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRAIDAYSLNPGKQLFEKMVSGMYLGELVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEKNKEGLHNAKEILTRLGVEPSDDDCVSVQHVCTIVSFRSANLVAATLGAILNRLRDNKGTPRLRTTVGVDGSLYKTHPQYSRRFHKTLRRLVPDSDVRFLLSESGSGKGAAMVTAVAYRLAE

>d1bg3a1 c.55.1.3 (A:1-222) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

MIAAQLLAYYFTELKDDQVKKIDKYLYAMRLSDEILIDILTRFKKEMKNGLSRDYNPTASVKMLPTFVRSIPDGSEKGDFIALDLGGSSFRILRVQVNHEKNQNVSMESEIYDTPENIVHGSGTQLFDHVADCLGDFMEKKKIKDKKLPVGFTFSFPCRQSKIDEAVLITWTKRFKASGVEGADVVKLLNKAIKKRGDYDANIVAVVNDTVGTMMTCGYDDQ

>d1bu6o1 c.55.1.4 (O:3-253) Glycerol kinase {Escherichia coli}

KKYIVALDQGTTSSRAVVMDHDANIISVSQREFEQIYPKPGWVEHDPMEIWATQSSTLVEVLTKADISSDQIAAIGITNQRETTIVWEKETGKPIYNAIVWQCRRTAEICEHLKRDGLEDYIRSNTGLVIDPYFSGTKVKWILDHVEGSRERARRGELLFGTVDTWLIWKMTQGRVHVTDYTNASRTMLFNIHTLDWDDKMLEVLDIPREMLPEVRRSSEVYGQTNIGGKGGTRIPISGIAGDQQAALFGQ

>d1bu6o2 c.55.1.4 (O:254-499) Glycerol kinase {Escherichia coli}

LCVKEGMAKNTYGTGCFMLMNTGEKAVKSENGLLTTIACGPTGEVNYALEGAVFMAGASIQWLRDEMKLINDAYDSEYFATKVQNTNGVYVVPAFTGLGAPYWDPYARGAIFGLTRGVNANHIIRATLESIAYQTRDVLEAMQADSGIRLHALRVDGGAVANNFLMQFQSDILGTRVERPEVREVTALGAAYLAGLAVGFWQNLDELQEKAVIEREFRPGIETTERNYRYAGWKKAVKRAMAWEEH

>d1chma1 c.55.2.1 (A:2-156) Creatinase {Pseudomonas putida}

QMPKTLRIRNGDKVRSTFSAQEYANRQARLRAHLAAENIDAAIFTSYHNINYYSDFLYCSFGRPYALVVTEDDVISISANIDGGQPWRRTVGTDNIVYTDWQRDNYFAAIQQALPKARRIGIEHDHLNLQNRDKLAARYPDAELVDVAAACMRMR

>d1az9\_1 c.55.2.1 (1-176) Aminopeptidase P {Escherichia coli}

SEISRQEFQRRRQALVEQMQPGSAALIFAAPEVTRSADSEYPYRQNSDFWYFTGFNEPEAVLVLIKSDDTHNHSVLFNRVRDLTAEIWFGRRLGQDAAPEKLGVDRALAFSEINQQLYQLLNGLDVVYHAQGEYAYADVIVNSALEKLRKGSRQNLTAPATMIDWRPVVHEMRLFK

>d1jl1a\_ c.55.3.1 (A:) RNase H (RNase HI) {Escherichia coli}

KQVEIFTAGSALGNPGPGGYGAILRYRGREKTFSAGYTRTTNNRMELMAAIVALEALKEHAEVILSTDSQYVRQGITQWIHNWKKRGWKTADKKPVKNVDLWQRLDAALGQHQIKWEWVKGHAGHPENERADELARAAAMNPTLEDTGYQVE

>d1ekea\_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Methanococcus jannaschii}

MIIIGIDEAGRGPVLGPMVVCAFAIEKEREEELKKLGVKDSKELTKNKRAYLKKLLENLGYVEKRILEAEEINQLMNSINLNDIEINAFSKVAKNLIEKLNIRDDEIEIYIDACSTNTKKFEDSFKDKIEDIIKERNLNIKIIAEHKADAKYPVVSAASIIAKAERDEIIDYYKKIYGDIGSGYPSDPKTIKFLEDYFKKHKKLPDIARTHWKTCKRILDKSKQT

>d1i39a\_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Archaeoglobus fulgidus}

MKAGIDEAGKGCVIGPLVVAGVACSDEDRLRKLGVKDSKKLSQGRREELAEEIRKICRTEVLKVSPENLDERMAAKTINEILKECYAEIILRLKPEIAYVDSPDVIPERLSRELEEITGLRVVAEHKADEKYPLVAAASIIAKVEREREIERLKEKFGDFGSGYASDPRTREVLKEWIASGRIPSCVRMRWKTVSNLRQK

>d1c9ra1 c.55.3.1 (A:430-558) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANAATKLGKAGYVTNKGRQKVVPLTNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPDKSESELVNQIIEALIKKEAVYLAWVPAHAGIGGNAAVDALVSAGIAA

>d1c0ma2 c.55.3.2 (A:49-216) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}

GVNPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAVQHHWATAIAVLGRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLLKDRIRVLAEGDGFMKRIPTSKQGELLAKAMYALNHKERGENTKTPIQKHWRPT

>d1c6va\_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Simian immunodeficiency virus}

NSDLGTWQMDCTHLEGKIVIVAVHVASGFIEAEVIPQETGRQTALFLLKLAGRWPITHLHTDNGANFASQEVKMVAWWAGIEHTFGVPYNPQSQGVVEAMNHHLKNQIDRIREQANSVETIVLMAVHCMNHKRRGGIGDMTPAERLINMITTEQEIQFQ

>d1kfsa1 c.55.3.5 (A:324-518) Exonuclease domain of prokaryotic DNA polymerase {Escherichia coli}

MISYDNYVTILDEETLKAWIAKLEKAPVFAFDTETDSLDNISANLVGLSFAIEPGVAAYIPVAHDYLDAPDQISRERALELLKPLLEDEKALKVGQNLKYDRGILANYGIELRGIAFDTMLESYILNSVAGRHDMDSLAERWLKHKTITFEEIAGKGKNQLTFNQIALEEAGRYAAEDADVTLQLHLKMWPDLQK

>d1qtma1 c.55.3.5 (A:293-422) Exonuclease domain of prokaryotic DNA polymerase {Thermus aquaticus}

ALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEG

>d1xwl\_1 c.55.3.5 (297-468) Exonuclease domain of prokaryotic DNA polymerase {Bacillus stearothermophilus, newly identified strain as yet unnamed}

AKMAFTLADRVTEEMLADKAALVVEVVEENYHDAPIVGIAVVNEHGRFFLRPETALADPQFVAWLGDETKKKSMFDSKRAAVALKWKGIELCGVSFDLLLAAYLLDPAQGVDDVAAAAKMKQYEAVRPDEAVYGKGAKRAVPDEPVLAEHLVRKAAAIWELERPFLDELRRN

>d1t7pa1 c.55.3.5 (A:1-210) Exonuclease domain of T7 DNA polymerase {Bacteriophage T7}

MIVSDIEANALLESVTKFHCGVIYDYSTAEYVSYRPSDFGAYLDALEAEVARGGLIVFHNGHKYDVPALTKLAKLQLNREFHLPRENCIDTLVLSRLIHSNLKDTDMGLLRSGKLPGALEAWGYRLGEMKGEYKDDFKRMLEEQGEEYVDGMEWWNFNEEMMDYNVQDVVVTKALLEKLLSDKHYFPPEIDFTDVGYTTFWSES

>d1ih7a1 c.55.3.5 (A:1-375) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage RB69}

MKEFYLTVEQIGDSIFERYIDSNGRERTREVEYKPSLFAHCPESQATKYFDIYGKPCTRKLFANMRDASQWIKRMEDIGLEALGMDDFKLAYLSDTYNYEIKYDHTKIRVANFDIEVTSPDGFPEPSQAKHPIDAITHYDSIDDRFYVFDLLNSPYGNVEEWSIEIAAKLQEQGGDEVPSEIIDKIIYMPFDNEKELLMEYLNFWQQKTPVILTGWNVESFDIPYVYNRIKNIFGESTAKRLSPHRKTRVKVIENMYGSREIITLFGISVLDYIDLYKKFSFTNQPSYSLDYISEFELNVGKLKYDGPISKLRESNHQRYISYNIIDVYRVLQIDAKRQFINLSLDMGYYAKIQIQSVFSPIKTWDAIIFNSLKE

>d1tgoa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus gorgonarius}

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLGRPIEVWKLYFTHPQDVPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFILGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERVARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRS

>d1fxxa\_ c.55.3.5 (A:) Exonuclease I {Escherichia coli}

QSTFLFHDYETFGTHPALDRPAQFAAIRTDSEFNVIGEPEVFYCKPADDYLPQPGAVLITGITPQEARAKGENEAAFAARIHSLFTVPKTCILGYNNVRFDDEVTRNIFYRNFYDPYAWSWQHDNSRWDLLDVMRACYALRPEGINWPENDDGLPSFRLEHLTKANGIEHSNAHDAMADVYATIAMAKLVKTRQPRLFDYLFTHRNKHKLMALIDVPQMKPLVHVSGMFGAWRGNTSWVAPLAWHPENRNAVIMVDLAGDISPLLELDSDTLRERLYTAKTDLGDNAAVPVKLVHINKCPVLAQANTLRPEDADRLGINRQHCLDNLKILRENPQVREKVVAIFAEAEPFTPSDNVDAQLYNGFFSDADRAAMKIVLETEPRNLPALDITFVDKRIEKLLFNYRARNFPGTLDYAEQQRWLEHRRQVFTPEFLQGYADELQMLVQQYADDKEKVALLKALWQYADEIVEH

>d1jj2m\_ c.55.4.1 (M:) Ribosomal protein L18 (L18p) {Archaeon Haloarcula marismortui}

ATGPRYKVPMRRRREARTDYHQRLRLLKSGKPRLVARKSNKHVRAQLVTLGPNGDDTLASAHSSDLAEYGWEAPTGNMPSAYLTGLLAGLRAQEAGVEEAVLDIGLNSPTPGSKVFAIQEGAIDAGLDIPHNDDVLADWQRTRGAHIAEYDEQLEEPLYSGDFDAADLPEHFDELRETLLDGDIEL

>d1fjgk\_ c.55.4.1 (K:) Ribosomal protein S11 {Thermus thermophilus}

KRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVIGYKGSRKGTPYAAQLAALDAAKKAMAYGMQSVDVIVRGTGAGREQAIRALQASGLQVKSIVDDTPVPHNGCRPKKKFRKAS

>d1ewqa3 c.55.6.1 (A:121-266) DNA repair protein MutS, domain II {Thermus aquaticus}

LLQESLLPREANYLAAIATGDGWGLAFLDVSTGEFKGTVLKSKSALYDELFRHRPAEVLLAPELLENGAFLDEFRKRFPVMLSEAPFEPEGEGPLALRRARGALLAYAQRTQGGALSLQPFRFYDPGAFMRLPEATLRALEVFEPL

>d1e3ma3 c.55.6.1 (A:117-269) DNA repair protein MutS, domain II {Escherichia coli}

GTISDEALLQERQDNLLAAIWQDSKGFGYATLDISSGRFRLSEPADRETMAAELQRTNPAELLYAEDFAEMSLIEGRRGLRRRPLWEFEIDTARQQLNLQFGTRDLVGFGVENAPRGLCAAGCLLQYAKDTQRTTLPHIRSITMEREQDSIIM

>d1sfe\_2 c.55.7.1 (12-92) Ada DNA repair protein {Escherichia coli}

LAVRYALADCELGRCLVAESERGICAILLGDDDATLISELQQMFPAADNAPADLMFQQHVREVIASLNQRDTPLTLPLDIR

>d1qnta2 c.55.7.1 (A:6-91) O6-alkylguanine-DNA alkyltransferase {Human (Homo sapiens)}

EMKRTTLDSPLGKLELSGCEQGLHEIKLLGKGTSAADAVEVPAPAAVLGGPEPLMQCTAWLNAYFHQPEAIEEFPVPALHHPVFQQ

>d1mgta2 c.55.7.1 (A:1-88) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus kodakaraensis}

MLSVEKFRVGERVVWIGVIFSGRVQGIAFAFDRGTLMKRIHDLAEHLGKRGVSISLDVQPSDYPEKVFKVLIGELDNASFLRELSFEG

>d1ulb\_\_ c.56.2.1 (-) Purine nucleoside phosphorylase, PNP {Human (Homo sapiens)}

MENGYTYEDYKNTAEWLLSHTKHRPQVAIICGSGLGGLTDKLTQAQIFDYSEIPNFPRSTVPGHAGRLVFGFLNGRACVMMQGRFHMYEGYPLWKVTFPVRVFHLLGVDTLVVTNAAGGLNPKFEVGDIMLIRDHINLPGFSGQNPLRGPNDERFGDRFPAMSDAYDRTMRQRALSTWKQMGEQRELQEGTYVMVAGPSFETVAECRVLQKLGADAVGMSTVPEVIVARHCGLRVFGFSLITNKVIMDYESLEKANHEEVLAAGKQAAQKLEQFVSILMASIPLPDKAS

>d1k9sa\_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Escherichia coli}

ATPHINAEMGDFADVVLMPGDPLRAKYIAETFLEDAREVNNVRGMLGFTGTYKGRKISVMGHGMGIPSCSIYTKELITDFGVKKIIRVGSCGAVLPHVKLRDVVIGMGACTDSKVNRIRFKDHDFAAIADFDMVRNAVDAAKALGIDARVGNLFSADLFYSPDGEMFDVMEKYGILGVEMEAAGIYGVAAEFGAKALTICTVSDHIRTHEQTTAAERQTTFNDMIKIALESVLLGDK

>d1qe5a\_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cellulomonas sp.}

PPLDDPATDPFLVARAAADHIAQATGVEGHDMALVLGSGWGGAAELLGEVVAEVPTHEIPGFSSVTRSIRVERADGSVRHALVLGSRTHLYEGKGVRAVVHGVRTAAATGAETLILTNGCGGLNQEWGAGTPVLLSDHINLTARSPLEGPTFVDLTDVYSPRLRELAHRVDPTLPEGVYAQFPGPHYETPAEVRMAGILGADLVGMSTTLEAIAARHCGLEVLGVSLVTNLAAGISPTPLSHAEVIEAGQAAGPRISALLADIAKR

>d1k3fa\_ c.56.2.1 (A:) Uridine phosphorylase {Escherichia coli}

MSKSDVFHLGLTKNDLQGATLAIVPGDPDRVEKIAALMDKPVKLASHREFTTWRAELDGKPVIVCSTGIGGPSTSIAVEELAQLGIRTFLRIGTTGAIQPHINVGDVLVTTASVRLDGASLHFAPLEFPAVADFECTTALVEAAKSIGATTHVGVTASSDTFYPGQERYDTYSGRVVRHFKGSMEEWQAMGVMNYEMESATLLTMCASQGLRAGMVAGVIVNRTQQEIPNAETMKQTESHAVKIVVEAARRLL

>d1cb0a\_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Human (Homo sapiens)}

AVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDALILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEIQPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLGLRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMATDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQFSVLLP

>d1je0a\_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Archaeon Sulfolobus solfataricus}

PVHILAKKGEVAERVLVVGDPGRARLLSTLLQNPKLTNENRGFLVYTGKYNGETVSIATHGIGGPSIAIVLEELAMLGANVFIRYGTTGALVPYINLGEYIIVTGASYNQGGLFYQYLRDNACVASTPDFELTNKLVTSFSKRNLKYYVGNVFSSDAFYAEDEEFVKKWSSRGNIAVEMECATLFTLSKVKGWKSATVLVVSDNLAKGGIWITKEELEKSVMDGAKAVLDTLTS

>d1a2za\_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Archaeon Thermococcus litoralis}

MKKVLITGFEPFGGDSKNPTEQIAKYFDRKQIGNAMVYGRVLPVSVKRATIELKRYLEEIKPEIVINLGLAPTYSNITVERIAVNIIDARIPDNDGYQPIDEKIEEDAPLAYMATLPVRAITKTLRDNGIPATISYSAGTYLCNYVMFKTLHFSKIEGYPLKAGFIHVPYTPDQVVNKFFLLGKNTPSMCLEAEIKAIELAVKVSLDYLEKDRDDIKIPL

>d1auga\_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Bacillus amyloliquefaciens}

MEKKVLLTGFDPFGGETVNPSWEAVKRLNGAAEGPASIVSEQVPTVFYKSLAVLREAIKKHQPDIIICVGQAGGRMQITPERVAINLNEARIPDNEGNQPVGEDISQGGPAAYWTGLPIKRIVEEIKKEGIPAAVSYTAGTFVCNHLFYGLMDEISRHHPHIRGGFIHIPYIPEQTLQKSAPSLSLDHITKALKIAAVTAAVHEDDIETG

>d1pca\_1 c.56.5.1 (1-308) Carboxypeptidase A {Pig (Sus scrofa)}

ARTTSTFNYATYHTLEEIYDFMDILVAEHPALVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWIDSGIHSREWITQASGVWFAKKITENYGQNSSFTAILDSMDIFLEIVTNPNGFAFTHSDNRLWRKTRSKASGSLCVGSDSNRNWDAGFGGAGASSSPCAETYHGKYPNSEVEVKSITDFVKNNGNIKAFISIHSYSQLLLYPYGYKTQSPADKSELNQIAKSAVAALKSLYGTSYKYGSIITVIYQASGGVIDWTYNQGIKYSFSFELRDTGRRGFLLPASQIIPTAQETWLALLTIMEHTLNNS

>d1h8la2 c.56.5.1 (A:4-304) Carboxypeptidase D, catalytic domain {Crested duck (Lophonetta specularioides)}

QAVQPVDFRHHHFSDMEIFLRRYANEYPSITRLYSVGKSVELRELYVMEISDNPGIHEAGEPEFKYIGNMHGNEVVGRELLLNLIEYLCKNFGTDPEVTDLVQSTRIHIMPSMNPDGYEKSQEGDRGGTVGRNNSNNYDLNRNFPDQFFQVTDPPQPETLAVMSWLKTYPFVLSANLHGGSLVVNYPFDDDEQGIAIYSKSPDDAVFQQLALSYSKENKKMYQGSPCKDLYPTEYFPHGITNGAQWYNVPGGMQDWNYLNTNCFEVTIELGCVKYPKAEELPKYWEQNRRSLLQFIKQVHR

>d1amp\_\_ c.56.5.4 (-) Aminopeptidase {Aeromonas proteolytica}

MPPITQQATVTAWLPQVDASQITGTISSLESFTNRFYTTTSGAQASDWIASEWQALSASLPNASVKQVSHSGYNQKSVVMTITGSEAPDEWIVIGGHLDSTIGSHTNEQSVAPGADDDASGIAAVTEVIRVLSENNFQPKRSIAFMAYAAEEVGLRGSQDLANQYKSEGKNVVSALQLDMTNYKGSAQDVVFITDYTDSNFTQYLTQLMDEYLPSLTYGFDTCGYACSDHASWHNAGYPAAMPFESKFNDYNPRIHTTQDTLANSDPTGSHAKKFTQLGLAYAIEMGSATG

>d1qq9a\_ c.56.5.4 (A:) Aminopeptidase {Streptomyces griseus}

APDIPLANVKAHLTQLSTIAANNGGNRAHGRPGYKASVDYVKAKLDAAGYTTTLQQFTSGGATGYNLIANWPGGDPNKVLMAGAHLDSVSSGAGINDNGSGSAAVLETALAVSRAGYQPDKHLRFAWWGAEELGLIGSKFYVNNLPSADRSKLAGYLNFDMIGSPNPGYFVYDDDPVIEKTFKNYFAGLNVPTEIETEGDGRSDHAPFKNVGVPVGGLFTGAGYTKSAAQAQKWGGTAGQAFDRCYHSSCDSLSNINDTALDRNSDAAAHAIWTLSS

>d1cg2a1 c.56.5.4 (A:26-213,A:327-414) Carboxypeptidase G2, catalytic domain {Pseudomonas sp., strain rs-16}

QKRDNVLFQAATDEQPAVIKTLEKLVNIETGTGDAEGIAAAGNFLEAELKNLGFTVTRSKSAGLVVGDNIVGKIKGRGGKNLLLMSHMDTVYLKGILAKAPFRVEGDKAYGPGIADDKGGNAVILHTLKLLKEYGVRDYGTITVLFNTDEEKGSFGSRDLIQEEAKLADYVLSFEPTSAGDEKLSLGTXFNAGEGGKKLVDKAVAYYKEAGGTLGVEERTGGGTDAAYAALSGKPVIESLGLPGFGYHSDKAEYVDISAIPRRLYMAARLIMDLGAG

>d1di6a\_ c.57.1.1 (A:) MogA {Escherichia coli}

ATLRIGLVSISDRASSGVYQDKGIPALEEWLTSALTTPFELETRLIPDEQAIIEQTLCELVDEMSCHLVLTTGGTGPARRDVTPDATLAVADREMPGFGEQMRQISLHFVPTAILSRQVGVIRKQALILNLPGQPKSIKETLEGVKDAEGNVVVHGIFASVPYCIQLLEGPYVETAPEVVAAFRPKSARR

>d1jlja\_ c.57.1.1 (A:) Gephyrin N-terminal domain {Human (Homo sapiens)}

HQIRVGVLTVSDSCFRNLAEDRSGINLKDLVQDPSLLGGTISAYKIVPDEIEEIKETLIDWCDEKELNLILTTGGTGFAPRDVTPEATKEVIEREAPGMALAMLMGSLNVTPLGMLSRPVCGIRGKTLIINLPGSKKGSQECFQFILPALPHAIDLLRDAIVKVKEVHD

>d1bgva2 c.58.1.1 (A:1-194) Glutamate dehydrogenase {Clostridium symbiosum}

SKYVDRVIAEVEKKYADEPEFVQTVEEVLSSLGPVVDAHPEYEEVALLERMVIPERVIEFRVPWEDDNGKVHVNTGYRVQFNGAIGPYKGGLRFAPSVNLSIMKFLGFEQAFKDSLTTLPMGGAKGGSDFDPNGKSDREVMRFCQAFMTELYRHIGPDIDVPAGDLGVGAREIGYMYGQYRKIVGGFYNGVLTG

>d1gtma2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}

ADPYEIVIKQLERAAQYMEISEEALEFLKRPQRIVEVTIPVEMDDGSVKVFTGFRVQHNWARGPTKGGIRWHPEETLSTVKALAAWMTWKTAVMDLPYGGGKGGIIVDPKKLSDREKERLARGYIRAIYDVISPYEDIPAPDVYTNPQIMAWMMDEYETISRRKTPAFGIITGKPLSI

>d1hwxa2 c.58.1.1 (A:1-208) Glutamate dehydrogenase {Cow (Bos taurus)}

ADREDDPNFFKMVEGFFDRGASIVEDKLVEDLKTRQTQEQKRNRVRGILRIIKPCNHVLSLSFPIRRDDGSWEVIEGYRAQHSHQRTPCKGGIRYSTDVSVDEVKALASLMTYKCAVVDVPFGGAKAGVKINPKNYTDEDLEKITRRFTMELAKKGFIGPGVDVPAPNMSTGEREMSWIADTYASTIGHYDINAHACVTGKPISQGGI

>d1leha2 c.58.1.1 (A:1-134) Leucine dehydrogenase {Bacillus sphaericus}

MEIFKYMEKYDYEQLVFCQDEASGLKAVIAIHDTTLGPALGGARMWTYNAEEEAIEDALRLARGMTYKNAAAGLNLGGGKTVIIGDPFADKNEDMFRALGRFIQGLNGRYITAEDVGTTVDDMDLIHQETDYVT

>d1c1da2 c.58.1.1 (A:1-148) Phenylalanine dehydrogenase {Rhodococcus sp., M4}

SIDSALNWDGEMTVTRFDAMTGAHFVIRLDSTQLGPAAGGTRAAQYSNLADALTDAGKLAGAMTLKMAVSNLPMGGGKSVIALPAPRHSIDPSTWARILRIHAENIDKLSGNYWTGPDVNTNSADMDTLNDTTEFVFGRSLERGGAGS

>d1a4ia2 c.58.1.2 (A:2-126) Tetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}

APAEILNGKEISAQIRARLKNQVTQLKEQVPGFTPRLAILQVGNRDDSNLYINVKLKAAEEIGIKATHIKLPRTTTESEVMKYITSLNEDSTVHGFLVQLPLDSENSINTEEVINAIAPEKDVDG

>d1edza2 c.58.1.2 (A:3-148) Tetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}

KPGRTILASKVAETFNTEIINNVEEYKKTHNGQGPLLVGFLANNDPAAKMYATWTQKTSESMGFRYDLRVIEDKDFLEEAIIQANGDDSVNGIMVYFPVFGNAQDQYLQQVVCKEKDVEGLNHVYYQNLYHNVRYLDKENRLKSIL

>d2uaga2 c.59.1.1 (A:298-437) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}

GLPHRFEVVLEHNGVRWINDSKATNVGSTEAALNGLHVDGTLHLLLGGDGKSADFSPLARYLNGDNVRLYCFGRDGAQLAALRPEVAEQTETMEQAMRLLAPRVQPGDMVLLSPACASLDQFKNFEQRGNEFARLAKELG

>d1e8ca2 c.59.1.1 (A:338-497) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

VCGRMEVFTAPGKPTVVVDYAHTPDALEKALQAARLHCAGKLWCVFGCGGDRDKGKRPLMGAIAEEFADVAVVTDDNPRTEEPRAIINDILAGMLDAGHAKVMEGRAEAVTCAVMQAKENDVVLVAGKGHEDYQIVGNQRLDYSDRVTVARLLGVIARSH

>d1gg4a1 c.59.1.1 (A:313-447) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

VPGRLFPIQLAENQLLLDDSYNANVGSMTAAVQVLAEMPGYRVLVVGDMAELGAESEACHVQVGEAAKAAGIDRVLSVGKQSHAISTASGVGEHFADKTALITRLKLLIAEQQVITILVKGSRSAAMEEVVRALQ

>d1fzta\_ c.60.1.1 (A:) Phosphoglycerate mutase {Yeast (Schizosaccharomyces pombe)}

MTTEAAPNLLVLTRHGESEWNKLNLFTGWKDPALSETGIKEAKLGGERLKSRGYKFDIAFTSALQRAQKTCQIILEEVGEPNLETIKSEKLNERYYGDLQGLNKDDARKKWGAEQVQIWRRSYDIAPPNGESLKDTAERVLPYYKSTIVPHILKGEKVLIAAHGNSLRALIMDLEGLTGDQIVKRELATGVPIVYHLDKDGKYVSKELIDN

>d1e58a\_ c.60.1.1 (A:) Phosphoglycerate mutase {Escherichia coli}

AVTKLVLVRHGESQWNKENRFTGWYDVDLSEKGVSEAKAAGKLLKEEGYSFDFAYTSVLKRAIHTLWNVLDELDQAWLPVEKSWKLNERHYGALQGLNKAETAEKYGDEQVKQWRRGFAVTPPELTKDDERYPGHDPRYAKLSEKELPLTESLALTIDRVIPYWNETILPRMKSGERVIIAAHGNSLRALVKYLDNMSEEEILELNIPTGVPLVYEFDENFKPLKRYYLGNADEIAAKAAAVANQGK

>d1ebba\_ c.60.1.1 (A:) Broad specificity phosphatase YhfR {Bacillus stearothermophilus}

ATTLYLTRHGETKWNVERRMQGWQDSPLTEKGRQDAMRLGKRLEAVELAAIYTSTSGRALETAEIVRGGRLIPIYQDERLREIHLGDWEGKTHDEIRQMDPIAFDHFWQAPHLYAPQRGERFCDVQQRALEAVQSIVDRHEGETVLIVTHGVVLKTLMAAFKDTPLDHLWSPPYMYGTSVTIIEVDGGTFHVAVEGDVSHIE

>d1ihp\_\_ c.60.1.3 (-) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus ficuum}

SCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA

>d1qfxa\_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus niger}

KQFSQEFRDGYSILKHYGGNGPYSERVSYGIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVYSINTTEYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPFFSSGYGRVIETARKFGEGFFGYNYSTNAALNIISESEVMGADSLTPTCDTDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMVMASFELNARPFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLTLLNQGPKEAGSLFFNFAHDTNITPILAALGVLIPNEDLPLDRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDCTSGPGYSCPLANYTSILNKNLPDYTTTCNVSASYPQYLSFWWNYNTTTELNYRSSPIACQEGDAMD

>d1dkla\_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Escherichia coli}

SEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL

>d1nula\_ c.61.1.1 (A:) Xantine-guanine PRTase (XPRTase) {Escherichia coli}

EKYIVTWDMLQIHARKLASRLMPSEQWKGIIAVSRGGLVPGALLARELGIRHVDTVCISSYDHDNQRELKVLKRAEGDGEGFIVIDDLVDTGGTAVAIREMYPKAHFVTIFAKPAGRPLVDDYVVDIPQDTWIEQPWDMGVVFVPPISGR

>d1fsga\_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Toxoplasma gondii}

GSHMASKPIEDYGKGKGRIEPMYIPDNTFYNADDFLVPPHCKPYIDKILLPGGLVKDRVEKLAYDIHRTYFGEELHIICILKGSRGFFNLLIDYLATIQKYSGRESSVPPFFEHYVRLKSYQNDNSTGQLTVLSDDLSIFRDKHVLIVEDIVDTGFTLTEFGERLKAVGPKSMRIATLVEKRTDRSNSLKGDFVGFSIEDVWIVGCCYDFNEMFRDFDHVAVLSDAARKKFEK

>d1ecfa1 c.61.1.1 (A:250-492) Glutamine PRPP amidotransferase, C-terminal domain {Escherichia coli}

NPCLFEYVYFARPDSFIDKISVYSARVNMGTKLGEKIAREWEDLDIDVVIPIPETSCDIALEIARILGKPYRQGFVKNRYVGRTFIMPGQQLRRKSVRRKLNANRAEFRDKNVLLVDDSIVRGTTSEQIIEMAREAGAKKVYLASAAPEIRFPNVYGIDMPSATELIAHGREVDEIRQIIGADGLIFQDLNDLIDAVRAENPDIQQFECSVFNGVYVTKDVDQGYLDFLDTLRNDDAKAVQRQ

>d1dqna\_ c.61.1.1 (A:) Guanine PRTase {Giardia lamblia}

MICSVTGKPVKDVLSTFFKDRNDVLESEVKKFHLLATFEECKALAADTARRMNEYYKDVAEPVTLVALLTGAYLYASLLTVHLTFPYTLHFVKVSSYKGTRQESVVFDEEDLKQLKEKREVVLIDEYVDSGHTIFSIQEQIKHAKICSCFVKDVDAIKKHSALADTKMFYGYTPMPKGSWLIGFGLDDNGLRRGWAHLFDINLSESEVTEFRRRLTEHIKGLNINGVNRY

>d1tc1a\_ c.61.1.1 (A:) Hypoxanthine PRTase {Trypanosoma cruzi}

YEFAEKILFTEEEIRTRIKEVAKRIADDYKGKGLRPYVNPLVLISVLKGSFMFTADLCRALCDFNVPVRMEFICVSSYGEGLTSSGQVRMLLDTRHSIEGHHVLIVEDIVDTALTLNYLYHMYFTRRPASLKTVVLLDKREGRRVPFSADYVVANIPNAFVIGYGLDYDDTYRELRDIVVLRPE

>d1qb7a\_ c.61.1.1 (A:) Adenine PRTase {Leishmania donovani}

PFKEVSPNSFLLDDSHALSQLLKKSYRWYSPVFSPRNVPRFADVSSITESPETLKAIRDFLVQRYRAMSPAPTHILGFDARGFLFGPMIAVELEIPFVLMRKADKNAGLLIRSEPYEKEYKEAAPEVMTIRYGSIGKGSRVVLIDDVLATGGTALSGLQLVEASDAVVVEMVSILSIPFLKAAEKIHSTANSRYKDIKFISLLSDDALTEENCGDSKNYTGPRVLSCGDVLAEHPH

>d1g2qa\_ c.61.1.1 (A:) Adenine PRTase {Baker's yeast (Saccharomyces cerevisiae)}

MPIASYAQELKLALHQYPNFPSEGILFEDFLPIFRNPGLFQKLIDAFKLHLEEAFPEVKIDYIVGLESRGFLFGPTLALALGVGFVPVRKAGKLPGECFKATYEKEYGSDLFEIQKNAIPAGSNVIIVDDIIATGGSAAAAGELVEQLEANLLEYNFVMELDFLKGRSKLNAPVFTLL

>d1oroa\_ c.61.1.1 (A:) Orotate PRTase {Escherichia coli}

MKPYQRQFIEFALSKQVLKFGEFTLKSGRKSPYFFNAGLFNTGRDLALLGRFYAEALVDSGIEFDLLFGPAYKGIPIATTTAVALAEHHDLDLPYCFNRKEAKDHGEGGNLVGSALQGRVMLVDDVITAGTAIRESMEIIQANGATLAGVLISLDRQERGRGEISAIQEVERDYNCKVISIITLKDLIAYLEEKPEMAEHLAAVKAYREEFGV

>d1a3c\_\_ c.61.1.1 (-) Uracil PRTase {Bacillus subtilis}

QKAVILDEQAIRRALTRIAHEMIERNKGMNNCILVGIKTRGIYLAKRLAERIEQIEGNPVTVGEIDITLYRDDLSKKTSNDEPLVKGADIPVDITDQKVILVDDVLYTGRTVRAGMDALVDVGRPSSIQLAVLVDRGHRELPIRADYIGKNIPTSKSEKVMVQLDEVDQNDLVAIYEN

>d1bd3a\_ c.61.1.1 (A:) Uracil PRTase {Toxoplasma gondii}

QEESILQDIITRFPNVVLMKQTAQLRAMMTIIRDKETPKEEFVFYADRLIRLLIEEALNELPFQKKEVTTPLDVSYHGVSFYSKICGVSIVRAGESMESGLRAVCRGVRIGKILIQRDETTAEPKLIYEKLPADIRERWVMLLDPMCATAGSVCKAIEVLLRLGVKEERIIFVNILAAPQGIERVFKEYPKVRMVTAAVDICLNSRYYIVPGIGDFGDRYFGTM

>d1dkra1 c.61.1.2 (A:8-166) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}

NLKIFSLNSNPELAKEIADIVGVQLGKCSVTRFSDGEVQINIEESIRGCDCYIIQSTSDPVNEHIMELLIMVDALKRASAKTINIVIPYYGYARQDRKARSREPITAKLFANLLETAGATRVIALDLHAPQIQGFFDIPIDHLMGVPILGEYFEGKNLE

>d1dkra2 c.61.1.2 (A:167-316) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}

DIVIVSPDHGGVTRARKLADRLKAPIAIIDKRRPRPNVAEVMNIVGNIEGKTAILIDDIIDTAGTITLAANALVENGAKEVYACCTHPVLSGPAVERINNSTIKELVVTNSIKLPEEKKIERFKQLSVGPLLAEAIIRVHEQQSVSYLFS

>d1lfaa\_ c.62.1.1 (A:) Integrin CD11a/CD18 (Leukocyte function associated antigen-1, LFA-1) {Human (Homo sapiens)}

GNVDLVFLFDGSMSLQPDEFQKILDFMKDVMKKLSNTSYQFAAVQFSTSYKTEFDFSDYVKRKDPDALLKHVKHMLLLTNTFGAINYVATEVFREELGARPDATKVLIIITDGEATDSGNIDAAKDIIRYIIGIGKHFQTKESQETLHKFASKPASEFVKILDTFEKLKDLFTELQKKIYVIE

>d1atza\_ c.62.1.1 (A:) von Willebrand factor A3 domain {Human (Homo sapiens)}

QPLDVILLLDGSSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITTIDVPWNVVPEKAHLLSLVDVMQREGGPSQIGDALGFAVRYLTSEMHGARPGASKAVVILVTDVSVDSVDAAADAARSNRVTVFPIGIGDRYDAAQLRILAGPAGDSNVVKLQRIEDLPTMVTLGNSFLHKL

>d1fnsa\_ c.62.1.1 (A:) von Willebrand factor A1 domain {Human (Homo sapiens)}

MYCSRLLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRVSQKWVRVAVVEYHDGSHAYIGLKDRKRPSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRIALLLMASQEPQRMSRNFVRYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVLSSVDELEQQRDEIVSYLCDLAPEAP

>d1ido\_\_ c.62.1.1 (-) Integrin CR3 (CD11b/CD18, Mac-1), alpha subunit {Human (Homo sapiens)}

DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREK

>d1aoxa\_ c.62.1.1 (A:) Integrin alpha2-beta1 {Human (Homo sapiens)}

SCPSLIDVVVVCDESNSIYPWDAVKNFLEKFVQGLDIGPTKTQVGLIQYANNPRVVFNLNTYKTKEEMIVATSQTSQYGGDLTNTFGAIQYARKYAYSAASGGRRSATKVMVVVTDGESHDGSMLKAVIDQCNHDNILRFGIAVLGYLNRNALDTKNLIKEIKAIASIPTERYFFNVSDEAALLEKAGTLGEQIFSIEGGT

>d1jv2b2 c.62.1.1 (B:107-354) Integrin beta A domain {Human (Homo sapiens)}

VEDYPVDIYYLMDLSYSMKDDLWSIQNLGTKLATQMRKLTSNLRIGFGAFVDKPVSPYMYISPPEALENPCYDMKTTCLPMFGYKHVLTLTDQVTRFNEEVKKQSVSRNRDAPEGGFDAIMQATVCDEKIGWRNDASHLLVFTTDAKTHIALDGRLAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEKLSQKNINLIFAVTENVVNLYQNYSELIPGTTVGVLSMDSSNVLQLIVDAYGKIRSK

>d1poia\_ c.63.1.1 (A:) Glutaconate-CoA transferase alpha {Acidaminococcus fermentans}

SKVMTLKDAIAKYVHSGDHIALGGFTTDRKPYAAVFEILRQGITDLTGLGGAAGGDWDMLIGNGRVKAYINCYTANSGVTNVSRRFRKWFEAGKLTMEDYSQDVIYMMWHAAALGLPFLPVTLMQGSGLTDEWGISKEVRKTLDKVPDDKFKYIDNPFKPGEKVVAVPVPQVDVAIIHAQQASPDGTVRIWGGKFQDVDIAEAAKYTIVTCEEIISDEEIRRDPTKNDIPGMCVDAVVLAPYGAHPSQCYGLYDYDNPFLKVYDKVSKTQEDFDAFCKEWVFDLKDHDEYLNKLGATRLINLKVVPGLGYHIDMTKE

>d1poib\_ c.63.1.1 (B:) Glutaconate-CoA transferase beta {Acidaminococcus fermentans}

DYTNYTNKEMQAVTIAKQIKNGQVVTVGTGLPLIGASVAKRVYAPDCHIIVESGLMDCSPVEVPRSVGDLRFMAHCGCIWPNVRFVGFEINEYLHKANRLIAFIGGAQIDPYGNVNSTSIGDYHHPKTRFTGSGGANGIATYSNTIIMMQHEKRRFMNKIDYVTSPGWIDGPGGRERLGLPGDVGPQLVVTDKGILKFDEKTKRMYLAAYYPTSSPEDVLENTGFDLDVSKAVELEAPDPAVIKLIREEIDPGQAFIQVP

>d1jkxa\_ c.65.1.1 (A:) Glycinamide ribonucleotide transformylase, GART {Escherichia coli}

MNIVVLISGNGSNLQAIIDACKTNKIKGTVRAVFSNKADAFGLERARQAGIATHTLIASAFDSREAYDRELIHEIDMYAPDVVVLAGFMRILSPAFVSHYAGRLLNIHPSLLPKYPGLHTHRQALENGDEEHGTSVHFVTDELDGGPVILQAKVPVFAGDSEDDITARVQTQEHAIYPLVISWFADGRLKMHENAAWLDGQRLPPQGYA

>d1fmta2 c.65.1.1 (A:1-206) Methionyl-tRNAfmet formyltransferase {Escherichia coli}

SESLRIIFAGTPDFAARHLDALLSSGHNVVGVFTQPDRPAGRGKKLMPSPVKVLAEEKGLPVFQPVSLRPQENQQLVAELQADVMVVVAYGLILPKAVLEMPRLGCINVHGSLLPRWRGAAPIQRSLWAGDAETGVTIMQMDVGLDTGDMLYKLSCPITAEDTSGTLYDKLAELGPQGLITTLKQLADGTAKPEVQDETLVTYAEK

>d1fp1d2 c.66.1.12 (D:129-372) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}

RGYLASFTTFLCYPALLQVWMNFKEAVVDEDIDLFKNVHGVTKYEFMGKDKKMNQIFNKSMVDVCATEMKRMLEIYTGFEGISTLVDVGGGSGRNLELIISKYPLIKGINFDLPQVIENAPPLSGIEHVGGDMFASVPQGDAMILKAVCHNWSDEKCIEFLSNCHKALSPNGKVIIVEFILPEEPNTSEESKLVSTLDNLMFITVGGRERTEKQYEKLSKLSGFSKFQVACRAFNSLGVMEFYK

>d1fp2a2 c.66.1.12 (A:109-352) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}

LCLAPMVECVLDPTLSGSYHELKKWIYEEDLTLFGVTLGSGFWDFLDKNPEYNTSFNDAMASDSKLINLALRDCDFVFDGLESIVDVGGGTGTTAKIICETFPKLKCIVFDRPQVVENLSGSNNLTYVGGDMFTSIPNADAVLLKYILHNWTDKDCLRILKKCKEAVTNDGKRGKVTIIDMVIDKKKDENQVTQIKLLMDVNMACLNGKERNEEEWKKLFIEAGFQHYKISPLTGFLSLIEIYP

>d1dl5a1 c.66.1.7 (A:1-213) Protein-L-isoaspartyl O-methyltransferase {Thermotoga maritima}

MREKLFWILKKYGVSDHIAKAFLEIPREEFLTKSYPLSYVYEDIVLVSYDDGEEYSTSSQPSLMALFMEWVGLDKGMRVLEIGGGTGYNAAVMSRVVGEKGLVVSVEYSRKICEIAKRNVERLGIENVIFVCGDGYYGVPEFSPYDVIFVTVGVDEVPETWFTQLKEGGRVIVPINLKLSRRQPAFLFKKKDPYLVGNYKLETRFITAGGNLG

>d1jg1a\_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Archaeon Pyrococcus furiosus}

EKELYEKWMRTVEMLKAEGIIRSKEVERAFLKYPRYLSVEDKYKKYAHIDEPLPIPAGQTVSAPHMVAIMLEIANLKPGMNILEVGTGSGWNAALISEIVKTDVYTIERIPELVEFAKRNLERAGVKNVHVILGDGSKGFPPKAPYDVIIVTAGAPKIPEPLIEQLKIGGKLIIPVGSYHLWQELLEVRKTKDGIKIKNHGGVAFVPLIGEYGWK

>d1kr5a\_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Human (Homo sapiens)}

ASHSELIHNLRKNGIIKTDKVFEVMLATDRSHYAKCNPYMDSPQSIGFQATISAPHMHAYALELLFDQLHEGAKALDVGSGSGILTACFARMVGCTGKVIGIDHIKELVDDSVNNVRKDDPTLLSSGRVQLVVGDGRMGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGRLILPVGPAGGNQMLEQYDKLQDGSIKMKPLMGVIYVPLTDKEKQWSR

>d3mag\_\_ c.66.1.9 (-) Polymerase regulatory subunit VP39 {Vaccinia virus}

MDVVSLDKPFMYFEEIDNELDYEPESANEVAKKLPYQGQLKLLLGELFFLSKLQRHGILDGATVVYIGSAPGTHIRYLRDHFYNLGVIIKWMLIDGRHHDPILNGLRDVTLVTRFVDEEYLRSIKKQLHPSKIILISDVRSPKRGGNESTADLLSNYALQNVMISILNPVASSLKWRCPFPDQWIKDFYIPHGNKMLQPFAPSYSAEMRLLSIYTGENMRLTRVTKSDAVNYEKKMYYLNKIVRNKVVVNFDYPNQEYDYFHMYFMLRTVYCNKTFPTTKAKVLFLQQSIFRFLNIP

>d1yub\_\_ c.66.1.9 (-) rRNA methyltransferase {Streptococcus pneumoniae, Ermam}

MNKNIKYSQNFLTSEKVLNQIIKQLNLKETDTVYEIGTGKGHLTTKLAKISKQVTSIELDSHLFNLSSEKLKLNTRVTLIHQDILQFQFPNKQRYKIVGNIPYHLSTQIIKKVVFESRASDIYLIVEEGFYKRTLDIHRTLGLLLHTQVSIQQLLKLPAECFHPKPKVNSVLIKLTRHTTDVPDKYWKLYTYFVSKWVNREYRQLFTKNQFHQAMKHAKVNNLSTITYEQVLSIFNSYLLFNGRK

>d1i4wa\_ c.66.1.9 (A:) Transcription factor sc-mtTFB {Baker's yeast (Saccharomyces cerevisiae)}

PIPGIKDISKLKFFYGFKYLWNPTVYNKIFDKLDLTKTYKHPEELKVLDLYPGVGIQSAIFYNKYCPRQYSLLEKRSSLYKFLNAKFEGSPLQILKRDPYDWSTYSNLIDEERIFVPEVQSSDHINDKFLTVANVTGEGSEGLIMQWLSCIGNKNWLYRFGKVKMLLWMPSTTARKLLARPGMHSRSKCSVVREAFTDTKLIAISDANELKGFDSQCIEEWDPILFSAAEIWPTKGKPIALVEMDPIDFDFDVDNWDYVTRHLMILKRTPLNTVMDSLGHGGQQYFNSRITDKDLLKKCPIDLTNDEFIYLTKLFMEWPFKP

>d6mhta\_ c.66.1.10 (A:) DNA methylase HhaI, coenzyme-binding domain {Haemophilus haemolyticus}

MIEIKDKQLTGLRFIDLFAGLGGFRLALESCGAECVYSNEWDKYAQEVYEMNFGEKPEGDITQVNEKTIPDHDILCAGFPCQAFSISGKQKGFEDSRGTLFFDIARIVREKKPKVVFMENVKNFASHDNGNTLEVVKNTMNELDYSFHAKVLNALDYGIPQKRERIYMICFRNDLNIQNFQFPKPFELNTFVKDLLLPDSEVEHLVIDRKDLVMTNQEIEQTTPKTVRLGIVGKGGQGERIYSTRGIAITLSAYGGGIFAKTGGYLVNGKTRKLHPRECARVMGYPDSYKVHPSTSQAYKQFGNSVVINVLQYIAYNIGSSLNFKPY

>d1g38a\_ c.66.1.10 (A:) DNA methylase TaqI, coenzyme-binding domain {Thermus aquaticus}

VETPPEVVDFMVSLAEAPRGGRVLEPACAHGPFLRAFREAHGTGYRFVGVEIDPKALDLPPWAEGILADFLLWEPGEAFDLILGNPPYGIVGEASKYPIHVFKAVKDLYKKAFSTWKGKYNLYGAFLEKAVRLLKPGGVLVFVVPATWLVLEDFALLREFLAREGKTSVYYLGEVFPQKKVSAVVIRFQKSGKGLSLWDTQESESGFTPILWAEYPHWEGEIIRFETEETRKLEISGMPLGDLFHIRFAARSPEFKKHPAVRKEPGPGLVPVLTGRNLKPGWVDYEKNHSGLWMPKERAKELRDFYATPHLVVAHTKGTRVVAAWDERAYPWREEFHLLPKEGVRLDPSSLVQWLNSEAMQKHVRTLYRDFVPHLTLRMLERLPVRREYGFHT

>d1dcta\_ c.66.1.10 (A:) DNA methylase HaeIII, coenzyme-binding domain {Haemophilus aegyptius}

MNLISLFSGAGGLDLGFQKAGFRIICANEYDKSIWKTYESNHSAKLIKGDISKISSDEFPKCDGIIGGPPCQSWSEGGSLRGIDDPRGKLFYEYIRILKQKKPIFFLAENVKGMMAQRHNKAVQEFIQEFDNAGYDVHIILLNANDYGVAQDRKRVFYIGFRKELNINYLPPIPHLIKPTFKDVIWDLKDNPIPALDKNKTNGNKCIYPNHEYFIGSYSTIFMSRNRVRQWNEPAFTVQASGRQCQLHPQAPVMLKVSKNLNKFVEGKEHLYRRLTVRECARVQGFPDDFIFHYESLNDGYKMIGNAVPVNLAYEIAKTIKSAL

>d2dpma\_ c.66.1.10 (A:) DpnM DNA adenine methyltransferase {Streptococcus pneumoniae}

TLQPFTKWTGGKRQLLPVIRELIPKTYNRYFEPFVGGGALFFDLAPKDAVINDFNAELINCYQQIKDNPQELIEILKVHQEYNSKEYYLDLRSADRDERIDMMSEVQRAARILYMLRVNFNGLYRVNSKNQFNVPYGRYKNPKIVDEELISAISVYINNNQLEIKVGDFEKAIVDVRTGDFVYFDPPYIPLSETSAFTSYTHEGFSFADQVRLRDAFKRLSDTGAYVMLSNSSSALVEELYKDFNIHYVEATRTNGAKSSSRGKISEIIVTNYEK

>d1g55a\_ c.66.1.10 (A:) DNMT2 {Human (Homo sapiens)}

EPLRVLELYSGVGGMHHALRESCIPAQVVAAIDVNTVANEVYKYNFPHTQLLAKTIEGITLEEFDRLSFDMILMSPPCQPFTRIGRQGDMTDSRTNSFLHILDILPRLQKLPKYILLENVKGFEVSSTRDLLIQTIENCGFQYQEFLLSPTSLGIPNSRLRYFLIAKLQSEPLPFQAPGQVLMEFPKIEIHRKNQQDSDLSVKMLKDFLEDDTDVNQYLLPPKSLLRYALLLDIVQPTCRRSVCFTKGYGSYIEGTGSVLQTAEDVQVENIYKSLTNLSQEEQITKLLILKLRYFTPKEIANLLGFPPEFGFPEKITVKQRYRLLGNSLNVHVVAKLIKILYE

>d1booa\_ c.66.1.11 (A:) m.PvuII N4 cytosine-specific DNA methyltransferase {Proteus vulgaris}

NFGKKPAYTTSNGSMYIGDSLELLESFPEESISLVMTSPPFALQRKKEYGNLEQHEYVDWFLSFAKVVNKKLKPDGSFVVDFGGAYMKGVPARSIYNFRVLIRMIDEVGFFLAEDFYWFNPSKLPSPIEWVNKRKIRVKDAVNTVWWFSKTEWPKSDITKVLAPYSDRMKKLIEDPDKFYTPKTRPSGHDIGKSFSKDNGGSIPPNLLQISNSESNGQYLANCKLMGIKAHPARFPAKLPEFFIRMLTEPDDLVVDIFGGSNTTGLVAERESRKWISFEMKPEYVAASAFRFLDNNISEEKITDIYNRILNGESLDLNSI

>d1eg2a\_ c.66.1.11 (A:) m.RsrI N6 adenosine-specific DNA methyltransferase {Rhodobacter sphaeroides}

GTTRHVYDVCDCLDTLAKLPDDSVQLIICDPPYNIMLADWDDHMDYIGWAKRWLAEAERVLSPTGSIAIFGGLQYQGEAGSGDLISIISHMRQNSKMLLANLIIWNYPNGMSAQRFFANRHEEIAWFAKTKKYFFDLDAVREPYDEETKAAYMKDKRLNPESVEKGRNPTNVWRMSRLNGNSLERVGHPTQKPAAVIERLVRALSHPGSTVLDFFAGSGVTARVAIQEGRNSICTDAAPVFKEYYQKQLTFLQDDGLIDKARSYEIVEGAANFGAALQR

>d1ajsa\_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Pig (Sus scrofa), cytosolic form}

APPSVFAEVPQAQPVLVFKLIADFREDPDPRKVNLGVGAYRTDDCQPWVLPVVRKVEQRIANNSSLNHEYLPILGLAEFRTCASRLALGDDSPALQEKRVGGVQSLGGTGALRIGAEFLARWYNGTNNKDTPVYVSSPTWENHNGVFTTAGFKDIRSYRYWDTEKRGLDLQGFLSDLENAPEFSIFVLHACAHNPTGTDPTPEQWKQIASVMKRRFLFPFFDSAYQGFASGNLEKDAWAIRYFVSEGFELFCAQSFSKNFGLYNERVGNLTVVAKEPDSILRVLSQMQKIVRVTWSNPPAQGARIVARTLSDPELFHEWTGNVKTMADRILSMRSELRARLEALKTPGTWNHITDQIGMFSFTGLNPKQVEYLINQKHIYLLPSGRINMCGLTTKNLDYVATSIHEAVTKIQ

>d2ay1a\_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Paracoccus denitrificans}

MLGNLKPQAPDKILALMGEFRADPRQGKIDLGVGVYKDATGHTPIMRAVHAAEQRMLETETTKTYAGLSGEPEFQKAMGELILGDGLKSETTATLATVGGTGALRQALELARMANPDLRVFVSDPTWPNHVSIMNFMGLPVQTYRYFDAETRGVDFEGMKADLAAAKKGDMVLLHGCCHNPTGANLTLDQWAEIASILEKTGALPLIDLAYQGFGDGLEEDAAGTRLIASRIPEVLIAASCSKNFGIYRERTGCLLALCADAATRELAQGAMAFLNRQTYSFPPFHGAKIVSTVLTTPELRADWMAELEAVRSGMLRLREQLAGELRDLSGSDRFGFVAEHRGMFSRLGATPEQVKRIKEEFGIYMVGDSRINIAGLNDNTIPILARAIIEVGV

>d3tata\_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Escherichia coli}

MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYYNEDGIIPQLQAVAEAEARLNAQPHGASLYLPMEGLNCYRHAIAPLLFGADHPVLKQQRVATIQTLGGSGALKVGADFLKRYFPESGVWVSDPTWENHVAIFAGAGFEVSTYPWYDEATNGVRFNDLLATLKTLPARSIVLLHPCCHNPTGADLTNDQWDAVIEILKARELIPFLDIAYQGFGAGMEEDAYAIRAIASAGLPALVSNSFSKIFSLYGERVGGLSVMCEDAEAAGRVLGQLKATVRRNYSSPPNFGAQVVAAVLNDEALKASWLAEVEEMRTRILAMRQELVKVLSTEMPERNFDYLLNQRGMFSYTGLSAAQVDRLREEFGVYLIASGRMCVAGLNTANVQRVAKAFAAVM

>d1gdea\_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Archaeon Pyrococcus horikoshii}

ALSDRLELVSASEIRKLFDIAAGMKDVISLGIGEPDFDTPQHIKEYAKEALDKGLTHYGPNIGLLELREAIAEKLKKQNGIEADPKTEIMVLLGANQAFLMGLSAFLKDGEEVLIPTPAFVSYAPAVILAGGKPVEVPTYEEDEFRLNVDELKKYVTDKTRALIINSPCNPTGAVLTKKDLEEIADFVVEHDLIVISDEVYEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGWRLGFVAAPSWIIERMVKFQMYNATCPVTFIQYAAAKALKDERSWKAVEEMRKEYDRRRKLVWKRLNEMGLPTVKPKGAFYIFPRIRDTGLTSKKFSELMLKEARVAVVPGSAFGKAGEGYVRISYATAYEKLEEAMDRMERVLKERKLV

>d1bw0a\_ c.67.1.1 (A:) Tyrosine aminotransferase (TAT) {Trypanosoma cruzi}

WDVSMSNHAGLVFNPIRTVSDNAKPSPSPKPIIKLSVGDPTLDKNLLTSAAQIKKLKEAIDSQECNGYFPTVGSPEAREAVATWWRNSFVHKEELKSTIVKDNVVLCSGGSHGILMAITAICDAGDYALVPQPGFPHYETVCKAYGIGMHFYNCRPENDWEADLDEIRRLKDDKTKLLIVTNPSNPCGSNFSRKHVEDIVRLAEELRLPLFSDEIYAGMVFKGKDPNATFTSVADFETTVPRVILGGTAKNLVVPGWRLGWLLYVDPHGNGPSFLEGLKRVGMLVCGPCTVVQAALGEALLNTPQEHLDQIVAKIEESAMYLYNHIGECIGLAPTMPRGAMYLMSRIDLEKYRDIKTDVEFFEKLLEEENVQVLPGTIFHAPGFTRLTTTRPVEVYREAVERIKAFCQRHAA

>d1fg7a\_ c.67.1.1 (A:) Histidinol-phosphate aminotransferase {Escherichia coli}

TVTITDLARENVRNLTPYQSARRLGGNGDVWLNANEYPTAVEFQLTQQTLNRYPECQPKAVIENYAQYAGVKPEQVLVSRGADEGIELLIRAFCEPGKDAILYCPPTYGMYSVSAETIGVECRTVPTLDNWQLDLQGISDKLDGVKVVYVCSPNNPTGQLINPQDFRTLLELTRGKAIVVADEAYIEFCPQASLAGWLAEYPHLAILRTLSKAFALAGLRCGFTLANEEVINLLMKVIAPYPLSTPVADIAAQALSPQGIVAMRERVAQIIAEREYLIAALKEIPCVEQVFDSETNYILARFKASSAVFKSLWDQGIILRDQNKQPSLSGCLRITVGTREESQRVIDALRAEQV

>d1kusa\_ c.67.1.1 (A:) L-threonine-O-3-phosphate decarboxylase CobD {Salmonella enterica}

HGGNIREPATVLGISPDQLLDFSANINPLGMPVSVKRALIDNLDCIERYPDADYFHLHQALARHHQVPASWILAGNGETESIFTVASGLKPRRAMIVTPGFAEYGRALAQSGCEIRRWSLREADGWQLTDAILEALTPDLDCLFLCTPNNPTGLLPERPLLQAIADRCKSLNINLILDEAFIDFIPHETGFIPALKDNPHIWVLRSLTKFYAIPGLRLGYLVNSDDAAMARMRRQQMPWSVNALAALAGEVALQDSAWQQATWHWLREEGARFYQALCQLPLLTVYPGRANYLLLRCEREDIDLQRRLLTQRILIRSCANYPGLDSRYYRVAIRSAAQNERLLAALRNVLTGIAP

>d1jg8a\_ c.67.1.1 (A:) Low-specificity threonine aldolase {Thermatoga maritima}

MIDLRSDTVTKPTEEMRKAMAQAEVGDDVYGEDPTINELERLAAETFGKEAALFVPSGTMGNQVSIMAHTQRGDEVILEADSHIFWYEVGAMAVLSGVMPHPVPGKNGAMDPDDVRKAIRPRNIHFPRTSLIAIENTHNRSGGRVVPLENIKEICTIAKEHGINVHIDGARIFNASIASGVPVKEYAGYADSVMFCLSKGLCAPVGSVVVGDRDFIERARKARKMLGGGMRQAGVLAAAGIIALTKMVDRLKEDHENARFLALKLKEIGYSVNPEDVKTNMVILRTDNLKVNAHGFIEALRNSGVLANAVSDTEIRLVTHKDVSRNDIEEALNIFEKLFRKFS

>d1cl1a\_ c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Escherichia coli}

KLDTQLVNAGRSKKYTLGAVNSVIQRASSLVFDSVEAKKHATRNRANGELFYGRRGTLTHFSLQQAMCELEGGAGCVLFPCGAAAVANSILAFIEQGDHVLMTNTAYEPSQDFCSKILSKLGVTTSWFDPLIGADIVKHLQPNTKIVFLESPGSITMEVHDVPAIVAAVRSVVPDAIIMIDNTWAAGVLFKALDFGIDVSIQAATKYLVGHSDAMIGTAVCNARCWEQLRENAYLMGQMVDADTAYITSRGLRTLGVRLRQHHESSLKVAEWLAEHPQVARVNHPALPGSKGHEFWKRDFTGSSGLFSFVLKKKLNNEELANYLDNFSLFSMAYSWGGYESLILANQPEHIAAIRPQGEIDFSGTLIRLHIGLEDVDDLIADLDAGFARIV

>d1ibja\_ c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Thale cress (Arabidopsis thaliana)}

ASVSTLLVNLDNKFDPFDAMSTPLYQTATFKQPSAIENGPYDYTRSGNPTRDALESLLAKLDKADRAFCFTSGMAALSAVTHLIKNGEEIVAGDDVYGGSDRLLSQVVPRSGVVVKRVNTTKLDEVAAAIGPQTKLVWLESPTNPRQQISDIRKISEMAHAQGALVLVDNSIMSPVLSRPLELGADIVMHSATKFIAGHSDVMAGVLAVKGEKLAKEVYFLQNSEGSGLAPFDCWLCLRGIKTMALRIEKQQENARKIAMYLSSHPRVKKVYYAGLPDHPGHHLHFSQAKGAGSVFSFITGSVALSKHLVETTKYFSIAVSFGSVKSLISMPCFMSHASIPAEVREARGLTEDLVRISAGIEDVDDLISDLDIAFKTFPL

>d1cs1a\_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Escherichia coli}

RKQATIAVRSGLNDDEQYGCVVPPIHLSSTYNFTGFNEPRAHDYSRRGNPTRDVVQRALAELEGGAGAVLTNTGMSAIHLVTTVFLKPGDLLVAPHDCYGGSYRLFDSLAKRGCYRVLFVDQGDEQALRAALAEKPKLVLVESPSNPLLRVVDIAKICHLAREVGAVSVVDNTFLSPALQNPLALGADLVLHSCTKYLNGHSDVVAGVVIAKDPDVVTELAWWANNIGVTGGAFDSYLLLRGLRTLVPRMELAQRNAQAIVKYLQTQPLVKKLYHPSLPENQGHEIAARQQKGFGAMLSFELDGDEQTLRRFLGGLSLFTLAESLGGVESLISHAATMTHAGMAPEARAAAGISETLLRISTGIEDGEDLIADLENGFRAANKG

>d1qgna\_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Common tobacco (Nicotiana tabacum)}

MKYASFLNSDGSVAIHAGERLGRGIVTDAITTPVVNTSAYFFNKTSELIDFKEKRRASFEYGRYGNPTTVVLEEKISALEGAESTLLMASGMCASTVMLLALVPAGGHIVTTTDCYRKTRIFIETILPKMGITATVIDPADVGALELALNQKKVNLFFTESPTNPFLRCVDIELVSKLCHEKGALVCIDGTFATPLNQKALALGADLVLHSATKFLGGHNDVLAGCISGPLKLVSEIRNLHHILGGALNPNAAYLIIRGMKTLHLRVQQQNSTALRMAEILEAHPKVRHVYYPGLQSHPEHHIAKKQMTGFGGAVSFEVDGDLLTTAKFVDALKIPYIAPSFGGCESIVDQPAIMSYWDLSQSDRAKYGIMDNLVRFSFGVEDFDDLKADILQALDSI

>d1e5ea\_ c.67.1.3 (A:) Methionine gamma-lyase, MGL {Trichomonas vaginalis}

ERMTPATACIHANPQKDQFGAAIPPIYQTSTFVFDNCQQGGNRFAGQESGYIYTRLGNPTVSNLEGKIAFLEKTEACVATSSGMGAIAATVLTILKAGDHLISDECLYGCTHALFEHALTKFGIQVDFINTAIPGEVKKHMKPNTKIVYFETPANPTLKIIDMERVCKDAHSQEGVLVIADNTFCSPMITNPVDFGVDVVVHSATKYINGHTDVVAGLICGKADLLQQIRMVGIKDITGSVISPHDAWLITRGLSTLNIRMKAESENAMKVAEYLKSHPAVEKVYYPGFEDHEGHDIAKKQMRMYGSMITFILKSGFEGAKKLLDNLKLITLAVSLGGCESLIQHPASMTHAVVPKEEREAAGITDGMIRLSVGIEDADELIADFKQGLDALLR

>d1d2fa\_ c.67.1.3 (A:) Modulator in mal gene expression, MalY {Escherichia coli}

LLPFTISDMDFATAPCIIEALNQRLMHGVFGYSRWKNDEFLAAIAHWFSTQHYTAIDSQTVVYGPSVIYMVSELIRQWSETGEGVVIHTPAYDAFYKAIEGNQRTVMPVALEKQADGWFCDMGKLEAVLAKPECKIMLLCSPQNPTGKVWTCDELEIMADLCERHGVRVISDEIHMDMVWGEQPHIPWSNVARGDWALLTSGSKSFNIPALTGAYGIIENSSSRDAYLSALKGRDGLSSPSVLALTAHIAAYQQGAPWLDALRIYLKDNLTYIADKMNAAFPELNWQIPQSTYLAWLDLRPLNIDDNALQKALIEQEKVAIMPGYTYGEEGRGFVRLNAGCPRSKLEKGVAGLINAIRAVR

>d1c7na\_ c.67.1.3 (A:) Cystalysin {Treponema denticola}

MIYDFTTKISRKNLGSLKWDLMYSQNPEVGNEVVPLSVADMEFKNPPELIEGLKKYLDETVLGYTGPTEEYKKTVKKWMKDRHQWDIQTDWIINTAGVVPAVFNAVREFTKPGDGVIIITPVYYPFFMAIKNQERKIIECELLEKDGYYTIDFQKLEKLSKDKNNKALLFCSPHNPVGRVWKKDELQKIKDIVLKSDLMLWSDEIHFDLIMPGYEHTVFQSIDEQLADKTITFTAPSKTFNIAGMGMSNIIIKNPDIRERFTKSRDATSGMPFTTLGYKACEICYKECGKWLDGCIKVIDKNQRIVKDFFEVNHPEIKAPLIEGTYLQWIDFRALKMDHKAMEEFMIHKAQIFFDEGYIFGDGGIGFERINLAAPSSVIQESLERLNKALKDLK

>d1eg5a\_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Thermotoga maritima}

MRVYFDNNATTRVDDRVLEEMIVFYREKYGNPNSAHGMGIEANLHMEKAREKVAKVLGVSPSEIFFTSCATESINWILKTVAETFEKRKRTIITTPIEHKAVLETMKYLSMKGFKVKYVPVDSRGVVKLEELEKLVDEDTFLVSIMAANNEVGTIQPVEDVTRIVKKKNKETLVHVDAVQTIGKIPFSLEKLEVDYASFSAHKFHGPKGVGITYIRKGVPIRPLIHGGGQERGLRSGTQNVPGIVGAARAMEIAVEELSEAAKHMEKLRSKLVSGLMNLGAHIITPLEISLPNTLSVSFPNIRGSTLQNLLSGYGIYVSTSSACTSKDERLRHVLDAMGVDRRIAQGAIRISLCKYNTEEEVDYFLKKIEEILSFL

>d1jf9a\_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Escherichia coli}

IFSVDKVRADFPVLSREVNGLPLAYLDSAASAQKPSQVIDAEAEFYRHGYAAVHRGIHTLSAQATEKMENVRKRASLFINARSAEELVFVRGTTEGINLVANSWGNSNVRAGDNIIISQMEHHANIVPWQMLCARVGAELRVIPLNPDGTLQLETLPTLFDEKTRLLAITHVSNVLGTENPLAEMITLAHQHGAKVLVDGAQAVMHHPVDVQALDCDFYVFSGHKLYGPTGIGILYVKEALLQEMPPWEGGGSMIATVSLSEGTTWTKAPWRFEAGTPNTGGIIGLGAALEYVSALGLNNIAEYEQNLMHYALSQLESVPDLTLYGPQNRLGVIAFNLGKHHAYDVGSFLDNYGIAVRTGHHCAMPLMAYYNVPAMCRASLAMYNTHEEVDRLVTGLQRIHRLLG

>d1elua\_ c.67.1.3 (A:) Cystine C-S lyase {Synechocystis sp.}

QFPGLANKTYFNFGGQGILPTVALEAITAMYGYLQENGPFSIAANQHIQQLIAQLRQALAETFNVDPNTITITDNVTTGCDIVLWGLDWHQGDEILLTDCEHPGIIAIVQAIAARFGITYRFFPVAATLNQGDAAAVLANHLGPKTRLVILSHLLWNTGQVLPLAEIMAVCRRHQGNYPVRVLVDGAQSAGSLPLDFSRLEVDYYAFTGHKWFAGPAGVGGLYIHGDCLGEINPTYVGWRSITYGAKGEPTGWAEGGKRFEVATSAYPQYAGLLAALQLHQRQGTAEERYQAICQRSEFLWRGLNQLPHVHCLATSAPQAGLVSFTVDSPLGHRAIVQKLEEQRIYLRTIADPDCIRACCHYITDEEEINHLLARLADFGP

>d2dkb\_\_ c.67.1.4 (-) Dialkylglycine decarboxylase {Pseudomonas cepacia}

LNDDATFWRNARHHLVRYGGTFEPMIIERAKGSFVYDADGRAILDFTSGQMSAVLGHCHPEIVSVIGEYAGKLDHLFSEMLSRPVVDLATRLANITPPGLDRALLLSTGAESNEAAIRMAKLVTGKYEIVGFAQSWHGMTGAAASATYSAGRKGVGPAAVGSFAIPAPFTYRPRFERNGAYDYLAELDYAFDLIDRQSSGNLAAFIAEPILSSGGIIELPDGYMAALKRKCEARGMLLILDEAQTGVGRTGTMFACQRDGVTPDILTLSKTLGAGLPLAAIVTSAAIEERAHELGYLFYTTHVSDPLPAAVGLRVLDVVQRDGLVARANVMGDRLRRGLLDLMERFDCIGDVRGRGLLLGVEIVKDRRTKEPADGLGAKITRECMNLGLSMNIVQLPGMGGVFRIAPPLTVSEDEIDLGLSLLGQAIERAL

>d2gsaa\_ c.67.1.4 (A:) Glutamate-1-semialdehyde aminomutase (aminotransferase) {Synechococcus sp., strain GR6}

FKTIKSDEIFAAAQKLMPGGVSSPVRAFKSVGGQPIVFDRVKDAYAWDVDGNRYIDYVGTWGPAICGHAHPEVIEALKVAMEKGTSFGAPCALENVLAEMVNDAVPSIEMVRFVNSGTEACMAVLRLMRAYTGRDKIIKFEGCYHGHADMFLVKAGSGVATLGLPSSPGVPKKTTANTLTTPYNDLEAVKALFAENPGEIAGVILEPIVGNSGFIVPDAGFLEGLREITLEHDALLVFDEVMTGFRIAYGGVQEKFGVTPDLTTLGKIIGGGLPVGAYGGKREIMQLVAPAGPMYQAGTLSGNPLAMTAGIKTLELLRQPGTYEYLDQITKRLSDGLLAIAQETGHAACGGQVSGMFGFFFTEGPVHNYEDAKKSDLQKFSRFHRGMLEQGIYLAPSQFEAGFTSLAHTEEDIDATLAAARTVMSAL

>d2oata\_ c.67.1.4 (A:) Ornithine aminotransferase {Human (Homo sapiens)}

GPPTSDDIFEREYKYGAHNYHPLPVALERGKGIYLWDVEGRKYFDFLSSYSAVNQGHCHPKIVNALKSQVDKLTLTSRAFYNNVLGEYEEYITKLFNYHKVLPMNTGVEAGETACKLARKWGYTVKGIQKYKAKIVFAAGNFWGRTLSAISSSTDPTSYDGFGPFMPGFDIIPYNDLPALERALQDPNVAAFMVEPIQGEAGVVVPDPGYLMGVRELCTRHQVLFIADEIQTGLARTGRWLAVDYENVRPDIVLLGKALSGGLYPVSAVLCDDDIMLTIKPGEHGSTYGGNPLGCRVAIAALEVLEEENLAENADKLGIILRNELMKLPSDVVTAVRGKGLLNAIVIKETKDWDAWKVCLRLRDNGLLAKPTHGDIIRFAPPLVIKEDELRESIEIINKTILSF

>d1gtxa\_ c.67.1.4 (A:) 4-aminobutyrate aminotransferase, GABA-aminotransferase {Pig (Sus scrofa)}

FDYDGPLMKTEVPGPRSRELMKQLNIIQNAEAVHFFCNYEESRGNYLVDVDGNRMLDLYSQISSIPIGYSHPALVKLVQQPQNVSTFINRPALGILPPENFVEKLRESLLSVAPKGMSQLITMACGSCSNENAFKTIFMWYRSKERGQSAFSKEELETCMINQAPGCPDYSILSFMGAFHGRTMGCLATTHSKAIHKIDIPSFDWPIAPFPRLKYPLEEFVKENQQEEARCLEEVEDLIVKYRKKKKTVAGIIVEPIQSEGGDNHASDDFFRKLRDISRKHGCAFLVDEVQTGGGSTGKFWAHEHWGLDDAADVMTFSKKMMTGGFFHKEEFRPNAPYRIFNTWLGDPSKNLLLAEVINIIKREDLLSNAAHAGKVLLTGLLDLQARYPQFISRVRGRGTFCSFDTPDESIRNKLISIARNKGVMLGGCGDKSIRFRPTLVFRDHHAHLFLNIFSDILADFK

>d1bt4a\_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Bacillus circulans, subsp. alkalophilus}

SERAYNFNAGPAALPLEVLERAQAEFVDYQHTGMSIMEMSHRGAVYEAVHNEAQARLLALLGNPTGYKVLFIQGGASTQFAMIPMNFLKEGQTANYVMTGSWASKALKEAKLIGDTHVAASSEASNYMTLPKLQEIQLQDNAAYLHLTSNETIEGAQFKAFPDTGSVPLIGDMSSDILSRPFDLNQFGLVYAGAQKNLGPSGVTVVIVREDLVAESPKHLPTMLRYDTYVKNNSLYNTPPSFGIYMVNEVLKWIEERGGLEGVQQANRKKASLIYDAIDQSGGFYRGCVDVDSRSDMNITFRLASEELEKEFVKASEQEGFVGLKGHRSVGGLRASIYNAVPYESCEALVQFMEHFKRSRG

>d1ejia\_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Mouse (Mus musculus)}

MADRDATLWASHEKMLSQPLKDSDAEVYSIIKKESNRQRVGLELIASENFASRAVLEALGSSLNNKYSEGYPGQRYYGGTEFIDELEMLCQKRALQAYHLDPQCWGVNVQPYSGSPANFAVYTALVEPHGRIMGLDLPDGGHLTHGFMTDKKKISATSIFFESMPYKVYPETGYINYDQLEENASLFHPKLIIAGTSCYSRNLDYARLRKIADDNGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTTTHKTLRGCRAGMIFYRKGVRSVDPKTGKETYYELESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTTEFKIYQLQVLANCRALSDALTELGYKIVTGGSDNHLILMDLRSKGTDGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLGTPALTSRGLLEEDFQKVAHFIHRGIELTLQIQSHMATKATLKEFKEKLAGDEKIQSAVATLREEVENFASNFSLPGLPDF

>d1b9ha\_ c.67.1.4 (A:) 3-amino-5-hydroxybenzoic acid synthase (AHBA synthase) {Amycolatopsis mediterranei}

KAPEFPAWPQYDDAERNGLVRALEQGQWWRMGGDEVNSFEREFAAHHGAAHALAVTNGTHALELALQVMGVGPGTEVIVPAFTFISSSQAAQRLGAVTVPVDVDAATYNLDPEAVAAAVTPRTKVIMPVHMAGLMADMDALAKISADTGVPLLQDAAHAHGARWQGKRVGELDSIATFSFQNGKLMTAGEGGAVVFPDGETEKYETAFLRHSCGRPRDDRRYFHKIAGSNMRLNEFSASVLRAQLARLDEQIAVRDERWTLLSRLLGAIDGVVPQGGDVRADRNSHYMAMFRIPGLTEERRNALVDRLVEAGLPAFAAFRAIYRTDAFWELGAPDESVDAIARRCPNTDAISSDCVWLHHRVLLAGEPELHATAEIIADAVARA

>d1fc4a\_ c.67.1.4 (A:) 2-amino-3-ketobutyrate CoA ligase {Escherichia coli}

GSHMRGEFYQQLTNDLETARAEGLFKEERIITSAQQADITVADGSHVINFCANNYLGLANHPDLIAAAKAGMDSHGFGMASVRFICGTQDSHKELEQKLAAFLGMEDAILYSSCFDANGGLFETLLGAEDAIISDALNHASIIDGVRLCKAKRYRYANNDMQELEARLKEAREAGARHVLIATDGVFSMDGVIANLKGVCDLADKYDALVMVDDSHAVGFVGENGRGSHEYCDVMGRVDIITGTLGKALGGASGGYTAARKEVVEWLRQRSRPYLFSNSLAPAIVAASIKVLEMVEAGSELRDRLWANARQFREQMSAAGFTLAGADHAIIPVMLGDAVVAQKFARELQKEGIYVTGFFYPVVPKGQARIRTQMSAAHTPEQITRAVEAFTRIGKQLGVIA

>d1bs0a\_ c.67.1.4 (A:) PLP-dependent acyl-CoA synthase (8-amino-7-oxonanoate synthase, AONS) {Escherichia coli}

SWQEKINAALDARRAADALRRRYPVAQGAGRWLVADDRQYLNFSSNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVSGYSVVHQALEEELAEWLGYSRALLFISGFAANQAVIAAMMAKEDRIAADRLSHASLLEAASLSPSQLRRFAHNDVTHLARLLASPCPGQQMVVTEGVFSMDGDSAPLAEIQQVTQQHNGWLMVDDAHGTGVIGEQGRGSCWLQKVKPELLVVTFGKGFGVSGAAVLCSSTVADYLLQFARHLIYSTSMPPAQAQALRASLAVIRSDEGDARREKLAALITRFRAGVQDLPFTLADSCSAIQPLIVGDNSRALQLAEKLRQQGCWVTAIRPPTVPAGTARLRLTLTAAHEMQDIDRLLEVLHGNG

>d1qj5a\_ c.67.1.4 (A:) Adenosylmethionine-8-amino-7-oxononanoate aminotransferase, BioA {Escherichia coli}

MTTDDLAFDQRHILHPYTSMTSPLPVYPVVSAEGCELILSDGRRLVDGMSSWWAAIHGYNHPQLNAAMKSQIDAMSHVMFGGITHAPAIELCRKLVAMTPQPLECVFLADSGSVAVEVAMKMALQYWQAKGEARQRFLTFRNGYHGDTFGAMSVCDPDNSMHSLWKGYLPENLFAPAPQSRMDGEWDERDMVGFARLMAAHRHEIAAVIIEPIVQGAGGMRMYHPEWLKRIRKICDREGILLIADEIATGFGRTGKLFACEHAEIAPDILCLGKALTGGTMTLSATLTTREVAETISNGEAGCFMHGPTFMGNPLACAAANASLAILESGDWQQQVADIEVQLREQLAPARDAEMVADVRVLGAIGVVETTHPVNMAALQKFFVEQGVWIRPFGKLIYLMPPYIILPQQLQRLTAAVNRAVQDETFFCQ

>d1b8ga\_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Apple (Malus domestica)}

MLSRNATFNSHGQDSSYFLGWQEYEKNPYHEVHNTNGIIQMGLAENQLCFDLLESWLAKNPEAAAFKKNGESIFAELALFQDYHGLPAFKKAMVDFMAEIRGNKVTFDPNHLVLTAGATSANETFIFCLADPGEAVLIPTPYYPGFDRDLKWRTGVEIVPIHCTSSNGFQITETALEEAYQEAEKRNLRVKGVLVTNPSNPLGTTMTRNELYLLLSFVEDKGIHLISDEIYSGTAFSSPSFISVMEVLKDRNCDENSEVWQRVHVVYSLSKDLGLPGFRVGAIYSNDDMVVAAATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRLKQRQKKLVSGLQKSGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNISPGSSCHCTEPGWFRVCFANLPERTLDLAMQRLKAFVG

>d1i52a\_ c.68.1.13 (A:) 4-diphosphocytidyl-2-c-methylerythritol (CDP-me) synthase (YgbP) {Escherichia coli}

HLDVCAVVPAAGFGRRMQTECPKQYLSIGNQTILEHSVHALLAHPRVKRVVIAISPGDSRFAQLPLANHPQITVVDGGDERADSVLAGLKAAGDAQWVLVHDAARPCLHQDDLARLLALSETSRTGGILAAPVRDTMKRAEPGKNAIAHTVDRNGLWHALTPQFFPRELLHDCLTRALNEGATITDEASALEYCGFHPQLVEGRADNIKVTRPEDLALAEFYLTR

>d1h7ea\_ c.68.1.13 (A:) CMP:2-keto-3-deoxy-manno-octonic acid (CMP-KDO)synthetase, KdsB {Escherichia coli}

SKAVIVIPARYGSSRLPGKPLLDIVGKPMIQHVYERALQVAGVAEVWVATDDPRVEQAVQAFGGKAIMTRNDHESGTDRLVEVMHKVEADIYINLQGDEPMIRPRDVETLLQGMRDDPALPVATLCHAISAAEAAEPSTVKVVVNTRQDALYFSRSPIPYPRNAEKARYLKHVGIYAYRRDVLQNYSQLPESMPEQAESLEQLRLMNAGINIRTFEVAATGPGVDTPACLEKVRALMAQELAENA

>d1jyka\_ c.68.1.13 (A:) CTP:phosphocholine cytidylytransferase LicC {Streptococcus pneumoniae}

EIRVKAIILAAGLGTRLRPLTENTPKALVQVNQKPLIEYQIEFLKEKGINDIIIIVGYLKEQFDYLKEKYGVRLVFNDKYADYNNFYSLYLVKEELANSYVIDADNYLFKNMFRNDLTRSTYFSVYREDCTNEWFLVYGDDYKVQDIIVDSKAGRILSGVSFWDAPTAEKIVSFIDKAYVSGEFVDLYWDNMVKDNIKELDVYVEELEGNSIYEIDSVQDYRKLEEILK

>d1maaa\_ c.69.1.1 (A:) Acetylcholinesterase {Mouse (Mus musculus)}

EDPQLLVRVRGGQLRGIRLKAPGGPVSAFLGIPFAEPPVGSRRFMPPEPKRPWSGVLDATTFQNVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRPASPTPVLIWIYGGGFYSGAASLDVYDGRFLAQVEGAVLVSMNYRVGTFGFLALPGSREAPGNVGLLDQRLALQWVQENIAAFGGDPMSVTLFGESAGAASVGMHILSLPSRSLFHRAVLQSGTPNGPWATVSAGEARRRATLLARLVGCPPGGAGGNDTELIACLRTRPAQDLVDHEWHVLPQESIFRFSFVPVVDGDFLSDTPEALINTGDFQDLQVLVGVVKDEGSYFLVYGVPGFSKDNESLISRAQFLAGVRIGVPQASDLAAEAVVLHYTDWLHPEDPTHLRDAMSAVVGDHNVVCPVAQLAGRLAAQGARVYAYIFEHRASTLTWPLWMGVPHGYEIEFIFGLPLDPSLNYTTEERIFAQRLMKYWTNFARTGDPNDPRDRKSPQWPPYTTAAQQYVSLNLKPLEVRRGLRAQTCAFWNRFLPKLLSAT

>d1dx4a\_ c.69.1.1 (A:) Acetylcholinesterase {Fruit fly (Drosophila melanogaster)}

DRLVVQTSSGPVRGRSVTVQGREVHVYTGIPYAKPPVEDLRFRKPVPAEPWHGVLDATGLSATCVQERYEYFPGFSGEEIWNPNTNVSEDCLYINVWAPAKARLRHGRGANGGEHPNGKQADTDHLIHNGNPQNTTNGLPILIWIYGGGFMTGSATLDIYNADIMAAVGNVIVASFQYRVGAFGFLHLAPEMPSEFAEEAPGNVGLWDQALAIRWLKDNAHAFGGNPEWMTLFGESAGSSSVNAQLMSPVTRGLVKRGMMQSGTMNAPWSHMTSEKAVEIGKALINDCNCNASMLKTNPAHVMSCMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAFLPADPMTLMKTADLKDYDILMGNVRDEGTYFLLYDFIDYFDKDDATALPRDKYLEIMNNIFGKATQAEREAIIFQYTSWEGNPGYQNQQQIGRAVGDHFFTCPTNEYAQALAERGASVHYYYFTHRTSTSLWGEWMGVLHGDEIEYFFGQPLNNSLQYRPVERELGKRMLSAVIEFAKTGNPAQDGEEWPNFSKEDPVYYIFSTDDKIEKLARGPLAARCSFWNDYLPKVRSW

>d2bce\_\_ c.69.1.1 (-) Bile-salt activated lipase (cholesterol esterase) {Cow (Bos taurus)}

AKLGSVYTEGGFVEGVNKKLSLFGDSVDIFKGIPFAAAPKALEKPERHPGWQGTLKAKSFKKRCLQATLTQDSTYGNEDCLYLNIWVPQGRKEVSHDLPVMIWIYGGAFLMGASQGANFLSNYLYDGEEIATRGNVIVVTFNYRVGPLGFLSTGDSNLPGNYGLWDQHMAIAWVKRNIEAFGGDPDNITLFGESAGGASVSLQTLSPYNKGLIKRAISQSGVGLCPWAIQQDPLFWAKRIAEKVGCPVDDTSKMAGCLKITDPRALTLAYKLPLGSTEYPKLHYLSFVPVIDGDFIPDDPVNLYANAADVDYIAGTNDMDGHLFVGMDVPAINSNKQDVTEEDFYKLVSGLTVTKGLRGANATYEVYTEPWAQDSSQETRKKTMVDLETDILFLIPTKIAVAQHKSHAKSANTYTYLFSQPSRMPIYPKWMGADHADDLQYVFGKPFATPLGYRAQDRTVSKAMIAYWTNFARTGDPNTGHSTVPANWDPYTLEDDNYLEINKQMDSNSMKLHLRTNYLQFWTQTYQALPTVTSAGASLLPPEDNSQASPVPPADNSGAPTEPSAGDSEVAQMPVVIGF

>d1qe3a\_ c.69.1.1 (A:) Thermophylic para-nitrobenzyl esterase (PNB esterase) {Bacillus subtilis}

THQIVTTQYGKVKGTTENGVHKWKGIPYAKPPVGQWRFKAPEPPEVWEDVLDATAYGPICPQPSDLLSLSYTELPRQSEDCLYVNVFAPDTPSQNLPVMVWIHGGAFYLGAGSEPLYDGSKLAAQGEVIVVTLNYRLGPFGFLHLSSFDEAYSDNLGLLDQAAALKWVRENISAFGGDPDNVTVFGESAGGMSIAALLAMPAAKGLFQKAIMESGASRTMTKEQAASTAAAFLQVLGINESQLDRLHTVAAEDLLKAADQLRIAEKENIFQLFFQPALDPKTLPEEPEKSIAEGAASGIPLLIGTTRDEGYLFFTPDSDVHSQETLDAALEYLLGKPLAEKAADLYPRSLESQIHMMTDLLFWRPAVAYASAQSHYAPVWMYRFDWHPEKPPYNKAFHALELPFVFGNLDGLERMAKAEITDEVKQLSHTIQSAWITFAKTGNPSTEAVNWPAYHEETRETVILDSEITIENDPESEKRQKLF

>d1jkma\_ c.69.1.2 (A:) Carboxylesterase {Bacillus subtilis, brefeldin A esterase}

PGRLGDESSGPRTDPRFSPAMVEALATFGLDAVAAAPPVSASDDLPTVLAAVGASHDGFQAVYDSIALDLPTDRDDVETSTETILGVDGNEITLHVFRPAGVEGVLPGLVYTHGGGMTILTTDNRVHRRWCTDLAAAGSVVVMVDFRNAWTAEGHHPFPSGVEDCLAAVLWVDEHRESLGLSGVVVQGESGGGNLAIATTLLAKRRGRLDAIDGVYASIPYISGGYAWDHERRLTELPSLVENDGYFIENGGMALLVRAYDPTGEHAEDPIAWPYFASEDELRGLPPFVVAVNELDPLRDEGIAFARRLARAGVDVAARVNIGLVHGADVIFRHWLPAALESTVRDVAGFAADRARLR

>d1jjia\_ c.69.1.2 (A:) Carboxylesterase {Archaeon Archaeoglobus fulgidus}

MLDMPIDPVYYQLAEYFDSLPKFDQFSSAREYREAINRIYEERNRQLSQHERVERVEDRTIKGRNGDIRVRVYQQKPDSPVLVYYHGGGFVICSIESHDALCRRIARLSNSTVVSVDYRLAPEHKFPAAVYDCYDATKWVAENAEELRIDPSKIFVGGDSAGGNLAAAVSIMARDSGEDFIKHQILIYPVVNFVAPTPSLLEFGEGLWILDQKIMSWFSEQYFSREEDKFNPLASVIFADLENLPPALIITAEYDPLRDEGEVFGQMLRRAGVEASIVRYRGVLHGFINYYPVLKAARDAINQIAALLVFD

>d1jjfa\_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase z {Clostridium thermocellum}

SLPTMPPSGYDQVRNGVPRGQVVNISYFSTATNSTRPARVYLPPGYSKDKKYSVLYLLHGIGGSENDWFEGGGRANVIADNLIAEGKIKPLIIVTPNTNAAGPGIADGYENFTKDLLNSLIPYIESNYSVYTDREHRAIAGLSMGGGQSFNIGLTNLDKFAYIGPISAAPNTYPNERLFPDGGKAAREKLKLLFIACGTNDSLIGFGQRVHEYCVANNINHVYWLIQGGGHDFNVWKPGLWNFLQMADEAGLTRD

>d1gkla\_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase y {Clostridium thermocellum}

SFKYESAVQYRPAPDSYLNPCPQAGRIVKETYTGINGTKSLNVYLPYGYDPNKKYNIFYLMHGGGENENTIFSNDVKLQNILDHAIMNGELEPLIVVTPTFNGGNCTAQNFYQEFRQNVIPFVESKYSTYAESTTPQGIAASRMHRGFGGFAMGGLTTWYVMVNCLDYVAYFMPLSGDYWYGNSPQDKANSIAEAINRSGLSKREYFVFAATGSEDIAYANMNPQIEAMKALPHFDYTSDFSKGNFYFLVAPGATHWWGYVRHYIYDALPYFFHELEHHHHHH

>g1wht.1 c.69.1.5 (A:,B:) Serine carboxypeptidase II {Wheat (Triticum vulgaris)}

GHAADRIARLPGQPAVDFDMYSGYITVDEGAGRSLFYLLQEAPEDAQPAPLVLWLNGGPGCSSVAYGASEELGAFRVKPRGAGLVLNEYRWNKVANVLFLDSPAGVGFSYTNTSSDIYTSGDNRTAHDSYAFLAKWFERFPHYKYRDFYIAGESYAGHYVPELSQLVHRSKNPVINLKGFMVGNGLIDDYHDYVGTFEFWWNHGIVSDDTYRRLKEACLHDSFIHPSPACDAATDVATAEQGNIDMYSLYTPVCNIXSYDPCTERYSTAYYNRRDVQMALHANVTGAMNYTWATCSDTINTHWHDAPRSMLPIYRELIAAGLRIWVFSGDTDAVVPLTATRYSIGALGLPTTTSWYPWYDDQEVGGWSQVYKGLTLVSVRGAGHEVPLHRPRQALVLFQYFLQGKPMPGQ

>d1cpy\_\_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (Saccharomyces cerevisiae)}

KIKDPKILGIDPNVTQYTGYLDVEDEDKHFFFWTFESRNDPAKDPVILWLNGGPGCSSLTGLFFALGPSSIGPDLKPIGNPYSWNSNATVIFLDQPVNVGFSYSGSSGVSNTVAAGKDVYNFLELFFDQFPEYVNKGQDFHIAGASYAGHYIPVFASEILSHKDRNFNLTSVLIGNGLTDPLTQYNYYEPMACGEGGEPSVLPSEECSAMEDSLERCLGLIESCYDSQSVWSCVPATIYCNNAQLAPYQRTGRNVYDIRKDCEGGNLCYPTLQDIDDYLNQDYVKEAVGAEVDHYESCNFDINRNFLFAGDWMKPYHTAVTDLLNQDLPILVYAGDKDFICNWLGNKAWTDVLPWKYDEEFASQKVRNWTASITDEVAGEVKSYKHFTYLRVFNGGHMVPFDVPENALSMVNEWIHGGFSL

>d1ac5\_\_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (Saccharomyces cerevisiae), kex1(delta)p}

LPSSEEYKVAYELLPGLSEVPDPSNIPQMHAGHIPLRSEDADEQDSSDLEYFFWKFTNNDSNGNVDRPLIIWLNGGPGCSSMDGALVESGPFRVNSDGKLYLNEGSWISKGDLLFIDQPTGTGFSVEQNKDEGKIDKNKFDEDLEDVTKHFMDFLENYFKIFPEDLTRKIILSGESYAGQYIPFFANAILNHNKFSKIDGDTYDLKALLIGNGWIDPNTQSLSYLPFAMEKKLIDESNPNFKHLTNAHENCQNLINSASTDEAAHFSYQECENILNLLLSYTRESSQKGTADCLNMYNFNLKDSYPSCGMNWPKDISFVSKFFSTPGVIDSLHLDSDKIDHWKECTNSVGTKLSNPISKPSIHLLPGLLESGIEIVLFNGDKDLICNNKGVLDTIDNLKWGGIKGFSDDAVSFDWIHKSKSTDDSEEFSGYVKYDRNLTFVSVYNASHMVPFDKSLVSRGIVDIYSNDVMIIDNNGKNVMITT

>d1ivya\_ c.69.1.5 (A:) Human 'protective protein', HPP {Human (Homo sapiens)}

APDQDEIQRLPGLAKQPSFRQYSGYLKSSGSKHLHYWFVESQKDPENSPVVLWLNGGPGCSSLDGLLTEHGPFLVQPDGVTLEYNPYSWNLIANVLYLESPAGVGFSYSDDKFYATNDTEVAQSNFEALQDFFRLFPEYKNNKLFLTGESYAGIYIPTLAVLVMQDPSMNLQGLAVGNGLSSYEQNDNSLVYFAYYHGLLGNRLWSSLQTHCCSQNKCNFYDNKDLECVTNLQEVARIVGNSGLNIYNLYAPCAGGVPSHFRYEKDTVVVQDLGNIFTRLPLKRMWHQALLRSGDKVRMDPPCTNTTAASTYLNNPYVRKALNIPEQLPQWDMCNFLVNLQYRRLYRSMNSQYLKLLSSQKYQILLYNGDVDMACNFMGDEWFVDSLNQKMEVQRRPWLVKYGDSGEQIAGFVKEFSHIAFLTIKGAGHMVPTDKPLAAFTMFSRFLNKQPY

>d1b6g\_\_ c.69.1.8 (-) Haloalkane dehalogenase {Xanthobacter autotrophicus}

MVNAIRTPDQRFSNLDQYPFSPNYLDDLPGYPGLRAHYLDEGNSDAEDVFLCLHGEPTWSYLYRKMIPVFAESGARVIAPDFFGFGKSDKPVDEEDYTFEFHRNFLLALIERLDLRNITLVVQDWGGFLGLTLPMADPSRFKRLIIMNACLMTDPVTQPAFSAFVTQPADGFTAWKYDLVTPSDLRLDQFMKRWAPTLTEAEASAYAAPFPDTSYQAGVRKFPKMVAQRDQACIDISTEAISFWQNDWNGQTFMAIGMKDKLLGPDVMYPMKALINGCPEPLEIADAGHFVQEFGEQVAREALKHFAETE

>d1cv2a\_ c.69.1.8 (A:) Haloalkane dehalogenase {Sphingomonas paucimobilis, UT26, LinB}

GAKPFGEKKFIEIKGRRMAYIDEGTGDPILFQHGNPTSSYLWRNIMPHCAGLGRLIACDLIGMGDSDKLDPSGPERYAYAEHRDYLDALWEALDLGDRVVLVVHDWGSALGFDWARRHRERVQGIAYMEAIAMPIEWADFPEQDRDLFQAFRSQAGEELVLQDNVFVEQVLPGLILRPLSEAEMAAYREPFLAAGEARRPTLSWPRQIPIAGTPADVVAIARDYAGWLSESPIPKLFINAEPGALTTGRMRDFCRTWPNQTEITVAGAHFIQEDSPDEIGAAIAAFVRRLRPA

>d1ek1a2 c.69.1.11 (A:226-544) Mammalian epoxide hydrolase, C-terminal domain {Mouse (Mus musculus)}

LPVPCNPNDVSHGYVTVKPGIRLHFVEMGSGPALCLCHGFPESWFSWRYQIPALAQAGFRVLAIDMKGYGDSSSPPEIEEYAMELLCKEMVTFLDKLGIPQAVFIGHDWAGVMVWNMALFYPERVRAVASLNTPFMPPDPDVSPMKVIRSIPVFNYQLYFQEPGVAEAELEKNMSRTFKSFFRASDETGFIAVHKATEIGGILVNTPEDPNLSKITTEEEIEFYIQQFKKTGFRGPLNWYRNTERNWKWSCKGLGRKILVPALMVTAEKDIVLRPEMSKNMEKWIPFLKRGHIEDCGHWTQIEKPTEVNQILIKWLQTE

>d1ehya\_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Agrobacterium radiobacter}

AIRRPEDFKHYEVQLPDVKIHYVREGAGPTLLLLHGWPGFWWEWSKVIGPLAEHYDVIVPDLRGFGDSEKPDLNDLSKYSLDKAADDQAALLDALGIEKAYVVGHDFAAIVLHKFIRKYSDRVIKAAIFDPIQPDFGPVYFGLGHVHESWYSQFHQLDMAVEVVGSSREVCKKYFKHFFDHWSYRDELLTEEELEVHVDNCMKPDNIHGGFNYYRANIRPDAALWTDLDHTMSDLPVTMIWGLGDTCVPYAPLIEFVPKYYSNYTMETIEDCGHFLMVEKPEIAIDRIKTAFR

>d1qo7a\_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Aspergillus niger}

KAFAKFPSSASISPNPFTVSIPDEQLDDLKTLVRLSKIAPPTYESLQADGRFGITSEWLTTMREKWLSEFDWRPFEARLNSFPQFTTEIEGLTIHFAALFSEREDAVPIALLHGWPGSFVEFYPILQLFREEYTPETLPFHLVVPSLPGYTFSSGPPLDKDFGLMDNARVVDQLMKDLGFGSGYIIQGGDIGSFVGRLLGVGFDACKAVHLNLCAMRAPPEGPSIESLSAAEKEGIARMEKFMTDGLAYAMEHSTRPSTIGHVLSSSPIALLAWIGEKYLQWVDKPLPSETILEMVSLYWLTESFPRAIHTYRETTPTASAPNGATMLQKELYIHKPFGFSFFPKDLCPVPRSWIATTGNLVFFRDHAEGGHFAALERPRELKTDLTAFVEQVW

>d1brt\_\_ c.69.1.12 (-) Bromoperoxidase A2 {Streptomyces aureofaciens}

PFITVGQENSTSIDLYYEDHGTGQPVVLIHGFPLSGHSWERQSAALLDAGYRVITYDRRGFGQSSQPTTGYDYDTFAADLNTVLETLDLQDAVLVGFSTGTGEVARYVSSYGTARIAKVAFLASLEPFLLKTDDNPDGAAPQEFFDGIVAAVKADRYAFYTGFFNDFYNLDENLGTRISEEAVRNSWNTAASGGFFAAAAAPTTWYTDFRADIPRIDVPALILHGTGDRTLPIENTARVFHKALPSAEYVEVEGAPHGLLWTHAEEVNTALLAFLAK

>d1a8q\_\_ c.69.1.12 (-) Bromoperoxidase A1 {Streptomyces aureofaciens}

PICTTRDGVEIFYKDWGQGRPVVFIHGWPLNGDAWQDQLKAVVDAGYRGIAHDRRGHGHSTPVWDGYDFDTFADDLNDLLTDLDLRDVTLVAHSMGGGELARYVGRHGTGRLRSAVLLSAIPPVMIKSDKNPDGVPDEVFDALKNGVLTERSQFWKDTAEGFFSANRPGNKVTQGNKDAFWYMAMAQTIEGGVRCVDAFGYTDFTEDLKKFDIPTLVVHGDDDQVVPIDATGRKSAQIIPNAELKVYEGSSHGIAMVPGDKEKFNRDLLEFLNK

>d1thta\_ c.69.1.13 (A:) Myristoyl-ACP-specific thioesterase {Vibrio harveyi}

QCKTIAHVLRVNNGQELHVWETPPKENVPFKNNTILIASGFARRMDHFAGLAEYLSTNGFHVFRYDSLHHVGLSSGSIDEFTMTTGKNSLCTVYHWLQTKGTQNIGLIAASLSARVAYEVISDLELSFLITAVGVVNLRDTLEKALGFDYLSLPIDELPNDLDFEGHKLGSEVFVRDCFEHHWDTLDSTLDKVANTSVPLIAFTANNDDWVKQEEVYDMLAHIRTGHCKLYSLLGSSHDLGENLVVLRNFYQSVTKAAIAMDGGSLEIDVDFIEPDFEQLTIATVNERRLKAEIENRTPEMA

>d1ei9a\_ c.69.1.13 (A:) Palmitoyl protein thioesterase 1 {Cow (Bos taurus)}

DPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIHVLSLEIGKTLREDVENSFFLNVNSQVTTVCQILAKDPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMVNLISVGGQHQGVFGLPRCPGESSHICDFIRKTLNAGAYNKAIQERLVQAEYWHDPIREDIYRNHSIFLADINQERGVNESYKKNLMALKKFVMVKFLNDTIVDPVDSEWFGFYRSGQAKETIPLQESTLYTQDRLGLKAMDKAGQLVFLALEGDHLQLSEEWFYAHIIPFLE

>d1auoa\_ c.69.1.14 (A:) Carboxylesterase {Pseudomonas fluorescens}

MTEPLILQPAKPADACVIWLHGLGADRYDFMPVAEALQESLLTTRFVLPQAPTRPVTINGGYEMPSWYDIKAMSPARSISLEELEVSAKMVTDLIEAQKRTGIDASRIFLAGFSQGGAVVFHTAFINWQGPLGGVIALSTYAPTFGDELELSASQQRIPALCLHGQYDDVVQNAMGRSAFEHLKSRGVTVTWQEYPMGHEVLPQEIHDIGAWLAARLG

>d1fj2a\_ c.69.1.14 (A:) Acyl protein thioesterase 1 {Human (Homo sapiens)}

MDPEFMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSSHIKYICPHAPVRPVTLNMNVAMPSWFDIIGLSPDSQEDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTALTTQQKLAGVTALSCWLPLRASFPQGPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLKTLVNPANVTFKTYEGMMHSSCQQEMMDVKQFIDKLLPPI

>d1tca\_\_ c.69.1.17 (-) Triacylglycerol lipase {Yeast (Candida antarctica), form b}

LPSGSDPAFSQPKSVLDAGLTCQGASPSSVSKPILLVPGTGTTGPQSFDSNWIPLSTQLGYTPCWISPPPFMLNDTQVNTEYMVNAITALYAGSGNNKLPVLTWSQGGLVAQWGLTFFPSIRSKVDRLMAFAPDYKGTVLAGPLDALAVSAPSVWQQTTGSALTTALRNAGGLTQIVPTTNLYSATDEIVQPQVSNSPLDSSYLFNGKNVQAQAVCGPLFVIDHAGSLTSQFSYVVGRSALRSTTGQARSADYGITDCNPLPANDLTPEQKVAAAALLAPAAAAIVAGPKQNCEPDLMPYARPFAVGKRTCSGIVTP

>d3tgl\_\_ c.69.1.17 (-) Triacylglycerol lipase {Rhizomucor miehei}

GIRAATSQEINELTYYTTLSANSYCRTVIPGATWDCIHCDATEDLKIIKTWSTLIYDTNAMVARGDSEKTIYIVFRGSSSIRNWIADLTFVPVSYPPVSGTKVHKGFLDSYGEVQNELVATVLDQFKQYPSYKVAVTGHSLGGATVLLCALDLYQREEGLSSSNLFLYTQGQPRVGDPAFANYVVSTGIPYRRTVNERDIVPHLPPAAFGFLHAGEEYWITDNSPETVQVCTSDLETSDCSNSIVPFTSVLDHLSYFGINTGLCT

>d1tia\_\_ c.69.1.17 (-) Triacylglycerol lipase {Penicillium camembertii}

DVSTSELDQFEFWVQYAAASYYEADYTAQVGDKLSCSKGNCPEVEATGATVSYDFSDSTITDTAGYIAVDHTNSAVVLAFRGSYSVRNWVADATFVHTNPGLCDGCLAELGFWSSWKLVRDDIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDLRGKGYPSAKLYAYASPRVGNAALAKYITAQGNNFRFTHTNDPVPKLPLLSMGYVHVSPEYWITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEAHIWYFVQVDAGKG

>d1thg\_\_ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Geotrichum candidum), ATCC 34614}

EAPTAVLNGNEVISGVLEGKVDTFKGIPFADPPLNDLRFKHPQPFTGSYQGLKANDFSPACMQLDPGNSLTLLDKALGLAKVIPEEFRGPLYDMAKGTVSMNEDCLYLNVFRPAGTKPDAKLPVMVWIYGGAFVYGSSAAYPGNSYVKESINMGQPVVFVSINYRTGPFGFLGGDAITAEGNTNAGLHDQRKGLEWVSDNIANFGGDPDKVMIFGESAGAMSVAHQLIAYGGDNTYNGKKLFHSAILQSGGPLPYHDSSSVGPDISYNRFAQYAGCDTSASANDTLECLRSKSSSVLHDAQNSYDLKDLFGLLPQFLGFGPRPDGNIIPDAAYELFRSGRYAKVPYISGNQEDEGTAFAPVALNATTTPHVKKWLQYIFYDASEASIDRVLSLYPQTLSVGSPFRTGILNALTPQFKRVAAILSDMLFQSPRRVMLSATKDVNRWTYLSTHLHNLVPFLGTFHGNELIFQFNVNIGPANSYLRYFISFANHHDPNVGTNLLQWDQYTDEGKEMLEIHMTDNVMRTDDYRIEGISNFETDVNLYG

>d1i6wa\_ c.69.1.18 (A:) Lipase A {Bacillus subtilis}

HNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKVANVVTLGGANRLTTGKALPGTDPNQKILYTSIYSSADMIVMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN

>d4lipd\_ c.69.1.18 (D:) Lipase {Burkholderia cepacia (formerly Pseudomonas cepacia)}

DNYAATRYPIILVHGLTGTDKYAGVLEYWYGIQEDLQQRGATVYVANLSGFQSDDGPNGRGEQLLAYVKTVLAATGATKVNLVGHSQGGLTSRYVAAVAPDLVASVTTIGTPHRGSEFADFVQGVLAYDPTGLSSTVIAAFVNVFGILTSSSNNTNQDALAALKTLTTAQAATYNQNYPSAGLGAPGSCQTGAPTETVGGNTHLLYSWAGTAIQPTISVFGVTGATDTSTIPLVDPANALDPSTLALFGTGTVMVNRGSGQNDGVVSKCSALYGQVLSTSYKWNHLDEINQLLGVRGANAEDPVAVIRTHANRLKLAGV

>d1ex9a\_ c.69.1.18 (A:) Lipase {Pseudomonas aeruginosa}

STYTQTKYPIVLAHGMLGFDNILGVDYWFGIPSALRRDGAQVYVTEVSQLDTSEVRGEQLLQQVEEIVALSGQPKVNLIGHSHGGPTIRYVAAVRPDLIASATSVGAPHKGSDTADFLRQIPPGSAGEAVLSGLVNSLGALISFLSSGSTGTQNSLGSLESLNSEGAARFNAKYPQGIPTSACGEGAYKVNGVSYYSWSGSSPLTNFLDPSDAFLGASSLTFKNGTANDGLVGTCSSHLGMVIRDNYRMNHLDEVNQVFGLTSLFETSPVSVYRQHANRLKNASL

>d2masa\_ c.70.1.1 (A:) Inosine-uridine nucleoside N-ribohydrolase, IU-NH {Crithidia fasciculata}

AKKIILDCDPGLDDAVAILLAHGNPEIELLAITTVVGNQTLAKVTRNAQLVADIAGITGVPIAAGCDKPLVRKIMTAGHIHGESGMGTVAYPAEFKNKVDERHAVNLIIDLVMSHEPKTITLVPTGGLTNIAMAARLEPRIVDRVKEVVLMGGGYHEGNATSVAEFNIIIDPEAAHIVFNESWQVTMVGLDLTHQALATPPILQRVKEVDTNPARFMLEIMDYYTKIYQSNRYMAAAAVHDPCAVAYVIDPSVMTTERVPVDIELTGKLTLGMTVADFRNPRPEHCHTQVAVKLDFEKFWGLVLDALERIGDP

>d1hoza\_ c.70.1.1 (A:) Inosine-adenosine-guanosine preferring nucleoside hydrolase {Trypanosoma vivax}

GSAKNVVLDHDGNLDDFVAMVLLASNTEKVRLIGALCTDADCFVENGFNVTGKIMCLMHNNMNLPLFPIGKSAATAVNPFPKEWRCLAKNMDDMPILNIPENVELWDKIKAENEKYEGQQLLADLVMNSEEKVTICVTGPLSNVAWCIDKYGEKFTSKVEECVIMGGAVDVRGNVFLPSTDGTAEWNIYWDPASAKTVFGCPGLRRIMFSLDSTNTVPVRSPYVQRFGEQTNFLLSILVGTMWAMCTHCELLRDGDGYYAWDALTAAYVVDQKVANVDPVPIDVVVDKQPNEGATVRTDAENYPLTFVARNPEAEFFLDMLLRSARAC

>d1ra9\_\_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Escherichia coli}

MISLIAALAVDRVIGMENAMPWNLPADLAWFKRNTLDKPVIMGRHTWESIGRPLPGRKNIILSSQPGTDDRVTWVKSVDEAIAACGDVPEIMVIGGGRVYEQFLPKAQKLYLTHIDAEVEGDTHFPDYEPDDWESVFSEFHDADAQNSHSYCFEILERR

>d3dfr\_\_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Lactobacillus casei}

TAFLWAQNRNGLIGKDGHLPWHLPDDLHYFRAQTVGKIMVVGRRTYESFPKRPLPERTNVVLTHQEDYQAQGAVVVHDVAAVFAYAKQHLDQELVIAGGAQIFTAFKDDVDTLLVTRLAGSFEGDTKMIPLNWDDFTKVSSRTVEDTNPALTHTYEVWQKKA

>d1df7a\_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Mycobacterium tuberculosis}

MVGLIWAQATSGVIGRGGDIPWRLPEDQAHFREITMGHTIVMGRRTWDSLPAKVRPLPGRRNVVLSRQADFMASGAEVVGSLEEALTSPETWVIGGGQVYALALPYATRCEVTEVDIGLPREAGDALAPVLDETWRGETGEWRFSRSGLRYRLYSYHRS

>d1d1ga\_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Thermotoga maritima}

AKVIFVLAMDVSGKIASSVESWSSFEDRKNFRKITTEIGNVVMGRITFEEIGRPLPERLNVVLTRRPKTSNNPSLVFFNGSPADVVKFLEGKGYERVAVIGGKTVFTEFLREKLVDELFVTVEPYVFGKGIPFFDEFEGYFPLKLLEMRRLNERGTLFLKYSVE

>d1vdra\_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Haloferax volcanii}

ELVSVAALAENRVIGRDGELPWPSIPADKKQYRSRIADDPVVLGRTTFESMRDDLPGSAQIVMSRSERSFSVDTAHRAASVEEAVDIAASLDAETAYVIGGAAIYALFQPHLDRMVLSRVPGEYEGDTYYPEWDAAEWELDAETDHEGFTLQEWVRS

>d8dfr\_\_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Chicken (Gallus gallus)}

VRSLNSIVAVCQNMGIGKDGNLPWPPLRNEYKYFQRMTSTSHVEGKQNAVIMGKKTWFSIPEKNRPLKDRINIVLSRELKEAPKGAHYLSKSLDDALALLDSPELKSKVDMVWIVGGTAVYKAAMEKPINHRLFVTRILHEFESDTFFPEIDYKDFKLLTEYPGVPADIQEEDGIQYKFEVYQKSV

>d1dyr\_\_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Fungus (Pneumocystis carinii)}

NQQKSLTLIVALTTSYGIGRSNSLPWKLKKEISYFKRVTSFVPTFDSFESMNVVLMGRKTWESIPLQFRPLKGRINVVITRNESLDLGNGIHSAKSLDHALELLYRTYGSESSVQINRIFVIGGAQLYKAAMDHPKLDRIMATIIYKDIHCDVFFPLKFRDKEWSSVWKKEKHSDLESWVGTKVPHGKINEDGFDYEFEMWTRDL

>d1aoea\_ c.71.1.1 (A:) Dihydrofolate reductases, eukaryotic type {Yeast (Candida albicans)}

MLKPNVAIIVAALKPALGIGYKGKMPWRLRKEIRYFKDVTTRTTKPNTRNAVIMGRKTWESIPQKFRPLPDRLNIILSRSYENEIIDDNIIHASSIESSLNLVSDVERVFIIGGAEIYNELINNSLVSHLLITEIEHPSPESIEMDTFLKFPLESWTKQPKSELQKFVGDTVLEDDIKEGDFTYNYTLWTRK

>d1ekqa\_ c.72.1.2 (A:) Hydroxyethylthiazole kinase (THZ kinase, ThiK) {Bacillus subtilis}

MDAQSAAKCLTAVRRHSPLVHSITNNVVTNFTANGLLALGASPVMAYAKEEVADMAKIAGALVLNIGTLSKESVEAMIIAGKSANEHGVPVILDPVGAGATPFRTESARDIIREVRLAAIRGNAAEIAHTVGVTDWLIKGVDAGEGGGDIIRLAQQAAQKLNTVIAITGEVDVIADTSHVYTLHNGHKLLTKVTGAGCLLTSVVGAFCAVEENPLFAAIAAISSYGVAAQLAAQQTADKGPGSFQIELLNKLSTVTEQDVQEWATIERV

>d1jxha\_ c.72.1.2 (A:) 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate kinase (HMP-phosphate kinase, ThiD) {Salmonella typhimurium}

MQRINALTIAGTDPSGGAGIQADLKTFSALGAYGCSVITALVAENTCGVQSVYRIEPDFVAAQLDSVFSDVRIDTTKIGMLAETDIVEAVAERLQRHHVRNVVLDTVMLAKSGDPLLSPSAIETLRVRLLPQVSLITPNLPEAAALLDAPHARTEQEMLAQGRALLAMGCEAVLMKGGHLEDAQSPDWLFTREGEQRFSAPRVNTKNTHGTGCTLSAALAALRPRHRSWGETVNEAKAWLSAALAQADTLEVGKGIGPVHHFHAWW

>d1rkd\_\_ c.72.1.1 (-) Ribokinase {Escherichia coli}

AGSLVVLGSINADHILNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGANIAFIACTGDDSIGESVRQQLATDNIDITPVSVIKGESTGVALIFVNGEGENVIGIHAGANAALSPALVEAQRERIANASALLMQLESPLESVMAAAKIAHQNKTIVALNPAPARELPDELLALVDIITPNETEAEKLTGIRVENDEDAAKAAQVLHEKGIRTVLITLGSRGVWASVNGEGQRVPGFRVQAVDTIAAGDTFNGALITALLEEKPLPEAIRFAHAAAAIAVTRKGAQPSVPWREEIDAFLDRQR

>d1bx4a\_ c.72.1.1 (A:) Adenosine kinase {Human (Homo sapiens)}

VRENILFGMGNPLLDISAVVDKDFLDKYSLKPNDQILAEDKHKELFDELVKKFKVEYHAGGSTQNSIKVAQWMIQQPHKAATFFGCIGIDKFGEILKRKAAEAHVDAHYYEQNEQPTGTCAACITGDNRSLIANLAAANCYKKEKHLDLEKNWMLVEKARVCYIAGFFLTVSPESVLKVAHHASENNRIFTLNLSAPFISQFYKESLMKVMPYVDILFGNETEAATFAREQGFETKDIKEIAKKTQALPKMNSKRQRIVIFTQGRDDTIMATESEVTAFAVLDQDQKEIIDTNGAGDAFVGGFLSQLVSDKPLTECIRAGHYAASIIIRRTGCTFPEKPDFH

>d1dgya\_ c.72.1.1 (A:) Adenosine kinase {Toxoplasma gondii}

GPMRVFAIGNPILDLVAEVPSSFLDEFFLKRGDATLATPEQMRIYSTLDQFNPTSLPGGSALNSVRVVQKLLRKPGSAGYMGAIGDDPRGQVLKELCDKEGLATRFMVAPGQSTGTCAVLINEKERTLCTHLGACGSFRIPENWTTFASGALIFYATAYTLTATPKNALEVAGYAHGIPNAIFTLNLSAPFCVELYKDAMQSLLLHTNILFGNEEEFAHLAKVHNLVAAEKVALSVANKEHAVEVCTGALRLLTAGQNTGATKLVVMTRGHNPVIAAEQTADGTVVVHEVGVPVVAAEKIVDTNGAGDAFVGGFLYGLSQGKTVKQCIMCGNACAQDVIQHVGFSLSF

>d2uaga3 c.72.2.1 (A:94-297) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}

DIELFCREAQAPIVAITGSNGKSTVTTLVGEMAKAAGVNVGVGGNIGLPALMLLDDECELYVLELSSFQLETTSSLQAVAATILNVTEDHMDRYPFGLQQYRAAKLRIYENAKVCVVNADDALTMPIRGADERCVSFGVNMGDYHLNHQQGETWLRVKGEKVLNVKEMKLSGQHNYTNALAALALADAAGLPRASSLKALTTFT

>d1e8ca3 c.72.2.1 (A:88-337) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

QLNERLSALAGRFYHEPSDNLRLVGVTGTNGKTTTTQLLAQWSQLLGEISAVMGTVGNGLLGKVIPTENTTGSAVDVQHELAGLVDQGATFCAMEVSSHGLVQHRVAALKFAASVFTNLSRDHLDYHGDMEHYEAAKWLLYSEHHCGQAIINADDEVGRRWLAKLPDAVAVSMEDHINPNCHGRWLKATEVNYHDSGATIRFSSSWGDGEIESHLMGAFNVSNLLLALATLLALGYPLADLLKTAARLQP

>d1gg4a4 c.72.2.1 (A:82-312) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

DTRLAFGELAAWVRQQVPARVVALTGSSGKTSVKEMTAAILSQCGNTLYTAGNLNNDIGVPMTLLRLTPEYDYAVIELGANHQGEIAWTVSLTRPEAALVNNLAAAHLEGFGSLAGVAKAKGEIFSGLPENGIAIMNADNNDWLNWQSVIGSRKVWRFSPNAANSDFTATNIHVTSHGTEFTLQTPTGSVDVLLPLPGRHNIANALAAAALSMSVGATLDAIKAGLANLKA

>d1ed8a\_ c.76.1.1 (A:) Alkaline phosphatase {Escherichia coli}

TPEMPVLENRAAQGDITAPGGARRLTGDQTAALRDSLSDKPAKNIILLIGDGMGDSEITAARNYAEGAGGFFKGIDALPLTGQYTHYALNKKTGKPDYVTDSAASATAWSTGVKTYNGALGVDIHEKDHPTILEMAKAAGLATGNVSTAELQDATPAALVAHVTSRKCYGPSATSEKCPGNALEKGGKGSITEQLLNARADVTLGGGAKTFAETATAGEWQGKTLREQAQARGYQLVSDAASLNSVTEANQQKPLLGLFADGNMPVRWLGPKATYHGNIDKPAVTCTPNPQRNDSVPTLAQMTDKAIELLSKNEKGFFLQVEGASIDKQDHAANPCGQIGETVDLDEAVQRALEFAKKEGNTLVIVTADHAHASQIVAPDTKAPGLTQALNTKDGAVMVMSYGNSEEDSQEHTGSQLRIAAYGPHAANVVGLTDQTDLFYTMKAALGLK

>d1ew2a\_ c.76.1.1 (A:) Alkaline phosphatase {Human (Homo sapiens)}

IIPVEEENPDFWNREAAEALGAAKKLQPAQTAAKNLIIFLGDGMGVSTVTAARILKGQKKDKLGPEIPLAMDRFPYVALSKTYNVDKHVPDSGATATAYLCGVKGNFQTIGLSAAARFNQCNTTRGNEVISVMNRAKKAGKSVGVVTTTRVQHASPAGTYAHTVNRNWYSDADVPASARQEGCQDIATQLISNMDIDVILGGGRKYMFRMGTPDPEYPDDYSQGGTRLDGKNLVQEWLAKRQGARYVWNRTELMQASLDPSVTHLMGLFEPGDMKYEIHRDSTLDPSLMEMTEAALRLLSRNPRGFFLFVEGGRIDHGHHESRAYRALTETIMFDDAIERAGQLTSEEDTLSLVTADHSHVFSFGGYPLRGSSIFGLAPGKARDRKAYTVLLYGNGPGYVLKDGARPDVTESESGSPEYRQQSAVPLDEETHAGEDVAVFARGPQAHLVHGVQEQTFIAHVMAFAACLEPYTACDLAPP

>d1auk\_\_ c.76.1.2 (-) Arylsulfatase A {Human (Homo sapiens)}

RPPNIVLIFADDLGYGDLGCYGHPSSTTPNLDQLAAGGLRFTDFYVPVSLCTPSRAALLTGRLPVRMGMYPGVLVPSSRGGLPLEEVTVAEVLAARGYLTGMAGKWHLGVGPEGAFLPPHQGFHRFLGIPYSHDQGPCQNLTCFPPATPCDGGCDQGLVPIPLLANLSVEAQPPWLPGLEARYMAFAHDLMADAQRQDRPFFLYYASHHTHYPQFSGQSFAERSGRGPFGDSLMELDAAVGTLMTAIGDLGLLEETLVIFTADNGPETMRMSRGGCSGLLRCGKGTTYEGGVREPALAFWPGHIAPGVTHELASSLDLLPTLAALAGAPLPNVTLDGFDLSPLLLGTGKSPRQSLFFYPSYPDEVRGVFAVRTGKYKAHFFTQGSAHSDTTADPACHASSSLTAHEPPLLYDLSKDPGENYNLLGGVAGATPEVLQALKQLQLLKAQLDAAVTFGPSQVARGEDPALQICCHPGCTPRPACCHCP

>d1fsu\_\_ c.76.1.2 (-) Arylsulfatase B (4-sulfatase) {Human (Homo sapiens)}

SRPPHLVFLLADDLGWNDVGFHGSRIRTPHLDALAAGGVLLDNYYTQPLXTPSRSQLLTGRYQIRTGLQHQIIWPCQPSCVPLDEKLLPQLLKEAGYTTHMVGKWHLGMYRKECLPTRRGFDTYFGYLLGSEDYYSHERCTLIDALNVTRCALDFRDGEEVATGYKNMYSTNIFTKRAIALITNHPPEKPLFLYLALQSVHEPLQVPEEYLKPYDFIQDKNRHHYAGMVSLMDEAVGNVTAALKSSGLWNNTVFIFSTDNGGQTLAGGNNWPLRGRKWSLWEGGVRGVGFVASPLLKQKGVKNRELIHISDWLPTLVKLARGHTNGTKPLDGFDVWKTISEGSPSPRIELLHNIDPNFVDSSPCPRNSMAPAKDDSSLPEYSAFNTSVHAAIRHGNWKLLTGYPGCGYWFPPPSQYNVSEIPSSDPPTKTLWLFDIDRDPEERHDLSREYPHIVTKLLSRLQFYHKHSVPVYFPAQDPRCDPKATGVWGPWM

>d1hdha\_ c.76.1.2 (A:) Arylsulfatase B (4-sulfatase) {Pseudomonas aeruginosa}

KRPNFLVIVADDLGFSDIGAFGGEIATPNLDALAIAGLRLTDFHTASTCSPTRSMLLTGTDHHIAGIGTMAEALTPELEGKPGYEGHLNERVVALPELLREAGYQTLMAGKWHLGLKPEQTPHARGFERSFSLLPGAANHYGFEPPYDESTPRILKGTPALYVEDERYLDTLPEGFYSSDAFGDKLLQYLKERDQSRPFFAYLPFSAPHWPLQAPREIVEKYRGRYDAGPEALRQERLARLKELGLVEADVEAHPVLALTREWEALEDEERAKSARAMEVYAAMVERMDWNIGRVVDYLRRQGELDNTFVLFMSDNGAEGALLEAFPKFGPDLLGFLDRHYDNSLENIGRANSYVWYGPRWAQAATAPSRLYKAFTTQGGIRVPALVRYPRLSRQGAISHAFATVMDVTPTLLDLAGVRHPGKRWRGREIAEPRGRSWLGWLSGETEAAHDENTVTGWELFGMRAIRQGDWKAVYLPAPVGPATWQLYDLARDPGEIHDLADSQPGKLAELIEHWKRYVSETGVV

>d1e4bp\_ c.74.1.1 (P:) L-fuculose-1-phosphate aldolase {Escherichia coli}

MERNKLARQIIDTCLEMTRLGLNQGTAGQVSVRYQDGMLITPTGIPYEKLTESHIVFIDGNGKHEEGKLPSSEWRFHMAAYQSRPDANAVVHNHAVHCTAVSILNRSIPAIHYMIAAAGGNSIPCAPYATFGTRELSEHVALALKNRKATLLQHHGLIACEVNLEKALWLAHEVEVLAQLYLTTLAITDPVPVLSDEEIAVVLEKF

>d1jdia\_ c.74.1.1 (A:) L-ribulose-5-phosphate 4-epimerase {Escherichia coli}

MLEDLKRQVLEANLALPKHNLVTLTWGNVSAVDRERGVFVIKPSGVDYSIMTADDMVVVSIETGEVVEGAKKPSSDTPTHRLLYQAFPSIGGIVHTHSRHATIWAQAGQSIPATGTTHADYFYGTIPCTRKMTDAEINGEYEWETGNVIVETFEKQGIDAAQMPGVLVHSHGPFAWGKNAEDAVHNAIVLEEVAYMGIFCRQLAPQLPDMQQTLLNKHYLRKH

>d1cnza\_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Salmonella typhimurium}

MSKNYHIAVLPGDGIGPEVMAQALKVMDAVRSRFDMRITTSHYDVGGIAIDNHGHPLPKATVEGCEQADAILFGSVGGPKWENLPPESQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCPLRADIAANGFDILCVRELTGGIYFGQPKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRRKVTSIDKANVLQSSILWREIVNDVAKTYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGKNIANPIAQILSLALLLRYSLDANDAATAIEQAINRALEEGVRTGDLARGAAAVSTDEMGDIIARYVAEGV

>d1hqsa\_ c.77.1.1 (A:) Isocitrate dehydrogenase, ICDH {Bacillus subtilis}

MAQGEKITVSNGVLNVPNNPIIPFIEGDGTGPDIWNAASKVLEAAVEKAYKGEKKITWKEVYAGEKAYNKTGEWLPAETLDVIREYFIAIKGPLTTPVGGGIRSLNVALRQELDLFVCLRPVRYFTGVPSPVKRPEDTDMVIFRENTEDIYAGIEYAKGSEEVQKLISFLQNELNVNKIRFPETSGIGIKPVSEEGTSRLVRAAIDYAIEHGRKSVTLVHKGNIMKFTEGAFKNWGYELAEKEYGDKVFTWAQYDRIAEEQGKDAANKAQSEAEAAGKIIIKDSIADIFLQQILTRPNEFDVVATMNLNGDYISDALAAQVGGIGIAPGANINYETGHAIFEATHGTAPKYAGLDKVNPSSVILSGVLLLEHLGWNEAADLVIKSMEKTIASKVVTYDFARLMDGATEVKCSEFGEELIKNMD

>d1ekxa1 c.78.1.1 (A:1-150) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}

ANPLYQKHIISINDLSRDDLNLVLATAAKLKANPQPELLKHKVIASCFFEASTRTRLSFETSMHRLGASVVGFSDSANTSLGKKGETLADTISVISTYVDAIVMRHPQEGAARLATEFSGNVPVLNAGDGSNQHPTQTLLDLFTIQETQG

>d1ekxa2 c.78.1.1 (A:151-310) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}

RLDNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPQYILDMLDEKGIAWSLHSSIEEVMAEVDILYMTRVQKERLDPSEYANVKAQFVLRASDLHNAKANMKVLHPLPRVDEIATDVDKTPHAWYFQQAGNGIFARQALLALVLNRDLVL

>d2at2a2 c.78.1.1 (A:145-295) Aspartate carbamoyltransferase catalytic subunit {Bacillus subtilis}

FKGLTVSIHGDIKHSRVARSNAEVLTRLGARVLFSGPSEWQDEENTFGTYVSMDEAVESSDVVMLLRIQNERHQSAVSQEGYLNKYGLTVERAERMKRHAIIMHPAPVNRGVEIDDSLVESEKSRIFKQMKNGVFIRMAVIQCALQTNVKR

>d1dxha2 c.78.1.1 (A:151-335) Ornithine transcarbamoylase {Pseudomonas aeruginosa}

KPLHDISYAYLGDARNNMGNSLLLIGAKLGMDVRIAAPKALWPHDEFVAQCKKFAEESGAKLTLTEDPKEAVKGVDFVHTDVWVSMGEPVEAWGERIKELLPYQVNMEIMKATGNPRAKFMHCLPAFHNSETKVGKQIAEQYPNLANGIEVTEDVFESPYNIAFEQAENRMHTIKAILVSTLADI

>d1otha1 c.78.1.1 (A:34-184) Ornithine transcarbamoylase {Human (Homo sapiens)}

KVQLKGRDLLTLKNFTGEEIKYMLWLSADLKFRIKQKGEYLPLLQGKSLGMIFEKRSTRTRLSTETGFALLGGHPCFLTTQDIHLGVNESLTDTARVLSSMADAVLARVYKQSDLDTLAKEASIPIINGLSDLYHPIQILADYLTLQEHYS

>d1otha2 c.78.1.1 (A:185-354) Ornithine transcarbamoylase {Human (Homo sapiens)}

SLKGLTLSWIGDGNNILHSIMMSAAKFGMHLQAATPKGYEPDASVTKLAEQYAKENGTKLLLTNDPLEAAHGGNVLITDTWISMGREEEKKKRLQAFQGYQVTMKTAKVAASDWTFLHCLPRKPEEVDDEVFYSPRSLVFPEAENRKWTIMAVMVSLLTDYSPQLQKPKF

>d1b74a1 c.78.2.1 (A:1-105) Glutamate racemase {Aquifex pyrophilus}

MKIGIFDSGVGGLTVLKAIRNRYRKVDIVYLGDTARVPYGIRSKDTIIRYSLECAGFLKDKGVDIIVVACNTASAYALERLKKEINVPVFGVIEPGVKEALKKSR

>d1b74a2 c.78.2.1 (A:106-252) Glutamate racemase {Aquifex pyrophilus}

NKKIGVIGTPATVKSGAYQRKLEEGGADVFAKACPLFAPLAEEGLLEGEITRKVVEHYLKEFKGKIDTLILGCTHYPLLKKEIKKFLGDAEVVDSSEALSLSLHNFIKDDGSSSLELFFTDLSPNLQFLIKLILGRDYPVKLAEGVF

>d1qopb\_ c.79.1.1 (B:) Tryptophan synthase, beta-subunit {Salmonella typhimurium}

TTLLNPYFGEFGGMYVPQILMPALNQLEEAFVSAQKDPEFQAQFADLLKNYAGRPTALTKCQNITAGTRTTLYLKREDLLHGGAHKTNQVLGQALLAKRMGKSEIIAETGAGQHGVASALASALLGLKCRIYMGAKDVERQSPNVFRMRLMGAEVIPVHSGSATLKDACNEALRDWSGSYETAHYMLGTAAGPHPYPTIVREFQRMIGEETKAQILDKEGRLPDAVIACVGGGSNAIGMFADFINDTSVGLIGVEPGGHGIETGEHGAPLKHGRVGIYFGMKAPMMQTADGQIEESYSISAGLDFPSVGPQHAYLNSIGRADYVSITDDEALEAFKTLCRHEGIIPALESSHALAHALKMMREQPEKEQLLVVNLSGRGDKDIFTVHDIL

>d1tdj\_1 c.79.1.1 (5-335) Allosteric threonine deaminase N-terminal domain {Escherichia coli}

QPLSGAPEGAEYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLDRVFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRGERLAHILSGANVNFHGLRYVSERCELGE

>d1e5xa\_ c.79.1.1 (A:) Threonine synthase {Mouse-ear cress (Arabidopsis thaliana)}

IETAVKPPHRTEDNIRDEARRNRSNAVNPFSAKYVPFNAAPGSTESYSLDEIVYRSRSGGLLDVEHDMEALKRFDGAYWRDLFDSRVGKSTWPYGSGVWSKKEWVLPEIDDDDIVSAFEGNSNLFWAERFGKQFLGMNDLWVKHCGISHTGSFKDLGMTVLVSQVNRLRKMKRPVVGVGCASTGDTSAALSAYCASAGIPSIVFLPANKISMAQLVQPIANGAFVLSIDTDFDGCMKLIREITAELPIYLANSLNSLRLEGQKTAAIEILQQFDWQVPDWVIVPGGNLGNIYAFYKGFKMCQELGLVDRIPRMVCAQAANANPLYLHYKSGWKDFKPMTASTTFASAIQIGDPVSIDRAVYALKKCNGIVEEATEEELMDAMAQADSTGMFICPHTGVALTALFKLRNQGVIAPTDRTVVVSTAHGLKFTQSKIDYHSNAIPDMACRFSNPPVDVKADFGAVMDVLKSYLGSNTLTS

>d1f2da\_ c.79.1.1 (A:) 1-aminocyclopropane-1-carboxylate deaminase {Yeast (Hansenula saturnus)}

AGVAKFAKYPLTFGPSPISNLNRLSQHLGSKVNVYAKREDCNSGLAFGGNKLRKLEYIVPDIVEGDYTHLVSIGGRQSNQTRMVAALAAKLGKKCVLIQEDWVPIPEAEKDVYNRVGNIELSRIMGADVRVIEDGFDIGMRKSFANALQELEDAGHKPYPIPAGCSEHKYGGLGFVGFADEVINQEVELGIKFDKIVVCCVTGSTTAGILAGMAQYGRQDDVIAIDASFTSEKTKEQTLRIANNTAKLIGVEHEFKDFTLDTRFAYPCYGVPNEGTIEAIRTCAEQEGVLTDPVYEGKSMQGLIALIKEDYFKPGANVLYVHLGGAPALSAYSSFFPTKTA

>d1jbqa\_ c.79.1.1 (A:) Cystathionine beta-synthase {Human (Homo sapiens)}

WIRPDAPSRCTWQLGRPASESPHHHTAPAKSPKILPDILKKIGDTPMVRINKIGKKFGLKCELLAKCEFFNAGGSVKDRISLRMIEDAERDGTLKPGDTIIEPTSGNTGIGLALAAAVRGYRCIIVMPEKMSSEKVDVLRALGAEIVRTPTNARFDSPESHVGVAWRLKNEIPNSHILDQYRNASNPLAHYDTTADEILQQCDGKLDMLVASVGTGGTITGIARKLKEKCPGCRIIGVDPEGSILAEPEELNQTEQTTYEVEGIGYDFIPTVLDRTVVDKWFKSNDEEAFTFARMLIAQEGLLCGGSAGSTVAVAVKAAQELQEGQRCVVILPDSVRNYMTKFLSDRWMLQKGFL

>d1iata\_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Human (Homo sapiens)}

AALTRDPQFQKLQQWYREHRSELNLRRLFDANKDRFNHFSLTLNTNHGHILVDYSKNLVTEDVMRMLVDLAKSRGVEAARERMFNGEKINYTEGRAVLHVALRNRSNTPILVDGKDVMPEVNKVLDKMKSFCQRVRSGDWKGYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPRVWYVSNIDGTHIAKTLAQLNPESSLFIIASKTFTTQETITNAETAKEWFLQAAKDPSAVAKHFVALSTNTTKVKEFGIDPQNMFEFWDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGAHWMDQHFRTTPLEKNAPVLLALLGIWYINCFGCETHAMLPYDQYLHRFAAYFQQGDMESNGKYITKSGTRVDHQTGPIVWGEPGTNGQHAFYQLIHQGTKMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMRGKSTEEARKELQAAGKSPEDLERLLPHKVFEGNRPTNSIVFTKLTPFMLGALVAMYEHKIFVQGIIWDINSFDQWGVELGKQLAKKIEPELDGSAQVTSHDASTNGLINFIKQQREARV

>d1c7qa\_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Bacillus stearothermophilus}

AISFDYSNALPFMQENELDYLSEFVKAAHHMLHERKGPGSDFLGWVDWPIRYDKNEFSRIKQAAERIRNHSDALVVIGIGGSYLGARAAIEALSHTFHNQMNDTTQIYFAGQNISSTYISHLLDVLEGKDLSINVISKSGTTTEPAIAFRIFRDYMEKKYGKEEARKRIYVTTDRTKGALKKLADQEGYETFVIPDNIGGRYSVLTAVGLLPIAVAGLNIDRMMEGAASAYHKYNNPDLLTNESYQYAAVRNILYRKGKAIELLVNYEPSLHYVSEWWKQLFGESEGKDQKGLFPASVDFTTDLHSMGQYVQEGRRNLIETVLHVKKPQIELTIQEDPENIDGLNFLAGKTLDEVNKKAFQGTLLAHVDGGVPNLIVELDEMNEYTFGEMVYFFEKACGISGHLLGVNPFDQPGVEAYKKNMFALLGKPGFEDEKAALMKRL

>d1aa6\_2 c.81.1.1 (1-564) Formate dehydrogenase H {Escherichia coli}

MKKVVTVCPYCASGCKINLVVDNGKIVRAEAAQGKTNQGTLCLKGYYGWDFINDTQILTPRLKTPMIRRQRGGKLEPVSWDEALNYVAERLSAIKEKYGPDAIQTTGSSRGTGNETNYVMQKFARAVIGTNNVDCCARVCHGPSVAGLHQSVGNGAMSNAINEIDNTDLVFVFGYNPADSHPIVANHVINAKRNGAKIIVCDPRKIETARIADMHIALKNGSNIALLNAMGHVIIEENLYDKAFVASRTEGFEEYRKIVEGYTPESVEDITGVSASEIRQAARMYAQAKSAAILWGMGVTQFYQGVETVRSLTSLAMLTGNLGKPHAGVNPVRGQNNVQGACDMGALPDTYPGYQYVKDPANREKFAKAWGVESLPAHTGYRISELPHRAAHGEVRAAYIMGEDPLQTDAELSAVRKAFEDLELVIVQDIFMTKTASAADVILPSTSWGEHEGVFTAADRGFQRFFKAVEPKWDLKTDWQIISEIATRMGYPMHYNNTQEIWDELRHLCPDFYGATYEKMGELGFIQWPCRDTSDADQGTSYLFKEKFDTPNGLAQFFTCDWVA

>d1tmo\_2 c.81.1.1 (5-631) Trimethylamine N-oxide reductase {Shewanella massilia}

NEDEWLTTGSHFGAFKMKRKNGVIAEVKPFDLDKYPTDMINGIRGMVYNPSRVRYPMVRLDFLLKGHKSNTHQRGDFRFVRVTWDKALTLFKHSLDEVQTQYGPSGLHAGQTGWRATGQLHSSTSHMQRAVGMHGNYVKKIGDYSTGAGQTILPYVLGSTEVYAQGTSWPLILEHSDTIVLWSNDPYKNLQVGWNAETHESFAYLAQLKEKVKQGKIRVISIDPVVTKTQAYLGCEQLYVNPQTDVTLMLAIAHEMISKKLYDDKFIQGYSLGFEEFVPYVMGTKDGVAKTPEWAAPICGVEAHVIRDLAKTLVKGRTQFMMGWCIQRQQHGEQPYWMAAVLATMIGQIGLPGGGISYGHHYSSIGVPSSGAAAPGAFPRNLDENQKPLFDSSDFKGASSTIPVARWIDAILEPGKTIDANGSKVVYPDIKMMIFSGNNPWNHHQDRNRMKQAFHKLECVVTVDVNWTATCRFSDIVLPACTTYERNDIDVYGAYANRGILAMQKMVEPLFDSLSDFEIFTRFAAVLGKEKEYTRNMGEMEWLETLYNECKAANAGKFEMPDFATFWKQGYVHFGDGEVWTRHADFRNDPEINPLGTPSGLIEIFSRKIDQFGYDDCKGHPTWMEKT

>d1g8ka2 c.81.1.1 (A:4-682) Arsenite oxidase large subunit {Alcaligenes faecalis}

NDRITLPPANAQRTNMTCHFCIVGCGYHVYKWPELEEGGRAPEQNALGLDFRKQLPPLAVTLTPAMTNVVTEHDGARYDIMVVPDKACVVNSGLSSTRGGKMASYMYTPTGDGKERLSAPRLYAADEWVDTTWDHAMALYAGLIKKTLDKDGPQGVFFSCFDHGGAGGGFENTWGTGKLMFSAIQTPMVRIHNRPAYNSECHATREMGIGELNNAYEDAQLADVIWSIGNNPYESQTNYFLNHWLPNLQGATTSKKKERFPNENFPQARIIFVDPRETPSVAIARHVAGNDRVLHLAIEPGTDTALFNGLFTYVVEQGWIDKPFIEAHTKGFDDAVKTNRLSLDECSNITGVPVDMLKRAAEWSYKPKASGQAPRTMHAYEKGIIWGNDNYVIQSALLDLVIATHNVGRRGTGCVRMGGHQEGYTRPPYPGDKKIYIDQELIKGKGRIMTWWGCNNFQTSNNAQALREAILQRSAIVKQAMQKARGATTEEMVDVIYEATQNGGLFVTSINLYPTKLAEAAHLMLPAAHPGEMNLTSMNGERRIRLSEKFMDPPGTAMADCLIAARIANALRDMYQKDGKAEMAAQFEGFDWKTEEDAFNDGFRRAGQPGAPAIDSQGGSTGHLVTYDRLRKSGNNGVQLPVVSWDESKGLVGTEMLYTEGKFDTDDGKAHFKPAPWNG

>d2napa2 c.81.1.1 (A:4-600) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}

RPEKWVKGVCRYCGTGCGVLVGVKDGKAVAIQGNPNNHNAGLLCLKGSLLIPVLNSKERVTQPLVRRHKGGKLEPVSWDEALDLMASRFRSSIDMYGPNSVAWYGSGQCLTEESYVANKIFKGGFGTNNVDGNPRLCMASAVGGYVTSFGKDEPMGTYADIDQATCFFIIGSNTSEAHPVLFRRIARRKQVEPGVKIIVADPRRTNTSRIADMHVAFRPGTDLAFMHSMAWVIINEELDNPRFWQRYVNFMDAEGKPSDFEGYKAFLENYRPEKVAEICRVPVEQIYGAARAFAESAATMSLWCMGINQRVQGVFANNLIHNLHLITGQICRPGATSFSLTGQPNACGGVRDGGALSHLLPAGRAIPNAKHRAEMEKLWGLPEGRIAPEPGYHTVALFEALGRGDVKCMIICETNPAHTLPNLNKVHKAMSHPESFIVCIEAFPDAVTLEYADLVLPPAFWCERDGVYGCGERRYSLTEKAVDPPGQCRPTVNTLVEFARRAGVDPQLVNFRNAEDVWNEWRMVSKGTTYDFWGMTRERLRKESGLIWPCPSEDHPGTSLRYVRGQDPCVPADHPDRFFFYGKPDGRAVIWMRPAKG

>d1ad3a\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus)}

SISDTVKRAREAFNSGKTRSLQFRIQQLEALQRMINENLKSISGALASDLGKNEWTSYYEEVAHVLEELDTTIKELPDWAEDEPVAKTRQTQQDDLYIHSEPLGVVLVIGAWNYPFNLTIQPMVGAVAAGNAVILKPSEVSGHMADLLATLIPQYMDQNLYLVVKGGVPETTELLKERFDHIMYTGSTAVGKIVMAAAAKHLTPVTLELGGKSPCYVDKDCDLDVACRRIAWGKFMNSGQTCVAPDYILCDPSIQNQIVEKLKKSLKDFYGEDAKQSRDYGRIINDRHFQRVKGLIDNQKVAHGGTWDQSSRYIAPTILVDVDPQSPVMQEEIFGPVMPIVCVRSLEEAIQFINQREKPLALYVFSNNEKVIKKMIAETSSGGVTANDVIVHITVPTLPFGGVGNSGMGAYHGKKSFETFSHRRSCLVKSLLNEEAHKARYPPSPA

>d1bi9a\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus), retinal type II}

MASLQLLPSPTPNLEIKYTKIFINNEWQNSESGRVFPVCNPATGEQVCEVQEADKVDIDKAVQAARLAFSLGSVWRRMDASERGRLLDKLADLVERDRATLATMESLNGGKPFLQAFYIDLQGVIKTLRYYAGWADKIHGMTIPVDGDYFTFTRHEPIGVCGQIIPWNFPLLMFTWKIAPALCCGNTVVIKPAEQTPLSALYMGALIKEAGFPPGVVNILPGYGPTAGAAIASHIGIDKIAFTGSTEVGKLIQEAAGRSNLKRVTLELGGKSPNIIFADADLDYAVEQAHQGVFFNQGQCCTAGSRIFVEESIYEEFVKRSVERAKRRIVGSPFDPTTEQGPQIDKKQYNKILELIQSGVAEGAKLECGGKGLGRKGFFIEPTVFSNVTDDMRIAKEEIFGPVQEILRFKTMDEVIERANNSDFGLVAAVFTNDINKALMVSSAMQAGTVWINCYNALNAQSPFGGFKMSGNGREMGEFGLREYSEVKTVTVKIPQKNS

>d1a4sa\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Baltic cod (Gadus callarias)}

AQLVDSMPSASTGSVVVTDDLNYWGGRRIKSKDGATTEPVFEPATGRVLCQMVPCGAEEVDQAVQSAQAAYLKWSKMAGIERSRVMLEAARIIRERRDNIAKLEVINNGKTITEAEYDIDAAWQCIEYYAGLAPTLSGQHIQLPGGAFAYTRREPLGVCAGILAWNYPFMIAAWKCAPALACGNAVVFKPSPMTPVTGVILAEIFHEAGVPVGLVNVVQGGAETGSLLCHHPNVAKVSFTGSVPTGKKVMEMSAKTVKHVTLELGGKSPLLIFKDCELENAVRGALMANFLTQGQVCTNGTRVFVQREIMPQFLEEVVKRTKAIVVGDPLLTETRMGGLISKPQLDKVLGFVAQAKKEGARVLCGGEPLTPSDPKLKNGYFMSPCVLDNCRDDMTCVKEEIFGPVMSVLPFDTEEEVLQRANNTTFGLASGVFTRDISRAHRVAANLEAGTCYINTYSISPVEVPFGGYKMSGFGRENGQATVDYYSQLKTVIVEMGDVDSLF

>d1euha\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Streptococcus mutans}

TKQYKNYVNGEWKLSENEIKIYEPASGAELGSVPAMSTEEVDYVYASAKKAQPAWRALSYIERAAYLHKVADILMRDKEKIGAILSKEVAKGYKSAVSEVVRTAEIINYAAEEGLRMEGEVLEGGSFEAASKKKIAVVRREPVGLVLAISPFNYPVNLAGSKIAPALIAGNVIAFKPPTQGSISGLLLAEAFAEAGLPAGVFNTITGRGSEIGDYIVEHQAVNFINFTGSTGIGERIGKMAGMRPIMLELGGKDSAIVLEDADLELTAKNIIAGAFGYSGQRCTAVKRVLVMESVADELVEKIREKVLALTIGNPEDDADITPLIDTKSADYVEGLINDANDKGATALTEIKREGNLICPILFDKVTTDMRLAWEEPFGPVLPIIRVTSVEEAIEISNKSEYGLQASIFTNDFPRAFGIAEQLEVGTVHINNKTQRGTDNFPFLGAKKSGAGIQGVKYSIEAMTTVKSVVFDIK

>d1ez0a\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Vibrio harveyi}

TDNVFYATNAFTGEALPLAFPVHTEVEVNQAATAAAKVARDFRRLNNSKRASLLRTIASELEARSDDIIARAHLETALPEVRLTGEIARTANQLRLFADVVNSGSYHQAILDTPNPTRAPLPKPDIRRQQIALGPVAVFGASNFPLAFSAAGGDTASALAAGCPVIVKGHTAHPGTSQIVAECIEQALKQEQLPQAIFTLLQGNQRALGQALVSHPEIKAVGFTGSVGGGRALFNLAHERPEPIPFYGELGAINPTFIFPSAMRAKADLADQFVASMTMGCGQFCTKPGVVFALNTPETQAFIETAQSLIRQQSPSTLLTPGIRDSYQSQVVSRGSDDGIDVTFSQAESPCVASALFVTSSENWRKHPAWEEEIFGPQSLIVVCENVADMLSLSEMLAGSLTATIHATEEDYPQVSQLIPRLEEIAGRLVFNGWPTGVEVGYAMVHGGPYPASTHSASTSVGAEAIHRWLRPVAYQALPESLLPDSLKAENPLEIARAVDGKAA

>d1kfia1 c.84.1.1 (A:3-205) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

QVIPAPRVQVTQPYAGQKPGTSGLRKKVSEATQPNYLENFVQSIFNTLRKDELKPKNVLFVGGDGRYFNRQAIFSIIRLAYANDISEVHVGQAGLMSTPASSHYIRKVNEEVGNCIGGIILTASHNPGGKEHGDFGIKFNVRTGAPAPEDFTDQIYTHTTKIKEYLTVDYEFEKHINLDQIGVYKFEGTRLEKSHFEVKVVDT

>d1kfia2 c.84.1.1 (A:206-323) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

VQDYTQLMQKLFDFDLLKGLFSNKDFSFRFDGMHGVAGPYAKHIFGTLLGCSKESLLNCDPSEDFGGGHPDPNLTYAHDLVELLDIHKKKDVGTVPQFGAACDGDADRNMILGRQFFV

>d1kfia3 c.84.1.1 (A:324-443) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

TPSDSLAVIAANANLIFKNGLLGAARSMPTSGALDKVAAKNGIKLFETPTGWKFFGNLMDAGLINLCGEESFGTGSNHIREKDGIWAVLAWLTILAHKNKNTDHFVTVEEIVTQYWQQFG

>d1k2yx1 c.84.1.1 (X:5-154) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

KAPTLPASIFRAYDIRGVVGDTLTAETAYWIGRAIGSESLARGEPCVAVGRDGRLSGPELVKQLIQGLVDCGCQVSDVGMVPTPVLYYAANVLEGKSGVMLTGAHNPPDYNGFKIVVAGETLANEQIQALRERIEKNDLASGVGSVEQVD

>d1k2yx2 c.84.1.1 (X:155-258) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

ILPRYFKQIRDDIAMAKPMKVVVDCGNGVAGVIAPQLIEALGCSVIPLYCEVDGNFPNHHPDPGKPENLKDLIAKVKAENADLGLAFDGDGDRVGVVTNTGTII

>d1k2yx3 c.84.1.1 (X:259-367) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

YPDRLLMLFAKDVVSRNPGADIIFDVKCTRRLIALISGYGGRPVMWKTGHSLIKKKMKETGALLAGEMSGHVFFKERWFGFDDGIYSAARLLEILSQDQRDSEHVFSAF

>d1k2yx4 c.84.1.1 (X:368-463) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

PSDISTPEINITVTEDSKFAIIEALQRDAQWGEGNITTLDGVRVDYPKGWGLVRASNTTPVLVLRFEADTEEELERIKTVFRNQLKAVDSSLPVPF

>d1fw8a\_ c.86.1.1 (A:) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SKYSLAPVAKELQSLLGKDVTFLNDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSRKVDGQKVKASKEDVQKFRHELSSLADVYINDAFGTAHRAHSSMVGFDLPQRAAGFLLEKELKYFGKALENPTRPFLAILGGAKVADKIQLIDNLLDKVDSIIIGGGMAFTFKKVLENTEIGDSIFDKAGAEIVPKLMEKAKAKGVEVVLPVDFIIADAFSADANTKTVTDKEGIPAGWQGLDNGPESRKLFAATVAKAKTIVWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKYGVTDKISHVSTGGGASLELLEGKELPGVAFLSEKKSLSSKLSVQDLDLKDKRVFIRVDFNVPLDGKKITSNQRIVAALPTIKYVLEHHPRYVVLASHLGRPNGERN

>d16pk\_\_ c.86.1.1 (-) Phosphoglycerate kinase {Trypanosoma brucei}

EKKSINECDLKGKKVLIRVDFNVPVKNGKITNDYRIRSALPTLKKVLTEGGSCVLMSHLGRPKGIPMAQAGKIRSTGGVPGFQQKATLKPVAKRLSELLLRPVTFAPDCLNAADVVSKMSPGDVVLLENVRFYKEEGSKKAKDREAMAKILASYGDVYISDAFGTAHRDSATMTGIPKILGNGAAGYLMEKEISYFAKVLGNPPRPLVAIVGGAKVSDKIQLLDNMLQRIDYLLIGGAMAYTFLKAQGYSIGKSKCEESKLEFARSLLKKAEDRKVQVILPIDHVCHTEFKAVDSPLITEDQNIPEGHMALDIGPKTIEKYVQTIGKCKSAIWNGPMGVFEMVPYSKGTFAIAKAMGRGTHEHGLMSIIGGGDSASAAELSGEAKRMSHVSTGGGASLELLEGKTLPGVTVLDDK

>d1ygpa\_ c.87.1.4 (A:) Glycogen phosphorylase {Baker's yeast (Saccharomyces cerevisiae)}

TRRLTGFLPQEIKSIDTMIPLLSRALWNKHQVKKFNKAEDFQDRFIDHVETTLARSLYNCDDMVAYEAASMSIRDNLVIDWNKTQQKFTTRDPKRVYYLSLEFLMGRALDNALINMKIEDPEDPAASKGKPREMIKGALDELGFKLEDVLDQEPDAGLGNGGLGRLAACFVDSMATEGIPAWGYGLRYEYGIFAQKIIDGYQVETPDYWLNSGNPWEIERNEVQIPVTFYGYVDRPEGGKTTLSASQWIGGERVLAVAYDFPVPGFKTSNVNNLRLWQARPTTEFDLNKFNNGDYKNSVAQQQRAESITAVLYPNDNFAQGKELRLKQQYFWCAASLHDILRRFKKSKRPWTEFPDQVAIQLNDTHPTLAIVELQRVLVDLEKLDWHEAWDIVTKTFAYTNHTVMQEALEKWPRRLFGHLLPRHLEIIYDINWFFLEDVAKKFPKDVDLLSRISIIEENSPERQIRMAFLAIVGSHKVNGVVELHSELIKTTIFKDFIKFYGPSKFVNVTNGITPRRWLKQANPSLAKLISETLNDPTEEYLLDMAKLTQLEKYVEDKEFLKKWNQVKLNNKIRLVDLIKKENDGVDIINREYLDDTLFDMQVKRIHEYKRQQLNVFGIIYRYLAMKNMLKNGASIEEVARKYPRKVSIFGGKSAPGYYMAKLIIKLINCVADIVNNDESIEHLLKVVFVADYNVSKAEIIIPASDLSEHISTAGTEASGTSNMKFVMNGGLIIGTVDGANVEITREIGEDNVFLFGNLSENVEELRYNHQYHPQDLPSSLDSVLSYIESGQFSPENPNEFKPLVDSIKYHGDYYLVSDDFESYLATHELVDQEFHNQRSEWLKKSVLSLANVGFFSSDRCIEEYSDTIWNVEPVT

>d1qm5a\_ c.87.1.4 (A:) Maltodextrin phosphorylase (MALP) {Escherichia coli}

SQPIFNDKQFQEALSRQWQRYGLNSAAEMTPRQWWLAVSEALAEMLRAQPFAKPVANQRHVNYISMEFLIGRLTGNNLLNLGWYQDVQDSLKAYDINLTDLLEEEIDPALGNGGLGRLAACFLDSMATVGQSATGYGLNYQYGLFRQSFVDGKQVEAPDDWHRSNYPWFRHNEALDVQVGIGGKVTKDGRWEPEFTITGQAWDLPVVGYRNGVAQPLRLWQATHAHPFDLTKFNDGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRLMQQYFQCACSVADILRRHHLAGRKLHELADYEVIQLNDTHPTIAIPELLRVLIDEHQMSWDDAWAITSKTFAYTNHTLMPEALERWDVKLVKGLLPRHMQIINEINTRFKTLVEKTWPGDEKVWAKLAVVHDKQVHMANLCVVGGFAVNGVAALHSDLVVKDLFPEYHQLWPNKFHNVTNGITPRRWIKQCNPALAALLDKSLQKEWANDLDQLINLEKFADDAKFRDQYREIKQANKVRLAEFVKVRTGIEINPQAIFDIQIKRLHEYKRQHLNLLHILALYKEIRENPQADRVPRVFLFGAKAAPGYYLAKNIIFAINKVADVINNDPLVGDKLKVVFLPDYCVSAAEKLIPAADISEQISTAGKEASGTGNMKLALNGALTVGTLDGANVEIAEKVGEENIFIFGHTVEQVKAILAKGYDPVKWRKKDKVLDAVLKELESGKYSDGDKHAFDQMLHSIGKQGGDPYLVMADFAAYVEAQKQVDVLYRDQEAWTRAAILNTARCGMFSSDRSIRDYQARIWQAKR

>d1ii2a1 c.91.1.1 (A:201-523) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}

HLCMHASANVGKQGDVTVFFGLSGTGKTTLSADPHRNLIGDDEHVWTDRGVFNIEGGCYAKAIGLNPKTEKDIYDAVRFGAVAENCVLDKRTGEIDFYDESICKNTRVAYPLSHIEGALSKAIAGHPKNVIFLTNDAFGVMPPVARLTSAQAMFWFVMGYTANVPGVEAGGTRTARPIFSSCFGGPFLVRHATFYGEQLAEKMQKHNSRVWLLNTGYAGGRADRGAKRMPLRVTRAIIDAIHDGTLDRTEYEEYPGWGLHIPKYVAKVPEHLLNPRKAWKDVRQFNETSKELVAMFQESFSARFAAKASQEMKSAVPRYVEFA

>d1khba1 c.91.1.1 (A:260-622) Cytosolic phosphoenolpyruvate carboxykinase (GTP-hydrolysing) {Human (Homo sapiens)}

WLAEHMLVLGITNPEGEKKYLAAAFPSACGKTNLAMMNPSLPGWKVECVGDDIAWMKFDAQGHLRAINPENGFFGVAPGTSVKTNPNAIKTIQKNTIFTNVAETSDGGVYWEGIDEPLASGVTITSWKNKEWSSEDGEPCAHPNSRFCTPASQCPIIDAAWESPEGVPIEGIIFGGRRPAGVPLVYEALSWQHGVFVGAAMRSEATAAAEHKGKIIMHDPFAMRPFFGYNFGKYLAHWLSMAQHPAAKLPKIFHVNWFRKDKEGKFLWPGFGENSRVLEWMFNRIDGKASTKLTPIGYIPKEDALNLKGLGHINMMELFSISKEFWDKEVEDIEKYLVDQVNADLPCEIEREILALKQRISQM

>d1ayl\_2 c.109.1.1 (1-227) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Escherichia coli}

MRVNNGLTPQELEAYGISDVHDIVYNPSYDLLYQEELDPSLTGYERGVLTNLGAVAVDTGIFTGRSPKDKYIVRDDTTRDTFWWADKGKGKNDNKPLSPETWQHLKGLVTRQLSGKRLFVVDAFCGANPDTRLSVRFITEVAWQAHFVKNMFIRPSDEELAGFKPDFIVMNGAKCTNPQWKEQGLNSENFVAFNLTERMQLIGGTWYGGEMKKGMFSMMNYLLPLKG

>d1ii2a2 c.109.1.1 (A:2-200) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}

PPTIHRNLLSPELVQWALKIEKDSRLTARGALAVMSYAKTGRSPLDKRIVDTDDVRENVDWGKVNMKLSEESFARVRKIAKEFLDTREHLFVVDCFAGHDERYRLKVRVFTTRPYHALFMRDMLIVPTPEELATFGEPDYVIYNAGECKADPSIPGLTSTTCVALNFKTREQVILGTEYAGEMKKGILTVMFELMPQMN

>d1khba2 c.109.1.1 (A:10-259) Cytosolic phosphoenolpyruvate carboxykinase (GTP-hydrolysing) {Human (Homo sapiens)}

NLSAKVVQGSLDSLPQAVREFLENNAELCQPDHIHICDGSEEENGRLLGQMEEEGILRRLKKYDNCWLALTDPRDVARIESKTVIVTQEQRDTVPIPKTGLSQLGRWMSEEDFEKAFNARFPGCMKGRTMYVIPFSMGPLGSPLSKIGIELTDSPYVVASMRIMTRMGTPVLEALGDGEFVKCLHSVGCPLPLQKPLVNNWPCNPELTLIAHLPDRREIISFGSGYGGNSLLGKKCFALRMASRLAKEEG

>d1doza\_ c.92.1.1 (A:) Ferrochelatase {Bacillus subtilis}

SRKKMGLLVMAYGTPYKEEDIERYYTHIRRGRKPEPEMLQDLKDRYEAIGGISPLAQITEQQAHNLEQHLNEIQDEITFKAYIGLKHIEPFIEDAVAEMHKDGITEAVSIVLAPHFSTFSVQSYNKRAKEEAEKLGGLTITSVESWYDEPKFVTYWVDRVKETYASMPEDERENAMLIVSAHSLPEKIKEFGDPYPDQLHESAKLIAEGAGVSEYAVGWQSEGNTPDPWLGPDVQDLTRDLFEQKGYQAFVYVPVGFVADHLEVLYDNDYECKVVTDDIGASYYRPEMPNAKPEFIDALATVVLKKLGR

>d1hrka\_ c.92.1.1 (A:) Ferrochelatase {Human (Homo sapiens)}

RKPKTGILMLNMGGPETLGDVHDFLLRLFLDRDLMTLPIQNKLAPFIAKRLTPKIQEQYRRIGGGSPIKIWTSKQGEGMVKLLDELSPNTAPHKYYIGFRYVHPLTEEAIEEMERDGLERAIAFTQYPQYSCSTTGSSLNAIYRYYNQVGRKPTMKWSTIDRWPTHHLLIQCFADHILKELDHFPLEKRSEVVILFSAHSLPMSVVNRGDPYPQEVSATVQKVMERLEYCNPYRLVWQSKVGPMPWLGPQTDESIKGLCERGRKNILLVPIAFTSDHIETLYELDIEYSQVLAKECGVENIRRAESLNGNPLFSKALADLVHSHIQSNELCSKQLTLSCPLCVNPVCRETKSFFTSQQL

>d1toaa\_ c.92.2.2 (A:) Periplasmic zinc binding protein TroA {Treponema pallidum}

GKPLVVTTIGMIADAVKNIAQGDVHLKGLMGPGVDPHLYTATAGDVEWLGNADLILYNGLHLETKMGEVFSKLRGSRLVVAVSETIPVSQRLSLEEAEFDPHVWFDVKLWSYSVKAVYESLCKLLPGKTREFTQRYQAYQQQLDKLDAYVRRKAQSLPAERRVLVTAHDAFGYFSRAYGFEVKGLQGVSTASEASAHDMQELAAFIAQRKLPAIFIESSIPHKNVEALRDAVQARGHVVQIGGELFSDAMGDAGTSEGTYVGMVTHNIDTIVAALAR

>d1psza\_ c.92.2.2 (A:) Pneumococcal surface antigen PssA {Pneumococcus (Streptococcus pneumoniae)}

KKDTTSGQKLKVVATNSIIADITKNIAGDKIDLHSIVPIGQDPHEYEPLPEDVKKTSEADLIFYNGINLETGGNAWFTKLVENAKKTENKDYFAVSDGVDVIYLEGQNEKGKEDPHAWLNLENGIIFAKNIAKQLSAKDPNNKEFYEKNLKEYTDKLDKLDKESKDKFNKIPAEKKLIVTSEGAFKYFSKAYGVPSAYIWEINTEEEGTPEQIKTLVEKLRQTKVPSLFVESSVDDRPMKTVSQDTNIPIYAQIFTDSIAEQGKEGDSYYSMMKYNLDKIAEGLAK

>d1mioa\_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}

SENLKDEILEKYIPKTKKTRSGHIVIKTEETPNPEIVANTRTVPGIITARGCAYAGCKGVVMGPIKDMVHITHGPIGCSFYTWGGRRFKSKPENGTGLNFNEYVFSTDMQESDIVFGGVNKLKDAIHEAYEMFHPAAIGVYATCPVGLIGDDILAVAATASKEIGIPVHAFSCEGYKGVSQSAGHHIANNTVMTDIIGKGNKEQKKYSINVLGEYNIGGDAWEMDRVLEKIGYHVNATLTGDATYEKVQNADKADLNLVQCHRSINYIAEMMETKYGIPWIKCNFIGVDGIVETLRDMAKCFDDPELTKRTEEVIAEEIAAIQDDLDYFKEKLQGKTACLYVGGSRSHTYMNMLKSFGVDSLVAGFEFAHRDDYEGREVIPTIKIDADSKNIPEITVTPDEQKYRVVIPEDKVEELKKAGVPLSSYGGMMKEMHDGTILIDDMNHHDMEVVLEKLKPDMFFAGIKEKFVIQKGGVLSKQLHSYDYNGPYAGFRGVVNFGHELVNGIYTPAWKMITPPWKKASSES

>d1miob\_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}

LDATPKEIVERKALRINPAKTCQPVGAMYAALGIHNCLPHSHGSQGCCSYHRTVLSRHFKEPAMASTSSFTEGASVFGGGSNIKTAVKNIFSLYNPDIIAVHTTCLSETLGDDLPTYISQMEDAGSIPEGKLVIHTNTPSYVGSHVTGFANMVQGIVNYLSENTGAKNGKINVIPGFVGPADMREIKRLFEAMDIPYIMFPDTSGVLDGPTTGEYKMYPEGGTKIEDLKDTGNSDLTLSLGSYASDLGAKTLEKKCKVPFKTLRTPIGVSATDEFIMALSEATGKEVPASIEEERGQLIDLMIDAQQYLQGKKVALLGDPDEIIALSKFIIELGAIPKYVVTGTPGMKFQKEIDAMLAEAGIEGSKVKVEGDFFDVHQWIKNEGVDLLISNTYGKFIAREENIPFVRFGFPIMDRYGHYYNPKVGYKGAIRLVEEITNVILDKIERECTEEDFEVVR

>d2minb\_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}

SQQVDKIKASYPLFLDQDYKDMLAKKRDGFEEKYPQDKIDEVFQWTTTKEYQELNFQREALTVNPAKACQPLGAVLCALGFEKTMPYVHGSQGCVAYFRSYFNRHFREPVSCVSDSMTEDAAVFGGQQNMKDGLQNCKATYKPDMIAVSTTCMAEVIGDDLNAFINNSKKEGFIPDEFPVPFAHTPSFVGSHVTGWDNMFEGIARYFTLKSMDDKVVGSNKKINIVPGFETYLGNFRVIKRMLSEMGVGYSLLSDPEEVLDTPADGQFRMYAGGTTQEEMKDAPNALNTVLLQPWHLEKTKKFVEGTWKHEVPKLNIPMGLDWTDEFLMKVSEISGQPIPASLTKERGRLVDMMTDSHTWLHGKRFALWGDPDFVMGLVKFLLELGCEPVHILCHNGNKRWKKAVDAILAASPYGKNATVYIGKDLWHLRSLVFTDKPDFMIGNSYGKFIQRDTLHKGKEFEVPLIRIGFPIFDRHHLHRSTTLGYEGAMQILTTLVNSILERLDEETRGMQATDYNHDLVR

>d1qgua\_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}

TNATGERNLALIQEVLEVFPETARKERRKHMMVSDPKMKSVGKCIISNRKSQPGVMTVRGCAYAGSKGVVFGPIKDMAHISHGPVGCGQYSRAGRRNYYTGVSGVDSFGTLNFTSDFQERDIVFGGDKKLSKLIEEMELLFPLTKGITIQSECPVGLIGDDISAVANASSKALDKPVIPVRCEGFRGVSQSLGHHIANDVVRDWILNNREGQPFETTPYDVAIIGDYNIGGDAWASRILLEEMGLRVVAQWSGDGTLVEMENTPFVKLNLVHCYRSMNYIARHMEEKHQIPWMEYNFFGPTKIAESLRKIADQFDDTIRANAEAVIARYEGQMAAIIAKYRPRLEGRKVLLYMGGLRPRHVIGAYEDLGMEIIAAGYEFAHNDDYDRTLPDLKEGTLLFDDASSYELEAFVKALKPDLIGSGIKEKYIFQKMGVPFRQMHSWDYSGPYHGYDGFAIFARDMDMTLNNPAWNELTAPWL

>d2dri\_\_ c.93.1.1 (-) D-ribose-binding protein {Escherichia coli, strain k-12}

KDTIALVVSTLNNPFFVSLKDGAQKEADKLGYNLVVLDSQNNPAKELANVQDLTVRGTKILLINPTDSDAVGNAVKMANQANIPVITLDRQATKGEVVSHIASDNVLGGKIAGDYIAKKAGEGAKVIELQGIAGTSAARERGEGFQQAVAAHKFNVLASQPADFDRIKGLNVMQNLLTAHPDVQAVFAQNDEMALGALRALQTAGKSDVMVVGFDGTPDGEKAVNDGKLAATIAQLPDQIGAKGVETADKVLKGEKVQAKYPVDLKLVVKQ

>d8abp\_\_ c.93.1.1 (-) L-arabinose-binding protein {Escherichia coli}

NLKLGFLVKQPEEPWFQTEWKFADKAGKDLGFEVIKIAVPDGEKTLNAIDSLAASGAKGFVICTPDPKLGSAIVAKARGYDMKVIAVDDQFVNAKGKPMDTVPLVMLAATKIGERQGQELYKEMQKRGWDVKESAVMAITANELDTARRRTTGSMDALKAAGFPEKQIYQVPTKSNDIPGAFDAANSMLVQHPEVKHWLIVGMNDSTVLGGVRATEGQGFKAADIIGIGINGVDAVSELSKAQATGFYGSLLPSPDVHGYKSSEMLYNWVAKDVEPPKFTEVTDVVLITRDNFKEELEKKGLGGK

>d1rpja\_ c.93.1.1 (A:) D-allose-binding protein {Escherichia coli}

AAEYAVVLKTLSNPFWVDMKKGIEDEAKTLGVSVDIFASPSEGDFQSQLQLFEDLSNKNYKGIAFAPLSSVNLVMPVARAWKKGIYLVNLDEKIDMDNLKKAGGNVEAFVTTDNVAVGAKGASFIIDKLGAEGGEVAIIEGKAGNASGEARRNGATEAFKKASQIKLVASQPADWDRIKALDVATNVLQRNPNIKAIYCANDTMAMGVAQAVANAGKTGKVLVVGTDGIPEARKMVEAGQMTATVAQNPADIGATGLKLMVDAEKSGKVIPLDKAPEFKLVDSILVTQ

>d2gbp\_\_ c.93.1.1 (-) Galactose/glucose-binding protein {Escherichia coli}

ADTRIGVTIYKYDDNFMSVVRKAIEQDAKAAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAINLVDPAAAGTVIEKARGQNVPVVFFNKEPSRKALDSYDKAYYVGTDSKESGIIQGDLIAKHWAANQGWDLNKDGQIQFVLLKGEPGHPDAEARTTYVIKELNDKGIKTEQLQLDTAMWDTAQAKDKMDAWLSGPNANKIEVVIANNDAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGALAGTVLNDANNQAKATFDLAKNLADGKGAADGTNWKIDNKVVRVPYVGVDKDNLAEFSKK

>d1pea\_\_ c.93.1.1 (-) Amide receptor/negative regulator of the amidase operon (AmiC) {Pseudomonas aeruginosa}

PLIGLLFSETGVTADIERSQRYGALLAVEQLNREGGVGGRPIETLSQDPGGDPDRYRLCAEDFIRNRGVRFLVGCYMSHTRKAVMPVVERADALLCYPTPYEGFEYSPNIVYGGPAPNQNSAPLAAYLIRHYGERVVFIGSDYIYPRESNHVMRHLYRQHGGTVLEEIYIPLYPSDDDLQRAVERIYQARADVVFSTVVGTGTAELYRAIARRYGDGRRPPIASLTTSEAEVAKMESDVAEGQVVVAPYFSSIDTPASRAFVQACHGFFPENATITAWAEAAYWQTLLLGRAAQAAGNWRVEDVQRHLYDIDIDAPQGPVRVERQNNHSRLSSRIAEIDARGVFQVRWQSPEPIRPDPYVVVHNLDDW

>d1jx6a\_ c.93.1.1 (A:) Quorum-sensing signal (autoinducer-2) binding protein LuxP {Vibrio harveyi}

GYWGYQEFLDEFPEQRNLTNALSEAVRAQPVPLSKPTQRPIKISVVYPGQQVSDYWVRNIASFEKRLYKLNINYQLNQVFTRPNADIKQQSLSLMEALKSKSDYLIFTLDTTRHRKFVEHVLDSTNTKLILQNITTPVREWDKHQPFLYVGFDHAEGSRELATEFGKFFPKHTYYSVLYFSEGYISDVRGDTFIHQVNRDNNFELQSAYYTKATKQSGYDAAKASLAKHPDVDFIYACSTDVALGAVDALAELGREDIMINGWGGGSAELDAIQKGDLDITVMRMNDDTGIAMAEAIKWDLEDKPVPTVYSGDFEIVTKADSPERIEALKKRAFRYSD

>d1dbqa\_ c.93.1.1 (A:) Purine repressor (PurR), C-terminal domain {Escherichia coli}

KSIGLLATSSEAAYFAEIIEAVEKNCFQKGYTLILGNAWNNLEKQRAYLSMMAQKRVDGLLVMCSEYPEPLLAMLEEYRHIPMVVMDWGEAKADFTDAVIDNAFEGGYMAGRYLIERGHREIGVIPGPLERNTGAGRLAGFMKAMEEAMIKVPESWIVQGDFEPESGYRAMQQILSQPHRPTAVFCGGDIMAMGALCAADEMGLRVPQDVSLIGYDNVRNARYFTPALTTIHQPKDSLGETAFNMLLDRIVNKREEPQSIEVHPRLIERRSVADGPFRDYRR

>d1tlfa\_ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}

SLLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERSGVEACKAAVHNLLAQRVSGLIINYPLDDQDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRLAGWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMRAITESGLRVGADISVVGYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRL

>d1byka\_ c.93.1.1 (A:) Trehalose repressor, C-terminal domain {Escherichia coli}

SDKVVAIIVTRLDSLSENLAVQTMLPAFYEQGYDPIMMESQFSPQLVAEHLGVLKRRNIDGVVLFGFTGITEEMLAHWQSSLVLLARDAKGFASVCYDDEGAIKILMQRLYDQGHRNISYLGVPHSDVTTGKRRHEAYLAFCKAHKLHPVAALPGLAMKQGYENVAKVITPETTALLCATDTLALGASKYLQEQRIDTLQLASVGNTPLMKFLHPEIVTVDPGYAEAGRQAACQLIAQVTGRSEPQQIIIPATLS

>d2lbp\_\_ c.93.1.1 (-) Leucine-binding protein {Escherichia coli}

DDIKVAVVGAMSGPIAQWGIMEFNGAEQAIKDINAKGGIKGDKLVGVEYDDACDPKQAVAVANKIVNDGIKYVIGHLCSSSTQPASDIYEDEGILMISPGATAPELTQRGYQHIMRTAGLDSSQGPTAAKYILETVKPQRIAIIHDKQQYGEGLARSVQDGLKAANANVVFFDGITAGEKDFSALIARLKKENIDFVYYGGYYPEMGQMLRQARSVGLKTQFMGPEGVGNASLSNIAGDAAEGMLVTMPKRYDQDPANQGIVDALKADKKDPSGPYVWITYAAVQSLATALERTGSDEPLALVKDLKANGANTVIGPLNWDEKGDLKGFDFGVFQWHADGSSTKAK

>d1dp4a\_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Rat (Rattus norvegicus)}

SDLTVAVVLPLTNTSYPWSWARVGPAVELALARVKARPDLLPGWTVRMVLGSSENAAGVCSDTAAPLAAVDLKWEHSPAVFLGPGCVYSAAPVGRFTAHWRVPLLTAGAPALGIGVKDEYALTTRTGPSHVKLGDFVTALHRRLGWEHQALVLYADRLGDDRPCFFIVEGLYMRVRERLNITVNHQEFVEGDPDHYPKLLRAVRRKGRVIYICSSPDAFRNLMLLALNAGLTGEDYVFFHLDVFGQSLKSAQGLVPQKPWERGDGQDRSARQAFQAAKIITYKEPDNPEYLEFLKQLKLLADKKFNFTVEDGLKNIIPASFHDGLLLYVQAVTETLAQGGTVTDGENITQRMWNRSFQGVTGYLKIDRNGDRDTDFSLWDMDPETGAFRVVLNYNGTSQELMAVSEHKLYWPLGYPPPDVPKCGF

>d1jdpa\_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Human (Homo sapiens)}

EALPPQKIEVLVLLPQDDSYLFSLTRVRPAIEYALRSVEGNGTGRRLLPPGTRFQVAYEDSDCGNRALFSLVDRVAAARGAKPDLILGPVCEYAAAPVARLASHWDLPMLSAGALAAGFQHKDSEYSHLTRVAPAYAKMGEMMLALFRHHHWSRAALVYSDDKLERNCYFTLEGVHEVFQEEGLHTSIYSFDETKDLDLEDIVRNIQASERVVIMCASSDTIRSIMLVAHRHGMTSGDYAFFNIELFNSSSYGDGSWKRGDKHDFEAKQAYSSLQTVTLLRTVKPEFEKFSMEVKSSVEKQGLNMEDYVNMFVEGFHDAILLYVLALHEVLRAGYSKKDGGKIIQQTWNRTFEGIAGQVSIDANGDRYGDFSVIAMTDVEAGTQEVIGDYFGKEGRFEMRP

>d1ewka\_ c.93.1.1 (A:) Metabotropic glutamate receptor subtype 1 {Rat (Rattus norvegicus)}

RSVARMDGDVIIGALFSVHHQPPAEKVPERKCGEIREQYGIQRVEAMFHTLDKINADPVLLPNITLGSEIRDSCWHSSVALEQSIEFIRDSLISIRDEKDGLNRCLPDGQTLPPGRTKKPIAGVIGPGSSSVAIQVQNLLQLFDIPQIAYSATSIDLSDKTLYKYFLRVVPSDTLQARAMLDIVKRYNWTYVSAVHTEGNYGESGMDAFKELAAQEGLCIAHSDKIYSNAGEKSFDRLLRKLRERLPKARVVVCFCEGMTVRGLLSAMRRLGVVGEFSLIGSDGWADRDEVIEGYEVEANGGITIKLQSPEVRSFDDYFLKLRLDTNTRNPWFPEFWQHRFQCRLPGHLLENPNFKKVCTGNESLEENYVQDSKMGFVINAIYAMAHGLQNMHHALCPGHVGLCDAMKPIDGRKLLDFLIKSSFVGVSGEEVWFDEKGDAPGRYDIMNLQYTEANRYDYVHVGTWHEGVLNIDDYKI

>d1jeta\_ c.94.1.1 (A:) Oligo-peptide binding protein (OPPA) {Salmonella typhimurium}

ADVPAGVQLADKQTLVRNNGSEVQSLDPHKIEGVPESNVSRDLFEGLLISDVEGHPSPGVAEKWENKDFKVWTFHLRENAKWSDGTPVTAHDFVYSWQRLADPNTASPYASYLQYGHIANIDDIIAGKKPATDLGVKALDDHTFEVTLSEPVPYFYKLLVHPSVSPVPKSAVEKFGDKWTQPANIVTNGAYKLKNWVVNERIVLERNPQYWDNAKTVINQVTYLPISSEVTDVNRYRSGEIDMTYNNMPIELFQKLKKEIPNEVRVDPYLCTYYYEINNQKAPFNDVRVRTALKLALDRDIIVNKVKNQGDLPAYSYTPPYTDGAKLVEPEWFKWSQQKRNEEAKKLLAEAGFTADKPLTFDLLYNTSDLHKKLAIAVASIWKKNLGVNVNLENQEWKTFLDTRHQGTFDVARAGWCADYNEPTSFLNTMLSDSSNNTAHYKSPAFDKLIADTLKVADDTQRSELYAKAEQQLDKDSAIVPVYYYVNARLVKPWVGGYTGKDPLDNIYVKNLYIIKH

>d1pda\_1 c.94.1.1 (3-219) Porphobilinogen deaminase (hydroxymethylbilane synthase), N-terminal domain {Escherichia coli}

DNVLRIATRQSPLALWQAHYVKDKLMASHPGLVVELVPMVTRGDVILDTPLAKVGGKGLFVKELEVALLENRADIAVHSMKDVPVEFPQGLGLVTICEREDPRDAFVSNNYDSLDALPAGSIVGTSSLRRQCQLAERRPDLIIRSLRGNVGTRLSKLDNGEYDAIILAVAGLKRLGLESRIRAALPPEISLPAVGQGAVGIECRLDDSRTRELLAAL

>d1lst\_\_ c.94.1.1 (-) Lysine-,arginine-,ornithine-binding (LAO) protein {Salmonella typhimurium}

ALPQTVRIGTDTTYAPFSSKDAKGEFIGFDIDLGNEMCKRMQVKCTWVASDFDALIPSLKAKKIDAIISSLSITDKRQQEIAFSDKLYAADSRLIAAKGSPIQPTLESLKGKHVGVLQGSTQEAYANDNWRTKGVDVVAYANQDLIYSDLTAGRLDAALQDEVAASEGFLKQPAGKEYAFAGPSVKDKKYFGDGTGVGLRKDDTELKAAFDKALTELRQDGTYDKMAKKYFDFNVYGDK

>d1sbp\_\_ c.94.1.1 (-) Sulphate-binding protein {Salmonella typhimurium}

KDIQLLNVSYDPTRELYEQYNKAFSAHWKQETGDNVVIDQSHGGSGKQATSVINGIEADTVTLALAYDVNAIAERGRIDKNWIKRLPDDSAPYTSTIVFLVRKGNPKQIHDWNDLIKPGVSVITPNPKSSGGARWNYLAAWGYALHHNNNDQAKAEDFVKALFKNVEVLDSGARGSTNTFVERGIGDVLIAWENEALLATNELGKDKFEIVTPSESILAEPTVSVVDKVVEKKDTKAVAEAYLKYLYSPEGQEIAAKNFYRPRDADVAKKYDDAFPKLKLFTIDEVFGGWAKAQKDHFADGGTFDQISK

>d1ixh\_\_ c.94.1.1 (-) Phosphate-binding protein {Escherichia coli}

EASLTGAGATFPAPVYAKWADTYQKETGNKVNYQGIGSSGGVKQIIANTVDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGNDGIAAFVQRLPGAIGYVEYAYAKQNNLAYTKLISADGKPVSPTEENFANAAKGADWSKTFAQDLTNQKGEDAWPITSTTFILIHKDQKKPEQGTEVLKFFDWAYKTGAKQANDLDYASLPDSVVEQVRAAWKTNIKDSSGKPLY

>d3mbp\_\_ c.94.1.1 (-) D-maltodextrin-binding protein, MBP {Escherichia coli}

KIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITK

>d1elja\_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Pyrococcus furiosus}

MKIEEGKVVIWHAMQPNELEVFQSLAEEYMALCPEVEIVFEQKPNLEDALKAAIPTGQGPDLFIWAHDWIGKFAEAGLLEPIDEYVTEDLLNEFAPMAQDAMQYKGHYYALPFAAETVAIIYNKEMVSEPPKTFDEMKAIMEKYYDPANEKYGIAWPINAYFISAIAQAFGGYYFDDKTEQPGLDKPETIEGFKFFFTEIWPYMAPTGDYNTQQSIFLEGRAPMMVNGPWSINDVKKAGINFGVVPLPPIIKDGKEYWPRPYGGVKLIYFAAGIKNKDAAWKFAKWLTTSEESIKTLALELGYIPVLTKVLDDPEIKNDPVIYGFGQAVQHAYLMPKSPKMSAVWGGVDGAINEILQDPQNADIEGILKKYQQEILNNMQ

>d1eu8a\_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Thermococcus litoralis}

IEEGKIVFAVGGAPNEIEYWKGVIAEFEKKYPGVTVELKRQATDTEQRRLDLVNALRGKSSDPDVFLMDVAWLGQFIASGWLEPLDDYVQKDNYDLSVFFQSVINLADKQGGKLYALPVYIDAGLLYYRKDLLEKYGYSKPPETWQELVEMAQKIQSGERETNPNFWGFVWQGKQYEGLVCDFVEYVYSNGGSLGEFKDGKWVPTLNKPENVEALQFMVDLIHKYKISPPNTYTEMTEEPVRLMFQQGNAAFERNWPYAWGLHNADDSPVKGKVGVAPLPHFPGHKSAATLGGWHIGISKYSDNKALAWEFVKFVESYSVQKGFAMNLGWNPGRVDVYDDPAVVSKSPHLKELRAVFENAVPRPIVPYYPQLSEIIQKYVNSALAGKISPQEALDKAQKEAEELVKQ

>d3thia\_ c.94.1.1 (A:) Thiaminase I {Paenibacillus thiaminolyticus}

ITLKVAIYPYVPDPARFQAAVLDQWQRQEPGVKLEFTDWDSYSADPPDDLDVFVLDSIFLSHFVDAGYLLPFGSQDIDQAEDVLPFALQGAKRNGEVYGLPQILCTNLLFYRKGDLKIGQVDNIYELYKKIGTSHSEQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPPLDPLNDKVIRGLRLLINMAGEKPSQYVPEDGDAYVRASWFAQGSGRAFIGYSESMMRMGDYAEQVRFKPISSSAGQDIPLFYSDVVSVNSKTAHPELAKKLANVMASADTVEQALRPQADGQYPQYLLPARHQVYEALMQDYPIYSELAQIVNKPSNRVFRLGPEVRTWLKDAKQVLPEALG

>d1mrp\_\_ c.94.1.1 (-) Ferric-binding protein {Haemophilus influenzae}

DITVYNGQHKEAATAVAKAFEQETGIKVTLNSGKSEQLAGQLKEEGDKTPADVFYTEQTATFADLSEAGLLAPISEQTIQQTAQKGVPLAPKKDWIALSGRSRVVVYDHTKLSEKDMEKSVLDYATPKWKGKIGYVSTSGAFLEQVVALSKMKGDKVALNWLKGLKENGKLYAKNSVALQAVENGEVPAALINNYYWYNLAKEKGVENLKSRLYFVRHQDPGALVSYSGAAVLKASKNQAEAQKFVDFLASKKGQEALVAARAEYPLRADVVSPFNLEPYEKLEAPVVSATTAQDKEHAIKLIEEAGLK

>d1dpe\_\_ c.94.1.1 (-) Dipeptide-binding protein {Escherichia coli}

KTLVYCSEGSPEGFNPQLFISGTTYDASSVPLYNRLVEFKIGTTEVIPGLAEKWEVSEDGKTYTFHLRKGVKWHDNKEFKPTRELNADDVVFSFDRQKNAQNPYHKVSGGSYEYFEGMGLPELISEVKKVDDNTVQFVLTRPEAPFLADLAMDFASILSKEYADAMMKAGTPEKLDLNPIGTGPFQLQQYQKDSRIRYKAFDGYWGTKPQIDTLVFSITPDASVRYAKLQKNECQVMPYPNPADIARMKQDKSINLMEMPGLNVGYLSYNVQKKPLDDVKVRQALTYAVNKDAIIKAVYQGAGVSAKNLIPPTMWGYNDDVQDYTYDPEKAKALLKEAGLEKGFSIDLWAMPVQRPYNPNARRMAEMIQADWAKVGVQAKIVTYEWGEYLKRAKDGEHQTVMMGWTGDNGDPDNFFATEFSCAASEQGSNYSKWCYKPFEDLIQPARATDDHNKRVELYKQAQVVMHDQAPALIIAHSTVFEPVRKEVKGYVVDPLGKHHFENVSIE

>d1pot\_\_ c.94.1.1 (-) Spermidine/putrescine-binding protein PotD {Escherichia coli}

NNTLYFYNWTEYVPPGLLEQFTKETGIKVIYSTYESNETMYAKLKTYKDGAYDLVVPSTYYVDKMRKEGMIQKIDKSKLTNFSNLDPDMLNKPFDPNNDYSIPYIWGATAIGVNGDAVDPKSVTSWADLWKPEYKGSLLLTDDAREVFQMALRKLGYSGNTTDPKEIEAAYNELKKLMPNVAAFNSDNPANPYMEGEVNLGMIWNGSAFVARQAGTPIDVVWPKEGGIFWMDSLAIPANAKNKEGALKLINFLLRPDVAKQVAETIGYPTPNLAARKLLSPEVANDKTLYPDAETIKNGEWQNDVGAASSIYEEYYQKLKAG

>d1a99a\_ c.94.1.1 (A:) Putrescine receptor (PotF) {Escherichia coli}

QKTLHIYNWSDYIAPDTVANFEKETGIKVVYDVFDSNEVLEGKLMAGSTGFDLVVPSASFLERQLTAGVFQPLDKSKLPEWKNLDPELLKLVAKHDPDNKFAMPYMWATTGIGYNVDKVKAVLGENAPVDSWDLILKPENLEKLKSCGVSFLDAPEEVFATVLNYLGKDPNSTKADDYTGPATDLLLKLRPNIRYFHSSQYINDLANGDICVAIGWAGDVWQASNRAKEAKNGVNVSFSIPKEGAMAFFDVFAMPADAKNKDEAYQFLNYLLRPDVVAHISDHVFYANANKAATPLVSAEVRENPGIYPPADVRAKLFTLKVQDPKIDRVRTRAWTKVKSG

>d1wdna\_ c.94.1.1 (A:) Glutamine-binding protein {Escherichia coli}

KLVVATDTAFVPFEFKQGDLYVGFDVDLWAAIAKELKLDYELKPMDFSGIIPALQTKNVDLALAGITITDERKKAIDFSDGYYKSGLLVMVKANNNDVKSVKDLDGKVVAVKSGTGSVDYAKANIKTKDLRQFPNIDNAYMELGTNRADAVLHDTPNILYFIKTAGNGQFKAVGDSLEAQQYGIAFPKGSDELRDKVNGALKTLRENGTYNEIYKKWFGTEPK

>d1ftka\_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Rat (Rattus norvegicus), GluR2}

KTVVVTTILESPYVMMKKNHEMLEGNERYEGYCVDLAAEIAKHCGFKYKLTIVGDGKYGARDADTKIWNGMVGELVYGKADIAIAPLTITLVREEVIDFSKPFMSLGISIMIKKPGTDGNPIESAEDLSKQTEIAYGTLDSGSTKEFFRRSKIAVFDKMWTYMRSAEPSVFVRTTAEGVARVRKSKGKYAYLLESTMNEYIEQRKPCDTMKVGGNLDSKGYGIATPKGSSLGNAVNLAVLKLNEQGLLDKLKNKWWYDKGEC

>d1ii5a\_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Synechocystis sp., GluR0}

GSAMALKVGVVGNPPFVFYGEGKNAAFTGISLDVWRAVAESQKWNSEYVRQNSISAGITAVAEGELDILIGPISVTPERAAIEGITFTQPYFSSGIGLLIPGTATPLFRSVGDLKNKEVAVVRDTTAVDWANFYQADVRETNNLTAAITLLQKKQVEAVMFDRPALIYYTRQNPNLNLEVTEIRVSLEPYGFVLKENSPLQKTINVEMLNLLYSRVIAEFTERWLG

>d1amf\_\_ c.94.1.1 (-) Molybdate-binding protein, ModA {Escherichia coli}

GKITVFAAASLTNAMQDIATQFKKEKGVDVVSSFASSSTLARQIEAGAPADLFISADQKWMDYAVDKKAIDTATRQTLLGNSLVVVAPKASVQKDFTIDSKTNWTSLLNGGRLAVGDPEHVPAGIYAKEALQKLGAWDTLSPKLAPAEDVRGALALVERNEAPLGIVYGSDAVASKGVKVVATFPEDSHKKVEYPVAVVEGHNNATVKAFYDYLKGPQAAEIFKRYGFTIK

>d1atg\_\_ c.94.1.1 (-) Molybdate-binding protein, ModA {Azotobacter vinelandii}

ELKVVTATNFLGTLEQLAGQFAKQTGHAVVISSGSSGPVYAQIVNGAPYNVFFSADEKSPEKLDNQGFALPGSRFTYAIGKLVLWSAKPGLVDNQGKVLAGNGWRHIAISNPQIAPYGLAGTQVLTHLGLLDKLTAQERIVEANSVGQAHSQTASGAADLGFVALAQIIQAAAKIPGSHWFPPANYYEPIVQQAVITKSTAEKANAEQFMSWMKGPKAVAIIKAAGYVLPQ

>d1al3\_\_ c.94.1.1 (-) Cofactor-binding fragment of CysB {Klebsiella aerogenes}

TWPDKGSLYVATTHTQARYALPGVIKGFIERYPRVSLHMHQGSPTQIAEAVSKGNADFAIATEALHLYDDLVMLPCYHWNRSIVVTPEHPLATKGSVSIEELAQYPLVTYTFGFTGRSELDTAFNRAGLTPRIVFTATDADVIKTYVRLGLGVGVIASMAVDPVSDPDLVKLDANGIFSHSTTKIGFRRSTFLRSYMYDFIQRFAPHLTRDVVDTAVALRSNEDIEAMFKDIKLPEK

>d1i6aa\_ c.94.1.1 (A:) Hydrogen peroxide-inducible genes activator OxyR, regulatory domain {Escherichia coli}

ETMSGPLHIGLIPTVGPYLLPHIIPMLHQTFPKLEMYLHEAQTHQLLAQLDSGKLDAVILALVKESEAFIEVPLFDEPMLLAIYEDHPWANREAVPMADLAGEKLLMLEDGHCLRDQAMGFCFEAGADEDTHFRATSLETLRNMVAAGSGITLLPALAVPPERKRDGVVYLPAIKPEPRRTIGLVYRPGSPLRSRYEQLAEAIRARMDGHFD

>d1kwha\_ c.94.1.1 (A:) Alginate-binding periplasmic protein AlgQ2 {Sphingomonas sp.}

KEATWVTDKPLTLKIHMHFRDKWVWDENWPVAKESFRLTNVKLQSVANKAATNSQEQFNLMMASGDLPDVVGGDNLKDKFIQYGQEGAFVPLNKLIDQYAPHIKAFFKSHPEVERAIKAPDGNIYFIPYVPDGVVARGYFIREDWLKKLNLKPPQNIDELYTVLKAFKEKDPNGNGKADEVPFIDRHPDEVFRLVNFWGARSSGSDNYMDFYIDNGRVKHPWAETAFRDGMKHVAQWYKEGLIDKEIFTRKAKAREQMFGGNLGGFTHDWFASTMTFNEGLAKTVPGFKLIPIAPPTNSKGQRWEEDSRQKVRPDGWAITVKNKNPVETIKFFDFYFSRPGRDISNFGVPGVTYDIKNGKAVFKDSVLKSPQPVNNQLYDMGAQIPIGFWQDYDYERQWTTPEAQAGIDMYVKGKYVMPGFEGVNMTREERAIYDKYWADVRTYMYEMGQAWVMGTKDVDKTWDEYQRQLKLRGLYQVLQMMQQAYDRQYKN

>d1cb6a2 c.94.1.2 (A:1335-1691) Lactoferrin {Human (Homo sapiens)}

EEEVAARRARVVWCAVGEQELRKCNQWSGLSEGSVTCSSASTTEDCIALVLKGEADAMSLDGGYVYTAGKCGLVPVLAENYKSQQSSDPDPNCVDRPVEGYLAVAVVRRSDTSLTWNSVKGKKSCHTAVDRTAGWNIPMGLLFNQTGSCKFDEYFSQSCAPGSDPRSNLCALCIGDEQGENKCVPNSNERYYGYTGAFRCLAENAGDVAFVKDVTVLQNTDGNNNEAWAKDLKLADFALLCLDGKRKPVTEARSCHLAMAPNHAVVSRMDKVERLKQVLLHQQAKFGRNGSDCPDKFCLFQSETKNLLFNDNTECLARLHGKTTYEKYLGPQYVAGITNLKKCSTSPLLEACEFLRK

>d1dot\_1 c.94.1.2 (1-334) Ovotransferrin {Duck (Anas platyrhynchos)}

APPKTTVRWCTISSAEEKKCNSLKDHMQQERVTLSCVQKATYLDCIKAISNNEADAISLDGGQVFEAGLAPYKLKPIAAEVYERSGGSTTSYYAVAVVKKGTDFMIKDLRGKTSCHTGLGRSAGWNIPIGTLIHREDIEWEGIESGISEQAVAKFFSASCVPGATIEQKLCRQCKGDAKTKCLRNGPYSGYSGAFQCLKDGKGDVAFVKHTTVQENAPEEKDEYELLCLDGSRQPVDSYKTCNWARVAAHAVVARDDSKIDDIWSFLGMQAYSLGVDTTSDFHLFGPPGKKDPVLKDLLFKDSAIMLKRVPELMDSQLYLGFEYYSAIQSLRKD

>d1afwa1 c.95.1.1 (A:25-293) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

KNSLLEKRPEDVVIVAANRSAIGKGFKGAFKDVNTDYLLYNFLNEFIGRFPEPLRADLNLIEEVACGNVLNVGAGATEHRAACLASGIPYSTPFVALNRQCSSGLTAVNDIANKIKVGQIDIGLALGVESMTNNYKNVNPLGMISSEELQKNREAKKCLIPMGITNENVAANFKISRKDQDEFAANSYQKAYKAKNEGLFEDEILPIKLPDGSICQSDEGPRPNVTAESLSSIRPAFIKDRGTTTAGNASQVSDGVAGVLLARRSVANQ

>d1afwa2 c.95.1.1 (A:294-417) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

LNLPVLGRYIDFQTVGVPPEIMGVGPAYAIPKVLEATGLQVQDIDIFEINEAFAAQALYCIHKLGIDLNKVNPRGGAIALGHPLGCTGARQVATILRELKKDQIGVVSMCIGTGMGAAAIFIKE

>d1qfla1 c.95.1.1 (A:4-268) Biosynthetic thiolase {Zoogloea ramigera}

SIVIASAARTAVGSFNGAFANTPAHELGATVISAVLERAGVAAGEVNEVILGQVLPAGEGQNPARQAAMKAGVPQEATAWGMNQLCGSGLRAVALGMQQIATGDASIIVAGGMESMSMAPHCAHLRGGVKMGDFKMIDTMIKDGLTDAFYGYHMGTTAENVAKQWQLSRDEQDAFAVASQNKAEAAQKDGRFKDEIVPFIVKGRKGDITVDADEYIRHGATLDSMAKLRPAFDKEGTVTAGNASGLNDGAAAALLMSEAEASRRG

>d1ek4a1 c.95.1.1 (A:1-253) Beta-ketoacyl-ACP synthase I {Escherichia coli}

MKRVVITGLGIVSSIGNNQQEVLASLREGRSGITFSQELKDSGMRSHVWGNVKLDTTGLIDRKVVRFMSDASIYAFLSMEQAIADAGLSPEAYQNNPRVGLIAGSGGGSPRFQVFGADAMRGPRGLKAVGPYVVTKAMASGVSACLATPFKIHGVNYSISSASATSAHCIGNAVEQIQLGKQDIVFAGGGEELCWEMACEFDAMGALSTKYNDTPEKASRTYDAHRDGFVIAGGGGMVVVEELEHALARGAHI

>d1kas\_1 c.95.1.1 (2-251) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KRRVVVTGLGMLSPVGNTVESTWKALLAGQSGISLIDHFDTSAYATKFAGLVKDFNCEDIISRKEQRKMDAFIQYGIVAGVQAMQDSGLEITEENATRIGAAIGSGIGGLGLIEENHTSLMNGGPRKISPFFVPSTIVNMVAGHLTIMYGLRGPSISIATACTSGVHNIGHAARIIAYGDADVMVAGGAEKASTPLGVGGFGAARALSTRNDNPQAASRPWDKERDGFVLGDGAGMLVLEEYEHAKKRGA

>d1kas\_2 c.95.1.1 (252-412) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KIYAELVGFGMSSDAYHMTSPPENGAGAALAMANALRDAGIEASQIGYVNAHGTSTPAGDKAEAQAVKTIFGEAASRVLVSSTKSMTGHLLGAAGAVESIYSILALRDQAVPPTINLDNPDEGCDLDFVPHEARQVSGMEYTLCNSFGFGGTNGSLIFKKI

>d1hnja2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}

ISTHLHADGSYGELLTLPNADRVNPENSIHLTMAGNEVFKVAVTELAHIVDETLAANNLDRSQLDWLVPHQANLRIISATAKKLGMSMDNVVVTLDRHGNTSAASVPCALDEAVRDGRIKPGQLVLLEAFGGGFTWGSALVRF

>d1hzpa1 c.95.1.1 (A:-10-174) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}

MTEIATTSGARSVGLLSVGAYRPERVVTNDEICQHIDSSDEWIYTRTGIKTRRFAADDESAASMATEACRRALSNAGLSAADIDGVIVTTNTHFLQTPPAAPMVAASLGAKGILGFDLSAGCAGFGYALGAAADMIRGGGAATMLVVGTEKLSPTIDMYDRGNCFIFADGAAAVVVGETPFQGI

>d1hzpa2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}

GPTVAGSDGEQADAIRQDIDWITFAQNPSGPRPFVRLEGPAVFRWAAFKMGDVGRRAMDAAGVRPDQIDVFVPHQANSRINELLVKNLQLRPDAVVANDIEHTGNTSAASIPLAMAELLTTGAAKPGDLALLIGYGAGLSYAAQVVRM

>d1bi5a1 c.95.1.2 (A:1-235) Chalcone synthase {Alfalfa (Medicago sativa)}

MVSVSEIRKAQRAEGPATILAIGTANPANCVEQSTYPDFYFKITNSEHKTELKEKFQRMCDKSMIKRRYMYLTEEILKENPNVCEYMAPSLDARQDMVVVEVPRLGKEAAVKAIKEWGQPKSKITHLIVCTTSGVDMPGADYQLTKLLGLRPYVKRYMMYQQGAFAGGTVLRLAKDLAENNKGARVLVVCSEVTAVTFRGPSDTHLDSLVGQALFGDGAAALIVGSDPVPEIEKP

>d1ee0a2 c.95.1.2 (A:236-395) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}

AVERPIFEIVSTDQTILPDTEKAMKLHLREGGLTFQLHRDVPLMVAKNIENAAEKALSPLGITDWNSVFWMVHPGGRAILDQVERKLNLKEDKLRASRHVLSEYGNLISACVLFIIDEVRKRSMAEGKSTTGEGLDCGVLFGFGPGMTVETVVLRSVRVT

>d1aln\_1 c.97.1.1 (1-150) Cytidine deaminase {Escherichia coli}

MHPRFQTAFAQLADNLQSALEPILADKYFPALLTGEQVSSLKSATGLDEDALAFALLPLAAACARTPLSNFNVGAIARGVSGTWYFGANMEFIGATMQQTVHAEQSAISHAWLSGEKALAAITVNYTPCGHCRQFMNELNSGLDLRIHLP

>d1aln\_2 c.97.1.1 (151-294) Cytidine deaminase {Escherichia coli}

GREAHALRDYLPDAFGPKDLEIKTLLMDEQDHGYALTGDALSQAAIAAANRSHMPYSKSPSGVALECKDGRIFSGSYAENAAFNPTLPPLQGALILLNLKGYDYPDIQRAVLAEKADAPLIQWDATSATLKALGCHSIDRVLLA

>d1fus\_\_ d.1.1.1 (-) RNase F1 {Fusarium moniliforme}

ESATTCGSTNYSASQVRAAANAACQYYQNDDTAGSSTYPHTYNNYEGFDFPVDGPYQEFPIKSGGVYTGGSPGADRVVINTNCEYAGAITHTGASGNNFVGCSGTN

>d1rtu\_\_ d.1.1.1 (-) RNase U2 {Ustilago sphaerogena}

CDIPQSTNCGGNVYSNDDINTAIQGALDDVANGDRPDNYPHQYYXEASEDITLCCGSGPWSEFPLVYNGPYYSSRDNYVSPGPDRVIYQTNTGEFCATVTHTGAASYDGFTQCS

>d1goua\_ d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}

AVINTFDGVADYLIRYKRLPNDYITKSQASALGWVASKGDLAEVAPGKSIGGDVFSNREGRLPSAGSRTWREADINYVSGFRNADRLVYSSDWLIYKTTDHYATFTRIR

>d0rst\_\_ d.1.1.1 (-) RNase St {Streptomyces erythreus}

QAPCGDTSGFEEVRLADLPPEATDTYELIEKGGPYPYPEDGTVFENREGILPDCAEGYYHEYTVKTPSGDDRGARRFVVGDGGEYFYTEDHYESFRLTIVN

>d1de3a\_ d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus giganteus), alpha-Sarcin}

AVTWTCLNDQKNPKTNKYETKRLLYNQNKAESNSHHAPLSDGKTGSSYPHWFTNGYDGDGKLPKGRTPIKFGKSDCDRPPKHSKDGNGKTDHYLLEFPTFPDGHDYKFDSKKPKENPGPARVIYTYPNKVFCGIIAHTKENQGELKLCSH

>d1lsg\_1 d.2.1.2 (1-144) Lysozyme {Chicken (Gallus gallus)}

MKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRLQQHHLGGAKQAGDV

>d1b9oa\_ d.2.1.2 (A:) alpha-Lactalbumin {Human (Homo sapiens)}

KQFTKCELSQLLKDIDGYGGIALPELICTMFHTSGYDTQAIVENDESTEYGLFQISNKLWCKSSQVPQSRNICDISCDKFLDDDITDDIMCAKKILDIKGIDYWLAHKALCTEKLEQWLCEKL

>d1qsaa2 d.2.1.6 (A:451-618) 70 kDa soluble lytic transglycosylase, SLT70 {Escherichia coli}

LAYNDLFKRYTSGKEIPQSYAMAIARQESAWNPKVKSPVGASGLMQIMPGTATHTVKMFSIPGYSSPGQLLDPETNINIGTSYLQYVYQQFGNNRIFSSAAYNAGPGRVRTWLGNSAGRIDAVAFVESIPFSETRGYVKNVLAYDAYYRYFMGDKPTLMSATEWGRRY

>d1qusa\_ d.2.1.6 (A:) 36 kDa soluble lytic transglycosylase, SLT35 {Escherichia coli}

MVEPQHNVMQMGGDFANNPNAQQFIDKMVNKHGFDRQQLQEILSQAKRLDSVLRLMDNQAPTTSVKPPSGPNGAWLRYRKKFITPDNVQNGVVFWNQYEDALNRAWQVYGVPPEIIVGIIGVETRWGRVMGKTRILDALATLSFNYPRRAEYFSGELETFLLMARDEQDDPLNLKGSFAGAMGYGQFMPSSYKQYAVDFSGDGHINLWDPVDAIGSVANYFKAHGWVKGDQVAVMANGQAPGLPNGFKTKYSISQLAAAGLTPQQPLGNHQQASLLRLDVGTGYQYWYGLPNFYTITRYNHSTHYAMAVWQLGQAVALARVQ

>d1chka\_ d.2.1.7 (A:) Endochitosanase {Streptomyces sp., strain N174}

AGAGLDDPHKKEIAMELVSSAENSSLDWKAQYKYIEDIGDGRGYTGGIIGFCSGTGDMLELVQHYTDLEPGNILAKYLPALKKVNGSASHSGLGTPFTKDWATAAKDTVFQQAQNDERDRVYFDPAVSQAKADGLRALGQFAYYDAIVMHGPGNDPTSFGGIRKTAMKKARTPAQGGDETTYLNGFLDARKAAMLTEAAHDDTSRVDTEQRVFLKAGNLDLNPPLKWKTYGDPYVINS

>d1qgia\_ d.2.1.7 (A:) Endochitosanase {Bacillus circulans}

ASPDDNFSPETLQFLRNNTGLDGEQWNNIMKLINKPEQDDLNWIKYYGYCEDIEDERGYTIGLFGATTGGSRDTHPDGPDLFKAYDAAKGASNPSADGALKRLGINGKMKGSILEIKDSEKVFCGKIKKLQNDAAWRKAMWETFYNVYIRYSVEQARQRGFTSAVTIGSFVDTALNQGATGGSDTLQGLLARSGSSSNEKTFMKNFHAKRTLVVDTNKYNKPPNGKNRVKQWDTLVDMGKMNLKNVDSEIAQVTDWEMK

>d1pcia\_ d.3.1.1 (A:) Caricain (protease omega) {Papaya (Carica papaya)}

LTSTERLIQLFNSWMLNHNKFYENVDEKLYRFEIFKDNLNYIDETNKKNNSYWLGLNEFADLSNDEFNEKYVGSLIDATIEQSYDEEFINEDIVNLPENVDWRKKGAVTPVRHQGSCGSCWAFSAVATVEGINKIRTGKLVELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKYPYKAKQGTCRAKQVGGPIVKTSGVGRVQPNNEGNLLNAIAKQPVSVVVESKGRPFQLYKGGIFEGPCGTKVDGAVTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPGVCGLYKSSYYPTKN

>d3gcb\_\_ d.3.1.1 (-) Bleomycin hydrolase {Baker's yeast (Saccharomyces cerevisiae), Gal6}

AFQGAMASSIDISKINSWNKEFQSDLTHQLATTVLKNYNADDALLNKTRLQKQDNRVFNTVVSTDSTPVTNQKSSGRAWLFAATNQLRLNVLSELNLKEFELSQAYLFFYDKLEKANYFLDQIVSSADQDIDSRLVQYLLAAPTEDGGQYSMFLNLVKKYGLIPKDLYGDLPYSTTASRKWNSLLTTKLREFAETLRTALKERSADDSIIVTLREQMQREIFRLMSLFMDIPPVQPNEQFTWEYVDKDKKIHTIKSTPLEFASKYAKLDPSTPVSLINDPRHPYGKLIKIDRLGNVLGGDAVIYLNVDNETLSKLVVKRLQNNKAVFFGSHTPKFMDKKTGVMDIELWNYPAIGYNLPQQKASRIRYHESLMTHAMLITGCHVDETSKLPLRYRVENSWGKDSGKDGLYVMTQKYFEEYCFQIVVDINELPKELASKFTSGKEEPIVLPIWDPMGALA

>d2cb5a\_ d.3.1.1 (A:) Bleomycin hydrolase {Human (Homo sapiens)}

SSSGLNSEKVAALIQKLNSDPQFVLAQNVGTTHDLLDICLKRATVQRAQHVFQHAVPQEGKPITNQKSSGRSWIFSCLNVMRLPFMKKLNIEEFEFSQSYLFFWDKVERCYFFLSAFVDTAQRKEPEDGRLVQFLLMNPANDGGQWDMLVNIVEKYGVIPKKCFPESYTTEATRRMNDILNHKMREFCIRLRNLVHSGATKGEISATQDVMMEEIFRVVCICLGNPPETFTWEYRDKDKNYEKIGPITPLEFYREHVKPLFNMEDKICLVNDPRPQHKHNKLYTVEYLSNMVGGRKTLYNNQPIDFLKKMVAASIKDGEAVWFGCDVGKHFNSKLGLSDMNLYDHELVFGVSLKNMNKAERLTFGESLMTHAMTFTAVSEKDDQDGAFTKWRVENSWGEDHGHKGYLCMTDEWFSEYVYEVVVDRKHVPEEVLAVLEQEPIILPAWDPMGALA

>d3pbh\_\_ d.3.1.1 (-) (Pro)cathepsin B {Human (Homo sapiens)}

MRSRPSFHPLSDELVNYVNKRNTTWQAGHNFYNVDMSYLKRLCGTFLGGPKPPQRVMFTEDLKLPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHTNAHVSVEVSAEDLLTCCGSMCGDGCNGGYPAEAWNFWTRKGLVSGGLYESHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYKQDKHYGYNSYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGGHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTD

>d1cs8a\_ d.3.1.1 (A:) (Pro)cathepsin L {Human (Homo sapiens)}

SLTFDHSLEAQWTKWKAMHNRLYGMNEEGWRRAVWEKNMKMIELHNQEYREGKHSFTMAMNAFGDMTSEEFRQVMNGFQNRKPRKGKVFQEPLFYEAPRSVDWREKGYVTPVKNQGQCGSCWAFSATGALEGQMFRKTGRLISLSEQNLVDCSGPQGNEGCNGGLMDYAFQYVQDNGGLDSEESYPYEATEESCKYNPKYSVANDAGFVDIPKQEKALMKAVATVGPISVAIDAGHESFLFYKEGIYFEPDCSSEDMDHGVLVVGYGFESTESDNNKYWLVKNSWGEEWGMGGYVKMAKDRRNHCGIASAASYPTV

>d1deua\_ d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}

RGQTCYRPLRGDGLAPLGRTTYPRPHEYLSPADLPKSWDWRNVDGVNYASITRNQHIPQYCGSCWAHASTSAMADRINIKRKGAWPSTLLSVQNVIDCGNAGSCEGGNDLSVWDYAHQHGIPDETCNNYQAKDQECDKFNQCGTCNEFKECHAIRNYTLWRVGDYGSLSGREKMMAEIYANGPISCGIMATERLANYTGGIYAEYQDTTYINHVVSVAGWGISDGTEYWIVRNSWGEPWGERGWLRIVTSTYKDGKGARYNLAIEEHCTFGDPIV

>d1cv8\_\_ d.3.1.1 (-) Staphopain {Staphylococcus aureus}

NEQYVNKLENFKIRETQGNNGWCAGYTMSALLNATYNTNKYHAEAVMRFLHPNLQGQQFQFTGLTPREMIYFGQTQGRSPQLLNRMTTYNEVDNLTKNNKGIAILGSRVESRNGMHAGHAMAVVGNAKLNNGQEVIIIWNPWDNGFMTQDAKNNVIPVSNGDHYQWYSSIYGY

>d1dkia\_ d.3.1.1 (A:) Streptococcal pyrogenic exotoxin B {Streptococcus pyogenes}

LDKVNLGGELSGSNMYVYNISTGGFVIVSGDKRSPEILGYSTSGSFDVNGKENIASFMESYVEQIKENKKLDSTYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGSVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRGDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVGIKP

>d1uch\_\_ d.3.1.6 (-) Ubiquitin C-terminal hydrolase UCH-l3 {Human (Homo sapiens)}

RWLPLEANPEVTNQFLKQLGLHPNWQFVDVYGMDPELLSMVPRPVCAVLLLFPITEKYEVFRTEEEEKIKSQGQDVTSSVYFMKQTISNACGTIGLIHAIANNKDKMHFESGSTLKKFLEESVSMSPEERARYLENYDAIRVTHETSAHEGQTEAPSIDEKVDLHFIALVHVDGHLYELDGRKPFPINHGETSDETLLEDAIEVCKKFMERDPDELRFNAIALSAA

>d1cmxa\_ d.3.1.6 (A:) Ubiquitin C-terminal hydrolase UCH-l3 {Synthetic, based on Saccharomyces cerevisiae sequence}

RAVVPIESNPEVFTNFAHKLGLKNEWAYFDIYSLTEPELLAFLPRPVKAIVLLFPINEDRKSSTSQQITSSYDVIWFKQSVKNACGLYAILHSLSNNQSLLEPGSDLDNFLKSQSDTSSSKNRFDDVTTDQFVLNVIKENVQTFSTGQSEAPEATADTNLHYITYVEENGGIFELDGRNLSGPLYLGKSDPTATDLIEQELVRVRVASYMENANEEDVLNFAMLGLGPN

>d1avpa\_ d.3.1.7 (A:) Human adenovirus 2 proteinase {Mastadenovirus H2}

MGSSEQELKAIVKDLGCGPYFLGTYDKRFPGFVSPHKLACAIVNTAGRETGGVHWMAFAWNPRSKTCYLFEPFGFSDQRLKQVYQFEYESLLRRSAIASSPDRCITLEKSTQSVQGPNSAACGLFCCMFLHAFANWPQTPMDHNPTMNLITGVPNSMLNSPQVQPTLRRNQEQLYSFLERHSPYFRSHSAQIRSATSFCHLKNM

>d1euva\_ d.3.1.7 (A:) Ulp1 protease C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

GSLVPELNEKDDDQVQKALASRENTQLMNRDNIEITVRDFKTLAPRRWLNDTIIEFFMKYIEKSTPNTVAFNSFFYTNLSERGYQGVRRWMKRKKTQIDKLDKIFTPINLNQSHWALGIIDLKKKTIGYVDSLSNGPNAMSFAILTDLQKYVMEESKHTIGEDFDLIHLDCPQQPNGYDCGIYVCMNTLYGSADAPLDFDYKDAIRMRRFIAHLILTDALK

>d1h8xa\_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSQKERHIIVACEGSPYVPVHFDASVE

>d1bc4\_\_ d.5.1.1 (-) Cytotoxic ribonuclease {Bullfrog (Rana catesbeiana)}

ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP

>d1hi2a\_ d.5.1.1 (A:) Eosinophil-derived neurotoxin (EDN) {Human (Homo sapiens)}

MKPPQFTWAQWFETQHINMTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGNPNMTCPSNKTRKNCHHSGSQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVHLDRII

>d1agi\_\_ d.5.1.1 (-) Angiogenin {Cow (Bos taurus)}

AQDDYRYIHFLTQHYDAKPKGRNDEYCFNMMKNRRLTRPCKDRNTFIHGNKNDIKAICEDRNGQPYRGDLRISKSEFQITICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHFDESFITPRH

>d1i4ma\_ d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}

GAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY

>d1i17a\_ d.6.1.1 (A:) Prion-like protein Doppel {Mouse (Mus musculus)}

RVAENRPGAFIKQGRKLDIDFGAEGNRYYAANYWQFPDGIYYEGCSEANVTKEMLVTSCVNATQAANQAEFSREKQDSKLHQRVLWRLIKEICSAKHCDFWLERGAA

>d1mgsa\_ d.9.1.1 (A:) Melanoma growth stimulating activity (MGSA) {Human (Homo sapiens)}

ASVATELRCQCLQTLQGIHPKNIQSVNVKSPGPHCAQTEVIATLKNGRKACLNPASPIVKKIIEKMLNSDKSN

>d1huna\_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens), 1-beta}

APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQEYVYDLELN

>d1ha6a\_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Mouse (Mus musculus), ccl20/mip-3a}

ASNYDCCLSYIQTPLPSRAIVGFTRQMADEACDINAIIFHTKKRKSVCADPKQNWVKRAVNLLSLRVKKM

>d1esra\_ d.9.1.1 (A:) Monocyte chemoattractant protein-2 (MCP-2) {Human (Homo sapiens)}

EPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTQRGKEVCADPKERWVRDSMKHLDQIFQNLKP

>d1el0a\_ d.9.1.1 (A:) CC chemokine I-309 {Human (Homo sapiens)}

SKSMQVPFSRCCFSFAEQEIPLRAILCYRNTSSICSNEGLIFKLKRGKEACALDTVGWVQRHRKMLRHCPSKRK

>d1eiha\_ d.9.1.1 (A:) Eotaxin-2 {Human (Homo sapiens)}

VVIPSPCCMFFVSKRIPENRVVSYQLSSRSTCLKAGVIFTTKKGQQSCGDPKQEWVQRYMKNLDAKQKKASPR

>d1j9oa\_ d.9.1.1 (A:) Lymphotactin {Human (Homo sapiens)}

VGSEVSDKRTCVSLTTQRLPVSRIKTYTITEGSLRAVIFITKRGLKVCADPQATWVRDVVRSMDRKSNTRNNMIQTKPTGTQQSTNTAVTLTG

>d1b2ta\_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}

MQHHGVTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVKDAMQHLDRQAAALTRNG

>d1a15a\_ d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}

KPVSLSYRCPCRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN

>d1g91a\_ d.9.1.1 (A:) Myeloid progenitor inhibitory factor-1 (MPIF-1) {Human (Homo sapiens)}

MDRFHATSADCCISYTPRSIPCSLLESYFETNSECSKPGVIFLTKKGRRFCANPSDKQVQVCMRMLKLDTRIKTRKN

>d1ap0\_\_ d.9.2.2 (-) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMVEEVLEEEEEEYVVEKVLDRRVVKGKVEYLLKWKGFSDEDNTWEPEENLDCPDLIAEFLQSQKTAHETDKS

>d1dz1a\_ d.9.2.2 (A:) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMKEESEKPRGFARGLEPERIIGATDSSGELMFLMKWKNSDEADLVPAKEANVKCPQVVISFYEERLTWH

>d1e0ba\_ d.9.2.2 (A:) HP1 homologue SWI6 {Fission yeast (Schizosaccharomyces pombe)}

QVENYDSWEDLVSSIDTIERKDDGTLEIYLTWKNGAISHHPSTITNKKCPQKMLQFYESHL

>d1g6za\_ d.9.2.2 (A:) Histone methyltransferase clr4 chromo domain {Fission yeast (Schizosaccharomyces pombe)}

ISSPKQEEYEVERIVDEKLDRNGAVKLYRIRWLNYSSRSDTWEPPENLSGCSAVLAEWKRRKRRLKGSNS

>d1qk9a\_ d.10.1.3 (A:) Methyl-CpG-binding protein 2, MECP2 {Human (Homo sapiens)}

ASASPKQRRSIIRDRGPMYDDPTLPEGWTRKLKQRKSGRSAGKYDVYLINPQGKAFRSKVELIAYFEKVGDTSLDPNDFDFTVTGRGSGSGC

>d1d9na\_ d.10.1.3 (A:) Methylation-dependent transcriptional repressor MBD1/PCM1 {Human (Homo sapiens)}

MAEDWLDCPALGPGWKRREVFRKSGATCGRSDTYYQSPTGDRIRSKVELTRYLGPACDLTLFDFKQGILCYPAPK

>d1k25a1 d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}

TESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQQVLLLSDK

>d1k25a2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}

VEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLGD

>d4rhn\_\_ d.13.1.1 (-) Histidine triad nucleotide-binding protein (HINT) {Rabbit (Oryctolagus cuniculus)}

RPGGDTIFGKIIRKEIPAKIIFEDDQCLAFHDISPQAPTHFLVIPKKHISQISAAEDADESLLGHLMIVGKKCAADLGLKKGYRMVVNEGSDGGQSVYHVHLHVLGGRQMNWPPG

>d1emsa1 d.13.1.1 (A:281-440) NIT-FHIT fusion protein, C-terminal domain {Nematode (Caenorhabditis elegans)}

RSDLYTLHINEKSSETGGLKFARFNIPADHIFYSTPHSFVFVNLKPVTDGHVLVSPKRVVPRLTDLTDAETADLFIVAKKVQAMLEKHHNVTSTTICVQDGKDAGQTVPHVHIHILPRRAGDFGDNEIYQKLASHDKEPERKPRSNEQMAEEAVVYRNLM

>d1guqa1 d.13.1.2 (A:2-177) Galactose-1-phosphate uridylyltransferase {Escherichia coli}

TQFNPVDHPHRRYNPLTGQWILVSPHRAKRPWQGAQETPAKQVLPAHDPDCFLCAGNVRVTGDKNPDYTGTYVFTNDFAALMSDTPDAPESHDPLMRCQSARGTSRVICFSPDHSKTLPELSVAALTEIVKTWQEQTAELGKTYPWVQVFENKGAAMGCSNPHPGGQIWANSFLPN

>d1guqa2 d.13.1.2 (A:178-348) Galactose-1-phosphate uridylyltransferase {Escherichia coli}

EAEREDRLQKEYFAEQKSPMLVDYVQRELADGSRTVVETEHWLAVVPYWAAWPFETLLLPKAHVLRITDLTDAQRSDLALALKKLTSRYDNLFQCSFPYSMGWHGAPFNGEENQHWQLHAHFYPPLLRSATVRKFMVGYEMLAETQRDLTAEQAAERLRAVSDIHFRESGV

>d1k6za\_ d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}

SFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSHNIFSQDILKPILSWDEVGGHPVLWNRQPLNSLDNNSLYTQLEMLVQGAERLQTSSLISPPRSFSHH

>d1jyoa\_ d.198.1.1 (A:) Virulence effector SptP secretion chaperone SicP {Salmonella typhimurium}

LQAHQDIIANIGEKLGLPLTFDDNNQCLLLLDSDIFTSIEAKDDIWLLNGMIIPLSPVCGDSIWRQIMVINGELAANNEGTLAYIDAAETLLLIHAITDLTNTYHIISQLESFVNQQEALKNILQEYAKV

>d1k3ea\_ d.198.1.1 (A:) Secretion chaperone CesT {Escherichia coli}

MSSRSELLLEKFAEKIGIGSISFNENRLCSFAIDEIYYISLSDANDEYMMIYGVCGKFPTDNSNFALEILNANLWFAENGGPYLCYEAGAQSLLLALRFPLDDATPEKLENEIEVVVKSMENLYLVLHNQGITLENEHMKIEEISS

>d1k3sa\_ d.198.1.1 (A:) Secretion chaperone SigE {Salmonella enterica}

MESLLNRLYDALGLDAPEDEPLLIIDDGIQVYFNESDHTLEMCCPFMPLPDDILTLQHFLRLNYTSAVTIGADADNTALVALYRLPQTSTEEEALTGFELFISNVKQLKEHYA

>d1k8kf\_ d.198.2.1 (F:) ARPC4 (20 kDa subunit) {Cow (Bos taurus)}

TATLRPYLSAVRATLQAALCLENFSSQVVERHNKPEVEVRSSKELLLQPVTISRNEKEKVLIEGSINSVRVSIAVKQADEIEKILCHKFMRFMMMRAENFFILRRKPVEGYDISFLITNFHTEQMYKHKLVDFVIHFMEEIDKEISEMKLSVNARARIVAEEFLKNF

>d1k8kd1 d.198.2.1 (D:1-120) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

MILLEVNNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTKVMVSISLKFYKELQAHGADELLKRVYGSYLVNPESGYNVSLLYDLENLPASKDSIVHQAGMLKRNC

>d1k8kd2 d.198.2.1 (D:121-284) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

FASVFEKYFQFQEEGKEGENRAVIHYRDDETMYVESKKDRVTVVFSTVFKDDDDVVIGKVFMQEFKEGRRASHTAPQVLFSHREPPLELKDTDAAVGDNIGYITFVLFPRHTNASARDNTINLIHTFRDYLHYHIKCSKAYIHTRMRAKTSDFLKVLNRARPDA

>d1dar\_3 d.14.1.1 (476-599) Elongation factor G (EF-G), domain IV {Thermus thermophilus}

VGKPQVAYRETITKPVDVEGKFIRQTGGRGQYGHVKIKVEPLPRGSGFEFVNAIVGGVIPKEYIPAVQKGIEEAMQSGPLIGFPVVDIKVTLYDGSYHEVDSSEMAFKIAGSMAIKEAVQKGDP

>d1fjge1 d.14.1.1 (E:74-154) Ribosomal protein S5, C-terminal domain {Thermus thermophilus}

GTIPHEIEVEFGASKIVLKPAAPGTGVIAGAVPRAILELAGVTDILTKELGSRNPINIAYATMEALRQLRTKADVERLRKG

>d1fjgi\_ d.14.1.1 (I:) Ribosomal protein S9 {Thermus thermophilus}

EQYYGTGRRKEAVARVFLRPGNGKVTVNGQDFNEYFQGLVRAVAALEPLRAVDALGRFDAYITVRGGGKSGQIDAIKLGIARALVQYNPDYRAKLKPLGFLTRDARVVERKKYGKHKARRAPQYSKR

>d1b63a1 d.14.1.3 (A:217-331) DNA mismatch repair protein MutL {Escherichia coli}

GTAFLEQALAIEWQHGDLTLRGWVADPNHTTPALAEIQYCYVNGRMMRDRLINHAIRQACEDKLGADQQPAFVLYLEIDPHQVDVNVHPAKHEVRFHQSRLVHDFIYQGVLSVLQ

>d1h7sa1 d.14.1.3 (A:232-365) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GQKQLQSLIPFVQLPPSDSVCEEYGLSCSDALHNLFYISGFISQCTHGVGRSSTDRQFFFINRRPCDPAKVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTPDKRQILLQEEKLLLAVLKTSLIGMFDS

>d1ei1a1 d.14.1.3 (A:221-392) DNA gyrase B {Escherichia coli}

GIKAFVEYLNKNKTPIHPNIFYFSTEKDGIGVEVALQWNDGFQENIYCFTNNIPQRDGGTHLAGFRAAMTRTLNAYMDKEGYSKKAKVSATGDDAREGLIAVVSVKVPDPKFSSQTKDKLVSSEVKSAVEQQMNELLAEYLLENPTDAKIVVGKIIDAARAREAARRAREMT

>d1e3ha2 d.14.1.4 (A:3-151) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}

NETHYAEAVIDNGAFGTRTIRFETGRLARQAAGSAVAYLDDDTMVLSATTASKNPKDQLDFFPLTVDVEERMYAAGKIPGSFFRREGRPSEDAILTCRLIDRPLRPSFKKGLRNEIQVVATIMALNPDHLYDVVAINAASASTQLAGLP

>d1e3ha3 d.14.1.4 (A:346-482) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}

TDIRTLAAEVEAIPRVHGSALFERGETQILGVTTLNMLRMEQQLDTLSPVTRKRYMHNYNFPPYSVGETGRVGSPKRREIGHGALAERAIVPVLPTREEFPYAIRQVSEALGSNGSTSMGSVCASTMSLLNAGVPLK

>d1h72c1 d.14.1.5 (C:5-167) Homoserine kinase {Archaeon Methanococcus jannaschii}

MKVRVKAPCTSANLGVGFDVFGLCLKEPYDVIEVEAIDDKEIIIEVDDKNIPTDPDKNVAGIVAKKMIDDFNIGKGVKITIKKGVKAGSGLGSSAASSAGTAYAINELFKLNLDKLKLVDYASYGELASSGAKHADNVAPAIFGGFTMVTNYEPLEVLHIPID

>d1fi4a1 d.14.1.5 (A:3-190) Mevalonate 5-diphosphate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

VYTASVTAPVNIATLKYWGKRDTKLNLPTNSSISVTLSQDDLRTLTSAATAPEFERDTLWLNGEPHSIDNERTQNCLRDLRQLRKEMESKDASLPTLSQWKLHIVSENNFPTAAGLASSAAGFAALVSAIAKLYQLPQSTSEISRIARKGSGSACRSLFGGYVAWEMGKAEDGHDSMAVQIADSSDWP

>d1c3ta\_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}

MQLFVKTLTGKTLTVELEPSDTVENLKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNLQKESTIHLVLRLRGG

>d1a5r\_\_ d.15.1.1 (-) SUMO-1 (smt3 homologue) {Human (Homo sapiens)}

GSMSDQEAKPSTEDLGDKKEGEYIKLKVIGQDSSEIHFKVKMTTHLKKLKESYCQRQGVPMNSLRFLFEGQRIADNHTPKELGMEEEDVIEVYQEQTGGHSTV

>d1vcba\_ d.15.1.1 (A:) Elongin B {Human (Homo sapiens)}

MDVFLMIRRHKTTIFTDAKESSTVFELKRIVEGILKRPPDEQRLYKDDQLLDDGKTLGECGFTSQTARPQAPATVGLAFRADDTFEALCIEPFSSPPE

>d1h8ca\_ d.15.1.2 (A:) Fas-assosiated factor 1, Faf1 {Human (Homo sapiens)}

NAEPVSKLRIRTPSGEFLERRFLASNKLQIVFDFVASKGFPWDEYKLLSTFPRRDVTQLDPNKSLLEVKLFPQETLFLEAKE

>d1i42a\_ d.15.1.2 (A:) p47 {Rat (Rattus norvegicus)}

KASSSILINEAEPTTNIQIRLADGGRLVQKFNHSHRISDIRLFIVDARPAMAATSFVLMTTFPNKELADENQTLKEANLLNAVIVQRLT

>d1gc7a3 d.15.1.4 (A:1-87) Radixin {Mouse (Mus musculus)}

MPKPINVRVTTMDAELEFAIQPNTTGKQLFDQVVKTVGLREVWFFGLQYVDSKGYSTWLKLNKKVTQQDVKKENPLQFKFRAKFFPE

>d1gg3a3 d.15.1.4 (A:1-81) Erythroid membrane protein 4.1R {Human (Homo sapiens)}

MHCKVSLLDDTVYECVVEKHAKGQDLLKRVCEHLNLLEEDYFGLAIWDNATSKTWLDSAKEIKKQVRGVPWNFTFNVKFYP

>d1c1yb\_ d.15.1.5 (B:) c-Raf1 RBD {Human (Homo sapiens)}

SNTIRVFLPNKQRTVVNVRNGMSLHDCLMKALKVRGLQPECCAVFRLLHEHKGKKARLDWNTDAASLIGEELQVDFL

>d1raxa\_ d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RalGDS {Human (Homo sapiens)}

QQVGDCCIIRVSLDVDNGNMYKSILVTSQDKAPAVIRKAMDKHNLEEEEPEDYELLQILSDDRKLKIPENANVFYAMNSTANYDFVLKKRTFT

>d1e8xa3 d.15.1.5 (A:142-321) Phoshoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}

AASEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDPALDEVRKE

>d1i35a\_ d.15.1.5 (A:) Protein kinase byr2 {Yest (Schizosaccharomyces pombe)}

CILRFIACNGQTRAVQSRGDYQKTLAIALKKFSLEDASKFIVCVSQSSRIKLITEEEFKQICFNSSSPERDRLIIVPKEKPCPSFEDLRRSWEIE

>d1d4ba\_ d.15.2.1 (A:) Cell death-inducing effector B (CIDE-B), N-terminal domain {Human (Homo sapiens)}

MEYLSALNPSDLLRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATRQELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLMVLQSGQSWSPTRSGVLHHHHHH

>d1c9fa\_ d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Mouse (Mus musculus)}

MCAVLRQPKCVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCFPGLPNDAELLLLTAGETWHGYVSD

>d1f2ri\_ d.15.2.1 (I:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Mouse (Mus musculus)}

MELSRGASAPDPDDVRPLKPCLLRRNHSRDQHGVAASSLEELRSKACELLAIDKSLTPITLVLAEDGTIVDDDDYFLCLPSNTKFVALACNEKWTYNDSD

>d1f0za\_ d.15.3.2 (A:) Thiamin biosynthesis sulfur carrier protein ThiS {Escherichia coli}

MQILFNDQAMQCAAGQTVHELLEQLDQRQAGAALAINQQIVPREQWAQHIVQDGDQILLFQVIAGG

>d1jsba\_ d.15.3.2 (A:) Hypothetical protein MTH1743 {Archaeon Methanobacterium thermoautotrophicum}

MVIGMKFTVITDDGKKILESGAPRRIKDVLGELEIPIETVVVKKNGQIVIDEEEIFDGDIIEVIRVIYGG

>d1frd\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Cyanobacterium (Anabaena sp.), pcc 7119 and 7120}

ASYQVRLINKKQDIDTTIEIDEETTILDGAEENGIELPFSCHSGSCSSCVGKVVEGEVDQSDQIFLDDEQMGKGFALLCVTYPRSNCTIKTHQEPYLA

>d1doi\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Archaeon Haloarcula marismortui}

PTVEYLNYEVVDDNGWDMYDDDVFGEASDMDLDDEDYGSLEVNEGEYILEAAEAQGYDWPFSCRAGACANCAAIVLEGDIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVKIVYNAKHLDYLQNRVI

>d1e9ma\_ d.15.4.1 (A:) Ferredoxin VI {Rhodobacter capsulatus}

AKIIFIEHNGTRHEVEAKPGLTVMEAARDNGVPGIDADCGGACACSTCHAYVDPAWVDKLPKALPTETDMIDFAYEPNPATSRLTCQIKVTSLLDGLVVHLPEKQI

>d1b9ra\_ d.15.4.1 (A:) Terpredoxin {Pseudomonas sp.}

PRVVFIDEQSGEYAVDAQDGQSLMEVATQNGVPGIVAECGGSCVCATCRIEIEDAWVEIVGEANPDENDLLQSTGEPMTAGTRLSCQVFIDPSMDGLIVRVPLPA

>d1ayfa\_ d.15.4.1 (A:) Adrenodoxin {Cow (Bos taurus)}

KITVHFINRDGETLTTKGKIGDSLLDVVVQNNLDIDGFGACEGTLACSTCHLIFEQHIFEKLEAITDEENDMLDLAYGLTDRSRLGCQICLTKAMDNMTVRVP

>d1feha2 d.15.4.2 (A:1-126) Fe-only hydrogenase, N-terminal domain {Clostridium pasteurianum}

MKTIIINGVQFNTDEDTTILKFARDNNIDISALCFLNNCNNDINKCEICTVEVEGTGLVTACDTLIEDGMIINTNSDAVNEKIKSRISQLLDIHEFKCGPCNRRENCEFLKLVIKYKARASKPFLP

>d1dgja2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio desulfuricans}

METKTLIVNGMARRLLVSPNDLLVDVLRSQLQLTSVKVGCGKGQCGACTVILDGKVVRACIIKMSRVAENASVTTLEGIG

>d1fo4a2 d.15.4.2 (A:3-92) Xanthine oxidase, N-terminal domain {Cow (Bos taurus)}

ADELVFFVNGKKVVEKNADPETTLLAYLRRKLGLRGTKLGCGEGGCGACTVMLSKYDRLQDKIIHFSANACLAPICTLHHVAVTTVEGIG

>d1ffva2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein, N-domain {Hydrogenophaga pseudoflava}

KKIITVNVNGKAQEKAVEPRTLLIHFLREELNLTGAHIGCETSHCGACTVDIDGRSVKSCTHLAVQCDGSEVLTVEGLA

>d2pia\_3 d.15.4.2 (224-321) Phthalate dioxygenase reductase, C-terminal domain {Pseudomonas cepacia, db01}

SFGATNTNARENTPFTVRLSRSGTSFEIPANRSILEVLRDANVRVPSSCESGTCGSCKTALCSGEADHRDMVLRDDEKGTQIMVCVSRAKSAELVLDL

>d1fumb2 d.15.4.2 (B:1-105) Fumarate reductase iron-sulfur protein, N-terminal domain {Escherichia coli}

AEMKNLKIEVVRYNPEVDTAPHSAFYEVPYDATTSLLDALGYIKDNLAPDLSYRWSCRMAICGSCGMMVNNVPKLACKTFLRDYTDGMKVEALANFPIERDLVVD

>d1qlab2 d.15.4.2 (B:1-106) Fumarate reductase iron-sulfur protein, N-terminal domain {Wolinella succinogenes}

MGRMLTIRVFKYDPQSAVSKPHFQEYKIEEAPSMTIFIVLNMIRETYDPDLNFDFVCRAGICGSCGMMINGRPSLACRTLTKDFEDGVITLLPLPAFKLIKDLSVD

>d1jq4a\_ d.15.4.2 (A:) Methane monooxygenase reductase N-terminal domain {Methylococcus capsulatus}

MQRVHTITAVTEDGESLRFECRSDEDVITAALRQNIFLMSSCREGGCATCKALCSEGDYDLKGCSVQALPPEEEEEGLVLLCRTYPKTDLEIELPYTH

>d1ssn\_\_ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}

SSSFDKGKYKKGDDASYFEPTGPYLMVNVTGVDSKGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITKVVIEKK

>d1bmlc1 d.15.5.1 (C:12-148) Streptokinase {Streptococcus equisimilis}

SVNNSQLVVSVAGTVEGTNQDISLKFFEIDLTSRPAHGGKTEQGLSPKSKPFATDSGAMPHKLEKADLLKAIQEQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEFLLSGHVRVRPYKE

>d1bmlc3 d.15.5.1 (C:285-372) Streptokinase {Streptococcus equisimilis}

DPFDRSHLKLFTIKYVDVNTNELLKSEQLLTASERNLDFRDLYDPRDKAKLLYNNLDAFGIMDYTLTGKVEDNHDDTNRIITVYMGKR

>d1qqra\_ d.15.5.1 (A:) Streptokinase {Streptococcus equisimilis}

IQNQAKSVDVEYTVQFTPLNPDDDFRPGLKLTKLLKTLAIGDTITSQELLAQAQSILNKNHPGYTIYERDSSIVTHDNDIFRTILPMDQEFTYRVKNREQAYRINKKSGLNEEINNTDLISEKYYVLKKGEKPYDPFD

>d1esfa2 d.15.6.1 (A:121-233) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}

EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQRGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS

>d1i4pa2 d.15.6.1 (A:121-239) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}

NHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTKNG

>d3tss\_2 d.15.6.1 (94-194) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}

LPTPIELPLKVKVHGKDSPLKYWPKFDKKQLAISTLDFKIRHQLTQTHGLYRSSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN

>d1enfa2 d.15.6.1 (A:102-213) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}

EKLAQERVIGANVWVDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKIYYKDSEISKGLIEFDMKTPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYT

>d1an8\_2 d.15.6.1 (96-208) Streptococcal superantigen Spe-C {Streptococcus pyogenes}

NKVNHKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNYKIYDATSPYVSGRIEIGTKDGKHEQIDLFDSPNEGTRSDIFAKYKDNRIINMKNFSHFDIYLEK

>d1et9a2 d.15.6.1 (A:96-204) Streptococcal superantigen Spe-H {Streptococcus pyogenes}

EKKEIKVPVNVWDKSKQQPPMFITVNKPKVTAQEVDIKVRKLLIKKYDIYNNREQKYSKGTVTLDLNSGKDIVFDLYYFGNGDFNSMLKIYSNNERIDSTQFHVDVSIS

>d1eu3a2 d.15.6.1 (A:97-209) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}

TSIPKNIPVNLWINGKQISVPYNEISTNKTTVTAQEIDLKVRKFLIAQHQLYSSGSSYKSGRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVYKDNKSFNIDKIGHLDIEIDS

>d1pgx\_\_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

ELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTEMVTEVPVA

>d2ptl\_\_ d.15.7.1 (-) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAG

>d1k0ia2 d.16.1.2 (A:174-275) p-Hydroxybenzoate hydroxylase (PHBH) {Pseudomonas aeruginosa}

LKVFERVYPFGWLGLLADTPPVSHELIYANHPRGFALCSQRSATRSQYYVQVPLSEKVEDWSDERFWTELKARLPSEVAEKLVTGPSLEKSIAPLRSFVVEP

>d1foha4 d.16.1.2 (A:241-341) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}

GEQTDYIWGVLDAVPASNFPDIRSRCAIHSAESGSIMIIPRENNLVRFYVQLQARAEKGGRVDRTKFTPEVVIANAKKIFHPYTFDVQQLDWFTAYHIGQR

>d1an9a2 d.16.1.3 (A:195-287) D-amino acid oxidase {Pig (Sus scrofa)}

LQPGRGQIIKVDAPWLKNFIITHDLERGIYNSPYIIPGLQAVTLGGTFQVGNWNEINNIQDHNTIWEGCCRLEPTLKDAKIVGEYTGFRPVRP

>d1c0pa2 d.16.1.3 (A:1194-1288) D-amino acid oxidase {Yeast (Rhodotorula gracilis)}

AEPIRGQTVLVKSPCKRCTMDSSDPASPAYIIPRPGGEVICGGTYGVGDWDLSVNPETVQRILKHCLRLDPTISSDGTIEGIEVLRHNVGLRPAR

>d1el8a2 d.16.1.3 (A:218-321) Sarcosine oxidase {Bacillus sp., strain b0618}

LQPYRQVVGFFESDESKYSNDIDFPGFMVEVPNGIYYGFPSFGGCGLKLGYHTFGQKIDPDTINREFGVYPEDESNLRAFLEEYMPGANGELKRGAVCMYTKTL

>d1b5qa2 d.16.1.5 (A:294-405) Polyamine oxidase {Maize (Zea mays)}

DMAVYTKIFLKFPRKFWPEGKGREFFLYASSRRGYYGVWQEFEKQYPDANVLLVTVTDEESRRIEQQSDEQTKAEIMQVLRKMFPGKDVPDATDILVPRWWSDRFYKGTFSN

>d1f8ra2 d.16.1.5 (A:320-432) L-amino acid oxidase {Malayan pit viper (Calloselasma rhodostoma)}

HYRSGTKIFLTCTTKFWEDDGIHGGKSTTDLPSRFIYYPNHNFTNGVGVIIAYGIGDDANFFQALDFKDCADIVFNDLSLIHQLPKKDIQSFCYPSVIQKWSLDKYAMGGITT

>d1gosa2 d.16.1.5 (A:290-401) Monoamine oxidase B {Human (Homo sapiens)}

PLGSVIKCIVYYKEPFWRKKDYCGTMIIDGEEAPVAYTLDDTKPEGNYAAIMGFILAHKARKLARLTKEERLKKLCELYAKVLGSLEALEPVHYEEKNWCEEQYSGGCYTTY

>d1eqka\_ d.17.1.2 (A:) Phytocystatin {Japanese rice (Oryza sativa), subsp. japonica, oryzacystatin-I}

MSSDGGPVLGGVEPVGNENDLHLVDLARFAVTEHNKKANSLLEFEKLVSVKQQVVAGTLYYFTIEVKEGDAKKLYEAKVWEKPWMDFKELQEFKPVDASANA

>d1dvd\_\_ d.17.1.2 (-) Cystatin A (stefin A) {Human (Homo sapiens)}

MIPGGLSEAKPATPEIQEIVDKVKPQLEEKTNETYGKLEAVQYKTQVVAGTNYYIKVRAGDNKYMHLKVFKSLPGQNEDLVLTGYQVDKNKDDELTGF

>d1g96a\_ d.17.1.2 (A:) Cystatin C {Human (Homo sapiens)}

VGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCTKTQPNLDNCPFHDQPHLKRKAFCSFQIYAVPWQGTMTLSKSTCQDA

>d1oaca2 d.17.2.1 (A:91-185) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

KRPHPLNALTADEIKQAVEIVKASADFKPNTRFTEISLLPPDKEAVWAFALENKPVDQPRKADVIMLDGKHIIEAVVDLQNNKLLSWQPIKDAHG

>d1oaca3 d.17.2.1 (A:186-300) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

MVLLDDFASVQNIINNSEEFAAAVKKRGITDAKKVITTPLTVGYFDGKDGLKQDARLLKVISYLDVGDGNYWAHPIENLVAVVDLEQKKIVKIEEGPVVPVPMTARPFDGRDRVA

>d1ksia2 d.17.2.1 (A:6-98) Copper amine oxidase, domains 1 and 2 {Pea seedling (Pisum sativum)}

VQHPLDPLTKEEFLAVQTIVQNKYPISNNRLAFHYIGLDDPEKDHVLRYETHPTLVSIPRKIFVVAIINSQTHEILINLRIRSIVSDNIHNGY

>d1ksia3 d.17.2.1 (A:99-206) Copper amine oxidase, domains 1 and 2 {Pea seedling (Pisum sativum)}

GFPILSVDEQSLAIKLPLKYPPFIDSVKKRGLNLSEIVCSSFTMGWFGEEKNVRTVRLDCFMKESTVNIYVRPITGITIVADLDLMKIVEYHDRDIEAVPTAENTEYQ

>d1av4\_2 d.17.2.1 (9-96) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ASPFRLASAGEISEVQGILRTAGLLGPEKRIAYLGVLDPARGAGSEAEDRRFRVFIHDVSGARPQEVTVSVTNGTVISAVELDTAATG

>d1av4\_3 d.17.2.1 (97-211) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ELPVLEEEFEVVEQLLATDERWLKALAARNLDVSKVRVAPLSAGVFEYAEERGRRILRGLAFVQDFPEDSAWAHPVDGLVAYVDVVSKEVTRVIDTGVFPVPAEHGNYTDPELTG

>d1a2va2 d.17.2.1 (A:18-115) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}

PARPAHPLDPLSTAEIKAATNTVKSYFAGKKISFNTVTLREPARKAYIQWKEQGGPLPPRLAYYVILEAGKPGVKEGLVDLASLSVIETRALETVQPI

>d1a2va3 d.17.2.1 (A:116-236) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}

LTVEDLCSTEEVIRNDPAVIEQCVLSGIPANEMHKVYCDPWTIGYDERWGTGKRLQQALVYYRSDEDDSQYSHPLDFCPIVDTEEKKVIFIDIPNRRRKVSKHKHANFYPKHMIEKVGAMR

>d1ouna\_ d.17.4.2 (A:) Nuclear transport factor-2 (NTF2) {Rat (Rattus norvegicus)}

GDKPIWEQIGSSFIQHYYQLFDNDRTQLGAIYIDASCLTWEGQQFQGKAAIVEKLSSLPFQKIQHSITAQDHQPTPDSCIISMVVGQLKADEDPIMGFHQMFLLKNINDAWVCTNDMFRLALHNF

>d1jkga\_ d.17.4.2 (A:) NTF2-related export protein 1 (p15) {Human (Homo sapiens)}

ASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRFQDWAS

>d1jkgb\_ d.17.4.2 (B:) NTF2-like domain of Tip associating protein, TAP {Human (Homo sapiens)}

APPCKGSYFGTENLKSLVLHFLQQYYAIYDSGDRQGLLDAYHDGACCSLSIPFIPQNPARSSLAEYFKDSRNVKKLKDPTLRFRLLKHTRLNVVAFLNELPKTQHDVNSFVVDISAQTSTLLCFSVNGVFKEVDGKSRDSLRAFTRTFIAVPASNSGLCIVNDELFVRNASSEEIQRAFAMPAPTP

>d1qjga\_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Comamonas testosteroni and Pseudomonas testosteroni}

MNTPEHMTAVVQRYVAALNAGDLDGIVALFADDATVENPVGSEPRSGTAAIREFYANSLKLPLAVELTQEVRAVANEAAFAFIVSFEYQGRKTVVAPIDHFRFNGAGKVVSMRALFGEKNIHAGA

>d1ea2a\_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Pseudomonas putida}

NLPTAQEVQGLMARFIELVDVGDIEAIVQMYADDATVEDPFGQPPIHGREQIAAFYRQGLGGGKVRACLTGPVRASHNGCGAMPFRVEMVWNGQPCALDVIDVMRFDEHGRIQTMQAYWSEVNLSV

>d3frua2 d.19.1.1 (A:1-178) Fc (IgG) receptor, alpha-1 and alpha-2 domains {Rat (Rattus norvegicus)}

AEPRLPLMYHLAAVSDLSTGLPSFWATGWLGAQQYLTYNNLRQEADPCGAWIWENQVSWYWEKETTDLKSKEQLFLEAIRTLENQINGTFTLQGLLGCELAPDNSSLPTAVFALNGEEFMRFNPRTGNWSGEWPETDIVGNLWMKQPEAARKESEFLLTSCPERLLGHLERGRQNLEW

>d1cd1a2 d.19.1.1 (A:7-185) CD1, alpha-1 and alpha-2 domains {Mouse (Mus musculus)}

NYTFRCLQMSSFANRSWSRTDSVVWLGDLQTHRWSNDSATISFTKPWSQGKLSNQQWEKLQHMFQVYRVSFTRDIQELVKMMSPKEDYPIEIQLSAGCEMYPGNASESFLHVAFQGKYVVRFWGTSWQTVPGAPSWLDLPIKVLNADQGTSATVQMLLNDTCPLFVRGLLEAGKSDLEK

>d1jk8a2 d.19.1.1 (A:2-84) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}

VADHVASYGVNLYQSYGPSGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTNIAVLKHNLNIVIKRSNSTAATN

>d1fnga2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

IKEEHTIIQAEFYLLPDKRGEFMFDFDGDEIFHVDIEKSETIWRLEEFAKFASFEAQGALANIAVDKANLDVMKERSNNTP

>d1i3rb2 d.19.1.1 (B:1-120) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

GKKVITAFNEGLKGGGGSLVGGGSGGGGSRPWFLEYCKSECHFYNGTQRVRLLVRYFYNLEENLRFDSDVGEFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRHNYEIFDNFLVPRR

>d1k8ia2 d.19.1.1 (A:11-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

QNHTFRHTLFCQDGIPNIGLSETYDEDELFSFDFSQNTRVPRLPDFAEWAQGQGDASAIAFDKSFCEMLMREVSPKLEGQIP

>d1k8ib2 d.19.1.1 (B:1-94) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

GFVAHVESTCVLNDAGTPQDFTYCVSFNKDLLACWDPDVGKIVPCEFGVLSRLAEIISNILNEQESLIHRLQNGLQDCATHTQPFWDVLTHRTR

>d1i4fa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-A2.1}

GSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQR

>d1de4a2 d.19.1.1 (A:4-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), hemochromatosis protein Hfe}

RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLD

>d1zaga2 d.19.1.1 (A:5-183) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}

DGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGMEDWKQDSQLQKAREDIFMETLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNILDR

>d1hyrc2 d.19.1.1 (C:0-180) MHC I homolog {Human (Homo sapiens), Mic-a}

MEPHSLRYNLTVLSWDGSVQSGFLTEVHLDGQPFLRCDRQKCRAKPQGQWAEDVLGNKTWDRETRDLTGNGKDLRMTLAHIKDQKEGLHSLQEIRVCEIHEDNSTRSSQHFYYDGELFLSQNLETKEWTMPQSSRAQTLAMNVRNFLKEDAMKTKTHYHAMHADCLQELRRYLKSGVVLRR

>d1kcgc\_ d.19.1.1 (C:) Class I MHC-related molecule Ulbp3 {Human (Homo sapiens)}

DAHSLWYNFTIIHLPRHGQQWCEVQSQVDQKNFLSYDCGSDKVLSMGHLEEQLYATDAWGKQLEMLREVGQRLRLELADTELEDFTPSGPLTLQVRMSCECEADGYIRGSWQFSFDGRKFLLFDSNNRKWTVVHAGARRMKEKWEKDSGLTTFFKMVSMRDCKSWLRDFLMHRKKRLE

>d1jfma\_ d.19.1.1 (A:) NK cell ligand RAE-1 beta {Mouse (Mus musculus)}

DAHSLRCNLTIKDPTPADPLWYEAKCFVGEILILHLSNINKTMTSGDPGETANATEVKKCLTQPLKNLCQKLRNKVSNTKVDTHKTNGYPHLQVTMIYPQSQGRTPSATWEFNISDSYFFTFYTENMSWRSANDESGVIMNKWKDDGEFVKQLKFLIHECSQKMDEFLKQSKEK

>d2ucz\_\_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc7}

SKTAQKRLLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPPDTPYADGVFNAKLEFPKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKILLSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

>d1jata\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc13}

AASLPKRIIKETEKLVSDPVPGITAEPHDDNLRYFQVTIEGPEQSPYEDGIFELELYLPDDYPMEAPKVRFLTKIYHPNIDRLGRICLDVLKTNWSPALQIRTVLLSIQALLASPNPNDPLANDVAEDWIKNEQGAKAKAREWTKLYAKKKP

>d1j7da\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), mms2}

GVKVPRNFRLLEELEEGQKGVGDGTVSWGLEDDEDMTLTRWTGMIIGPPRTNYENRIYSLKVECGPKYPEAPPSVRFVTKINMNGINNSSGMVDARSIPVLAKWQNSYSIKVVLQELRRLMMSKENMKLPQPPEGQTYNN

>d1c4zd\_ d.20.1.1 (D:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch7}

SRRLMKELEEIRKCGMKNFRNIQVDEANLLTWQGLIVPDNPPYDKGAFRIEINFPAEYPFKPPKITFKTKIYHPNIDEKGQVCLPVISAENWKPATKTDQVIQSLIALVNDPQPEHPLRADLAEEYSKDRKKFCKNAEEFTKKY

>d1u9aa\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc9}

LNMSGIALSRLAQERKAWRKDHPFGFVAVPTKNPDGTMNLMNWECAIPGKKGTPWEGGLFKLRMLFKDDYPSSPPKCKFEPPLFHPNVYPSGTVCLSILEEDKDWRPAITIKQILLGIQELLNEPNIQDPAQAEAYTIYCQNRVEYEKRVRAQAKKFAPS

>d2e2c\_\_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Clam (Spisula solidissima), E-2C}

MTTSKERHSVSKRLQQELRTLLMSGDPGITAFPDGDNLFKWVATLDGPKDTVYESLKYKLTLEFPSDYPYKPPVVKFTTPCWHPNVDQSGNICLDILKENWTASYDVRTILLSLQSLLGEPNNASPLNAQAADMWSNQTEYKKVLHEKYKTAQSDK

>d1bwza1 d.21.1.1 (A:1-130) Diaminopimelate epimerase {Haemophilus influenzae}

MQFSKMHGLGNDFVVVDGVTQNVFFTPETIRRLANRHCGIGFDQLLIVEAPYDPELDFHYRIFNADGSEVSQCGNGARCFARFVTLKGLTNKKDISVSTQKGNMVLTVKDMNQIRVNMGEPIWEPAKIPF

>d1bwza2 d.21.1.1 (A:131-274) Diaminopimelate epimerase {Haemophilus influenzae}

TANKFEKNYILRTDIQTVLCGAVSMGNPHCVVQVDDIQTANVEQLGPLLESHERFPERVNAGFMQIINKEHIKLRVYERGAGETQACGSGACAAVAVGIMQGLLNNNVQVDLPGGSLMIEWNGVGHPLYMTGEATHIYDGFITL

>d1h6ra\_ d.22.1.1 (A:) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}

SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFIVTTGKLPVPWPTLVTTFAYGLQCFARYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHCVYIVADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLCYQSALSKDPNEKRDHMVLLEFVTAAGITH

>d1ggxa\_ d.22.1.1 (A:) Red fluorescent protein (fp583 or dsred(clontech)) {Coral (Discosoma sp.)}

VIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL

>d2pil\_\_ d.24.1.1 (-) Pilin {Gc (Neisseria gonorrhoeae)}

FTLIELMIVIAIVGILAAVALPAYQDYTARAQVSEAILLAEGQKSAVTEYYLNHGKWPENNTSAGVASPPSDIKGKYVKEVEVKNGVVTATMLSSGVNNEIKGKKLSLWARRENGSVKWFCGQPVTRTDDDTVADAKDGKEIDTKHLPSTCRDNFDAK

>d1hpwa\_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa}

ALEGTEFARAQLSEAMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADNKYLPKTCQTATTTTP

>d1dzoa\_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa, type IV pilin, pak pilin}

GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCSR

>d1rot\_\_ d.26.1.1 (-) FKBP59-I, N-terminal domain {Rabbit (Oryctolagus cuniculus)}

GVDISPKQDEGVLKVIKREGTGTETPMIGDRVFVHYTGWLLDGTKFDSSLDRKDKFSFDLGKGEVIKAWDIAVATMKVGELCRITCKPEYAYGSAGSPPKIPPNATLVFEVELFEFKG

>d1pina2 d.26.1.1 (A:45-163) Mitotic rotamase PIN1, domain 2 {Human (Homo sapiens)}

GKNGQGEPARVRCSHLLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKARGDLGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILRTE

>d1eq3a\_ d.26.1.1 (A:) Parvulin {Human (Homo sapiens), hpar14}

NAVKVRHILCEKHGKIMEAMEKLKSGMRFNEVAAQYSEDKARQGGDLGWMTRGSMVGPFQEAAFALPVSGMDKPVFTDPPVKTKFGYHIIMVEGRK

>d1fd9a\_ d.26.1.1 (A:) Macrophage infectivity potentiator protein (MIP) {Legionella pneumophila}

TDKDKLSYSIGADLGKNFKNQGIDVNPEAMAKGMQDAMSGAQLALTEQQMKDVLNKFQKDLMAKRTAEFNKKADENKVKGEAFLTENKNKPGVVVLPSGLQYKVINSGNGVKPGKSDTVTVEYTGRLIDGTVFDSTEKTGKPATFQVSQVIPGWTEALQLMPAGSTWEIYVPSGLAYGPRSVGGPIGPNETLIFKIHLISVKKS

>d1edqa3 d.26.3.1 (A:444-516) Chitinase A {Serratia marcescens}

YGRGWTGVNGYQNNIPFTGTATGPVKGTWENGIVDYRQIAGQFMSGEWQYTYDATAEAPYVFKPSTGDLITFD

>d1goia3 d.26.3.1 (A:292-379) Chitinase B {Serratia marcescens}

YGRAFKGVSGGNGGQYSSHSTPGEDPYPSTDYWLVGCEECVRDKDPRIASYRQLEQMLQGNYGYQRLWNDKTKTPYLYHAQNGLFVTY

>d1d2ka2 d.26.3.1 (A:293-354) Chitinase 1 {Fungus (Coccidioides immitis)}

YGRAFASTDGIGTSFNGVGGGSWENGVWDYKDMPQQGAQVTELEDIAASYSYDKNKRYLISY

>d1e9la2 d.26.3.1 (A:267-336) Chitinase-like lectin ym1 {Mouse (Mus musculus)}

YGHTFILSDPSKTGIGAPTISTGPPGKYTDESGLLAYYEVCTFLNEGATEVWDAPQEVPYAYQGNEWVGY

>d1qcsa2 d.31.1.1 (A:86-201) C-terminal domain of NSF-N, NSF-Nc {Hamster (Cricetulus griseus)}

DKAKQCIGTMTIEIDFLQKKNIDSNPYDTDKMAAEFIQQFNNQAFSVGQQLVFSFNDKLFGLLVKDIEAMDPSILKGEPASGKRQKIEVGLVVGNSQVAFEKAENSSLNLIGKAKT

>d1cr5a2 d.31.1.1 (A:108-210) C-terminal domain of NSF-N, NSF-Nc {Baker's yeast (Saccharomyces cerevisiae), sec18p}

SGKQSYLGSIDIDISFRARGKAVSTVFDQDELAKQFVRCYESQIFSPTQYLIMEFQGHFFDLKIRNVQAIDLGDIEPTSAVATGIETKGILTKQTQINFFKGR

>d1cz4a2 d.31.1.1 (A:92-185) C-terminal domain of VAT-N, VAT-Nc {Archaeon Thermoplasma acidophilum}

TEIAKKVTLAPIIRKDQRLKFGEGIEEYVQRALIRRPMLEQDNISVPGLTLAGQTGLLFKVVKTLPSKVPVEIGEETKIEIREEPASEVLEEGG

>d1e32a3 d.31.1.1 (A:107-200) Membrane fusion atpase p97 domain 2, P97-Nc {Mouse (Mus musculus)}

DVKYGKRIHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIRKGDIFLVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGEPIKREDEEESLNE

>d1qipa\_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Human (Homo sapiens)}

GGLTDEAALSCCSDADPSTKDFLLQQTMLRVKDPKKSLDFYTRVLGMTLIQKCDFPIMKFSLYFLAYEDKNDIPKEKDEKIAWALSRKATLELTHNWGTEDDETQSYHNGNSDPRGFGHIGIAVPDVYSACKRFEELGVKFVKKPDDGKMKGLAFIQDPDGYWIEILNPNKMATLM

>d1f9za\_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Escherichia coli}

MRLLHTMLRVGDLQRSIDFYTKVLGMKLLRTSENPEYKYSLAFVGYGPETEEAVIELTYNWGVDKYELGTAYGHIALSVDNAAEACEKIRQNGGNVTREAGPVKGGTTVIAFVEDPDGYKIELIEEKDAGRGLGN

>d1qtoa\_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptomyces verticillus}

MVKFLGAVPVLTAVDVPANVSFWVDTLGFEKDFGDRDFAGVRRGDIRLHISRTEHQIVADNTSAWIEVTDPDALHEEWARAVSTDYADTSGPAMTPVGESPAGREFAVRDPAGNCVHFTAGE

>d1ecsa\_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Klebsiella pneumoniae}

TDQATPNLPSRDFDSTAAFYERLGFGIVFRDAGWMILQRGDLMLEFFAHPGLDPLASWFSCCLRLDDLAEFYRQCKSVGIQETSSGYPRIHAPELQGWGGTMAALVDPDGTLLRLIQNEL

>d1gdga1 d.32.1.3 (A:1-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Pseudomonas sp.}

SIERLGYLGFAVKDVPAWDHFLTKSVGLMAAGSAGDAALYRADQRAWRIAVQPGELDDLAYAGLEVDDAAALERMADKLRQAGVAFTRGDEALMQQRKVMGLLCLQDPFGLPLEIYYGPAEIFHEPFLPSAP

>d1han\_2 d.32.1.3 (133-289) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Burkholderia cepacia (formerly Pseudomonas cepacia)}

AVSGFLTGEQGLGHFVRCVPDSDKALAFYTDVLGFQLSDVIDMKMGPDVTVPAYFLHCNERHHTLAIAAFPLPKRIHHFMLEVASLDDVGFAFDRVDADGLITSTLGRHTNDHMVSFYASTPSGVEVEYGWSARTVDRSWVVVRHDSPSMWGHKSVR

>d1mpya1 d.32.1.3 (A:1-145) Catechol 2,3-dioxygenase (metapyrocatechase) {Pseudomonas putida, mt2}

MNKGVMRPGHVQLRVLDMSKALEHYVELLGLIEMDRDDQGRVYLKAWTEVDKFSLVLREADEPGMDFMGFKVVDEDALRQLERDLMAYGCAVEQLPAGELNSCGRRVRFQAPSGHHFELYADKEYTGKWGLNDVNPEAWPRDLKG

>d1mpya2 d.32.1.3 (A:146-307) Catechol 2,3-dioxygenase (metapyrocatechase) {Pseudomonas putida, mt2}

MAAVRFDHALMYGDELPATYDLFTKVLGFYLAEQVLDENGTRVAQFLSLSTKAHDVAFIHHPEKGRLHHVSFHLETWEDLLRAADLISMTDTSIDIGPTRHGLTHGKTIYFFDPSGNRNEVFCGGDYNYPDHKPVTWTTDQLGKAIFYHDRILNERFMTVLT

>d1cjxa1 d.32.1.3 (A:4-153) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas fluorescens}

YENPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEPNSIASYFAAEHGPSVCGMAFRVKDSQKAYNRALELGAQPIHIDTGPMELNLPAIKGIGGAPLYLIDRFGEGSSIYDIDFVYLEGVERNPVG

>d1cjxa2 d.32.1.3 (A:154-356) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas fluorescens}

AGLKVIDHLTHNVYRGRMVYWANFYEKLFNFREARYFDIKGEYTGLTSKAMSAPDGMIRIPLNEESSKGAGQIEEFLMQFNGEGIQHVAFLTDDLVKTWDALKKIGMRFMTAPPDTYYEMLEGRLPDHGEPVDQLQARGILLDGSSVEGDKRLLLQIFSETLMGPVFFEFIQRKGDDGFGEGNFKALFESIERDQVRRGVLAT

>d1b3ob2 d.37.1.1 (B:112-159) Type II inosine monophosphate dehydrogenase {Human (Homo sapiens)}

QGFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIIS

>d1jr1a3 d.37.1.1 (A:178-232) Type II inosine monophosphate dehydrogenase {Chinese hamster (Cricetulus griseus)}

IMTKREDLVVAPAGITLKEANEILQRSKKGKLPIVNENDELVAIIARTDLKKNRD

>d1zfja2 d.37.1.1 (A:95-158) Type II inosine monophosphate dehydrogenase {Streptococcus pyogenes}

NGVIIDPFFLTPEHKVSEAEELMQRYRISGVPIVETLANRKLVGIITNRDMRFISDYNAPISEH

>d1zfja3 d.37.1.1 (A:159-220) Type II inosine monophosphate dehydrogenase {Streptococcus pyogenes}

MTSEHLVTAAVGTDLETAERILHEHRIEKLPLVDNSGRLSGLITIKDIEKVIEFPHAAKDEF

>d1c8ua1 d.38.1.3 (A:2-115) Thioesterase II (TesB) {Escherichia coli}

SQALKNLLTLLNLEKIEEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPEERLVHSFHSYFLRPGDSKKPIIYDVETLRDGNSFSARRVAAIQNGKPIFYMTASFQAPEAGF

>d1c8ua2 d.38.1.3 (A:116-286) Thioesterase II (TesB) {Escherichia coli}

EHQKTMPSAPAPDGLPSETQIAQSLAHLLPPVLKDKFICDRPLEVRPVEFHNPLKGHVAEPHRQVWIRANGSVPDDLRVHQYLLGYASDLNFLPVALQPHGIGFLEPGIQIATIDHSMWFHRPFNLNEWLLYSVESTSASSARGFVRGEFYTQDGVLVASTVQEGVMRNHN

>d1egl\_\_ d.40.1.1 (-) Eglin C {Leech (Hirudo medicinalis)}

TEFGSELKSFPEVVGKTVDQAREYFTLHYPQYDVYFLPEGSPVTLDLRYNRVRVFYNPGTNVVNHVPHVG

>d1ypci\_ d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}

MKTEWPELVGKSVAAAKKVILQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAQVPRVG

>d1dwma\_ d.40.1.1 (A:) Trypsin inhibitor LUTI {Flax (Linum usitatissimum)}

SRRCPGKNAWPELVGKSGNMAAATVERENRNVHAIVLKEGSAMTKDFRCDRVWVIVNDHGVVTSVPHIT

>d1dgja3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio desulfuricans}

EFGADAALRMPENTLHLALAQAKVSHALIKGIDTSEAEKMPGVYKVLTHKDVKGKNRITGLITFPTNKGDGWERPILNDSKIFQYGDALAIVCADSEANARAAAEKVKFDLELLPEY

>d1fo4a3 d.41.1.1 (A:537-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}

KLDPTYTSATLLFQKHPPANIQLFQEVPNGQSKEDTVGRPLPHLAAAMQASGEAVYCDDIPRYENELFLRLVTSTRAHAKIKSIDVSEAQKVPGFVCFLSADDIPGSNETGLFNDETVFAKDTVTCVGHIIGAVVADTPEHAERAAHVVKVTYEDLPA

>d1jrob1 d.41.1.1 (B:2-123) Xanthine dehydrogenase chain B, N-terminal domain {Rhodobacter capsulatus}

SVGKPLPHDSARAHVTGQARYLDDLPCPANTLHLAFGLSTEASAAITGLDLEPVRESPGVIAVFTAADLPHDNDASPAPSPEPVLATGEVHFVGQPIFLVAATSHRAARIAARKARITYAPR

>d1ffvb1 d.41.1.1 (B:7-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {Hydrogenophaga pseudoflava}

DAEARELALAGMGASRLRKEDARFIQGKGNYVDDIKMPGMLHMDIVRAPIAHGRIKKIHKDAALAMPGVHAVLTAEDLKPLKLHWMPTLAGDVAAVLADEKVHFQMQEVAIVIADDRYIAADAVEAVKVEYDELPVVIDP

>d1qapa2 d.41.2.1 (A:8-129) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Salmonella typhimurium}

DDRRDALLERINLDIPAAVAQALREDLGGEVDAGNDITAQLLPADTQAHATVITREDGVFCGKRWVEEVFIQLAGDDVRLTWHVDDGDAIHANQTVFELQGPARVLLTGERTALNFVQTLSG

>d1qpoa2 d.41.2.1 (A:2-116) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Mycobacterium tuberculosis}

GLSDWELAAARAAIARGLDEDLRYGPDVTTLATVPASATTTASLVTREAGVVAGLDVALLTLNEVLGTNGYRVLDRVEDGARVPPGEALMTLEAQTRGLLTAERTMLNLVGHLSG

>d2tpt\_3 d.41.3.1 (336-440) Thymidine phosphorylase {Escherichia coli}

TAMLTKAVYADTEGFVSEMDTRALGMAVVAMGGGRRQASDTIDYSVGFTDMARLGDQVDGQRPLAVIHAKDENNWQEAAKAVKAAIKLADKAPESTPTVYRRISE

>d1brwa3 d.41.3.1 (A:331-433) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}

KAAYTSTVTAAADGYVAEMAADDIGTAAMWLGAGRAKKEDVIDLAVGIVLHKKIGDRVQKGEALATIHSNRPDVLDVKEKIEAAIRLSPQPVARPPLIYETIV

>d1buoa\_ d.42.1.1 (A:) Promyelocytic leukemia zinc finger (PLZF) protein BTB domain {Human (Homo sapiens)}

MGMIQLQNPSHPTGLLCKANQMRLAGTLCDVVIMVDSQEFHAHRTVLACTSKMFEILFHRNSQHYTLDFLSPKTFQQILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLETIQ

>d1vcbb\_ d.42.1.1 (B:) Elongin C {Human (Homo sapiens)}

MYVKLISSDGHEFIVKREHALTSGTIKAMLSGPGQFAENETNEVNFREIPSHVLSKVCMYFTYKVRYTNSSTEIPEFPIAPEIALELLMAANFLDC

>d1hv2a\_ d.42.1.1 (A:) Elongin C {Baker's yeast (Saccharomyces cerevisiae)}

MSQDFVTLVSKDDKEYEISRSAAMISPTLKAMIEGPFRESKGRIELKQFDSHILEKAVEYLNYNLKYSGVSEDDDEIPEFEIPTEMSLELLLAADYLSI

>d1t1da\_ d.42.1.2 (A:) Shaker potassium channel {California sea hare (Aplysia californica)}

ERVVINVSGLRFETQLKTLNQFPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGRLRRPVNVPLDVFSEEIKFYELGENAFERYREDEGF

>d3kvt\_\_ d.42.1.2 (-) akv3.1 voltage-gated potassium channel {California sea hare (Aplysia californica)}

ENRVIINVGGIRHETYKATLKKIPATRLSRLTEGMLNYDPVLNEYFFDRHPGVFAQIINYYRSGKLHYPTDVCGPLFEEELEFWGLDSNQVEPCCWMTYTAHR

>d1fs1b2 d.42.1.2 (B:2-68) Cyclin A/CDK2-associated p45, Skp1 {Human (Homo sapiens)}

PSIKLQSSDGEIFEVDVEIAKQSVTIKTMLEDLGMDPVPLPNVNAAILKKVIQWCTHHKDD

>d1efub2 d.43.1.1 (B:140-282) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}

DVLGSYQHGARIGVLVAAKGADEELVKHIAMHVAASKPEFIKPEDVSAEVVEKEYQVQLDIAMQSGKPKEIAEKMVEGRMKKFTGEVSLTGQPFVMEPSKTVGQLLKEHNAEVTGFIRFEVGEGIEKVETDFAAEVAAMSKQS

>d1efub4 d.43.1.1 (B:55-139) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}

VAADGVIKTKIDGNYGIILEVNCQTDFVAKDAGFQAFADKVLDAAVAGKITDVEVLKAQFEEERVALVAKIGENINIRRVAALEG

>d1tfe\_\_ d.43.1.1 (-) Elongation factor Ts (EF-Ts), dimerisation domain {Thermus thermophilus}

AREGIIGHYIHHNQRVGVLVELNCETDFVARNELFQNLAKDLAMHIAMMNPRYVSAEEIPAEELEKERQIYIQAALNEGKPQQIAEKIAEGRLKKYLEEVVLLEQPFVKDDKVKVKELIQQAIAKIGENIVVRRFCRFELGA

>d1kkca2 d.44.1.1 (A:98-213) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}

EKSGGGKIDQAPVLKAAIEQRWGSFDKFKDAFNTTLLGIQGSGWGWLVTDGPKGKLDITTTHDQDPVTGAAPVFGVDMWEHAYYLQYLNDKASYAKGIWNVINWAEAENRYIAGDK

>d1isaa2 d.44.1.1 (A:83-192) Fe superoxide dismutase (FeSOD) {Escherichia coli}

NAGGEPTGKVAEAIAASFGSFADFKAQFTDAAIKNFGSGWTWLVKNSDGKLAIVSTSNAGTPLTTDATPLLTVDVWEHAYYIDYRNARPGYLEHFWALVNWEFVAKNLAA

>d1coja2 d.44.1.1 (A:91-212) Fe superoxide dismutase (FeSOD) {Aquifex pyrophilus}

GGKGEPSEALKKKIEEDIGGLDACTNELKAAAMAFRGWAILGLDIFSGRLVVNGLDAHNVYNLTGLIPLIVIDTYEHAYYVDYKNKRPPYIDAFFKNINWDVVNERFEKAMKAYEALKDFIK

>d1b06a2 d.44.1.1 (A:93-210) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus acidocaldarius}

PAGKGGGKPGGALADLIDKQYGSFDRFKQVFSESANSLPGSGWTVLYYDNESGNLQIMTVENHFMNHIAELPVILIVDEFEHAYYLQYKNKRGDYLNAWWNVVNWDDAEKRLQKYLNK

>d1di2a\_ d.50.1.1 (A:) Double-stranded RNA-binding protein A, second dsRBD {Xenopus laevis}

MPVGSLQELAVQKGWRLPEYTVAQESGPPHKREFTITCRVETFVETGSGTSKQVAKRVAAEKLLTKFKT

>d1ekza\_ d.50.1.1 (A:) Staufen, domain III {Fruit fly (Drosophila melanogaster)}

MDEGDKKSPISQVHEIGIKRNMTVHFKVLREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVELQKL

>d1qu6a1 d.50.1.1 (A:1-90) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}

GSHMEMAGDLSAGFFMEELNTYRQKQGVVLKYQELPNSGPPHDRRFTFQVIIDGREFPEGEGRSKKEAKNAAAKLAVEILNKEKKAVSPL

>d1qu6a2 d.50.1.1 (A:91-179) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}

LLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQCASGVHGPEGFHYKCKMGQKEYSIGTGSTKQEAKQLAAKLAYLQILSEETGSGC

>d1ec6a\_ d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}

MKELVEIAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRRVTITGSPAATQAAQYLISQRVTYEQGVRASNPQKV

>d1vig\_\_ d.51.1.1 (-) Vigilin, KH6 {Human (Homo sapiens)}

INRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSVRIPPDSEKSNLIRIEGDPQGVQQAKRELLELAS

>d2fmr\_\_ d.51.1.1 (-) Fragile X protein, KH1 {Human (Homo sapiens)}

ASRFHEQFIVREDLMGLAIGTHGANIQQARKVPGVTAIDLDEDTCTFHIYGEDQDAVKKARSFLE

>d1khma\_ d.51.1.1 (A:) HnRNP K, KH3 {Human (Homo sapiens)}

GSPNSYGDLGGPIITTQVTIPKDLARSIIGKGGQRIKQIRHESGASIKIDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVKQYSGKFF

>d1k1ga\_ d.51.1.1 (A:) RNA splicing factor 1 {Human (Homo sapiens)}

TRVSDKVMIPQDEYPEINFVGLLIGPRGNTLKNIEKECNAKIMIRGKGSVKEGKVGRKDGQMLPGEDEPLHALVTANTMENVKKAVEQIRNILKQGIETPEDQNDLRKMQLRELARLNGTLR

>d3proc1 d.52.1.1 (C:6-85) Alpha-lytic protease prodomain {Lysobacter enzymogenes}

PQLKFAMQRDLGIFPTQLPQYLQTEKLARTQAAAIEREFGAQFAGSWIERNEDGSFKLVAATSGARKSSTLGGVEVRNVR

>d3proc2 d.52.1.1 (C:86-163) Alpha-lytic protease prodomain {Lysobacter enzymogenes}

YSLKQLQSAMEQLDAGANARVKGVSKPLDGVQSWYVDPRSNAVVVKVDDGATDAGVDFVALSGADSAQVRIESSPGKL

>d1fjgc1 d.52.3.1 (C:2-106) Ribosomal protein S3 N-terminal domain {Thermus thermophilus}

GNKIHPIGFRLGITRDWESRWYAGKKQYRHLLLEDQRIRGLLEKELYSAGLARVDIERAADNVAVTVHVAKPGVVIGRGGERIRVLREELAKLTGKNVALNVQEV

>d1egaa2 d.52.3.1 (A:183-295) GTPase Era C-terminal domain {Escherichia coli}

DYITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIERFVSNERGGYDINGLILVEREGQKKMVIGNKGAKIKTIGIEARKDMQEMFEAPVHLELWVKVKSGWADDERALRSL

>d1hh2p3 d.52.3.1 (P:277-344) Transcription factor NusA, C-terminal domains {Thermotoga maritima}

DDPKQLIANALAPATVIEVEILDKENKAARVLVPPTQLSLAIGKGGQNARLAAKLTGWKIDIKPIMNL

>d1k0ra2 d.52.3.1 (A:184-262) Transcription factor NusA, C-terminal domains {Mycobacterium tuberculosis}

THPNLVRKLFSLEVPEIADGSVEIVAVAREAGHRSKIAVRSNVAGLNAKGACIGPMGQRVRNVMSELSGEKIDIIDYDD

>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}

MNIGLLEALDQLEEEKGISKEEVIPILEKALVSAYRKNFGNSKNVEVVIDRNTGNIKVYQLLEVVEEVEDPATQISLEEAKKIDPLAEVGSIVKKELNVKNFGRIAAQTAKQVLIQRIRELEKEKQ

>d1k0ra4 d.202.1.1 (A:-4-99) Transcription factor NusA, N-terminal domain {Mycobacterium tuberculosis}

VSRRHMNIDMAALHAIEVDRGISVNELLETIKSALLTAYRHTQGHQTDARIEIDRKTGVVRVIARETDEAGNLISEWDDTPEGFGRIAATTARQVMLQRFRDAE

>d1onea2 d.54.1.1 (A:1-141) Enolase {Baker's yeast (Saccharomyces cerevisiae)}

AVSKVYARSVYDSRGNPTVEVELTTEKGVFRSIVPSGASTGVHEALEMRDGDKSKWMGKGVLHAVKNVNDVIAPAFVKANIDVKDQKAVDDFLISLDGTANKSKLGANAILGVSLAASRAAAAEKNVPLYKHLADLSKSKT

>d1ec7a2 d.54.1.1 (A:5-137) D-glucarate dehydratase {Escherichia coli}

FTTPVVTEMQVIPVAGHDSMLMNLSGAHAPFFTRNIVIIKDNSGHTGVGEIPGGEKIRKTLEDAIPLVVGKTLGEYKNVLTLVRNTFADRDAGGRGLQTFDLRTTIHVVTGIEAAMLDLLGQHLGVNVASLLG

>d1fhua2 d.54.1.1 (A:1-99) O-succinylbenzoate synthase {Escherichia coli}

MRSAQVYRWQIPMDAGVVLRDRRLKTRDGLYVCLREGEREGWGEISPLPGFSQETWEEAQSVLLAWVNNWLAGDCELPQMPSVAFGVSCALAELTDTLP

>d1muca2 d.54.1.1 (A:4-130) Muconate-lactonizing enzyme (cis muconate cycloisomerase) {Pseudomonas putida}

ALIERIDAIIVDLPTIRPHKLAMHTMQQQTLVVLRVRCSDGVEGIGEATTIGGLAYGYESPEGIKANIDAHLAPALIGLAADNINAAMLKLDKLAKGNTFAKSGIESALLDAQGKRLGLPVSELLGG

>d2mnr\_2 d.54.1.1 (3-132) Mandelate racemase {Pseudomonas putida}

EVLITGLRTRAVNVPLAYPVHTAVGTVGTAPLVLIDLATSAGVVGHSYLFAYTPVALKSLKQLLDDMAAMIVNEPLAPVSLEAMLAKRFCLAGYTGLIRMAAAGIDMAAWDALGKVHETPLVKLLGANAR

>d1jpdx2 d.54.1.1 (X:-2-113) L-Ala-D/L-Glu epimerase {Escherichia coli}

GSHMRTVKVFEEAWPLHTPFVIARGSRSEARVVVVELEEEGIKGTGECTPYPRYGESDASVMAQIMSVVPQLEKGLTREELQKILPAGAARNALDCALWDLAARRQQQSLADLIGI

>d1jpma2 d.54.1.1 (A:1-125) L-Ala-D/L-Glu epimerase {Bacillus subtilis}

MKIIRIETSRIAVPLTKPFKTALRTVYTAESVIVRITYDSGAVGWGEAPPTLVITGDSMDSIESAIHHVLKPALLGKSLAGYEAILHDIQHLLTGNMSAKAAVEMALYDGWAQMCGLPLYQMLGG

>d1kcza2 d.54.1.1 (A:1-160) beta-Methylaspartase {Clostridium tetanomorphum}

MKIVDVLCTPGLTGFYFDDQRAIKKGAGHDGFTYTGSTVTEGFTQVRQKGESISVLLVLEDGQVAHGDCAAVQYSGAGGRDPLFLAKDFIPVIEKEIAPKLIGREITNFKPMAEEFDKMTVNGNRLHTAIRYGITQAILDAVAKTRKVTMAEVIRDEYNP

>d1bxea\_ d.55.1.1 (A:) Ribosomal protein L22 {Thermus aquaticus, subsp. Thermus thermophilus}

MEAKAIARYVRISPRKVRLVVDLIRGKSLEEARNILRYTNKRGAYFVAKVLESAAANAVNNHDMLEDRLYVKAAYVDEGPALKRVLPRARGRADIIKKRTSHITVILGEK

>d1jj2q\_ d.55.1.1 (Q:) Ribosomal protein L22 {Archaeon Haloarcula marismortui}

GISYSVEADPDTTAKAMLRERQMSFKHSKAIAREIKGKTAGEAVDYLEAVIEGDQPVPFKQHNSGVGHKSKVDGWDAGRYPEKASKAFLDLLENAVGNADHQGFDGEAMTIKHVAAHKVGEQQGRKPRAMGRASAWNSPQVDVELILEEP

>d1h6ha\_ d.189.1.1 (A:) p40phox NADPH oxidase {Human (Homo sapiens)}

AVAQQLRAESDFEQLPDDVAISANIADIEEKRGFTSHFVFVIEVKTKGGSKYLIYRRYRQFHALQSKLEERFGPDSKSSALACTLPTLPAKVYVGVKQEIAEMRIPALNAYMKSLLSLPVWVLMDEDVRIFFYQSPYDSEQVP

>d1gd5a\_ d.189.1.1 (A:) p47phox NADPH oxidase {Human (Homo sapiens)}

GSMGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRPDDLKLP

>d1vjw\_\_ d.58.1.4 (-) Ferredoxin {Thermotoga maritima}

MKVRVDADACIGCGVCENLCPDVFQLGDDGKAKVLQPETDLPCAKDAADSCPTGAISVE

>d1fxra\_ d.58.1.4 (A:) Ferredoxin I {Sulfate-reducing bacteria (Desulfovibrio africanus)}

ARKFYVDQDECIACESCVEIAPGAFAMDPEIEKAYVKDVEGASQEEVEEAMDTCPVQCIHWEDE

>d1iqza\_ d.58.1.4 (A:) Ferredoxin {Bacillus thermoproteolyticus}

PKYTIVDKETCIACGACGAAAPDIYDYDEDGIAYVTLDDNQGIVEVPDILIDDMMDAFEGCPTDSIKVADEPFDGDPNKFE

>d1jb0c\_ d.58.1.4 (C:) Photosystem I iron-sulfur protein PsaC {Synechococcus elongatus}

AHTVKIYDTCIGCTQCVRACPTDVLEMVPWDGCKAGQIASSPRTEDCVGCKRCETACPTDFLSIRVYLGAETTRSMGLAY

>d1feha3 d.58.1.5 (A:127-209) Fe-only hydrogenase, second domain {Clostridium pasteurianum}

KDKTEYVDERSKSLTVDRTKCLLCGRCVNACGKNTETYAMKFLNKNGKTIIGAEDEKCFDDTNCLLCGQCIIACPVAALSEKS

>d1hfel2 d.58.1.5 (L:2-86) Fe-only hydrogenase larger subunit, N-domain {Desulfovibrio desulfuricans}

SRTVMERIEYEMHTPDPKADPDKLHFVQIDEAKCIGCDTCSQYCPTAAIFGEMGEPHSIPHIEACINCGQCLTHCPENAIYEAQS

>d1keka5 d.58.1.5 (A:669-785) Pyruvate-ferredoxin oxidoreductase, PFOR, domain V {Desulfovibrio africanus}

TSQFEKRGVAINVPQWVPENCIQCNQCAFVCPHSAILPVLAKEEELVGAPANFTALEAKGKELKGYKFRIQINTLDCMGCGNCADICPPKEKALVMQPLDTQRDAQVPNLEYAARIP

>d1h7wa5 d.58.1.5 (A:845-1017) Dihydropyrimidine dehydrogenase, C-terminal domain {Pig (Sus scrofa)}

ELQGWDGQSPGTESHQKGKPVPRIAELMGKKLPNFGPYLEQRKKIIAEEKMRLKEQNAAFPPLERKPFIPKKPIPAIKDVIGKALQYLGTFGELSNIEQVVAVIDEEMCINCGKCYMTCNDSGYQAIQFDPETHLPTVTDTCTGCTLCLSVCPIIDCIRMVSRTTPYEPKRGL

>d1jnrb\_ d.58.1.5 (B:) Adenylylsulfate reductase B subunit {Archaeon Archaeoglobus fulgidus}

PSFVNPEKCDGCKALERTACEYICPNDLMTLDKEKMKAYNREPDMCWECYSCVKMCPQGAIDVRGYVDYSPLGGACVPMRGTSDIMWTVKYRNGKVLRFKFAIRTTPWGSIQPFEGFPEPTEEALKSELLAGEPEIIGTSEFPQVKKKA

>d1pca\_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Pig (Sus scrofa)}

KEDFVGHQVLRISVDDEAQVQKVKELEDLEHLQLDFWRGPARPGFPIDVRVPFPSIQAVKVFLEAHGIRYTIMIEDVQLLLDEEQEQMFASQGR

>d1nsa\_2 d.58.3.1 (7A-95A) Procarboxypeptidase B {Pig (Sus scrofa)}

FEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVEDFLEQNELQYEVLINNLRSVLEAQFDSVSR

>d1spbp\_ d.58.3.2 (P:) Subtilisin prosegment {Bacillus amyloliquefaciens}

EKKYIVGFKQTMSTMSAAKKKDVISEKGGKVQKQFKYVDAASATLNEKAVKELKKDPSVAYVEEDHVAHAY

>d1itpa\_ d.58.3.2 (A:) Proteinase A inhibitor 1, POIA1 {Oyster mushroom (Pleurotus ostreatus)}

GSAGKFIVIFKNDVSEDKIRETKDEVIAEGGTITNEYNMPGMKGFAGELTPQSLTKFQGLQGDLIDSIEEDGIVTTQ

>d1ha1\_1 d.58.7.1 (8-92) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}

EPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE

>d2up1a2 d.58.7.1 (A:99-190) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}

GAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVIQKYHTVNGHNCEVRKALSKQEMASAS

>d1fht\_\_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}

AVPETRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALRSMQGFPFYDKPMRIQYAKTDSDIIAKMKGTFVERDRKREKRKPKSQE

>d2u1a\_\_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}

MAPAQPLSENPPNHILFLTNLPEETNELMLSMLFNQFPGFKEVRLVPGRHDIAFVEFDNEVQAGAARDALQGFKITQNNAMKISFAKK

>d1u2fa\_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}

ARRLYVGNIPFGITEEAMMDFFNAQMRLGGLTQAPGNPVLAVQINQDKNFAFLEFRSVDETTQAMAFDGIIFQGQSLKIRRPHDYQPLPG

>d2u2fa\_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}

AHKLFIGGLPNYLNDDQVKELLTSFGPLKAFNLVKDSATGLSKGYAFCEYVDINVTDQAIAGLNGMQLGDKKLLVQRASVGAKNA

>d1sxl\_\_ d.58.7.1 (-) Sex-lethal protein {Drosophila melanogaster}

MSYARPGGESIKDTNLYVTNLPRTITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKREEAQEAISALNNVIPEGGSQPLSVRLAEEHGK

>d1d8za\_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}

MDSKTNLIVNYLPQNMTQDEFKSLFGSIGDIESCKLVRDKITGQSLGYGFVNYSDPNDADKAINTLNGLKLQTKTIKVSYARPSSASIR

>d1cvja1 d.58.7.1 (A:11-90) Poly(A)-binding protein {Human (Homo sapiens)}

ASLYVGDLHPDVTEAMLYEKFSPAGPILSIRVCRDMITRRSLGYAYVNFQQPADAERALDTMNFDVIKGKPVRIMWSQRD

>d1cvja2 d.58.7.1 (A:91-179) Poly(A)-binding protein {Human (Homo sapiens)}

PSLRKSGVGNIFIKNLDKSIDNKALYDTFSAFGNILSCKVVCDENGSKGYGFVHFETQEAAERAIEKMNGMLLNDRKVFVGRFKSRKER

>d1qm9a1 d.58.7.1 (A:1-110) Polypyrimidine tract-binding protein {Human (Homo sapiens)}

MGNSVLLVSNLNPERVTPQSLFILFGVYGDVQRVKILFNKKENALVQMADGNQAQLAMSHLNGHKLHGKPIRITLSKHQNVQLPREGQEDQGLTKDYGNSPLHRFKKPGS

>d1qm9a2 d.58.7.1 (A:111-198) Polypyrimidine tract-binding protein {Human (Homo sapiens)}

KNFQNIFPPSATLHLSNIPPSVSEEDLKVLFSSNGGVVKGFKFFQKDRKMALIQMGSVEEAVQALIDLHNHDLGENHHLRVSFSKSTI

>d1fj7a\_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}

GSHMLEDPVEGSESTTPFNLFIGNLNPNKSVAELKVAISELFAKNDLAVVDVRTGTNRKFGYVDFESAEDLEKALELTGLKVFGNEIKLEKPKGRDGTRGC

>d1fjca\_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}

SHMLEDPCTSKKVRAARTLLAKNLSFNITEDELKEVFEDALEIRLVSQDGKSKGIAYIEFKSEADAEKNLEEKQGAEIDGRSVSLYYTGEKGGTRG

>d1h6kx\_ d.58.7.1 (X:) CBP20, 20KDa nuclear cap-binding protein {Human (Homo sapiens)}

KSCTLYVGNLSFYTTEEQIYELFSKSGDIKKIIMGLDKMTACGFCFVEYYSRADAENAMRYINGTRLDDRIIRTDWDAG

>d1dbda\_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}

RRTTNDGFHLLKAGGSCFALISGTANQVKCYRFRVKKNHRHRYENCTTTWFTVADNGAERQGQAQILITFGSPSQRQDFLKHVPLPPGMNISGFTASLDF

>d1a7ge\_ d.58.8.1 (E:) Papillomavirus-1 E2 protein {Human papillomavirus type 31}

ATTPIIHLKGDANILKCLRYRLSKYKQLYEQVSSTWHWTCTDGKHKNAIVTLTYISTSQRDDFLNTVVIPNTVSVSTGYMTI

>d1b3ta\_ d.58.8.1 (A:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}

KGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLP

>d1bwva2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

RIKNSRYESGVIPYAKMGYWNPDYQVKDTDVLALFRVTPQPGVDPIEAAAAVAGESSTATWTVVWTDLLTAADLYRAKAYKVDQVPNNPEQYFAYIAYELDLFEEGSIANLTASIIGNVFGFKAVKALRLEDMRLPLAYLKTFQ

>d5ruba2 d.58.9.1 (A:2-137) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Rhodospirillum rubrum}

DQSSRYVNLALKEEDLIAGGEHVLCAYIMKPKAGYGYVATAAHFAAESSTGTNVEVCTTDDFTRGVDALVYEVDEARELTKIAYPVALFDRNITDGKAMIASFLTLTMGNNQGMGDVEYAKMHDFYVPEAYRALFD

>d1dar\_4 d.58.11.1 (600-689) Elongation factor G (EF-G), domains III and V {Thermus thermophilus}

VILEPIMRVEVTTPEEYMGDVIGDLNARRGQILGMEPRGNAQVIRAFVPLAEMFGYATDLRSKTQGRGSFVMFFDHYQEVPKQVQEKLIK

>d1fnma4 d.58.11.1 (A:404-482) Elongation factor G (EF-G), domains III and V {Thermus thermophilus}

VPEPVIDVAIEPKTKADQEKLSQALARLAEEDPTFRVSTHPETGQTIISGMGELHLEIIVDRLKREFKVDANVGKPQVA

>d1b64\_\_ d.58.12.1 (-) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Human (Homo sapiens)}

MLVAKSSILLDVKPWDDETDMAKLEECVRSIQADGLVWGSSKLVPVGYGIKKLQIQCVVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI

>d1gh8a\_ d.58.12.1 (A:) aEF-1beta {Archaeon Methanobacterium thermoautotrophicum}

MGDVVATIKVMPESPDVDLEALKKEIQERIPEGTELHKIDEEPIAFGLVALNVMVVVGDAEGGTEAAEESLSGIEGVSNIEVTDVRRLM

>d1fa0a1 d.58.16.1 (A:352-523) Poly(A) polymerase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

NDFFFRYKFYLEITAYTRGSDEQHLKWSGLVESKVRLLVMKLEVLAGIKIAHPFTKPFESSYCCPTEDDYEMIQDKYGSHKTETALNALKLVTDENKEEESIKDAPKAYLSTMYIGLDFNIENKKEKVDIHIPCTEFVNLCRSFNEDYGDHKVFNLALRFVKGYDLPDEVFD

>d1f5aa1 d.58.16.1 (A:365-498) Poly(A) polymerase, C-terminal domain {Cow (Bos taurus)}

PNFFQKYKHYIVLLASAPTEKQRLEWVGLVESKIRILVGSLEKNEFITLAHVNPQSFPAPKENPDKEEFRTMWVIGLVFKKTENSENLSVDLTYDIQSFTDTVYRQAINSKMFEVDMKIAAMHVKRKQLHQLLP

>d1afj\_\_ d.58.17.1 (-) Mercuric ion binding protein MerP {Shigella flexneri}

ATQTVTLAVPGMTCAACPITVKKALSKVEGVSKVDVGFEKREAVVTFDDTKASVQKLTKATADAGYPSSVKQ

>d1fvqa\_ d.58.17.1 (A:) Copper transporter domain ccc2a {Baker's yeast (Saccharomyces cerevisiae)}

AREVILAVHGMTCSACTNTINTQLRALKGVTKCDISLVTNECQVTYDNEVTADSIKEIIEDCGFDCEILRDS

>d1aw0\_\_ d.58.17.1 (-) Menkes copper-transporting ATPase {Human (Homo sapiens)}

LTQETVINIDGMTCNSCVQSIEGVISKKPGVKSIRVSLANSNGTVEYDPLLTSPETLRGAIEDMGFDATLSD

>d1cc8a\_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Baker's yeast (Saccharomyces cerevisiae)}

AEIKHYQFNVVMTCSGCSGAVNKVLTKLEPDVSKIDISLEKQLVDVYTTLPYDFILEKIKKTGKEVRSGKQL

>d1cpza\_ d.58.17.1 (A:) Copper chaperone {Enterococcus hirae}

AQEFSVKGMSCNHCVARIEEAVGRISGVKKVKVQLKKEKAVVKFDEANVQATEICQAINELGYQAEVI

>d1k0va\_ d.58.17.1 (A:) Copper chaperone {Bacillus subtilis, CopZ}

MEQKTLQVEGMSCQHCVKAVETSVGELDGVSAVHVNLEAGKVDVSFDADKVSVKDIADAIEDQGYDVAKIEGR

>d1qupa2 d.58.17.1 (A:2-73) Copper chaperone for superoxide dismutase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TTNDTYEATYAIPMHCENCVNDIKACLKNVPGINSLNFDIEQQIMSVESSVAPSTIINTLRNCGKDAIIRGA

>d1gmua2 d.58.38.1 (A:71-138) Urease metallochaperone UreE, C-terminal domain {Klebsiella aerogenes}

DEEVSVVRCDDPFMLAKACYALGNRHVPLQIMPGELRYHHDHVLDDMLRQFGLTVTFGQLPFEPEAGA

>d1eara2 d.58.38.1 (A:75-142) Urease metallochaperone UreE, C-terminal domain {Bacillus pasteurii}

LEKVYVIKPQTMQEMGKMAFEIGNRHTMCIIEDDEILVRYDKTLEKLIDEVGVSYEQSERRFKEPFKY

>d1tdj\_2 d.58.18.2 (336-423) Allosteric threonine deaminase C-terminal domain {Escherichia coli}

QREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNYRFADAKNACIFVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVRYMV

>d1tdj\_3 d.58.18.2 (424-514) Allosteric threonine deaminase C-terminal domain {Escherichia coli}

GGRPSHPLQERLYSFEFPESPGALLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFELGDHEPDFETRLNELGYDCHDETNNPAFRFFLAG

>d1dqaa1 d.58.20.1 (A:587-703) NAD-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

GMTRGPVVRLPRACDSAEVKAWLETSEGFAVIKEAFDSTSRFARLQKLHTSIAGRNLYIRFQSRSGDAMGMNMISKGTEKALSKLHEYFPEMQILAVSGNYCTDKKPAAINWIEGRG

>d1qaxa1 d.58.20.1 (A:111-220) NAD-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

LMHAQVQIVGIQDPLNARLSLLRRKDEIIELANRKDQLLNSLGGGCRDIEVHTFADTPRGPMLVAHLIVDVRDAMGANTVNTMAEAVAPLMEAITGGQVRLRILSNLADL

>d1azsa\_ d.58.29.1 (A:) Adenylyl cyclase VC1, domain C1a {Dog (Canis familiaris)}

DMMFHKIYIQKHDNVSILFADIEGFTSLASQCTAQELVMTLNELFARFDKLAAENHCLRIKILGDCYYCVSGLPEARADHAHCCVEMGMDMIEAISLVREMTGVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHMEAGGKAGRIHITKATLSYLNGDYEVEPGCGGERNAYLKEHSIETFLIL

>d1azsb\_ d.58.29.1 (B:) Adenylyl cyclase IIC1, domain C2a {Rat (Rattus norvegicus)}

HQSYDCVCVMFASIPDFKEFYTESDVNKEGLECLRLLNEIIADFDDLLSKPKFSGVEKIKTIGSTYMAATGLSAIPSQEHAQEPERQYMHIGTMVEFAYALVGKLDAINKHSFNDFKLRVGINHGPVIAGVIGAQKPQYDIWGNTVNVASRMDSTGVLDKIQVTEETSLILQTLGYTCTCRGIINVKGKGDLKTYFVNT

>d1fx2a\_ d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}

NNNRAPKEPTDPVTLIFTDIESSTALWAAHPDLMPDAVAAHHRMVRSLIGRYKCYEVKTVGDSFMIASKSPFAAVQLAQELQLCFLHHDWGTNALDDSYREFEEQRAEGECEYTPPTAHMDPEVYSRLWNGLRVRVGIHTGLCDIRHDEVTKGYDYYGRTPNMAARTESVANGGQVLMTHAAYMSLSAEDRKQIDVTALGDVALRGVSDPVKMYQLNTVPSRNFAALRLDREYFD

>d1e6ya2 d.58.31.2 (A:1002-1283) Alpha chain {Archaeon Methanosarcina barkeri}

AADIFSKFKKDMEVKFAQEFGSNKQTGGDITDKTAKFLRLGPEQDPRKVEMIKAGKEIAEKRGIAFYNPMMHSGAPLGQRAITPYTISGTDIVCEPDDLHYVNNAAMQQMWDDIRRTCIVGLDMAHETLEKRLGKEVTPETINHYLEVLNHAMPGAAVVQEMMVETHPALVDDCYVKVFTGDDALADEIDKQFLIDINKEFSEEQAAQIKASIGKTSWQAIHIPTIVSRTTDGAQTSRWAAMQIGMSFISAYAMCAGEAAVADLSFAAKHAALVSMGEMLPA

>d1hbnb2 d.58.31.2 (B:2-188) Beta chain {Archaeon Methanobacterium thermoautotrophicum}

AKFEDKVDLYDDRGNLVEEQVPLEALSPLRNPAIKSIVQGIKRTVAVNLEGIENALKTAKVGGPACKIMGRELDLDIVGNAESIAAAAKEMIQVTEDDDTNVELLGGGKRALVQVPSARFDVAAEYSAAPLVTATAFVQAIINEFDVSMYDANMVKAAVLGRYPQSVEYMGANIATMLDIPQKLEGP

>d1e8ga1 d.58.32.1 (A:274-560) Vanillyl-alcohol oxidase {Fungus (Penicillium simplicissimum)}

GGYQSYLITLPKDGDLKQAVDIIRPLRLGMALQNVPTIRHILLDAAVLGDKRSYSSRTEPLSDEELDKIAKQLNLGRWNFYGALYGPEPIRRVLWETIKDAFSAIPGVKFYFPEDTPENSVLRVRDKTMQGIPTYDELKWIDWLPNGAHLFFSPIAKVSGEDAMMQYAVTKKRCQEAGLDFIGTFTVGMREMHHIVCIVFNKKDLIQKRKVQWLMRTLIDDCAANGWGEYRTHLAFMDQIMETYNWNNSSFLRFNEVLKNAVDPNGIIAPGKSGVWPSQYSHVTWKL

>d1diqa1 d.58.32.1 (A:243-521) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}

PVFKPFEVIFEDEADIVEIVDALRPLRMSNTIPNSVVIASTLWEAGSAHLTRAQYTTEPGHTPDSVIKQMQKDTGMGAWNLYAALYGTQEQVDVNWKIVTDVFKKLGKGRIVTQEEAGDTQPFKYRAQLMSGVPNLQEFGLYNWRGGGGSMWFAPVSEARGSECKKQAAMAKRVLHKYGLDYVAEFIVAPRDMHHVIDVLYDRTNPEETKRADACFNELLDEFEKEGYAVYRVNTRFQDRVAQSYGPVKRKLEHAIKRAVDPNNILAPGRSGIDLNNDF

>d1ftra1 d.58.33.1 (A:1-148) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon Methanopyrus kandleri}

MEINGVEIEDTFAEAFEAKMARVLITAASHKWAMIAVKEATGFGTSVIMCPAEAGIDCGYVPPEETPDGRPGVTIMIGHNDEDELKEQLLDRIGQCVMTAPTASAFDAMPEAEKEDEDRVGYKLSFFGDGYQEEDELDGRKVWKIPVV

>d1ftra2 d.58.33.1 (A:149-296) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon Methanopyrus kandleri}

EGEFIVEDSFGITTGVAGGNFYIMAESQPAGLQAAEAAVDAIKGVEGAYAPFPGGIVASASKVGSKQYDFLPASTNDAYCPTVEDNELPEGVKCVYEIVINGLNEEAVKEAMRVGIEAACQQPGVVKISAGNFGGKLGQYEIHLHDLF

>d1qd1a1 d.58.34.1 (A:2-180) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}

SQLVECVPNFSEGKNQEVIDAISRAVAQTPGCVLLDVDSGPSTNRTVYTFVGRPEDVVEGALNAARAAYQLIDMSRHHGEHPRMGALDVCPFIPVRGVTMDECVRCAQAFGQRLAEELGVPVYLYGEAARTAGRQSLPALRAGEYEALPEKLKQAEWAPDFGPSAFVPSWGATVAGARK

>d1qd1a2 d.58.34.1 (A:181-326) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}

FLLAFNINLLSTREQAHRIALDLREQGRGKDQPGRLKKVQAIGWYLDEKNLAQVSTNLLDFEVTGLHTVFEETCREAQELSLPVVGSQLVGLVPLKALLDAAAFYCEKENLFLLQDEHRIRLVVNRLGLDSLAPFKPKERIIEYLV

>d1dj0a1 d.58.35.1 (A:7-114) Pseudouridine synthase I {Escherichia coli}

PPVYKIALGIEYDGSKYYGWQRQNEVRSVQEKLEKALSQVANEPITVFCAGRTDAGVHGTGQVVHFETTALRKDAAWTLGVNANLPGDIAVRWVKTVPDDFHARFSAT

>d1dj0a2 d.58.35.1 (A:115-270) Pseudouridine synthase I {Escherichia coli}

ARRYRYIIYNHRLRPAVLSKGVTHFYEPLDAERMHRAAQCLLGENDFTSFRAVQCQSRTPWRNVMHINVTRHGPYVVVDIKANAFVHHMVRNIVGSLMEVGAHNQPESWIAELLAAKDRTLAAATAKAEGLYLVAVDYPDRYDLPKPPMGPLFLAD

>d1k8wa1 d.58.35.2 (A:9-73) Pseudouridine synthase II TruB {Escherichia coli}

MDINGVLLLDKPQGMSSNDALQKVKRIYNANRAGHTGALDPLATGMLPICLGEATKFSQYLLDSD

>d1k8wa2 d.58.35.2 (A:74-312) Pseudouridine synthase II TruB {Escherichia coli}

KRYRVIARLGQRTDTSDADGQIVEERPVTFSAEQLAAALDTFRGDIEQIPSMYSALKYQGKKLYEYARQGIEVPREARPITVYELLFIRHEGNELELEIHCSKGTYIRTIIDDLGEKLGCGAHVIYLRRLAVSKYPVERMVTLEHLRELVEQAEQQDIPAAELLDPLLMPMDSPASDYPVVNLPLTSSVYFKNGNPVRTSGAPLEGLVRVTEGENGKFIGMGEIDDEGRVAPRRLVVEY

>d1aop\_1 d.58.36.1 (81-145) Sulfite reductase, domains 1 and 3 {Escherichia coli}

LLRCRLPGGVITTKQWQAIDKFAGENTIYGSIRLTNRQTFQFHGILKKNVKPVHQMLHSVGLDAL

>d1aop\_2 d.58.36.1 (346-425) Sulfite reductase, domains 1 and 3 {Escherichia coli}

IGWVKGIDDNWHLTLFIENGRILDYPARPLKTGLLEIAKIHKGDFRITANQNLIIAGVPESEKAKIEKIAKESGLMNAVT

>d1bxya\_ d.59.1.1 (A:) Prokaryotic ribosomal protein L30 {Thermus thermophilus}

MPRLKVKLVKSPIGYPKDQKAALKALGLRRLQQERVLEDTPAIRGNVEKVAHLVRVEVVE

>d1jj2v\_ d.59.1.1 (V:) Archaeal L30 (L30a) {Archaeon Haloarcula marismortui}

MHALVQLRGEVNMHTDIQDTLEMLNIHHVNHCTLVPETDAYRGMVAKVNDFVAFGEPSQETLETVLATRAEPLEGDADVDDEWVAEHTDYDDISGLAFALLSEETTLREQGLSPTLRLHPPRGGHDGVKHPVKEGGQLGKHDTEGIDDLLEAMR

>d2if1\_\_ d.64.1.1 (-) Eukaryotic translation initiation factor eIF-1 (SUI1) {Human (Homo sapiens)}

MRGSHHHHHHTDPMSAIQNLHSFDPFADASKGDDLLPAGTEDYIHIRIQQRNGRKTLTTVQGIADDYDKKKLVKAFKKKFACNGTVIEHPEYGEVIQLQGDQRKNICQFLVEIGLAKDDQLKVHGF

>d1d1ra\_ d.64.1.1 (A:) YciH {Escherichia coli}

KGDGVVRIQRQTSGRKGKGVCLITGVDLDDAELTKLAAELKKKCGCGGAVKDGVIEIQGDKRDLLKSLLEAKGMKVKLAGGLE

>d1f7ua3 d.67.2.1 (A:2-135) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Baker's yeast (Saccharomyces cerevisiae)}

ASTANMISQLKKLSIAEPAVAKDSHPDVNIVDLMRNYISQELSKISGVDSSLIFPALEWTNTMERGDLLIPIPRLRIKGANPKDLAVQWAEKFPCGDFLEKVEANGPFIQFFFNPQFLAKLVIPDILTRKEDYG

>d1iq0a3 d.67.2.1 (A:1-96) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Thermus thermophilus}

MLRRALEEAIAQALKEMGVPVRLKVARAPKDKPGDYGVPLFALAKELRKPPQAIAQELKDRLPLPEFVEEAVPVGGYLNFRLRTEALLREALRPKA

>d1j98a\_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Bacillus subtilis}

VESFELDHNAVVAPYVRHCGVHKVGTDGVVNKFDIRFCQPNKQAMKPDTIHTLEHLLAFTIRSHAEKYDHFDIIDISPMGCQTGYYLVVSGETTSAEIVDLLEDTMKEAVEITEIPAANEKQCGQAKLHDLEGAKRLMRFWLSQDKEELLKVFG

>d1j6wa\_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Haemophilus influenzae}

LLDSFKVDHTKMNAPAVRIAKTMLTPKGDNITVFDLRFCIPNKEILSPKGIHTLEHLFAGFMRDHLNGDSIEIIDISPMGCRTGFYMSLIGTPNEQKVSEAWLASMQDVLGVQDQASIPELNIYQCGSYTEHSLEDAHEIAKNVIARGIGVNKNEDLSLDN

>d1hr6b2 d.185.1.1 (B:246-462) Mitochondrial processing peptidase (MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}

GPLPVFCRGERFIKENTLPTTHIAIALEGVSWSAPDYFVALATQAIVGNWDRAIGTGTNSPSPLAVAASQNGSLANSYMSFSTSYADSGLWGMYIVTDSNEHNVRLIVNEILKEWKRIKSGKISDAEVNRAKAQLKAALLLSLDGSTAIVEDIGRQVVTTGKRLSPEEVFEQVDKITKDDIIMWANYRLQNKPVSMVALGNTSTVPNVSYIEEKLNQ

>d1hr6a1 d.185.1.1 (A:14-233) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}

ARTDNFKLSSLANGLKVATSNTPGHFSALGLYIDAGSRFEGRNLKGCTHILDRLAFKSTEHVEGRAMAETLELLGGNYQCTSSRENLMYQASVFNQDVGKMLQLMSETVRFPKITEQELQEQKLSAEYEIDEVWMKPELVLPELLHTAAYSGETLGSPLICPRGLIPSISKYYLLDYRNKFYTPENTVAAFVGVPHEKALELTGKYLGDWQSTHPPITKK

>d1hr6a2 d.185.1.1 (A:234-470) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}

VAQYTGGESCIPPAPVFGNLPELFHIQIGFEGLPIDHPDIYALATLQTLLGGGGSFSAGGPGKGMYSRLYTHVLNQYYFVENCVAFNHSYSDSGIFGISLSCIPQAAPQAVEVIAQQMYNTFANKDLRLTEDEVSRAKNQLKSSLLMNLESKLVELEDMGRQVLMHGRKIPVNEMISKIEDLKPDDISRVAEMIFTGNVNNAGNGKGRATVVMQGDRGSFGDVENVLKAYGLGNSSS

>d1be3a1 d.185.1.1 (A:1-233) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}

TATYAQALQSVPETQVSQLDNGLRVASEQSSQPTCTVGVWIDAGSRYESEKNNGAGYFVEHLAFKGTKNRPGNALEKEVESMGAHLNAYSTREHTAYYIKALSKDLPKAVELLADIVQNCSLEDSQIEKERDVILQELQENDTSMRDVVFNYLHATAFQGTPLAQSVEGPSENVRKLSRADLTEYLSRHYKAPRMVLAAAGGLEHRQLLDLAQKHFSGLSGTYDEDAVPTLSP

>d1be3a2 d.185.1.1 (A:234-446) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}

CRFTGSQICHREDGLPLAHVAIAVEGPGWAHPDNVALQVANAIIGHYDCTYGGGAHLSSPLASIAATNKLCQSFQTFNICYADTGLLGAHFVCDHMSIDDMMFVLQGQWMRLCTSATESEVLRGKNLLRNALVSHLDGTTPVCEDIGRSLLTYGRRIPLAEWESRIAEVDARVVREVCSKYFYDQCPAVAGFGPIEQLPDYNRIRSGMFWLRF

>d1ezva1 d.185.1.1 (A:27-239) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}

AEVTQLSNGIVVATEHNPAHTASVGVVFGSGAANENPYNNGVSNLWKNIFLSKENSAVAAKEGLALSSNISRDFQSYIVSSLPGSTDKSLDFLNQSFIQQKANLLSSSNFEATKKSVLKQVQDFEDNDHPNRVLEHLHSTAFQNTPLSLPTRGTLESLENLVVADLESFANNHFLNSNAVVVGTGNIKHEDLVNSIESKNLSLQTGTKPVLKK

>d1ezva2 d.185.1.1 (A:240-456) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}

KAAFLGSEVRLRDDTLPKAWISLAVEGEPVNSPNYFVAKLAAQIFGSYNAFEPASRLQGIKLLDNIQEYQLCDNFNHFSLSYKDSGLWGFSTATRNVTMIDDLIHFTLKQWNRLTISVTDTEVERAKSLLKLQLGQLYESGNPVNDANLLGAEVLIKGSKLSLGEAFKKIDAITVKDVKAWAGKRLWDQDIAIAGTGQIEGLLDYMRIRSDMSMMRW

>d1be3b2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}

KAKYHGGEIREQNGDSLVHAALVAESAAIGSAEANAFSVLQHVLGAGPHVKRGSNATSSLYQAVAKGVHQPFDVSAFNASYSDSGLFGFYTISQAASAGDVIKAAYNQVKTIAQGNLSNPDVQAAKNKLKAGYLMSVESSEGFLDEVGSQALAAGSYTPPSTVLQQIDAVADADVINAAKKFVSGRKSMAASGNLGHTPFIDEL

>d1bccb1 d.185.1.1 (B:18-235) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}

PPHPQDLEITKLPNGLVIASLENYSPGSTIGVFIKAGSRYENSSNLGTSHLLRLASSLTTKGASSFKITRGIEAVGGKLSVESTRENMAYTVECLRDDVEILMEFLLNVTTAPEFRPWEVADLQPQLKIDKAVAFQNPQTHVIENLHAAAYRNALADSLYCPDYRIGKVTSVELHDFVQNHFTSARMALVGLGVSHPVLKNVAEQLLNIRGGLGLSGA

>d1ezvb1 d.185.1.1 (B:17-218) Cytochrome bc1 core subunit 2 {Baker's yeast (Saccharomyces cerevisiae)}

LTVSARDAPTKISTLAVKVHGGSRYATKDGVAHLLNRFNFQNTNTRSALKLVRESELLGGTFKSTLDREYITLKATFLKDDLPYYVNALADVLYKTAFKPHELTESVLPAARYDYAVAEQCPVKSAEDQLYAITFRKGLGNPLLYDGVERVSLQDIKDFADKVYTKENLEVSGENVVEADLKRFVDESLLSTLPAGKSLVSK

>d1ezvb2 d.185.1.1 (B:219-368) Cytochrome bc1 core subunit 2 {Baker's yeast (Saccharomyces cerevisiae)}

SEPKFFLGEENRVRFIGDSVAAIGIPVNKASLAQYEVLANYLTSALSELSGLISSAKLDKFTDGGLFTLFVRDQDSAVVSSNIKKIVADLKKGKDLSPAINYTKLKNAVQNESVSSPIELNFDAVKDFKLGKFNYVAVGDVSNLPYLDEL

>d1ejda\_ d.68.2.2 (A:) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ) {Enterobacter cloacae}

MDKFRVQGPTRLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLTQLGTKVERXGSVWIDASNVNNFSAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCAIGARPVDLHIFGLEKLGAEIKLEEGYVKASVNGRLKGAHIVMDKVSVGATVTIMSAATLAEGTTIIENAAREPEIVDTANFLVALGAKISGQGTDRITIEGVERLGGGVYRVLPDRIETGTFLVAAAISGGKIVCRNAQPDTLDAVLAKLREAGADIETGEDWISLDMHGKRPKAVTVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITETIFENRFMHVPELIRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVDRIYHIDRGYERIEDKLRALGANIERVKGE

>d1g6sa\_ d.68.2.2 (A:) 5-enol-pyruvyl shikimate-3-phosphate(EPSP) synthase {Escherichia coli}

MESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDDVRHMLNALTALGVSYTLSADRTRCEIIGNGGPLHAEGALELFLGNAGTAMRPLAAALCLGSNDIVLTGEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQGGFTGGNVDVDGSVSSQFLTALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMKTFGVEIENQHYQQFVVKGGQSYQSPGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDYISCTRGELNAIDMDMNHIPDAAMTIATAALFAKGTTTLRNIYNWRVKETDRLFAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILDPKCTAKTFPDYFEQLARISQAA

>d1bwvs\_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

VRITQGTFSFLPDLTDEQIKKQIDYMISKKLAIGIEYTNDIHPRNAYWEIWGLPLFDVTDPAAVLFEINACRKARSNFYIKVVGFSSVRGIESTIISFIVNRPKHEPGFNLMRQEDKSRSIKYTIHSYESYKPEDERY

>d1gk8i\_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

MVWTPVNNKMFETFSYLPPLTDEQIAAQVDYIVANGWIPCLEFAEADKAYVSNESAIRFGSVSCLYYDNRYWTMWKLPMFGCRDPMQVLREIVACTKAFPDAYVRLVAFDNQKQVQIMGFLVQRP

>d1xxaa\_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Escherichia coli}

LKNLVLDIDYNDAVVVIHTSPGAAQLIARLLDSLGKAEGILGTIAGDDTIFTTPANGFTVKDLYEAILELF

>d1b4ba\_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Bacillus stearothermophilus}

ALVDVFIKLDGTGNLLVLRTLPGNAHAIGVLLDNLDWDEIVGTICGDDTCLIICRTPKDAKKVSNQLLSML

>d1bdfa1 d.74.3.1 (A:2-52,A:179-232) RNA polymerase alpha {Escherichia coli}

QGSVTEFLKPRLVDIEQVSSTHAKVTLEPLERGFGHTLGNALRAILLSSMPXPVERIAYNVEAARVEQRTDLDKLVIEMETNGTIDPEEAIRRAATILAEQLEAFV

>d1i50c1 d.74.3.1 (C:3-41,C:173-268) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

EEGPQVKIREASKDNVDFILSNVDLAMANSLRRVMIAEIXAAAIEFEYDPWNKLKHTDYWYEQDSAKEWPQSKNCEYEDPPNEGDPFDYKAQADTFYMNVESVGSIPVDQVVVRGIDTLQKKVASILLALTQMDQD

>d1c0aa2 d.74.4.1 (A:288-420) Prokaryotic AspRS, insert domain {Escherichia coli}

NPMELTDVADLLKSVEFAVFAGPANDPKGRVAALRVPGGASLTRKQIDEYGNFVKIYGAKGLAYIKVNERAKGLEGINSPVAKFLNAEIIEDILDRTAAQDGDMIFFGADNKKIVADAMGALRLKVGKDLGLT

>d1g51a2 d.74.4.1 (A:295-414) Prokaryotic AspRS, insert domain {Thermus thermophilus}

FGLELKEVGPLFRQSGFRVFQEAESVKALALPKALSRKEVAELEEVAKRHKAQGLAWARVEEGGFSGGVAKFLEPVREALLQATEARPGDTLLFVAGPRKVAATALGAVRLRAADLLGLK

>d1ewqa4 d.75.2.1 (A:1-120) DNA repair protein MutS, domain I {Thermus aquaticus}

MEGMLKGEGPGPLPPLLQQYVELRDQYPDYLLLFQVGDFYECFGEDAERLARALGLVLTHKTSKDFTTPMAGIPLRAFEAYAERLLKMGFRLAVADQVEPAEEAEGLVRREVTQLLTPGT

>d1e3ma4 d.75.2.1 (A:2-116) DNA repair protein MutS, domain I {Escherichia coli}

SAIENFDAHTPMMQQYLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPMAGIPYHAVENYLAKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTP

>d1iq4a\_ d.77.1.1 (A:) Ribosomal protein L5 {Bacillus stearothermophilus}

MNRLKEKYLNEVVPALMSKFNYKSIMQVPKIEKIVINMGVGDAVQNPKALDSAVEELTLIAGQRPVVTRAKKSIAGFRLRQGMPIGAKVTLRGERMYEFLDKLISVSLPRARDFRGVSKKSFDGRGNYTLGIKEQLIFPEIDYDKVNKVRGMDIVIVTTANTDEEARELLALLGMPFQK

>d1jj2d\_ d.77.1.1 (D:) Ribosomal protein L5 {Archaeon Haloarcula marismortui}

FHEMREPRIEKVVVHMGIGHGGRDLANAEDILGEITGQMPVRTKAKRTVGEFDIREGDPIGAKVTLRDEMAEEFLQTALPLAELATSQFDDTGNFSFGVEEHTEFPSQEYDPSIGIYGLDVTVNLVRPGYRVAKRDKASRSIPTKHRLNPADAVAFIESTYDVEV

>d1fsz\_2 d.79.2.1 (232-356) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}

INVDFADVKAVMNNGGLAMIGIGESDSEKRAKEAVSMALNSPLLDVDIDGATGALIHVMGPEDLTLEEAREVVATVSSRLDPNATIIWGATIDENLENTVRVLLVITGVQSRIEFTDTGLKRKKL

>d1tuba2 d.79.2.1 (A:246-440) Tubulin alpha-subunit {Pig (Sus scrofa)}

GALNVDLTEFQTNLVPYPRGHFPLATYAPVISAEKAYHEQLSVAEITNACFEPANQMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYEPPTVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYEEVGVDSV

>d1tubb2 d.79.2.1 (B:246-437) Tubulin beta-subunit {Pig (Sus scrofa)}

GQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPPRGLKMSATFIGNSTAIQELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQD

>d1ck9a\_ d.79.3.1 (A:) Eukaryotic ribosomal protein L30 (L30e) {Baker's yeast (Saccharomyces cerevisiae)}

APVKSQESINQKLALVIKSGKYTLGYKSTVKSLRQGKSKLIIIAANTPVLRKSELEYYAMLSKTKVYYFQGGNNELGTAVGKLFRVGVVSILEAGDSDILTTLA

>d1jj2f\_ d.79.3.1 (F:) Ribosomal protein L7ae {Archaeon Haloarcula marismortui}

PVYVDFDVPADLEDDALEALEVARDTGAVKKGTNETTKSIERGSAELVFVAEDVQPEEIVMHIPELADEKGVPFIFVEQQDDLGHAAGLEVGSAAAAVTDAGAAATVLEEIADKVEELR

>d1e7ka\_ d.79.3.1 (A:) Spliceosomal 15.5kd protein {Human (Homo sapiens)}

ADVNPKAYPLADAHLTKKLLDLVQQSCNYKQLRKGANEATKTLNRGISEFIVMAADAEPLEIILHLPLLCEDKNVPYVFVRSKQALGRACGVSRPVIACSVTIKEGSQLKQQIQSIQQSIERLLV

>d1gd0a\_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Human (Homo sapiens)}

PMFIVNTNVPRASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGGSSEPCALCSLHSIGKIGGAQNRSYSKLLCGLLAERLRISPDRVYINYYDMNAANVGWNNSTFALEHH

>d1dpta\_ d.80.1.3 (A:) D-dopachrome tautomerase {Human (Homo sapiens)}

PFLELDTNLPANRVPAGLEKRLCAAAASILGKPADRVNVTVRPGLAMALSGSTEPCAQLSISSIGVVGTAEDNRSHSAHFFEFLTKELALGQDRILIRFFPLESWQIGKIGTVMTFL

>d1cf2o2 d.81.1.1 (O:139-303) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Methanothermus fervidus}

SCNTTGLCRTLKPLHDSFGIKKVRAVIVRRGADPAQVSKGPINAIIPNPPKLPSHHGPDVKTVLDINIDTMAVIVPTTLMHQHNVMVEVEETPTVDDIIDVFEDTPRVILISAEDGLTSTAEIMEYAKELGRSRNDLFEIPVWRESITVVDNEIYYMQAVHQESD

>d1ggaa2 d.81.1.1 (A:165-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Trypanosoma brucei brucei, glycosome}

CTTNCLAPLVHVLVKEGFGISTGLMTTVHSYTATQKTVDGVSVKDWRGGRAAALNIIPSTTGAAKAVGMVIPSTQGKLTGMAFRVPTADVSVVDLTFIATRDTSIKEIDAALKRASKTYMKNILGYTDEELVSADFISDSRSSIYDSKATLQNNLPNERRFFKIVSWYD

>d1gl3a2 d.81.1.1 (A:134-354) Aspartate beta-semialdehyde dehydrogenase {Escherichia coli}

NCTVSLMLMSLGGLFANDLVDWVSVATYQAASGGGARHMRELLTQMGHLYGHVADELATPSSAILDIERKVTTLTRSGELPVDNFGVPLAGSLIPWIDKQLDNGQSREEWKGQAETNKILNTSSVIPVDGLCVRVGALRCHSQAFTIKLKKDVSIPTVEELLAAHNPWAKVVPNDREITMRELTPAAVTGTLTTPVGRLRKLNMGPEFLSAFTVGDQLLWG

>d1ebfa2 d.81.1.2 (A:151-340) Homoserine dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

PIISFLREIIQTGDEVEKIEGIFSGTLSYIFNEFSTSQANDVKFSDVVKVAKKLGYTEPDPRDDLNGLDVARKVTIVGRISGVEVESPTSFPVQSLIPKPLESVKSADEFLEKLSDYDKDLTQLKKEAATENKVLRFIGKVDVATKSVSVGIEKYDYSHPFASLKGSDNVISIKTKRYTNPVVIQGAGAG

>d1e5qa2 d.81.1.2 (A:125-391) Saccharopine reductase {Rice blast fungus (Magnaporthe grisea)}

LDPGIDHLYAIKTIEEVHAAGGKIKTFLSYCGGLPAPESSDNPLGYKFSWSSRGVLLALRNAASFYKDGKVTNVAGPELMATAKPYFIYPGFAFVAYPNRDSTPYKERYQIPEADNIVRGTLRYQGFPQFIKVLVDIGFLSDEEQPFLKEAIPWKEATQKIVKASSASEQDIVSTIVSNATFESTEEQKRIVAGLKWLGIFSDKKITPRGNALDTLCATLEEKMQFEEGERDLVMLQHKFEIENKDGSRETRTSSLCEYGAPIGSGG

>d1f06a2 d.81.1.3 (A:119-268) Diaminopimelic acid dehydrogenase (DAPDH) {Corynebacterium glutamicum}

WDPGMFSINRVYAAAVLAEHQQHTFWGPGLSQGHSDALRRIPGVQKAVQYTLPSEDALEKARRGEAGDLTGKQTHKRQCFVVADAADHERIENDIRTMPDYFVGYEVEVNFIDEATFDSEHTGMPHGGHVITTGDTGGFNHTVEYILKLD

>d1dih\_2 d.81.1.3 (131-240) Dihydrodipicolinate reductase {Escherichia coli}

VGVNVMLKLLEKAAKVMGDYTDIEIIEAHHRHKVDAPSGTALAMGEAIAHALDKDLKDCAVYSREGHTGERVPGTIGFATVRAGDIVGEHTAMFADIGERLEITHKASSR

>d1k5ha3 d.81.1.3 (A:126-274) 1-deoxy-D-xylulose-5-phosphate reductoisomerase {Escherichia coli}

ESLVTCGRLFMDAVKQSKAQLLPVDSEHNAIFQSLPQPIQHNLGYADLEQNGVVSILLTGSGGPFRETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIEARWLFNASASQMEVLIHPQSVIHSMVRYQDGSVLAQLGEP

>d1h6da2 d.81.1.5 (A:213-374) Glucose-fructose oxidoreductase {Zymomonas mobilis}

DPMNRAAVKLIRENQLGKLGMVTTDNSDVMDQNDPAQQWRLRRELAGGGSLMDIGIYGLNGTRYLLGEEPIEVRAYTYSDPNDERFVEVEDRIIWQMRFRSGALSHGASSYSTTTTSRFSVQGDKAVLLMDPATGYYQNLISVQTPGHANQSMMPQFIMPAN

>d1dpga2 d.81.1.5 (A:182-412,A:427-485) Glucose 6-phosphate dehydrogenase {Leuconostoc mesenteroides}

KEMVQNIAALRFGNPIFDAAWNKDYIKNVQVTLSEVLGVEERAGYYDTAGALLDMIQNHTMQIVGWLAMEKPESFTDKDIRAAKNAAFNALKIYDEAEVNKYFVRAQYGAGDSADFKPYLEELDVPADSKNNTFIAGELQFDLPRWEGVPFYVRSGKRLAAKQTRVDIVFKAGTFNFGSEQEAQEAVLSIIIDPKGAIELKLNAKSVEDAFNTRTIDLGWTVSDEDKKNTPXGSNFADWNGVSIAWKFVDAISAVYTADKAPLETYKSGSMGPEASDKLLAANGDAWVFKG

>d1qkia2 d.81.1.5 (A:200-434,A:450-511) Glucose 6-phosphate dehydrogenase {Human (Homo sapiens)}

DHYLGKEMVQNLMVLRFANRIFGPIWNRDNIACVILTFKEPFGTEGRGGYFDEFGIIRDVMQNHLLQMLCLVAMEKPASTNSDDVRDEKVKVLKCISEVQANNVVLGQYVGNPDGEGEATKGYLDDPTVPRGSTTATFAAVVLYVENERWDGVPFILRCGKALNERKAEVRLQFHDVAGDIFHQQCKRNELVIRVQPNEAVYTKMMTKKPGMFFNPEESELDLTYGNRYKNVKLPXMHFVRSDELLEAWRIFTPLLHQIELEKPKPIPYIYGSRGPTEADELMKRVGFQYEGTYKWVN

>d1ekga\_ d.82.2.1 (A:) C-terminal domain of frataxin {Human (Homo sapiens)}

LDETTYERLAEETLDSLAEFFEDLADKPYTFEDYDVSFGSGVLTVKLGGDLGTYVINKQTPNKQIWLSSPSSGPKRYDWTGKNWVYSHDGVSLHELLAAELTKALKTKLDLSSLAYSGK

>d1ew4a\_ d.82.2.1 (A:) CyaY {Escherichia coli}

MNDSEFHRLADQLWLTIEERLDDWDGDSDIDCEINGGVLTITFENGSKIIINRQEPLHQVWLATKQGGYHFDLKGDEWICDRSGETFWDLLEQAATQQAGETVSFR

>d1ewfa1 d.83.1.1 (A:1-217) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

VNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSELQPYFQTLPVMTKIDSVAGINYGLVAPPATTA

>d1ewfa2 d.83.1.1 (A:218-456) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

ETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAFAVLPNSALASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADVVYK

>d1e6ta\_ d.85.1.1 (A:) MS2 virus coat protein {Bacteriophage MS2}

ASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQNRKYTIKVEVPKVATQTVGGVELPVAAWRSYLNMELTIPIFATNSDCELIVKAMQGLLKDGNPIPSAIAANSGIY

>d1qbea\_ d.85.1.1 (A:) Qbeta coat protein {Bacteriophage Qbeta}

AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

>d1dwna\_ d.85.1.1 (A:) PP7 coat protein {Bacteriophage PP7}

SKTIVLSVGEATRTLTEIQSTADRQIFEEKVGPLVGRLRLTASLRQNGAKTAYRVNLKLDQADVVDCSTSVCGELPKVRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLVVNLVPLGR

>d1ej1a\_ d.86.1.1 (A:) Translation initiation factor eIF4e {Mouse (Mus musculus)}

KHPLQNRWALWFFKNDKSKTWQANLRLISKFDTVEDFWALYNHIQLSSNLMPGCDYSLFKDGIEPMWEDEKNKRGGRWLITLNKQQRRSDLDRFWLETLLCLIGESFDDYSDDVCGAVVNVRAKGDKIAIWTTECENRDAVTHIGRVYKERLGLPPKIVIGYQSHADTATKSGSTTKNRFVV

>d1ap8\_\_ d.86.1.1 (-) Translation initiation factor eIF4e {Baker's yeast (Saccharomyces cerevisiae)}

MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHFDVKHPLNTKWTLWYTKPAVDKSESWSDLLRPVTSFQTVEEFWAIIQNIPEPHELPLKSDYHVFRNDVRPEWEDEANAKGGKWSFQLRGKGADIDELWLRTLLAVIGETIDEDDSQINGVVLSIRKGGNKFALWTKSEDKEPLLRIGGKFKQVLKLTDDGHLEFFPHSSANGRHPQPSITL

>d1aoga3 d.87.1.1 (A:358-487) Trypanothione reductase {Trypanosoma cruzi}

DHTRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPLMHKVSGSKYKTFVAKIITNHSDGTVLGVHLLGDNAPEIIQGIGICLKLNAKISDFYNTIGVHPTSAEELCSMRTPSYYYVKGEKMEKP

>d1h6va3 d.87.1.1 (A:367-499) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

YDNVPTTVFTPLEYGCCGLSEEKAVEKFGEENIEVYHSFFWPLEWTVPSRDNNKCYAKVICNLKDNERVVGFHVLGPNAGEVTQGFAAALKCGLTKQQLDSTIGIHPVCAEIFTTLSVTKRSGGDILQSGCCG

>d1nhp\_3 d.87.1.1 (322-447) NADH peroxidase {Enterococcus faecalis}

GVQGSSGLAVFDYKFASTGINEVMAQKLGKETKAVTVVEDYLMDFNPDKQKAWFKLVYDPETTQILGAQLMSKADLTANINAISLAIQAKMTIEDLAYADFFFQPAFDKPWNIINTAALEAVKQER

>d1d7ya3 d.87.1.1 (A:309-405) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}

TAPGYAELPWYWSDQGALRIQVAGLASGDEEIVRGEVSLDAPKFTLIELQKGRIVGATCVNNARDFAPLRRLLAVGAKPDRAALADPATDLRKLAAA

>d1lvl\_3 d.87.1.1 (336-458) Dihydrolipoamide dehydrogenase {Pseudomonas putida}

PAAIAAVCFTDPEVVVVGKTPEQASQQGLDCIVAQFPFAANGRAMSLESKSGFVRVVARRDNHLILGWQAVGVAVSELSTAFAQSLEMGACLEDVAGTIHAHPTLGEAVQEAALRALGHALHI

>d1lpfa3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}

YDLIPSVIYTHPEIAWVGKTEQTLKAEGVEVNVGTFPFAASGRAMAANDTTGLVKVIADAKTDRVLGVHVIGPSAAELVQQGAIGMEFGTSAEDLGMMVFSHPTLSEALHEAALAVNGHAIHIA

>d1ojt\_3 d.87.1.1 (471-598) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

ARVIPGVAYTSPEVAWVGETELSAKASARKITKANFPWAASGRAIANGCDKPFTKLIFDAETGRIIGGGIVGPNGGDMIGEVCLAIEMGCDAADIGKTIHPHPTLGESIGMAAEVALGTCTDLPPQKK

>d1fcda3 d.87.1.1 (A:328-401) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}

PGTPSYLNTCYSILAPAYGISVAAIYRPNADGSAIESVPDSGGVTPVDAPDWVLEREVQYAYSWYNNIVHDTFG

>d1ffvc1 d.87.2.1 (C:178-287) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {Hydrogenophaga pseudoflava}

GTGWAYEKLKRKTGDWATAGCAVVMRKSGNTVSHIRIALTNVAPTALRAEAAEAALLGKAFTKEAVQAAADAAIAICEPAEDLRGDADYKTAMAGQMVKRALNAAWARCA

>d1fo4a4 d.87.2.1 (A:415-531) Xanthine oxidase, domain 4 (?) {Cow (Bos taurus)}

DEFFSAFKQASRREDDIAKVTCGMRVLFQPGSMQVKELALCYGGMADRTISALKTTQKQLSKFWNEKLLQDVCAGLAEELSLSPDAPGGMIEFRRTLTLSFFFKFYLTVLKKLGKDS

>d1jroa3 d.87.2.1 (A:346-462) Xanthine dehydrogenase chain A, domain 4 {Rhodobacter capsulatus}

PGLRCYKLSKRFDQDISAVCGCLNLTLKGSKIETARIAFGGMAGVPKRAAAFEAALIGQDFREDTIAAALPLLAQDFTPLSDMRASAAYRMNAAQAMALRYVRELSGEAVAVLEVMP

>d1mnma\_ d.88.1.1 (A:) MCM1 transcriptional regulator {Baker's yeast (Saccharomyces cerevisiae)}

QKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFELSVLTGTQVLLLVVSETGLVYTFSTPKFEPIVTQQEGRNLIQACLNAPDD

>d1egwa\_ d.88.1.1 (A:) Mef2a core {Human (Homo sapiens)}

GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEY

>d1nox\_\_ d.90.1.1 (-) NADH oxidase {Thermus thermophilus, HB8}

PVLDAKTAALKRRSIRRYRKDPVPEGLLREILEAALRAPSAWNLQPWRIVVVRDPATKRALREAAFGQAHVEEAPVVLVLYADLEDALAHLDEVIHPGVQGERREAQKQAIQRAFAAMGQEARKAWASGQSYILLGYLLLLLEAYGLGSVPMLGFDPERVRAILGLPSRAAIPALVALGYPAEEGYPSHRLPLERVVLWR

>d1vfra\_ d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio fischeri}

THPIIHDLENRYTSKKYDPSKKVSQEDLAVLLEALRLSASSINSQPWKFIVIESDAAKQRMHDSFANMHQFNQPHIKACSHVILFANKLSYTRDDYDVVLSKAVADKRITEEQKEAAFASFKFVELNCDENGEHKAWTKPQAYLALGNALHTLARLNIDSTTMEGIDPELLSEIFADELKGYECHVALAIGYHHPSEDYNASLPKSRKAFEDVITIL

>d1kqba\_ d.90.1.1 (A:) Nitroreductase {Enterobacter cloacae}

DIISVALKRHSTKAFDASKKLTAEEAEKIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGTYVFNERKMLDASHVVVFCAKTAMDDAWLERVVDQEEADGRFNTPEAKAANHKGRTYFADMHRVDLKDDDQWMAKQVYLNVGNFLLGVGAMGLDAVPIEGFDAAILDEEFGLKEKGFTSLVVVPVGHHSVEDFNATLPKSRLPLSTIVTEC

>d1f5va\_ d.90.1.1 (A:) Nitroreductase {Escherichia coli, oxygen-insensitive form}

MTPTIELICGHRSIRHFTDEPISEAQREAIINSARATSSSSFLQCSSIIRITDKALREELVTLTGGQKHVAQAAEFWVFCADFNRHLQICPDAQLGLAEQLLLGVVDTAMMAQNALIAAESLGLGGVYIGGLRNNIEAVTKLLKLPQHVLPLFGLCLGWPADNPDLKPRLPASILVHENSYQPLDKGALAQYDEQLAEYYLTRGSNNRRDTWSDHIRRTIIKESRPFILDYLHKQGWATR

>d1g12a\_ d.92.1.12 (A:) Fungal zinc peptidase {Grifola frondosa}

TYNGCSSSEQSALAAAASAAQSYVAESLSYLQTHTAATPRYTTWFGSYISSRHSTVLQHYTDMNSNDFSSYSFDCTCTAAGTFAYVYPNRFGTVYLCGAFWKAPTTGTDSQAGTLVHESSHFTRNGGTKDYAYGQAAAKSLATMDPDKAVMNADNHEYFSENNPAQS

>d1eb6a\_ d.92.1.12 (A:) Fungal zinc peptidase {Aspergillus oryzae, deuterolysin}

TEVTDCKGDAESSLTTALSNAAKLANQAAEAAESGDESKFEEYFKTTDQQTRTTVAERLRAVAKEAGSTSGGSTTYHCNDPYGYCEPNVLAYTLPSKNEIANCDIYYSELPPLAQKCHAQDQATTTLHEFTHAPGVYQPGTEDLGYGYDAATQLSAQDALNNADSYALYANAIELKC

>d1ezm\_\_ d.92.1.2 (-) Elastase {Pseudomonas aeruginosa}

AEAGGPGGNQKIGKYTYGSDYGPLIVNDRCEMDDGNVITVDMNSSTDDSKTTPFRFACPTNTYKQVNGAYSPLNDAHFFGGVVFKLYRDWFGTSPLTHKLYMKVHYGRSVENAYWDGTAMLFGDGATMFYPLVSLDVAAHEVSHGFTEQNSGLIYRGQSGGMNEAFSDMAGEAAEFYMRGKNDFLIGYDIKKGSGALRYMDQPSRDGRSIDNASQYYNGIDVHHSSGVYNRAFYLLANSPGWDTRKAFEVFVDANRYYWTATSNYNSGACGVIRSAQNRNYSAADVTRAFSTVGVTCP

>d1npc\_\_ d.92.1.2 (-) Neutral protease {Bacillus cereus, strain dsm 3101}

VTGTNKVGTGKGVLGDTKSLNTTLSGSSYYLQDNTRGATIFTYDAKNRSTLPGTLWADADNVFNAAYDAAAVDAHYYAGKTYDYYKATFNRNSINDAGAPLKSTVHYGSNYNNAFWNGSQMVYGDGDGVTFTSLSGGIDVIGHELTHAVTENSSNLIYQNESGALNEAISDIFGTLVEFYDNRNPDWEIGEDIYTPGKAGDALRSMSDPTKYGDPDHYSKRYTGSSDNGGVHTNSGIINKQAYLLANGGTHYGVTVTGIGKDKLGAIYYRANTQYFTQSTTFSQARAGAVQAAADLYGANSAEVAAVKQSFSAVGVN

>d1j7na1 d.92.1.14 (A:27-263) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}

ERNKTQEEHLKEIMKHIVKIEVKGEEAVKKEAAEKLLEKVPSDVLEMYKAIGGKIYIVDGDITKHISLEALSEDKKKIKDIYGKDALLHEHYVYAKEGYEPVLVIQSSEDYVENTEKALNVYYEIGKILSRDILSKINQPYQKFLDVLNTIKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLYAPEAFNYMDKFNEQEINLSLEELKDQR

>d1j7na2 d.92.1.14 (A:551-773) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}

PKSKIDTKIQEAQLNINQEWNKALGLPKYTKLITFNVHNRYASNIVESAYLILNEWKNNIQSDLIKKVTNYLVDGNGRFVFTDITLPNIAEQYTHQDEIYEQVHSKGLYVPESRSILLHGPSKGVELRNDSEGFIHEFGHAVDDYAGYLLDKNQSDLVTNSKKFIDIFKEEGSNLTSYGRTNEAEFFAEAFRLMHSTDHAERLKVQKNAPKTFQFINDQIKFI

>d3btaa3 d.92.1.7 (A:1-546) Botulinum neurotoxin {Clostridium botulinum, serotype A}

PFVNKQFNYKDPVNGVDIAYIKIPNVGQMQPVKAFKIHNKIWVIPERDTFTNPEEGDLNPPPEAKQVPVSYYDSTYLSTDNEKDNYLKGVTKLFERIYSTDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHEVLNLTRNGYGSTQYIRFSPDFTFGFEESLEVDTNPLLGAGKFATDPAVTLAHELIHAGHRLYGIAINPNRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNKFKDIASTLNKAKSIVGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLKFDKLYKMLTEIYTEDNFVKFFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLRNTNLAANFNGQNTEINNMNFTKLKNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIENLSSDIIGQLELMPNIERFPNGKKYELDK

>d1epwa3 d.92.1.7 (A:1-533) Botulinum neurotoxin {Clostridium botulinum, serotype B}

PVTINNFNYNDPIDNNNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCEYYDPDYLNTNDKKNIFLQTMIKLFNRIKSKPLGEKLLEMIINGIPYLGDRRVPLEEFNTNIASVTVNKLISNPGEVERKKGIFANLIIFGPGPVLNENETIDIGIQNHFASREGFGGIMQMKFCPEYVSVFNNVQENKGASIFNRRGYFSDPALILMHELIHVLHGLYGIKVDDLPIVPNEKKFFMQSTDAIQAEELYTFGGQDPSIITPSTDKSIYDKVLQNFRGIVDRLNKVLVCISDPNININIYKNKFKDKYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYFSDSLPPVKIKNLLDNEIYTIEEGFNISDKDMEKEYRGQNKAINKQAYEEISKEHLAVYKIQMCKSVKAPGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLTDFNVDVPVYEKQPAIKKIFTDE

>d1qba\_4 d.92.2.1 (201-337) Bacterial chitobiase, Domain 2 {Serratia marcescens}

SNADLQTLPAGALRGKIVPTPMQVKVHAQDADLRKGVALDLSTLVKPAADVVSQRFALLGVPVQTNGYPIKTDIQPGKFKGAMAVSGAYELKIGKKEAQVIGFDQAGVFYGLQSILSLVPSDGSGKIATLDASDAPR

>d1jaka2 d.92.2.1 (A:8-150) beta-N-acetylhexosaminidase, N-terminal domain {Streptomyces plicatus}

DRKAPVRPTPLDRVIPAPASVDPGGAPYRITRGTHIRVDDSREARRVGDYLADLLRPATGYRLPVTAHGHGGIRLRLAGGPYGDEGYRLDSGPAGVTITARKAAGLFHGVQTLRQLLPPAVEKDSAQPGPWLVAGGTIEDTPR

>d1fhs\_\_ d.93.1.1 (-) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo sapiens)}

GIEMKPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKVLRDGAGKYFLWVVKFNSLNELVDYHRSTSVSRNQQIFLRDIEQVPQQPTYVQA

>d1mil\_\_ d.93.1.1 (-) Shc adaptor protein {Human (Homo sapiens)}

GSQLRGEPWFHGKLSRREAEALLQLNGDFLVRESTTTPGQYVLTGLQSGQPKHLLLVDPEGVVRTKDHRFESVSHLISYHMDNHLPIISAGSELCLQQPVERKL

>d1pica\_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Human (Homo sapiens)}

GSPIPHHDEKTWNVGSSNRNKAENLLRGKRDGTFLVRESSKQGCYACSVVVDGEVKHCVINKTATGYGFAEPYNLYSSLKELVLHYQHTSLVQHNDSLNVTLAYPVYAQQRR

>d1fu6a\_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Rat (Rattus norvegicus)}

GMNNNMSLQDAEWYWGDISREEVNEKLRDTADGTFLVRDASTKMHGDYTLTLRKGGNNKSIKIFHRDGKYGFSDPLTFNSVVELINHYRNESLAQYNPKLDVKLLYPVSKY

>d1ab2\_\_ d.93.1.1 (-) Proto-oncogen tyrosine kinase {Human (Homo sapiens)}

GSGNSLEKHSWYHGPVSRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLYVSSESRFNTLAELVHHHSTVADGLITTLHYPAPKRGIHRD

>d1a81a1 d.93.1.1 (A:9-137) Syk tyrosine kinase {Human (Homo sapiens)}

SANHLPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHYTIERELNGTYAIAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPQGVQPKTGPFEDLKENLIREYVKQTWN

>d1a81a2 d.93.1.1 (A:138-262) Syk tyrosine kinase {Human (Homo sapiens)}

LQGQALEQAIISQKPQLEKLIATTAHEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHYRIDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKI

>d2plda\_ d.93.1.1 (A:) Phospholipase C-gamma-1 {Cow (Bos taurus)}

GSPGIHESKEWYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAISFRAEGKIKHCRVQQEGQTVMLGNSEFDSLVDLISYYEKHPLYRKMKLRYPINEENSS

>d1blk\_\_ d.93.1.1 (-) P55 Blk protein tyrosine kinase {Mouse (Mus musculus)}

GSVAPVETLEVEKWFFRTISRKDAERQLLAPMNKAGSFLIRESESNKGAFSLSVKDITTQGEVVKHYKIRSLDNGGYYISPRITFPTLQALVQHYSKKGDGLCQKLTLPCVNLA

>d1jwoa\_ d.93.1.1 (A:) Csk homologous kinase Chk {Human (Homo sapiens)}

LSLMPWFHGKISGQEAVQQLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHLTIDEAVFFCNLMDMVEHYSKDKGAICTKLVRPKRK

>d1bg1a3 d.93.1.1 (A:576-716) STAT3b {Mouse (Mus musculus)}

ILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDISGSTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPF

>d2cbla3 d.93.1.1 (A:264-351) Cbl {Human (Homo sapiens)}

THPGYMAFLTYDEVKARLQKFIHKPGSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKPLFQALIDGFREGFYLFPDGRNQNPDLTG

>d2shpa2 d.93.1.1 (A:2-110) Tyrosine phoshatase shp-2 {Human (Homo sapiens)}

KSRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDLTLSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLAELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSE

>d1d4ta\_ d.93.1.1 (A:) The Xlp protein Sap {Human (Homo sapiens)}

MDAVAVYHGKISRETGEKLLLATGLDGSYLLRDSESVPGVYCLCVLYHGYIYTYRVSQTETGSWSAETAPGVHKRYFRKIKNLISAFQKPDQGIVIPLQYPVEK

>d1ptf\_\_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Enterococcus faecalis}

MEKKEFHIVAETGIHARPATLLVQTASKFNSDINLEYKGKSVNLKSIMGVMSLGVGQGSDVTITVDGADEAEGMAAIVETLQKEGLA

>d1opd\_\_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Escherichia coli}

MFEQEVTITAPNGLHTRPAAQFVKEAKGFTSEITVTSNGKSASAKDLFKLQTLGLTQGTVVTISAEGEDEQKAVEHLVKLMAELE

>d1pch\_\_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Mycoplasma capricolum}

AKFSAIITDKVGLHARPASVLAKEASKFSSNITIIANEKQGNLKSIMNVMAMAIKTGTEITIQADGNDADQAIQAIKQTMIDTALIQG

>d1g9za\_ d.95.2.1 (A:) DNA endonuclease I-CreI {Chlamydomonas reinhardtii}

NTKYNKEFLLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLDKLVDEIGVGYVRDRGSVSDYILSEIKPLHNFLTQLQPFLKLKQKQANLVLKIIEQLPSAKESPDKFLEVCTWVDQIAALNDSKTRKTTSETVRAVLD

>d1b24a1 d.95.2.1 (A:7-99) I-dmoI {Archaeon Desulfurococcus mobilis}

VSGISAYLLGLIIGDGGLYKLKYKGNRSEYRVVITQKSENLIKQHIAPLMQFLIDELNVKSKIQIVKGDTRYELRVSSKKLYYYFANMLERIR

>d1b24a2 d.95.2.1 (A:100-179) I-dmoI {Archaeon Desulfurococcus mobilis}

LFNMREQIAFIKGLYVAEGDKTLKRLRIWNKNKALLEIVSRWLNNLGVRNTIHLDDHRHGVYVLNISLRDRIKFVHTILS

>d1dfaa2 d.95.2.2 (A:181-298) PI-SceI {Baker's yeast (Saccharomyces cerevisiae)}

PILYENDHFFDYMQKSKFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEKLNLCAEYKDRKEPQVAKTVNLYSKVVRGNGIRNNLNTENPLWDAIVGLGFLKD

>d1dfaa3 d.95.2.2 (A:299-415) PI-SceI {Baker's yeast (Saccharomyces cerevisiae)}

GVKNIPSFLSTDNIGTRETFLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGLVVSVNAEPAKVDMNGTKHKISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAAFARE

>d1dq3a3 d.95.2.2 (A:129-226) PI-Pfui intein {Archaeon Pyrococcus furiosus}

PDGEDYKFIFDYWLAGFIAGDGCFDKYHSHVKGHEYIYDRLRIYDYRIETFEIINDYLEKTFGRKYSIQKDRNIYYIDIKARNITSHYLKLLEGIDNG

>d1dq3a4 d.95.2.2 (A:227-335) PI-Pfui intein {Archaeon Pyrococcus furiosus}

IPPQILKEGKNAVLSFIAGLFDAEGHVSNKPGIELGMVNKRLIEDVTHYLNALGIKARIREKLRKDGIDYVLHVEEYSSLLRFYELIGKNLQNEEKREKLEKVLSNHKG

>d1a8ra\_ d.96.1.1 (A:) GTP cyclohydrolase I {Escherichia coli}

PSLSKEAALVHEALVARGLETPLRPPVHEMDNETRKSLIAGHMTEIMQLLNLDLADDSLMETPHRIAKMYVDEIFSGLDYANFPKITLIENKMKVDEMVTVRDITLTSTCESHFVTIDGKATVAYIPKDSVIGLSKINRIVQFFAQRPQVQERLTQQILIALQTLLGTNNVAVSIDAVHYCVKARGIRDATSATTTTSLGGLFKSSQNTRHEFLRAVRHHN

>d1is8a\_ d.96.1.1 (A:) GTP cyclohydrolase I {Rat (Rattus norvegicus)}

RPRSEEDNELNLPNLAAAYSSILRSLGEDPQRQGLLKTPWRAATAMQFFTKGYQETISDVLNDAIFDEDHDEMVIVKDIDMFSMCEHHLVPFVGRVHIGYLPNKQVLGLSKLARIVEIYSRRLQVQERLTKQIAVAITEALQPAGVGVVIEATHMCMVMRGVQKMNSKTVTSTMLGVFREDPKTREEFLTLIRS

>d1dhn\_\_ d.96.1.3 (-) 7,8-dihidroneopterin aldolase {Staphylococcus aureus}

MQDTIFLKGMRFYGYHGALSAENEIGQIFKVDVTLKVDLSEAGRTDNVIDTVHYGEVFEEVKSIMEGKAVNLLEHLAERIANRINSQYNRVMETKVRITKENPPIPGHYDGVGIEIVRENK

>d1b9la\_ d.96.1.3 (A:) 7,8-dihydroneopterin triphosphate epimerase {Escherichia coli}

AQPAAIIRIKNLRLRTFIGIKEEEINNRQDIVINVTIHYPADKARTSEDINDALNYRTVTKNIIQHVENNRFSLLEKLTQDVLDIAREHHWVTYAEVEIDKLHALRYADSVSMTLSWQR

>d1uox\_1 d.96.1.4 (1-136) Urate oxidase (uricase) {Aspergillus flavus}

SAVKAARYGKDNVRVYKVHKDEKTGVQTVYEMTVCVLLEGEIETSYTKADNSVIVATDSIKNTIYITAKQNPVTPPELFGSILGTHFIEKYNHIHAAHVNIVCHRWTRMDIDGKPHPHSFIRDSEEKRNVQVDVVE

>d1uox\_2 d.96.1.4 (137-295) Urate oxidase (uricase) {Aspergillus flavus}

GKGIDIKSSLSGLTVLKSTNSQFWGFLRDEYTTLKETWDRILSTDVDATWQWKNFSGLQEVRSHVPKFDATWATAREVTLKTFAEDNSASVQATMYKMAEQILARQQLIETVEYSLPNKHYFEIDLSWHKGLQNTGKNAEVFAPQSDPNGLIKCTVGRS

>d1e3ha5 d.101.1.1 (A:152-262) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5 {Streptomyces antibioticus}

FSGPIGGVRVALIRGQWVAFPTHTELEDAVFDMVVAGRVLEDGDVAIMMVEAEATEKTIQLVKDGAEAPTEEVVAAGLDAAKPFIKVLCKAQADLAAKAAKPTGEFPVFLD

>d1e3ha6 d.101.1.1 (A:483-578) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5 {Streptomyces antibioticus}

APVAGIAMGLISQEINGETHYVALTDILGAEDAFGDMDFKVAGTKEFVTALQLDTKLDGIPASVLAAALKQARDARLHILDVMMEAIDTPDEMSPN

>d1seta2 d.104.1.1 (A:111-421) Seryl-tRNA synthetase (SerRS) {Thermus thermophilus, strain hb27}

VGGEEANREIKRVGGPPEFSFPPLDHVALMEKNGWWEPRISQVSGSRSYALKGDLALYELALLRFAMDFMARRGFLPMTLPSYAREKAFLGTGHFPAYRDQVWAIAETDLYLTGTAEVVLNALHSGEILPYEALPLRYAGYAPAFRSEAGSFGKDVRGLMRVHQFHKVEQYVLTEASLEASDRAFQELLENAEEILRLLELPYRLVEVATGDMGPGKWRQVDIEVYLPSEGRYRETHSCSALLDWQARRANLRYRDPEGRVRYAYTLNNTALATPRILAMLLENHQLQDGRVRVPQALIPYMGKEVLEPCG

>d1e1oa2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysU}

DQEVRYRQRYLDLIANDKSRQTFVVRSKILAAIRQFMVARGFMEVETPMMQVIPGGASARPFITHHNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGISVRHNPEFTMMELYMAYADYHDLIELTESLFRTLAQEVLGTTKVTYGEHVFDFGKPFEKLTMREAIKKYRPETDMADLDNFDAAKALAESIGITVEKSWGLGRIVTEIFDEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGGREIGNGFSELNDAEDQAERFQEQVNAKAAGDDEAMFYDEDYVTALEYGLPPTAGLGIGIDRMIMLFTNSHTIRDVILFPAMRP

>d1qe0a2 d.104.1.1 (A:1-325) Histidyl-tRNA synthetase (HisRS) {Staphylococcus aureus}

MIKIPRGTQDILPEDSKKWRYIENQLDELMTFYNYKEIRTPIFESTDLFARGVGDSTDVVQKEMYTFKDKGDRSITLRPEGTAAVVRSYIEHKMQGNPNQPIKLYYNGPMFRYERKQKGRYRQFNQFGVEAIGAENPSVDAEVLAMVMHIYQSFGLKHLKLVINSVGDMASRKEYNEALVKHFEPVIHEFCSDCQSRLHTDPMRILDCKVDRDKEAIKTAPRITDFLNEESKAYYEQVKAYLDDLGIPYTEDPNLVRGLDYYTHTAFELMMDNPNYDGAITTLCGGGRYNGLLELLDGPSETGIGFALSIERLLLALEEEGIELD

>d1atia2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}

AASSLDELVALCKRRGFIFQSSEIYGGLQGVYDYGPLGVELKNNLKQAWWRRNVYERDDMEGLDASVLTHRLVLHYSGHEATFADPMVDNRITKKRYRLDHLLKEQPEEVLKRLYRAMEVEEENLHALVQAMMQAPERAGGAMTAAGVLDPASGEPGDWTPPRYFNMMFQDLRGPRGGRGLLAYLRPETAQGIFVNFKNVLDATSRKLGFGIAQIGKAFRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVEERLKWWQEMGLSRENLVPYQQPPESSAHYAKATVDILYRFPHGSLELEGIAQRTDFDLGSHTKDQEALGITARVLRNEHSTQRLAYRDPETGKWFVPYVIEPSAGVDRGVLALLAEAFTREELPNGEERIVLKLKP

>d1qf6a4 d.104.1.1 (A:242-532) Threonyl-tRNA synthetase (ThrRS) {Escherichia coli}

RDHRKIGKQLDLYHMQEEAPGMVFWHNDGWTIFRELEVFVRSKLKEYQYQEVKGPFMMDRVLWEKTGHWDNYKDAMFTTSSENREYCIKPMNCPGHVQIFNQGLKSYRDLPLRMAEFGSCHRNEPSGSLHGLMRVRGFTQDDAHIFCTEEQIRDEVNGCIRLVYDMYSTFGFEKIVVKLSTRPEKRIGSDEMWDRAEADLAVALEENNIPFEYQLGEGAFYGPKIEFTLYDCLDRAWQCGTVQLDFSLPSRLSASYVGEDNERKVPVMIHRAILGSMERFIGILTEEFAGF

>d1eova2 d.104.1.1 (A:205-557) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}

PILLEDASRSEAEAEAAGLPVVNLDTRLDYRVIDLRTVTNQAIFRIQAGVCELFREYLATKKFTEVHTPKLLGAPSEGGSSVFEVTYFKGKAYLAQSPQFNKQQLIVADFERVYEIGPVFRAENSNTHRHMTEFTGLDMEMAFEEHYHEVLDTLSELFVFIFSELPKRFAHEIELVRKQYPVEEFKLPKDGKMVRLTYKEGIEMLRAAGKEIGDFEDLSTENEKFLGKLVRDKYDTDFYILDKFPLEIRPFYTMPDPANPKYSNSYDFFMRGEEILSGAQRIHDHALLQERMKAHGLSPEDPGLKDYCDGFSYGCPPHAGGGIGLERVVMFYLDLKNIRRASLFPRDPKRLRP

>d1g51a3 d.104.1.1 (A:105-294,A:415-580) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}

TPPFPVDAGWRGEEEKEASEELRLKYRYLDLRRRRMQENLRLRHRVIKAIWDFLDREGFVQVETPFLTKSTPEGARDFLVPYRHEPGLFYALPQSPQLFKQMLMVAGLDRYFQIARCFRDEDLRADRQPDFTQLDLEMSFVEVEDVLELNERLMAHVFREALGVELPLPFPRLSYEEAMERYGSDKPDLRXREGFRFLWVVDFPLLEWDEEEEAWTYMHHPFTSPHPEDLPLLEKDPGRVRALAYDLVLNGVEVGGGSIRIHDPRLQARVFRLLGIGEEEQREKFGFFLEALEYGAPPHGGIAWGLDRLLALMTGSPSIREVIAFPKNKEGKDPLTGAPSPVPEEQLRELGLMVVRP

>d1jjca\_ d.104.1.1 (A:) Phenyl-tRNA synthetase (PheRS) alpha subunit, PheS {Thermus thermophilus and (Thermus aquaticus)}

RVDVSLPGASLFSGGLHPITLMERELVEIFRALGYQAVEGPEVESEFFNFDALNIPEHHPARDMWDTFWLTGEGFRLEGPLGEEVEGRLLLRTHTSPMQVRYMVAHTPPFRIVVPGRVFRFEQTDATHEAVFHQLEGLVVGEGIAMAHLKGAIYELAQALFGPDSKVRFQPVYFPFVEPGAQFAVWWPEGGKWLELGGAGMVHPKVFQAVDAYRERLGLPPAYRGVTGFAFGLGVERLAMLRYGIPDIRYFFGGRLKFLEQFKGVL

>d1jjcb5 d.104.1.1 (B:475-681) Phenyl-tRNA synthetase (PheRS) beta subunit, PheT, central domain {Thermus thermophilus (Thermus aquaticus)}

ALPAFFPAPDNRGVEAPYRKEQRLREVLSGLGFQEVYTYSFMDPEDARRFRLDPPRLLLLNPLAPEKAALRTHLFPGLVRVLKENLDLDRPERALLFEVGRVFREREETHLAGLLFGEGVGLPWAKERLSGYFLLKGYLEALFARLGLAFRVEAQAFPFLHPGVSGRVLVEGEEVGFLGALHPEIAQELELPPVHLFELRLPLPDKP

>d1hc7a2 d.104.1.1 (A:5-276) Prolyl-tRNA synthetase (ProRS) {Thermus thermophilus}

KGLTPQSQDFSEWYLEVIQKAELADYGPVRGTIVVRPYGYAIWENIQQVLDRMFKETGHQNAYFPLFIPMSFLRKEAEHVEGFSPELAVVTHAGGEELEEPLAVRPTSETVIGYMWSKWIRSWRDLPQLLNQWGNVVRWEMRTRPFLRTSEFLWQEGHTAHATREEAEEEVRRMLSIYARLAREYAAIPVIEGLKTEKEKFAGAVYTTTIEALMKDGKALQAGTSHYLGENFARAFDIKFQDRDLQVKYVHTTSWGLSWRFIGAIIMTHGDD

>d1g5ha2 d.104.1.1 (A:41-330) The aaRS-like accessory subunit of mitochondrial polymerase gamma, N-terminal domain {Mouse (Mus musculus)}

EALVDLCRRRHFLSGTPQQLSTAALLSGCHARFGPLGVELRKNLASQWWSSMVVFREQVFAVDSLHQEPGSSQPRDSAFRLVSPESIREILQDREPSKEQLVAFLENLLKTSGKLRATLLHGALEHYVNCLDLVNRKLPFGLAQIGVCFHPVSNSNQTPSSVTRVGEKTEASLVWFTPTRTSSQWLDFWLRHRLLWWRKFAMSPSNFSSADCQDELGRKGSKLYYSFPWGKEPIETLWNLGDQELLHTYPGNVSTIQGRDGRKNVVPCVLSVSGDVDLGTLAYLYDSFQL

>d12asa\_ d.104.1.1 (A:) Asparagine synthetase {Escherichia coli}

AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVQVKVKALPDAQFEVVHSLAKWKRQTLGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVMGDGERQFSTLKSTVEAIWAGIKATEAAVSEEFGLAPFLPDQIHFVHSQELLSRYPDLDAKGRERAIAKDLGAVFLVGIGGKLSDGHRHDVRAPDYDDWSTPSELGHAGLNGDILVWNPVLEDAFELSSMGIRVDADTLKHQLALTGDEDRLELEWHQALLRGEMPQTIGGGIGQSRLTMLLLQLPHIGQVQAGVWPAAVRESVPSLL

>d1qtsa2 d.105.1.1 (A:825-938) Alpa-adaptin AP2, C-terminal subdomain {Mouse (Mus musculus)}

FFQPTEMASQDFFQRWKQLSNPQQEVQNIFKAKHPMDTEITKAKIIGFGSALLEEVDPNPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKDTVSQRLCELLSEQF

>d1e42a2 d.105.1.1 (A:825-937) Beta2-adaptin AP2, C-terminal subdomain {Human (Homo sapiens)}

LFVEDGKMERQVFLATWKDIPNENELQFQIKECHLNADTVSSKLQNNNVYTIAKRNVEGQDMLYQSLKLTNGIWILAELRIQPGNPNYTLSLKCRAPEVSQYIYQVYDSILKN

>d1c44a\_ d.106.1.1 (A:) Sterol carrier protein 2 (SCP2) {Rabbit (Oryctolagus cuniculus)}

SSAGDGFKANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDKKADCTITMADSDLLALMTGKMNPQSAFFQGKLKITGNMGLAMKLQNLQLQPGKAKL

>d1ikta\_ d.106.1.1 (A:) SCP2-like domain of MFE-2 {Human (Homo sapiens)}

LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAKGAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIMLSQKLQMILKDYAKL

>d1b87a\_ d.108.1.1 (A:) Aminoglycoside 6'-N-acetyltransferase {Enterococcus faecium}

MIISEFDRNNPVLKDQLSDLLRLTWPEEYGDSSAEEVEEMMNPERIAVAAVDQDELVGFIGAIPQYGITGWELHPLVVESSRRKNQIGTRLVNYLEKEVASRGGITIYLGTDDLDHGTTLSQTDLYEHTFDKVASIQNLREHPYEFYEKLGYKIVGVLPNANGWDKPDIWMAKTIIPRPDS

>d1bo4a\_ d.108.1.1 (A:) Aminoglycoside 3-N-acetyltransferase {Serratia marcescens}

GIIRTCRLGPDQVKSMRAALDLFGREFGDVATYSQHQPDSDYLGNLLRSKTFIALAAFDQEAVVGALAAYVLPKFEQPRSEIYIYDLAVSGEHRRQGIATALINLLKHEANALGAYVIYVQADYGDDPAVALYTKLG

>d1ygha\_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Baker's yeast (Saccharomyces cerevisiae)}

KIEFRVVNNDNTKENMMVLTGLKNIFQKQLPKMPKEYIARLVYDRSHLSMAVIRKPLTVVGGITYRPFDKREFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIKYFLTYADNYAIGYFKKQGFTKEITLDKSIWMGYIKDYEGGTLMQCSMLPRIRYLD

>d1qsma\_ d.108.1.1 (A:) Histone acetyltransferase HPA2 {Baker's yeast (Saccharomyces cerevisiae)}

DNITVRFVTENDKEGWQRLWKSYQDFYEVSFPDDLDDFNFGRFLDPNIKMWAAVAVESSSEKIIGMINFFNHMTTWDFKDKIYINDLYVDENSRVKGAGGKLIQFVYDEADKLGTPSVYWCTDESNHRAQLLYVKVGYKAPKILYKRKGY

>d1bob\_\_ d.108.1.1 (-) Histone acetyltransferase HAT1 {Baker's yeast (Saccharomyces cerevisiae)}

FKPETWTSSANEALRVSIVGENAVQFSPLFTYPIYGDSEKIYGYKDLIIHLAFDSVTFKPYVNVKYSAKLGDDNIVDVEKKLLSFLPKDDVIVRDEAKWVDCFAEERKTHNLSDVFEKVSEYSLNGEEFVVYKSSLVDDFARRMHRRVQIFSLLFIEAANYIDETDPSWQIYWLLNKKTKELIGFVTTYKYWHYLGAKSFDEDIDKKFRAKISQFLIFPPYQNKGHGSCLYEAIIQSWLEDKSITEITVEDPNEAFDDLRDRNDIQRLRKLGYDAVFQKHSDLSDEFLESSRKSLKLEERQFNRLVEMLLLLNNS

>d1fy7a\_ d.108.1.1 (A:) Histone acetyltransferase ESA1 {Baker's yeast (Saccharomyces cerevisiae)}

ARVRNLNRIIMGKYEIEPWYFSPYPIELTDEDFIYIDDFTLQYFGSKKQYERYRKKCTLRHPPGNEIYRDDYVSFFEIDGRKQRTWCRNLCLLSKLFLDHKTLYYDVDPFLFYCMTRRDELGHHLVGYFSKEKESADGYNVACILTLPQYQRMGYGKLLIEFSYELSKKENKVGSPEKPLSDLGLLSYRAYWSDTLITLLVEHQKEITIDEISSMTSMTTTDILHTAKTLNILRYYKGQHIIFLNEDILDRYNRLKAKKRRTIDPNRLIWKPP

>d1cjwa\_ d.108.1.1 (A:) Serotonin N-acetyltranferase {Sheep (Ovis aries)}

HTLPANEFRCLTPEDAAGVFEIEREAFISVSGNCPLNLDEVQHFLTLCPELSLGWFVEGRLVAFIIGSLWDEERLTQESLALHRPRGHSAHLHALAVHRSFRQQGKGSVLLWRYLHHVGAQPAVRRAVLMCEDALVPFYQRFGFHPAGPCAIVVGSLTFTEMHCSL

>d1i12a\_ d.108.1.1 (A:) Glucosamine-phoshate N-acetyltransferase GNA1 {Baker's yeast (Saccharomyces cerevisiae)}

LPDGFYIRRMEEGDLEQVTETLKVLTTVGTITPESFCKLIKYWNEATVWNDNEDKKIMQYNPMVIVDKRTETVAATGNIIIERKIIHELGLCGHIEDIAVNSKYQGQGLGKLLIDQLVTIGFDYGCYKIILDCDEKNVKFYEKCGFSNAGVEMQIRK

>d1iica1 d.108.1.2 (A:34-218) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces cerevisiae)}

AMKDHKFWRTQPVKDFDEKVVEEGPIDKPKTPEDISDKPLPLLSSFEWCSIDVDNKKQLEDVFVLLNENYVEDRDAGFRFNYTKEFFNWALKSPGWKKDWHIGVRVKETQKLVAFISAIPVTLGVRGKQVPSVEINFLCVHKQLRSKRLTPVLIKEITRRVNKCDIWHALYTAGIVLPAPVSTCR

>d1iica2 d.108.1.2 (A:219-455) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces cerevisiae)}

YTHRPLNWKKLYEVDFTGLPDGHTEEDMIAENALPAKTKTAGLRKLKKEDIDQVFELFKRYQSRFELIQIFTKEEFEHNFIGEESLPLDKQVIFSYVVEQPDGKITDFFSFYSLPFTILNNTKYKDLGIGYLYYYATDADFQFKDRFDPKATKALKTRLCELIYDACILAKNANMDVFNALTSQDNTLFLDDLKFGPGDGFLNFYLFNYRAKPITGGLNPDNSNDIKRRSNVGVVML

>d2vik\_\_ d.109.1.1 (-) Villin, domain 1 (res. 1-126) {Chicken (Gallus gallus)}

VELSKKVTGKLDKTTPGIQIWRIENMEMVPVPTKSYGNFYEGDCYVLLSTRKTGSGFSYNIHYWLGKNSSQDEQGAAAIYTTQMDEYLGSVAVQHREVQGHESETFRAYFKQGLIYKQGGVASGMK

>d1svy\_\_ d.109.1.1 (-) Severin, domain 2 {Dictyostelium discoideum}

EYKPRLLHISGDKNAKVAEVPLATSSLNSGDCFLLDAGLTIYQFNGSKSSPQEKNKAAEVARAIDAERKGLPKVEVFCETDSDIPAEFWKLLGGKGAIAAKH

>d1d0na2 d.109.1.1 (A:153-262) Gelsolin {Horse (Equus caballus)}

VPNEVVVQRLLQVKGRRVVRATEVPVSWESFNNGDCFILDLGNNIYQWCGSKSNRFERLKATQVSKGIRDNERSGRAQVSVFEEGAEPEAMLQVLGPKPTLPEATEDTVK

>d1d0na3 d.109.1.1 (A:263-383) Gelsolin {Horse (Equus caballus)}

EDAANRKLAKLYKVSNGAGPMVVSLVADENPFAQGALRSEDCFILDHGKDGKIFVWKGKQANMEERKAALKTASDFISKMDYPKQTQVSVLPEGGETPLFRQFFKNWRDPDQTEGLGLAYL

>d1d0na4 d.109.1.1 (A:384-532) Gelsolin {Horse (Equus caballus)}

SSHIAHVERVPFDAATLHTSTAMAAQHGMDDDGTGQKQIWRVEGSNKVPVDPATYGQFYGGDSYIILYNYRHGSRQGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSRVVQGKEPAHLMSLFGGKPMIVYKGGTSREGGQTA

>d1d0na5 d.109.1.1 (A:533-628) Gelsolin {Horse (Equus caballus)}

PASTRLFQVRASSSGATRAVEIIPKAGALNSNDAFVLKTPSAAYLWVGAGASEAEKTGAQELLRVLRAQPVQVAEGSEPDSFWEALGGKATYRTSP

>d1d0na6 d.109.1.1 (A:629-755) Gelsolin {Horse (Equus caballus)}

RLKDKKMDAHPPRLFACSNKIGRFVIEEVPGEFMQEDLATDDVMLLDTWDQVFVWVGKDSQDEEKTEALTSAKRYIDTDPAHRDRRTPITVVKQGFEPPSFVGWFLGWDDSYWSVDPLDRALAELAA

>d1cnua\_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Amoeba (Acanthamoeba castellanii), actophorin}

GIAVSDDCVQKFNELKLGHQHRYVTFKMNASNTEVVVEHVGGPNATYEDFKSQLPERDCRYAIFDYEFQVDGGQRNKITFILWAPDSAPIKSKMMYTSTKDSIKKKLVGIQVEVQATDAAEISEDAVSERAKKD

>d1hqz1\_ d.109.1.2 (1:) Cofilin-like domain of actin-binding protein abp1p {Baker's yeast (Saccharomyces cerevisiae)}

LEPIDYTTHSREIDAEYLKIVRGSDPDTTWLIISPNAKKEYEPESTGSSFHDFLQLFDETKVQYGLARVSPPGSDVEKIIIIGWCPDSAPLKTRASFAANFAAVANNLFKGYHVQVTARDEDDLDENELLMKISNAAGA

>d1ak7\_\_ d.109.1.2 (-) Destrin {Human and pig (Homo sapiens) and (Sus scrofa)}

TMITPSSGNSASGVQVADEVCRIFYDMKVRKCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTITDPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELAPLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLGGSLIVAFEGCPV

>d1pne\_\_ d.110.1.1 (-) Profilin (actin-binding protein) {Cow (Bos taurus)}

AGWNAYIDNLMADGTCQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVGILVGKDRSSFFVNGLTLGGQKCSVIRDSLLQDGEFTMDLRTKSTGGAPTFNITVTMTAKTLVLLMGKEGVHGGMINKKCYEMASHLRRSQY

>d1ypra\_ d.110.1.1 (A:) Profilin (actin-binding protein) {Baker's yeast (Saccharomyces cerevisiae)}

SWQAYTDNLIGTGKVDKAVIYSRAGDAVWATSGGLSLQPNEIGEIVQGFDNPAGLQSNGLHIQGQKFMLLRADDRSIYGRHDAEGVVCVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLIGVQY

>d1cqa\_\_ d.110.1.1 (-) Profilin (actin-binding protein) {Birch (Betula verrucosa)}

SWQTYVDEHLMCDIDGQGEELAASAIVGHDGSVWAQSSSFPQFKPQEITGIMKDFEEPGHLAPTGLHLGGIKYMVIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEEPVTPGQCNMVVERLGDYLIDQGL

>d1ifqa\_ d.110.4.1 (A:) Sec22b {Mouse (Mus musculus)}

SVLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKLNEQSPTRCTLEAGAMTFHYIIEQGVCYLVLCEAAFPKKLAFAYLEDLHSEFDEQHGKKVPTVSRPYSFIEFDTFIQKTKKLYI

>d1h8ma\_ d.110.4.1 (A:) Synaptobrevin homolog 1 ykt6 {Baker's yeast (Saccharomyces cerevisiae)}

MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSVGQFMTFFAETVASRTGAGERQSIEEGNYIGHVYARSEGICGVLITDKQYPVRPAYTLLNKILDEYLVAHPKEEWADVTETNDALKMKQLDTYISKYQDPSQADA

>d1cfe\_\_ d.111.1.1 (-) Pathogenesis-related protein 1 (PR1) {Tomato (Lycopersicon esculentum), P14a}

QNSPQDYLAVHNDARAQVGVGPMSWDANLASRAQNYANSRAGDCNLIHSGAGENLAKGGGDFTGRAAVQLWVSERPSYNYATNQCVGGKKCRHYTQVVWRNSVRLGCGRARCNNGWWFISCNYDPVGNWIGQRPY

>d1qnxa\_ d.111.1.1 (A:) Insect allergen 5 (AG5) {Yellow jacket (Vespula vulgaris), Ves v 5}

AEAEFNNYCKIKCLKGGVHTACKYGSLKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLETRGNPGPQPPAKNMKNLVWNDELAYVAQVWANQCQYGHDTCRDVAKYQVGQNVALTGSTAAKYDDPVKLVKMWEDEVKDYNPKKKFSGNDFLKTGHYTQMVWANTKEVGCGSIKYIQEKWHKHYLVCNYGPSGNFKNEELYQTK

>d1a6ja\_ d.112.1.1 (A:) Nitrogen regulatory bacterial protein IIa-ntr {Escherichia coli}

LQLSSVLNRECTRSRVHCQSKKRALEIISELAAKQLSLPPQVVFEAILTREKMGSTGIGNGIAIPHGKLEEDTLRAVGVFVQLETPIAFDAIDNQPVDLLFALLVPADQTKTHLHTLSLVAKRLADKTICRRLRAAQSDEELYQIITDTE

>d1a3aa\_ d.112.1.1 (A:) Phosphotransferase IIa-mannitol {Escherichia coli}

LFKLGAENIFLGRKAATKEEAIRFAGEQLVKGGYVEPEYVQAMLDREKLTPTYLGESIAVPHGTVEAKDRVLKTGVVFCQYPEGVRFGEEEDDIARLVIGIAARNNEHIQVITSLTNALDDESVIERLAHTTSVDEVLELLAGRK

>d1mut\_\_ d.113.1.1 (-) Nucleoside triphosphate pyrophosphorylase (MutT) {Escherichia coli}

MKKLQIAVGIIRNENNEIFITRRAADAHMANKLEFPGGKIEMGETPEQAVVRELQEEVGITPQHFSLFEKLEYEFPDRHITLWFWLVERWEGEPWGKEGQPGEWMSLVGLNADDFPPANEPVIAKLKRL

>d1g0sa\_ d.113.1.1 (A:) ADP-ribose pyrophosphatase {Escherichia coli}

MLKPDNLPVTFGKNDVEIIARETLYRGFFSLDLYRFRHRLFNGQMSHEVRREIFERGHAAVLLPFDPVRDEVVLIEQIRIAAYDTSETPWLLEMVAGMIEEGESVEDVARREAIEEAGLIVKRTKPVLSFLASPGGTSERSSIMVGEVDATTASGIHGLADENEDIRVHVVSREQAYQWVEEGKIDNAASVIALQWLQLHHQALKNEWA

>d1jkna\_ d.113.1.1 (A:) Diadenosine tetraphosphate hydrolase {Narrow-leaved blue lupine (Lupinus angustifolius)}

GPLGSMDSPPEGYRRNVGICLMNNDKKIFAASRLDIPDAWQMPQGGIDEGEDPRNAAIRELREETGVTSAEVIAEVPYWLTYDFPPKVREKLNIQWGSDWKGQAQKWFLFKFTGQDQEINLLGDGSEKPEFGEWSWVTPEQLIDLTVEFKKPVYKEVLSVFAPHL

>d1tsy\_\_ d.117.1.1 (-) Thymidylate synthase {Lactobacillus casei}

MLEQPYLDLAKKVLDEGHFKPDRTHTGTYSIFGHQMRFDLSKGFPLLTTKKVPFGLIKSELLWFLHGDTNIRFLLQHRNHIWDEWAFEKWVKSDEYHGPDMTDFGHRSQKDPEFAAVYHEEMAKFDDRVLHDDAFAAKYGDLGLVYGSQWRAWHTSKGDTIDQLGDVIEQIKTHPYSRKLIVSAWNPEDVPTMALPPCHTLYQFYVNDGKLSLQLYQRSADIFLGVPFNIASYALLTHLVAHECGLEVGEFIHTFGDAHLYVNHLDQIKEQLSRTPRPAPTLQLNPDKHDIFDFDMKDIKLLNYDPYPAIKAPVAV

>d1bkpa\_ d.117.1.1 (A:) Thymidylate synthase {Bacillus subtilis}

TQFDKQYNSIIKDIINNGISDEEFDVRTKWDSDGTPAHTLSVISKQMRFDNSEVPILTTKKVAWKTAIKELLWIWQLKSNDVNDLNMMGVHIWDQWKQEDGTIGHAYGFQLGKKNRSLNGEKVDQVDYLLHQLKNNPSSRRHITMLWNPDELDAMALTPCVYETQWYVKHGKLHLEVRARSNDMALGNPFNVFQYNVLQRMIAQVTGYELGEYIFNIGDCHVYTRHIDNLKIQMEREQFEAPELWINPEVKDFYDFTIDDFKLINYKHGDKLLFEVAV

>d1f28a\_ d.117.1.1 (A:) Thymidylate synthase {Pneumocystis carinii}

NAEEQQYLNLVQYIINHGEDRPDRTGTGTLSVFAPSPLKFSLRNKTFPLLTTKRVFIRGVIEELLWFIRGETDSLKLREKNIHIWDANGSREYLDSIGLTKRQEGDLGPIYGFQWRHFGAEYIDCKTNYIGQGVDQLANIIQKIRTSPYDRRLILSAWNPADLEKMALPPCHMFCQFYVHIPSNNHRPELSCQLYQRSCDMGLGVPFNIASYALLTCMIAHVCDLDPGDFIHVMGDCHIYKDHIEALQQQLTRSPRPFPTLSLNRSITDIEDFTLDDFNIQNYHPYETIKMKMSI

>d1b5ea\_ d.117.1.1 (A:) dCMP hydroxymethylase {Bacteriophage T4}

MISDSMTVEEIRLHLGLALKEKDFVVDKTGVKTIEIIGASFVADEPFIFGALNDEYIQRELEWYKSKSLFVKDIPGETPKIWQQVASSKGEINSNYGWAIWSEDNYAQYDMCLAELGQNPDSRRGIMIYTRPSMQFDYNKDGMSDFMCTNTVQYLIRDKKINAVVNMRSNDVVFGFRNDYAWQKYVLDKLVSDLNAGDSTRQYKAGSIIWNVGSLHVYSRHFYLVDHWWKTGETHISKKDY

>d1axx\_\_ d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}

DKDVKYYTLEEIQKHKDSKSTWVILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTDARELSKTYIIGELHPDDRSKIAKPSETL

>d1cxya\_ d.120.1.1 (A:) Cytochrome b558 {Ectothiorhodospira vacuolata}

TLPVFTLEQVAEHHSPDDCWMAIHGKVYDLTPYVPNHPGPAGMMLVWCGQESTEAWETKSYGEPHSSLAARLLQRYLIGTL

>d1ltda2 d.120.1.1 (A:10-97) Flavocytochrome b2, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

KISPAEVAKHNKPDDCWVVINGYVYDLTRFLPNHPGGQDVIKFNAGKDVTAIFEPLHAPNVIDKYIAPEKKLGPLQGSMPPELVCPPY

>d1soxa2 d.120.1.1 (A:3-93) Sulfite oxidase, N-terminal domain {Chicken (Gallus gallus)}

SYPEYTREEVGRHRSPEERVWVTHGTDVFDVTDFVELHPGGPDKILLAAGGALEPFWALYAVHGEPHVLELLQQYKVGELSPDEAPAAPDA

>d1ei1a2 d.122.1.2 (A:2-220) DNA gyrase B {Escherichia coli}

SNSSDSSSIKVLKGLDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDEALAGHCKEIIVTIHADNSVSVQDDGRGIPTGIHPEEGVSAAEVIMTVLHAGGKFDDNSYKVSGGLHGVGVSVVNALSQKLELVIQREGKIHRQIYEHGVPQAPLAVTGETEKTGTMVRFWPSLETFTNVTEFEYEILAKRLRELSFLDSGVSIRLRDKRDGKEDHFHYEG

>d1b63a2 d.122.1.2 (A:-2-216) DNA mismatch repair protein MutL {Escherichia coli}

SHMPIQVLPPQLANQIAAGEVVERPASVVKELVENSLDAGATRIDIDIERGGAKLIRIRDNGCGIKKDELALALARHATSKIASLDDLEAIISLGFRGEALASISSVSRLTLTSRTAEQQEAWQAYAEGRDMNVTVKPAAHPVGTTLEVLDLFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNGKIVRQYRAVPEGGQKERRLGAIC

>d1h7sa2 d.122.1.2 (A:29-231) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GQVVLSLSTAVKELVENSLDAGATNIDLKLKDYGVDLIEVSDNGCGVEEENFEGLTLKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDVTISTCHASAKVGTRLMFDHNGKIIQKTPYPRPRGTTVSVQQLFSTLPVRHKEFQRNIKKEYAKMVQVLHAYCIISAGIRVSCTNQLGQGKRQPVVCTGGSPSIKENIGSVF

>d1bxda\_ d.122.1.3 (A:) Histidine kinase domain of the osmosensor EnvZ {Escherichia coli}

TGQEMPMEMADLNAVLGEVIAAESGYEREIETALYPGSIEVKMHPLSIKRAVANMVVNAARYGNGWIKVSSGTEPNRAWFQVEDDGPGIAPEQRKHLFQPFVRGDSARTISGTGLGLAIVQRIVDNHNGMLELGTSERGGLSIRAWLPVPVTRAQGTTKEG

>d1i58a\_ d.122.1.3 (A:) Histidine kinase CheA {Thermotoga maritima}

GSHMVPISFVFNRFPRMVRDLAKKMNKEVNFIMRGEDTELDRTFVEEIGEPLLHLLRNAIDHGIEPKEERIAKGKPPIGTLILSARHEGNNVVIEVEDDGRGIDKEKIIRKAIEKGLIDESKAATLSDQEILNFLFVPGFSTKEKVSEVSGRGVGMDVVKNVVESLNGSISIESEKDKGTKVTIRLPLT

>d1id0a\_ d.122.1.3 (A:) Histidine kinase PhoQ domain {Escherichia coli}

RELHPVAPLLDNLTSALNKVYQRKGVNISLDISPEISFVGEQNDFVEVMGNVLDNACKYCLEFVEISARQTDEHLYIVVEDDGPGIPLSKREVIFDRGQRVDTLRPGQGVGLAVAREITEQYEGKIVAGESMLGGARMEVIFGRQH

>d1gkza2 d.122.1.4 (A:186-378) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (Rattus norvegicus)}

DFVGIICTRLSPKKIIEKWVDFARRLCEHKYGNAPRVRINGHVAARFPFIPMPLDYILPELLKNAMRATMESHLDTPYNVPDVVITIANNDVDLIIRISDRGGGIAHKDLDRVMDYHFTTAEASTQDPRISPLFGHLDMHSGGQSGPMHGFGFGLPTSRAYAEYLGGSLQLQSLQGIGTDVYLRLRHIDGREE

>d1jm6a2 d.122.1.4 (A:1177-1366) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus), isozyme 2}

PKHIGSIDPNCSVSDVVKDAYDMAKLLCDKYYMASPDLEIQEVNATNATQPIHMVYVPSHLYHMLFELFKNAMRATVESHESSLTLPPIKIMVALGEEDLSIKMSDRGGGVPLRKIERLFSYMYSTAPTPQPGTGGTPLAGFGYGLPISRLYAKYFQGDLQLFSMEGFGTDAVIYLKALSTDSVERLPVY

>d1bola\_ d.124.1.1 (A:) Ribonuclease Rh {Rhizopus niveus}

SSCSSTALSCSNSANSDTCCSPEYGLVVLNMQWAPGYGPDNAFTLHGLWPDKCSGAYAPSGGCDSNRASSSIASVIKSKDSSLYNSMLTYWPSNQGNNNVFWSHEWSKHGTCVSTYDPDCYDNYEEGEDIVDYFQKAMDLRSQYNVYKAFSSNGITPGGTYTATEMQSAIESYFGAKAKIDCSSGTLSDVALYFYVRGRDTYVITDALSTGSCSGDVEYPTK

>d1dixa\_ d.124.1.1 (A:) RNase LE {Tomatoes (Lycopersicon esculentum)}

ASGSKDFDFFYFVQQWPGSYCDTKQSCCYPTTGKPAADFGIHGLWPNNNDGTYPSNCDPNSPYDQSQISDLISSMQQNWPTLACPSGSGSTFWSHEWEKHGTCAESVLTNQHAYFKKALDLKNQIDLLSILQGADIHPDGESYDLVNIRNAIKSAIGYTPWIQCNVDQSGNSQLYQVYICVDGSGSSLIECPIFPGGKCGTSIEFPTF

>d1iqqa\_ d.124.1.1 (A:) S3-RNase {Japanese pear (Pyrus pyrifolia)}

YDYFQFTQQYQLAVCNSNRTLCKDPPDKLFTVHGLWPSNMVGPDPSKCPIKNIRKREKLLEHQLEIIWPNVFDRTKNNLFWDKEWMKHGSCGYPTIDNENHYFETVIKMYISKKQNVSRILSKAKIEPDGKKRALLDIENAIRNGADNKKPKLKCQKKGTTTELVEITLCSDKSGEHFIDCPHPFEPISPHYCPTNNIKY

>d1g61a\_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Archaeon Methanococcus jannaschii}

MIIRKYFSGIPTIGVLALTTEEITLLPIFLDKDDVNEVSEVLETKCLQTNIGGSSLVGSLSVANKYGLLLPKIVEDEELDRIKNFLKENNLDLNVEIIKSKNTALGNLILTNDKGALISPELKDFKKDIEDSLNVEVEIGTIAELPTVGSNAVVTNKGCLTHPLVEDDELEFLKSLFKVEYIGKGTANKGTTSVGACIIANSKGAVVGGDTTGPELLIIEDALGL

>d1g62a\_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Baker's yeast (Saccharomyces cerevisiae)}

MATRTQFENSNEIGVFSKLTNTYCLVAVGGSENFYSAFEAELGDAIPIVHTTIAGTRIIGRMTAGNRRGLLVPTQTTDQELQHLRNSLPDSVKIQRVEERLSALGNVICCNDYVALVHPDIDRETEELISDVLGVEVFRQTISGNILVGSYCSLSNQGGLVHPQTSVQDQEELSSLLQVPLVAGTVNRGSSVVGAGMVVNDYLAVTGLDTTAPELSVIESIFRL

>d1jdw\_\_ d.126.1.2 (-) L-arginine: glycine amidinotransferase {Human (Homo sapiens)}

CPVSSYNEWDPLEEVIVGRAENACVPPFTIEVKANTYEKYWPFYQKQGGHYFPKDHLKKAVAEIEEMCNILKTEGVTVRRPDPIDWSLKYKTPDFESTGLYSAMPRDILIVVGNEIIEAPMAWRSRFFEYRAYRSIIKDYFHRGAKWTTAPKPTMADELYNQDYPIHSVEDRHKLAAQGKFVTTEFEPCFDAADFIRAGRDIFAQRSQVTNYLGIEWMRRHLAPDYRVHIISFKDPNPMHIDATFNIIGPGIVLSNPDRPCHQIDLFKKAGWTIITPPTPIIPDDHPLWMSSKWLSMNVLMLDEKRVMVDANEVPIQKMFEKLGITTIKVNIRNANSLGGGFHCWTCDVRRRGTLQSYLD

>d1bwda\_ d.126.1.2 (A:) L-arginine: inosamine-phosphate amidinotransferase {Streptomyces griseus}

RSLVSVHNEWDPLEEVIVGTAVGARVPTADRSVFAVEYAGDYESQEQIPSGAYPDRVLKETEEELHVLAAELTKLGVTVRRPGPRDHSALIKTPDWETDGFHDYCPRDGLLSVGQTIIETPMALRSRFLESLAYKDLLLEYFASGSRWLSAPKPRLTDDSYAPQAPAGERLTDEEPVFDAANVLRFGTDLLYLVSDSGNELGAKWLQSAVGDTYTVHPCRKLYASTHVDSTIVPLRPGLVLTNPSRVNDENMPDFLRSWENITCPELVDIGFTGDKPHCSVWIGMNLLVVRPDLAVVDRRQTALIRLLEKHGMNVLPLQLTHSRTLGGGFHCATLDVRRTGALETYQF

>d1chma2 d.127.1.1 (A:157-402) Creatinase, catalytic (C-terminal) domain {Pseudomonas putida}

MIKSAEEHVMIRHGARIADIGGAAVVEALGDQVPEYEVALHATQAMVRAIADTFEDVELMDTWTWFQSGINTDGAHNPVTTRKVNKGDILSLNCFPMIAGYYTALERTLFLDHCSDDHLRLWQVNVEVHEAGLKLIKPGARCSDIARELNEIFLKHDVLQYRTFGYGHSFGTLSHYYGREAGLELREDIDTVLEPGMVVSMEPMIMLPEGLPGAGGYREHDILIVNENGAENITKFPYGPEKNIIR

>d1c22a\_ d.127.1.1 (A:) Methionine aminopeptidase {Escherichia coli}

AISIKTPEDIEKMRVAGRLAAEVLEMIEPYVKPGVSTGELDRICNDYIVNEQHAVSACLGYHGYPKSVCISINEVVCHGIPDDAKLLKDGDIVNIDVTVIKDGFHGDTSKMFIVGKPTIMGERLCRITQESLYLALRMVKPGINLREIGAAIQKFVEAEGFSVVREYCGHGIGQGFHEEPQVLHYDSRETNVVLKPGMTFTIEPMVNAGKKEIRTMKDGWTVKTKDRSLSAQYEHTIVVTDNGCEILTLRKDDTIPAIISHD

>d1xgsa2 d.127.1.1 (A:1-194,A:272-295) Methionine aminopeptidase {Archaeon Pyrococcus furiosus}

MDTEKLMKAGEIAKKVREKAIKLARPGMLLLELAESIEKMIMELGGKPAFPVNLSINEIAAHYTPYKGDTTVLKEGDYLKIDVGVHIDGFIADTAVTVRVGMEEDELMEAAKEALNAAISVARAGVEIKELGKAIENEIRKRGFKPIVNLSGHKIERYKLHAGISIPNIYRPHDNYVLKEGDVFAIEPFATIGAXRNGIVAQFEHTIIVEKDSVIVTTE

>d1b6a\_2 d.127.1.1 (110-374,449-478) Methionine aminopeptidase {Human (Homo sapiens)}

KVQTDPPSVPICDLYPNGVFPKGQECEYPPTQDGRTAAWRTTSEEKKALDQASEEIWNDFREAAEAHRQVRKYVMSWIKPGMTMIEICEKLEDCSRKLIKENGLNAGLAFPTGCSLNNCAAHYTPNAGDTTVLQYDDICKIDFGTHISGRIIDCAFTVTFNPKYDTLLKAVKDATNTGIKCAGIDVRLCDVGEAIQEVMESYEVEIDGKTYQVKPIRNLNGHSIGQYRIHAGKTVPIVKGGEATRMEEGEVYAIETFGSTGKGVVXDIKGSYTAQFEHTILLRPTCKEVVSRGDDY

>d1az9\_2 d.127.1.1 (177-440) Aminopeptidase P, C-terminal domain {Escherichia coli}

SPEEIAVLRRAGEITAMAHTRAMEKCRPGMFEYHLEGEIHHEFNRHGARYPSYNTIVGSGENGCILHYTENECEMRDGDLVLIDAGCEYKGYAGDITRTFPVNGKFTQAQREIYDIVLESLETSLRLYRPGTSILEVTGEVVRIMVSGLVKLGILKGDVDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYGQDRSRILEPGMVLTVEPGLYIAPDAEVPEQYRGIGIRIEDDIVITETGNENLTASVVKKPEEIEALMVAARKQ

>d1qnaa1 d.129.1.1 (A:17-115) TATA-box binding protein (TBP), C-terminal domain {Arabidopsis thaliana}

HPSGIVPTLQNIVSTVNLDCKLDLKAIALQARNAEYNPKRFAAVIMRIREPKTTALIFASGKMVCTGAKSEDFSKMAARKYARIVQKLGFPAKFKDFKI

>d1qnaa2 d.129.1.1 (A:116-198) TATA-box binding protein (TBP), C-terminal domain {Arabidopsis thaliana}

QNIVGSCDVKFPIRLEGLAYSHAAFSSYEPELFPGLIYRMKVPKIVLLIFVSGKIVITGAKMRDETYKAFENIYPVLSEFRKI

>d1aisa1 d.129.1.1 (A:1-92) TATA-box binding protein (TBP), C-terminal domain {Archaeon Pyrococcus woesei}

MVDMSKVKLRIENIVASVDLFAQLDLEKVLDLCPNSKYNPEEFPGIICHLDDPKVALLIFSSGKLVVTGAKSVQDIERAVAKLAQKLKSIGV

>d1aisa2 d.129.1.1 (A:93-181) TATA-box binding protein (TBP), C-terminal domain {Archaeon Pyrococcus woesei}

KFKRAPQIDVQNMVFSGDIGREFNLDVVALTLPNCEYEPEQFPGVIYRVKEPKSVILLFSSGKIVCSGAKSEADAWEAVRKLLRELDKY

>d1mpga2 d.129.1.2 (A:1-99) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {Escherichia coli}

MYTLNWQPPYDWSWMLGFLAARAVSSVETVADSYYARSLAVGEYRGVVTAIPDIARHTLHINLSAGLEPVAAECLAKMSRLFDLQCNPQIVNGALGRLG

>d1ko9a2 d.129.1.2 (A:12-135) 8-oxoguanine glycosylase {Human (Homo sapiens)}

GHRTLASTPALWASIPCPRSELRLDLVLPSGQSFRWREQSPAHWSGVLADQVWTLTQTEEQLHCTVYRGDKSQASRPTPDELEAVRKYFQLDVTLAQLYHHWGSVDSHFQEVAQKFQGVRLLRQ

>d1mxa\_1 d.130.1.1 (1-102) S-adenosylmethionine synthetase {Escherichia coli}

AKHLFTSESVSEGHPDKIADQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSAWVDIEEITRNTVREIGYVHSDMGFDANSCAVLSAIGKQSPDI

>d1mxa\_2 d.130.1.1 (108-231) S-adenosylmethionine synthetase {Escherichia coli}

RADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHRLVQRQAEVRKNGTLPWLRPDAKSQVTFQYDDGKIVGIDAVVLSTQHSEEIDQKSLQEAVMEEIIKPILPAEWLTSATKFFINPTGRFV

>d1mxa\_3 d.130.1.1 (232-383) S-adenosylmethionine synthetase {Escherichia coli}

IGGPMGDCGLTGRKIIVDTYGGMARHGGGAFSGKDPSKVDRSAAYAARYVAKNIVAAGLADRCEIQVSYAIGVAEPTSIMVETFGTEKVPSEQLTLLVREFFDLRPYGLIQMLDLLHPIYKETAAYGHFGREHFPWEKTDKAQLLRDAAGLK

>d2pola1 d.131.1.1 (A:1-122) DNA polymerase III, beta subunit {Escherichia coli}

MKFTVEREHLLKPLQQVSGPLGGRPTLPILGNLLLQVADGTLSLTGTDLEMEMVARVALVQPHEPGATTVPARKFFDICRGLPEGAEIAVQLEGERMLVRSGRSRFSLSTLPAADFPNLDDW

>d2pola2 d.131.1.1 (A:123-244) DNA polymerase III, beta subunit {Escherichia coli}

QSEVEFTLPQATMKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTVATDGHRLAVCSMPIGQSLPSHSVIVPRKGVIELMRMLDGGDNPLRVQIGSNNIRAHVGDFIFTSKLVDGRFPDY

>d2pola3 d.131.1.1 (A:245-366) DNA polymerase III, beta subunit {Escherichia coli}

RRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLYVSENQLKITANNPEQEEAEEILDVTYSGAEMEIGFNVSYVLDVLNALKCENVRMMLTDSVSSVQIEDAASQSAAYVVMPMRL

>d1b77a1 d.131.1.2 (A:1-110) gp45 sliding clamp {Bacteriophage RB69}

MKLSKDTIAILKNFASINSGILLSQGKFIMTRAVNGTTYAEANISDEIDFDVALYDLNSFLSILSLVSDDAEISMHTDGNIKIADTRSTVYWPAADKSTIVFPNKPIQFP

>d1b77a2 d.131.1.2 (A:111-228) gp45 sliding clamp {Bacteriophage RB69}

VASVITEIKAEDLQQLLRVSRGLQIDTIAITNKDGKIVINGYNKVEDSGLTRPKYSLTLTDYDGSNNFNFVINMANMKIQPGNYKVMLWGAGDKVAAKFESSQVSYVIAMEADSTHDF

>d1dmla1 d.131.1.2 (A:29-169) UL42 {Human herpes virus type 1}

APCQVVLQGAELNGILQAFAPLRTSLLDSLLVMGDRGILIHNTIFGEQVFLPLEHSQFSRYRWRGPTAAFLSLVDQKRSLLSVFRANQYPDLRRVELAITGQAPFRTLVQRIWTTTSDGEAVELASETLMKRELTSFVVLV

>d1dmla2 d.131.1.2 (A:170-319) UL42 {Human herpes virus type 1}

PQGTPDVQLRLTRPQLTKVLNATGADSATPTTFELGVNGKFSVFTTSTCVTFAAREEGVSSSTSTQVQILSNALTKAGQAAANAKTVYGENTHRTFSVVVDDCSMRAVLRRLQVGGGTLKFFLTTPVPSLCVTATGPNAVSAVFLLKPQK

>d1plq\_1 d.131.1.2 (1-126) Prolifirating cell nuclear antigen (PCNA) {Baker's yeast (Saccharomyces cerevisiae)}

MLEAKFEEASLFKRIIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEYRCDHPVTLGMDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIAEYSLKLMDIDADFL

>d1plq\_2 d.131.1.2 (127-258) Prolifirating cell nuclear antigen (PCNA) {Baker's yeast (Saccharomyces cerevisiae)}

KIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSVIIKPFVDMEHPETSIKLEMDQPVDLTFGAKYLLDIIKGSSLSDRVGIRLSSEAPALFQFDLKSGFLQFFLAPKFNDEE

>d1axca1 d.131.1.2 (A:1-126) Prolifirating cell nuclear antigen (PCNA) {Human (Homo sapiens)}

MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSSHVSLVQLTLRSEGFDTYRCDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKLMDLDVEQL

>d1axca2 d.131.1.2 (A:127-255) Prolifirating cell nuclear antigen (PCNA) {Human (Homo sapiens)}

GIPEQEYSCVVKMPSGEFARICRDLSHIGDAVVISCAKDGVKFSASGELGNGNIKLSQTSNVDKEEEAVTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLSMSADVPLVVEYKIADMGHLKYYLAPKI

>d1ge8a1 d.131.1.2 (A:2-117) Prolifirating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}

PFEIVFEGAKEFAQLIDTASKLIDEAAFKVTEDGISMRAMDPSRVVLIDLNLPSSIFSKYEVVEPETIGVNLDHLKKILKRGKAKDTLILKKGEENFLEITIQGTATRTFRVPLID

>d1ge8a2 d.131.1.2 (A:126-247) Prolifirating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}

PELPFTAKVVVLGEVLKDAVKDASLVSDSIKFIARENEFIMKAEGETQEVEIKLTLEDEGLLDIEVQEETKSAYGVSYLSDMVKGLGKADEVTIKFGNEMPMQMEYYIRDEGRLTFLLAPRV

>d1hlra4 d.133.1.1 (A:311-907) Aldehyde oxidoreductase {Desulfovibrio gigas}

MSGPAAAAEDAIEIHPGTPNVYFEQPIVKGEDTGPIFASADVTVEGDFYVGRQPHMPIEPDVAFAYMGDDGKCYIHSKSIGVHLHLYMIAPGVGLEPDQLVLVANPMGGTFGYKFSPTSEALVAVAAMATGRPVHLRYNYQQQQQYTGKRSPWEMNVKFAAKKDGTLLAMESDWLVDHGPYSEFGDLLTLRGAQFIGAGYNIPNIRGLGRTVATNHVWGSAFRGYGAPQSMFASECLMDMLAEKLGMDPLELRYKNAYRPGDTNPTGQEPEVFSLPDMIDQLRPKYQAALEKAQKESTATHKKGVGISIGVYGSGLDGPDASEAWAELNADGTITVHTAWEDHGQGADIGCVGTAHEALRPMGVAPEKIKFTWPNTATTPNSGPSGGSREQVMTGNAIRVACENLLKACEKPGGGYYTYDELKAADKPTKITGNWTASGATHCDAVTGLGKPFVVYMYGVFMAEVTVDVATGQTTVDGMTLMADLGSLCNQLATDGQIYGGLAQGIGLALSEDFEDIKKHATLVGAGFPFIKQIPDKLDIVYVNHPRPDGPFGASGVGELPLTSPHAAIINAIKSATGVRIYRLPAYPEKVLEALKA

>d1fo4a5 d.133.1.1 (A:695-1332) Xanthine oxidase, C-terminal domain {Cow (Bos taurus)}

IITIEDAIKNNSFYGSELKIEKGDLKKGFSEADNVVSGELYIGGQDHFYLETHCTIAIPKGEEGEMELFVSTQNAMKTQSFVAKMLGVPVNRILVRVKRMGGGFGGKETRSTLVSVAVALAAYKTGHPVRCMLDRNEDMLITGGRHPFLARYKVGFMKTGTIVALEVDHYSNAGNSRDLSHSIMERALFHMDNCYKIPNIRGTGRLCKTNLSSNTAFRGFGGPQALFIAENWMSEVAVTCGLPAEEVRWKNMYKEGDLTHFNQRLEGFSVPRCWDECLKSSQYYARKSEVDKFNKENCWKKRGLCIIPTKFGISFTVPFLNQAGALIHVYTDGSVLVSHGGTEMGQGLHTKMVQVASKALKIPISKIYISETSTNTVPNSSPTAASVSTDIYGQAVYEACQTILKRLEPFKKKNPDGSWEDWVMAAYQDRVSLSTTGFYRTPNLGYSFETNSGNAFHYFTYGVACSEVEIDCLTGDHKNLRTDIVMDVGSSLNPAIDIGQVEGAFVQGLGLFTLEELHYSPEGSLHTRGPSTYKIPAFGSIPTEFRVSLLRDCPNKKAIYASKAVGEPPLFLGASVFFAIKDAIRAARAQHTNNNTKELFRLDSPATPEKIRNACVDKFTTLCVTGAPGNCKPWSLRV

>d1jrob2 d.133.1.1 (B:124-777) Xanthine dehydrogenase chain B, C-terminal domain {Rhodobacter capsulatus}

PAILTLDQALAADSRFEGGPVIWARGDVETALAGAAHLAEGCFEIGGQEHFYLEGQAALALPAEGGVVIHCSSQHPSEIQHKVAHALGLAFHDVRVEMRRMGGGFGGKESQGNHLAIACAVAARATGRPCKMRYDRDDDMVITGKRHDFRIRYRIGADASGKLLGADFVHLARCGWSADLSLPVCDRAMLHADGSYFVPALRIESHRLRTNTQSNTAFRGFGGPQGALGMERAIEHLARGMGRDPAELRALNFYDPPERGGLSAPPSPPEPIATKKTQTTHYGQEVADCVLGELVTRLQKSANFTTRRAEIAAWNSTNRTLARGIALSPVKFGISFTLTHLNQAGALVQIYTDGSVALNHGGTEMGQGLHAKMVQVAAAVLGIDPVQVRITATDTSKVPNTSATAASSGADMNGMAVKDACETLRGRLAGFVAAREGCAARDVIFDAGQVQASGKSWRFAEIVAAAYMARISLSATGFYATPKLSWDRLRGQGRPFLYFAYGAAITEVVIDRLTGENRILRTDILHDAGASLNPALDIGQIEGAYVQGAGWLTTEELVWDHCGRLMTHAPSTYKIPAFSDRPRIFNVALWDQPNREETIFRSKAVGEPPFLLGISAFLALHDACAACGPHWPDLQAPATPEAVLAAVRRAEGRA

>d1qj2b2 d.133.1.1 (B:147-809) Carbon monoxide (CO) dehydrogenase molybdoprotein {Pseudomonas carboxydovorans}

VDPFKAMEPDAPLLREDIKDKMTGAHGARKHHNHIFRWEIGDKEGTDATFAKAEVVSKDMFTYHRVHPSPLETCQCVASMDKIKGELTLWGTFQAPHVIRTVVSLISGLPEHKIHVIAPDIGGGFGNKVGAYSGYVCAVVASIVLGVPVKWVEDRMENLSTTSFARDYHMTTELAATKDGKILAMRCHVLADHGAFDACADPSKWPAGFMNICTGSYDMPVAHLAVDGVYTNKASGGVAYRXSFRVTEAVYAIERAIETLAQRLEMDSADLRIKNFIQPEQFPYMAPLGWEYDSGNYPLAMKKAMDTVGYHQLRAEQKAKQEAFKRGETREIMGIGISFFTEIVGAGPSKNCDILGVSMFDSAEIRIHPTGSVIARMGTKSQGQGHETTYAQIIATELGIPADDIMIEEGNTDTAPYGLGTYGSRSTPTAGAATAVAARKIKAKAQMIAAHMLEVHEGDLEWDVDRFRVKGLPEKFKTMKELAWASYNSPPPNLEPGLEAVNYYDPPNMTYPFGAYFCIMDIDIDTGVAKTRRFYALDDCGTRINPMIIEGQVHGGLTEAFAVAMGQEIRYDEQGNVLGASFMDFFLPTAVETPKWETDYTVTPSPHHPIGAKGVGESPHVGGVPCFSNAVNDAYAFLNAGHIQMPHDAWRLWKVGEQLGLHV

>d1aop\_3 d.134.1.1 (149-345) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4 {Escherichia coli}

NDMNRNVLCTSNPYESQLHAEAYEWAKKISEHLLPRTRAYAEIWLDQEKVATTDEEPILGQTYLPRKFKTTVVIPPQNDIDLHANDMNFVAIAENGKLVGFNLLVGGGLSIEHGNKKTYARTASEFGYLPLEHTLAVAEAVVTTQRDWGNRTDRKNAKTKYTLERVGVETFKAEVERRAGIKFEPIRPYEFTGRGDR

>d1aop\_4 d.134.1.1 (426-570) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4 {Escherichia coli}

PQRENSMACVSFPTCPLAMAEAERFLPSFIDNIDNLMAKHGVSDEHIVMRVTGCPNGCGRAMLAEVGLVGKAPGRYNLHLGGNRIGTRIPRMYKENITEPEILASLDELIGRWAKEREAGEGFGDFTVRAGIIRPVLDPARDLWD

>d1f0ia1 d.136.1.2 (A:6-263) Phospholipase D {Streptomyces sp.}

AATPHLDAVEQTLRQVSPGLEGDVWERTSGNKLDGSAADPSDWLLQTPGCWGDDKCADRVGTKRLLAKMTENIGNATRTVDISTLAPFPNGAFQDAIVAGLKESAAKGNSLKVRILVGAAPVYHMNGIPSKYRDKLTAKLGKAAENITLNVASMTTSKTAFSWNHSKILVVDGQSALTGGINSWKDDYLDTTHPVSDVDLALTGPAAGSAGRYLDTLWTWTCKNKSNIASVWFAASGNAGCMPTMHKDTNPKASPATG

>d1f0ia2 d.136.1.2 (A:264-514) Phospholipase D {Streptomyces sp.}

NVPVIAVGGLGVGIKDVDPKSTFRPDLPTASDTKCVVGLHDNTNADRDYDTVNPEESALRALVASAKGHIEISQQDLNATCPPLPRYDIRLYDALAAKMAAGVKVRIVVSDPANRGAVGSGGYSQIKSLSEISDTLRNRLANITGGQQAAKTAMCSNLQLATFRSSPNGKWADGHPYAQHHKLVSVDSSTFYIGSKNLYPSWLQDFGYIVESPEAAKQLDAKLLDPQWKYSQETATVDYARGICGA

>d1jy1a1 d.136.1.3 (A:145-350) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}

LEDPGEGQDIWDMLDKGNPFQFYLTRVSGVKPKYNSGALHIKDILSPLFGTLVSSAQFNYCFDVDWLVKQYPPEFRKKPILLVHGDKREAKAHLHAQAKPYENISLCQAKLDIAFGTHHTKMMLLLYEEGLRVVIHTSNLIHADWHQKTQGIWLSPLYPRIADGTHKSGESPTHFKANLISYLTAYNAPSLKEWIDVIHKHDLSET

>d1jy1a2 d.136.1.3 (A:351-608) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}

NVYLIGSTPGRFQGSQKDNWGHFRLKKLLKDHASSMPNAESWPVVGQFSSVGSLGADESKWLCSEFKESMLTLGKESKTPGKSSVPLYLIYPSVENVRTSLEGYPAGGSLPYSIQTAEKQNWLHSYFHKWSAETSGRSNAMPHIKTYMRPSPDFSKIAWFLVTSANLSKAAWGALEKNGTQLMIRSYELGVLFLPSALGLDSFKVKQKFFAGSQEPMATFPVPYDLPPELYGSKDRPWIWNIPYVKAPDTHGNMWVPS

>d1ckv\_\_ d.137.1.1 (-) Soluble methane monooxygenase regulatory protein B {Escherichia coli}

MSVNSNAYDAGIMGLKGKDFADQFFADENQVVHESDTVVLVLKKSDEINTFIEEILLTDYKKNVNPTVNVEDRAGYWWIKANGKIEVDCDEISELLGRQFNVYDFLVDVSSTIGRAYTLGNKFTITSELMGLDRKLEDYHA

>d1g10a\_ d.137.1.1 (A:) Toluene-4-monooxygenase catalytic effector protein {Pseudomonas mendocina}

STLADQALHNNNVGPIIRAGDLVEPVIETAEIDNPGKEITVEDRRAYVRIAAEGELILTRKTLEEQLGRPFNMQELEINLASFAGQIQADEDQIRFYFDKTM

>d1hqi\_\_ d.137.1.1 (-) Phenol hydroxylase P2 protein {Pseudomonas sp., CF600}

MSSLVYIAFQDNDNARYVVEAIIQDNPHAVVQHHPAMIRIEAEKRLEIRRETVEENLGRAWDVQEMLVDVITIGGNVDEDDDRFVLEWKN

>d1i94h\_ d.140.1.1 (H:) Ribosomal protein S8 {Thermus thermophilus}

MLTDPIADMLTRIRNATRVYKESTEVPASRFKEEILKILAREGFIKGYERVEVDGKPYLRIHLKYGPRRQGPDPRPEQVIKHIRRISRPGRRVYVGVKEIPRVRRGLGIAILSTPKGVLTDREARKLGVGGELICEVW

>d1i6ua\_ d.140.1.1 (A:) Ribosomal protein S8 {Archaeon Methanococcus jannaschii}

SLMDPLANALNHISNCERVGKKVVYIKPASKLIGRVLKVMQDNGYIGEFEFIEDGRAGIFKVELIGKINKCGAIKPRFPVKKFGYEKFEKRYLPARDFGILIVSTTQGVMSHEEAKKRGLGGRLLAYVY

>d1rl6a1 d.141.1.1 (A:7-81) Ribosomal protein L6 {Bacillus stearothermophilus}

PIEIPAGVTVTVNGNTVTVKGPKGELTRTFHPDMTITVEGNVITVTRPSDEKHHRALHGTTRSLLANMVEGVSKG

>d1rl6a2 d.141.1.1 (A:82-170) Ribosomal protein L6 {Bacillus stearothermophilus}

YEKALELVGVGYRASKQGKKLVLSVGYSHPVEIEPEEGLEIEVPSQTKIIVKGADKQRVGELAANIRAVRPPEPYKGKGIRYEGELVRL

>d1jj2e1 d.141.1.1 (E:1-79) Ribosomal protein L6 {Archaeon Haloarcula marismortui}

PRVELEIPEDVDAEQDHLDITVEGDNGSVTRRLWYPDIDVSVDGDTVVIESDEDNAKTMSTIGTFQSHIENMFHGVTEG

>d1jj2e2 d.141.1.1 (E:80-172) Ribosomal protein L6 {Archaeon Haloarcula marismortui}

WEYGMEVFYSHFPMQVNVEGDEVVIENFLGEKAPRRTTIHGDTDVEIDGEELTVSGPDIEAVGQTAADIEQLTRINDKDVRVFQDGVYITRKP

>d1gsa\_2 d.142.1.1 (123-314) Glutathione synthetase {Escherichia coli}

NEKLFTAWFSDLTPETLVTRNKAQLKAFWEKHSDIILKPLDGMGGASIFRVKEGDPNLGVIAETLTEHGTRYCMAQNYLPAIKDGDKRVLVVDGEPVPYCLARIPQGGETRGNLAAGGRGEPRPLTESDWKIARQIGPTLKEKGLIFVGLDIIGDRLTEINVTSPTCIREIEAEFPVSITGMLMDAIEARLQ

>d1iow\_2 d.142.1.1 (97-306) D-ala-D-ala ligase {Escherichia coli, gene ddlB}

KLRSKLLWQGAGLPVAPWVALTRAEFEKGLSDKQLAEISALGLPVIVKPSREGSSVGMSKVVAENALQDALRLAFQHDEEVLIEKWLSGPEFTVAILGEEILPSIRIQPSGTFYDYEAKFLSDETQYFCPAGLEASQEANLQALVLKAWTTLGCKGWGRIDVMLDSDGQFYLLEANTSPGMTSHSLVPMAARQAGMSFSQLVVRILELAD

>d1ehia2 d.142.1.1 (A:135-362) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}

DKALTKELLTVNGIRNTKYIVVDPESANNWSWDKIVAELGNIVFVKAANQGSSVGISRVTNAEEYTEALSDSFQYDYKVLIEEAVNGARELEVGVIGNDQPLVSEIGAHTVPNQGSGDGWYDYNNKFVDNSAVHFQIPAQLSPEVTKEVKQMALDAYKVLNLRGEARMDFLLDENNVPYLGEPNTLPGFTNMSLFKRLWDYSDINNAKLVDMLIDYGFEDFAQNKKLS

>d1e4ea2 d.142.1.1 (A:132-342) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}

DKSLTYIVAKNAGIATPAFWVINKDDRPVAATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCAVLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETVKKIYKTLGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGISLPELIDRLIVLALK

>d1dv1a3 d.142.1.2 (A:115-330) Biotin carboxylase subunit of acetyl-CoA carboxylase {Escherichia coli}

DKVSAIAAMKKAGVPCVPGSDGPLGDDMDKNRAIAKRIGYPVIIKASGGGGGRGMRVVRGDAELAQSISMTRAEAKAAFSNDMVYMEKYLENPRHVEIQVLADGQGNAIYLAERDCSMQRRHQKVVEEAPAPGITPELRRYIGERCAKACVDIGYRGAGTFEFLFENGEFYFIEMNTRIQVEHPVTEMITGVDLIKEQLRIAAGQPLSIKQEEVHV

>d1gsoa3 d.142.1.2 (A:104-327) Glycinamide ribonucleotide synthetase (GAR-syn) {Escherichia coli}

SKAFTKDFLARHKIPTAEYQNFTEVEPALAYLREKGAPIVIKADGLAAGKGVIVAMTLEEAEAAVHDMLAGNAFGDAGHRIVIEEFLDGEEASFIVMVDGEHVLPMATSQDHKRVGDKDTGPNTGGMGAYSPAPVVTDDVHQRTMERIIWPTVKGMAAEGNTYTGFLYAGLMIDKQGNPKVIEFNCRFGDLETQPIMLRMKSDLVELCLAACESKLDEKTSEWD

>d1b6ra3 d.142.1.2 (A:79-276) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

DRLTQKQLFDKLHLPTAPWQLLAERSEWPAVFDRLGELAIVKRRTGGYDGRGQWRLRANETEQLPAECYGECIVEQGINFSGEVSLVGARGFDGSTVFYPLTHNLHQDGILRTSVAFPQANAQQQARAEEMLSAIMQELGYVGVMAMECFVTPQGLLINELAPRVHNSGHWTQNGASISQFELHLRAITDLPLPQPVV

>d1eyza3 d.142.1.2 (A:113-318) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

NREGIRRLAAEELQLPTSTYRFADSESLFREAVADIGYPCIVKPVMSSSGKGQTFIRSAEQLAQAWKYAQQGGRAGAGRVIVEGVVKFDFEITLLTVSAVDGVHFCAPVGHRQEDGDYRESWQPQQMSPLALERAQEIARKVVLALGGYGLFGVELFVCGDEVIFSEVSPRPHDTGMVTLISQDLSEFALHVRAFLGLPVGGIRQY

>d1a9xa5 d.142.1.2 (A:128-402) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

DRRRFDVAMKKIGLETARSGIAHTMEEALAVAADVGFPCIIRPSFTMGGSGGGIAYNREEFEEICARGLDLSPTKELLIDESLIGWKEYEMEVVRDKNDNCIIVCSIENFDAMGIHTGDSITVAPAQTLTDKEYQIMRNASMAVLREIGVETGGSNVQFAVNPKNGRLIVIEMNPRVSRSSALASKATGFPIAKVAAKLAVGYTLDELMNDITGGRTPASFEPSIDYVVTKIPRFNFEKFAGANDRLTTQMKSVGEVMAIGRTQQESLQKALRGL

>d1a9xa6 d.142.1.2 (A:677-935) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

RFQHAVERLKLKQPANATVTAIEMAVEKAKEIGYPLVVRAAMEIVYDEADLRRYFQTAVLLDHFLDDAVEVDVDAICDGEMVLIGGIMEHIEQAGVHSGDSACSLPAYTLSQEIQDVMRQQVQKLAFELQVRGLMNVQFAVKNNEVYLIEVNPRAARTVPFVSKATGVPLAKVAARVMAGKSLAEQGVTKEVIPPYYSVKEVVLPFNKFPGVDPLLGPEMRSTGEVMGVGRTFAEAFAKAQLGS

>d1jkjb2 d.142.1.4 (B:1-238) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Escherichia coli}

MNLHEYQAKQLFARYGLPAPVGYACTTPREAEEAASKIGAGPWVVKCQVHAGGRGKAGGVKVVNSKEDIRAFAENWLGKRLVTYQTDANGQPVNQILVEAATDIAKELYLGAVVDRSSRRVVFMASTEGGVEIEKVAEETPHLIHKVALDPLTGPMPYQGRELAFKLGLEGKLVQQFTKIFMGLATIFLERDLALIEINPLVITKQGDLICLDGKLGADGNALFRQPDLREMRDQSQE

>d1eucb2 d.142.1.4 (B:0-245) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Pig (Sus scrofa)}

MVNLQEYQSKKLMSDNGVKVQRFFVADTANEALEAAKRLNAKEIVLKAQILAGGRGKGVFSSGLKGGVHLTKDPEVVGQLAKQMIGYNLATKQTPKEGVKVNKVMVAEALDISRETYLAILMDRSCNGPVLVGSPQGGVDIEEVAASNPELIFKEQIDIIEGIKDSQAQRMAENLGFLGPLQNQAADQIKKLYNLFLKIDATQVEVNPFGETPEGQVVCFDAKINFDDNAEFRQKDIFAMDDKSEN

>d2hgsa2 d.142.1.6 (A:304-474) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TKKVQQELSRPGMLEMLLPGQPEAVARLRATFAGLYSLDVGEEGDQAIAEALAAPSRFVLKPQREGGGNNLYGEEMVQALKQLKDSEERASYILMEKIEPEPFENCLLRPGSPARVVQCISELGIFGVYVRQEKTLVMNKHVGHLLRTKAIEHADGGVAAGVAVLDNPYPV

>d2hgsa3 d.142.1.6 (A:3-201) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TNWGSLLQDKQQLEELARQAVDRALAEGVLLRTSQEPTSSEVVSYAPFTLFPSLVPSALLEQAYAVQMDFNLLVDAVSQNAAFLEQTLSSTIKQDDFTARLFDIHKQVLKEGIAQTVFLGLNRSDYMFQRSADGSPALKQIEINTISASFGGLASRTPAVHRHVLSVLSKTKEAGKILSNNPSKGLALGIAKAWELYGS

>d1a0i\_2 d.142.2.1 (2-240) ATP-dependent DNA ligase, N-terminal domain {Bacteriophage T7}

VNIKTNPFKAVSFVESAIKKALDNAGYLIAEIKYDGVRGNICVDNTANSYWLSRVSKTIPALEHLNGFDVRWKRLLNDDRCFYKDGFMLDGELMVKGVDFNTGSGLLRTKWTDTKNQEFHEELFVEPIRKKDKVPFKLHTGHLHIKLYAILPLHIVESGEDCDVMTLLMQEHVKNMLPLLQEYFPEIEWQAAESYEVYDMVELQQLYEQKRAEGHEGLIVKDPMCIYKRGKKSGWWKMK

>d1fvia2 d.142.2.1 (A:2-189) ATP-dependent DNA ligase, N-terminal domain {Chlorella virus, PBCV-1}

AITKPLLAATLENIEDVQFPCLATPKIAGIRSVKQTQMLSRTFKPIRNSVMNRLLTELLPEGSDGEISIEGATFQDTTSAVMTGHKMYNAKFSYYWFDYVTDDPLKKYIDRVEDMKNYITVHPHILEHAQVKIIPLIPVEINNITELLQYERDVLSKGFEGVMIRKPDGKYKFGRSTLKEGILLKMKQ

>d1blxa\_ d.144.1.1 (A:) Cyclin-dependent PK (CDK, different isozymes) {Human (Homo sapiens)}

GLCRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTGEEGMPLSTIREVAVLRHLETFEHPNVVRLFDVCTVSRTDRETKLTLVFEHVDQDLTTYLDKVPEPGVPTETIKDMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTSVVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRDVALPRQAFHSKSAQPIEKFVTDIDELGKDLLLKCLTFNPAKRISAYSALSHPYFQDLERCKEN

>d1apme\_ d.144.1.1 (E:) cAMP-dependent PK, catalytic subunit {Mouse (Mus musculus)}

SEQESVKEFLAKAKEDFLKKWETPSQNTAQLDQFDRIKTLGTGSFGRVMLVKHKESGNHYAMKILDKQKVVKLKQIEHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMVMEYVAGGEMFSHLRRIGRFAEPHARFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDQQGYIQVTDFGFAKRVKGRTWTLCGTPEYLAPEIILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFPSHFSSDLKDLLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATTDWIAIYQRKVEAPFIPKFKGPGDTSNFDDYEEEEIRVSINEKCGKEFTEF

>d1a06\_\_ d.144.1.1 (-) Calmodulin-dependent protein kinase {Rat (Rattus norvegicus)}

WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAVKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKSKWKQAFNATAVVRHM

>d1ia8a\_ d.144.1.1 (A:) Cell cycle checkpoint kinase chk1 {Human (Homo sapiens)}

AVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVAVKIVDMKRAVDCPENIKKEICINKMLNHENVVKFYGHRREGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFFHQLMAGVVYLHGIGITHRDIKPENLLLDERDNLKISDFGLATVFRYNNRERLLNKMCGTLPYVAPELLKRREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKKTYLNPWKKIDSAPLALLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRP

>d1phk\_\_ d.144.1.1 (-) gamma-subunit of glycogen phosphorylase kinase (Phk) {Rabbit (Oryctolagus cuniculus)}

FYENYEPKEILGRGVSSVVRRCIHKPTCKEYAVKIIDVTGGGSFSAEEVQELREATLKEVDILRKVSGHPNIIQLKDTYETNTFFFLVFDLMKKGELFDYLTEKVTLSEKETRKIMRALLEVICALHKLNIVHRDLKPENILLDDDMNIKLTDFGFSCQLDPGEKLREVCGTPSYLAPEIIECSMNDNHPGYGKEVDMWSTGVIMYTLLAGSPPFWHRKQMLMLRMIMSGNYQFGSPEWDDYSDTVKDLVSRFLVVQPQKRYTAEEALAHPFFQQYV

>d1h8fa\_ d.144.1.1 (A:) Glycogen synthase kinase-3 beta (Gsk3b) {Human (Homo sapiens)}

SKVTTVVATPGQGPDRPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQGKAFKNRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFAFPQIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKLPNGRDTPALFNFTTQELSSNPPLATILIPPHARIQA

>d1tkia\_ d.144.1.1 (A:) Titin, kinase domain {Human (Homo sapiens)}

KELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKGTDQVLVKKEISILNIARHRNILHLHESFESMEELVMIFEFISGLDIFERINTSAFELNEREIVSYVHQVCEALQFLHSHNIGHFDIRPENIIYQTRRSSTIKIIEFGQARQLKPGDNFRLLFTAPEYYAPEVHQHDVVSTATDMWSLGTLVYVLLSGINPFLAETNQQIIENIMNAEYTFDEEAFKEISIEAMDFVDRLLVKERKSRMTASEALQHPWLKQKIERVSTKVIRTLKHRRYYHTLIKKDLNMVVSAARISCGGAIRSQKGVSVAKVKVASI

>d1koba\_ d.144.1.1 (A:) Twitchin, kinase domain {California sea hare (Aplysia californica), twk43}

INDYDKFYEDIWKKYVPQPVEVKQGSVYDYYDILEELGSGAFGVVHRCVEKATGRVFVAKFINTPYPLDKYTVKNEISIMNQLHHPKLINLHDAFEDKYEMVLILEFLSGGELFDRIAAEDYKMSEAEVINYMRQACEGLKHMHEHSIVHLDIKPENIMCETKKASSVKIIDFGLATKLNPDEIVKVTTATAEFAAPEIVDREPVGFYTDMWAIGVLGYVLLSGLSPFAGEDDLETLQNVKRCDWEFDEDAFSSVSPEAKDFIKNLLQKEPRKRLTVHDALEHPWLKGDHSNLTSRIPSSRYNKIRQKIKEKYADWPAPQPAIGRIANFSSLRKHRPQEYQIYDSYFDRKEAV

>d1jnk\_\_ d.144.1.1 (-) c-jun N-terminal kinase (jnk3s) {Human (Homo sapiens)}

DNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFQNQTHAKRAYRELVLMKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYIDQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKELIYKEVMN

>d1ckia\_ d.144.1.1 (A:) Casein kinase-1, CK1 {Rat (Rattus norvegicus)}

MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLHIESKIYKMMQGGVGIPTIRWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDFGLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRRDDLESLGYVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFATYLNFCRSLRFDDKPDYSYLRQLFRNLFHRQGFSYDYVFDWNMLKFGASR

>d1a6o\_\_ d.144.1.1 (-) Protein kinase CK2, alpha subunit {Maize (Zea mays)}

SKARVYADVNVLRPKEYWDYEALTVQWGEQDDYEVVRKVGRGKYSEVFEGINVNNNEKCIIKILKPVKKKKIKREIKILQNLCGGPNIVKLLDIVRDQHSKTPSLIFEYVNNTDFKVLYPTLTDYDIRYYIYELLKALDYCHSQGIMHRDVKPHNVMIDHELRKLRLIDWGLAEFYHPGKEYNVRVASRYFKGPELLVDLQDYDYSLDMWSLGCMFAGMIFRKEPFFYGHDNHDQLVKIAKVLGTDGLNVYLNKYRIELDPQLEALVGRHSRKPWLKFMNADNQHLVSPEAIDFLDKLLRYDHQERLTALEAMTHPYFQQVRAAENS

>d1b6cb\_ d.144.1.1 (B:) Type I TGF-beta receptor R4 {Human (Homo sapiens)}

TTLKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARLTALRIKKTLSQLSQQEG

>d1f3mc\_ d.144.1.1 (C:) pak1 {Human (Homo sapiens)}

SDEEILEKLRSIVSVGDPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIRQMNLQQQPKKELIINEILVMRENKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDVVTETCMDEGQIAAVCRECLQALEFLHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVVTRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRDFLNRCLDMDVEKRGSAKELLQHQFLKIAKPLSSLTPLIAAAKEATK

>d1howa\_ d.144.1.1 (A:) Sky1p {Baker's yeast (Saccharomyces cerevisiae)}

FHPAFKGEPYKDARYILVRKLGWGHFSTVWLAKDMVNNTHVAMKIVRGDKVYTEAAEDEIKLLQRVNDADNTKEDSMGANHILKLLDHFNHKGPNGVHVVMVFEVLGENLLALIKKYEHRGIPLIYVKQISKQLLLGLDYMHRRCGIIHTDIKPENVLMEIVDSPENLIQIKIADLGNACWYDEHYTNSIQTREYRSPEVLLGAPWGCGADIWSTACLIFELITGDFLFEPDEGHSYTKDDDHIAQIIELLGELPSYLLRNGKYTRTFFNSRGLLRNISKLKFWPLEDVLTEKYKFSKDEAKEISDFLSPMLQLDPRKRADAGGLVNHPWLKDTLGMEEIRVPDRELYGSGSDIPGWFEEVR

>d1vr2a\_ d.144.1.2 (A:) Vascular endothelial growth factor receptor 2 (kdr) {Human (Homo sapiens)}

LPYDASKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKVAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANA

>d1ir3a\_ d.144.1.2 (A:) Insulin receptor {Human (Homo sapiens)}

SSVFVPDEWEVSREKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFLNEASVMKGFTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMAAEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPVRWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDNCPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENK

>d1byga\_ d.144.1.2 (A:) C-terminal src kinase (csk) {Human (Homo sapiens)}

GWALNMKELKLLQTIGKGEFGDVMLGDYRGNKVAVKCIKNDATAQAFLAEASVMTQLRHSNLVQLLGVIVEEKGGLYIVTEYMAKGSLVDYLRSRGRSVLGGDCLLKFSLDVCEAMEYLEGNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALREKKFSTKSDVWSFGILLWEIYSFGRVPYPRIPLKDVVPRVEKGYKMDAPDGCPPAVYEVMKNCWHLDAAMRPSFLQLREQLEHIKTHEL

>d1jpaa\_ d.144.1.2 (A:) ephb2 receptor tyrosine kinase {Mouse (Mus musculus)}

KIFIDPFTFEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGKREIFVAIKTLKSGYTEKQRRDFLSEASIMGQFDHPNVIHLEGVVTKSTPVMIITEFMENGSLDSFLRQNDGQFTVIQLVGMLRGIAAGMKYLADMNYVHRDLAARNILVNSNLVCKVSDFGLSRFLEDDTSDPTYTSALGGKIPIRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMTNQDVINAIEQDYRLPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIRNPNSLKA

>d1fvra\_ d.144.1.2 (A:) Tie2 kinase {Human (Homo sapiens)}

PTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAE

>d1e8ga2 d.145.1.1 (A:6-273) Vanillyl-alcohol oxidase {Fungus (Penicillium simplicissimum)}

EFRPLTLPPKLSLSDFNEFIQDIIRIVGSENVEVISSKDQIVDGSYMKPTHTHDPTHVMDQDYFLASAIVAPRNVADVQSIVGLANKFSFPLWPISIGRNSGYGGAAPRVSGSVVLDMGKNMNRVLEVNVEGAYCVVEPGVTYHDLHNYLEANNLRDKLWLDVPDLGGGSVLGNAVERGVGYTPYGDHWMMHSGMEVVLANGELLRTGMGALPDPKRPETMGLKPEDQPWSKIAHLFPYGFGPYIDGLFSQSNMGIVTKIGIWLMPNP

>d1f0xa2 d.145.1.1 (A:9-273) D-lactate dehydrogenase {Escherichia coli}

NKAFLNELARLVGSSHLLTDPAKTARYRKGFRSGQGDALAVVFPGSLLELWRVLKACVTADKIILMQAANTGLTEGSTPNGNDYDRDVVIISTLRLDKLHVLGKGEQVLAYPGTTLYSLEKALKPLGREPHSVIGSSCIGASVIGGICNNSGGSLVQRGPAYTEMSLFARINEDGKLTLVNHLGIDLGETPEQILSKLDDDRIKDDDVRHDGRHAHDYDYVHRVRDIEADTPARYNADPDRLFESSGCAGKLAVFAVRLDTFEAE

>d1i19a2 d.145.1.1 (A:57-273) Cholesterol oxidase {Brevibacterium sterolicum}

VAPLPTPPNFPNDIALFQQAYQNWSKEIMLDATWVCSPKTPQDVVRLANWAHEHDYKIRPRGAMHGWTPLTVEKGANVEKVILADTMTHLNGITVNTGGPVATVTAGAGASIEAIVTELQKHDLGWANLPAPGVLSIGGALAVNAHGAALPAVGQTTLPGHTYGSLSNLVTELTAVVWNGTTYALETYQRNDPRITPLLTNLGRCFLTSVTMQAGPN

>d1uxy\_1 d.145.1.2 (3-200) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Escherichia coli}

HSLKPWNTFGIDHNAQHIVCAEDEQQLLNAWQYATAEGQPVLILGEGSNVLFLEDYRGTVIINRIKGIEIHDEPDAWYLHVGAGENWHRLVKYTLQEGMPGLENLALIPGCVGSSPIQNIGAYGVELQRVCAYVDSVELATGKQVRLTAKECRFGYRDSIFKHEYQDRFAIVAVGLRLPKEWQPVLTYGDLTRLDPTT

>d1hska1 d.145.1.2 (A:15-208) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Staphylococcus aureus}

NKDIYQALQQLIPNEKIKVDEPLKRYTYTKTGGNADFYITPTKNEEVQAVVKYAYQNEIPVTYLGNGSNIIIREGGIRGIVISLLSLDHIEVSDDAIIAGSGAAIIDVSRVARDYALTGLEFACGIPGSIGGAVYMNAGAYGGEVKDCIDYALCVNEQGSLIKLTTKELELDYRNSIIQKEHLVVLEAAFTLAP

>d1qj2c2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Pseudomonas carboxydovorans}

MIPGSFDYHRPKSIADAVALLTKLGEDARPLAGGHSLIPIMKTRLATPEHLVDLRDIGDLVGIREEGTDVVIGAMTTQHALIGSDFLAAKLPIIRETSLLIADPQIRYMGTIGGNAANGDPGNDMPALMQCLGAAYELTGPEGARIVAARDYYQGAYFTAIEPGELLTAIRIPVPPT

>d1fo4a6 d.145.1.3 (A:192-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}

SPSLFNPEEFMPLDPTQEPIFPPELLRLKDVPPKQLRFEGERVTWIQASTLKELLDLKAQHPEAKLVVGNTEIGIEMKFKNQLFPMIICPAWIPELNAVEHGPEGISFGAACALSSVEKTLLEAVAKLPTQKTEVFRGVLEQLRWFAGKQVKSVASLGGNIITASPISDLNPVFMASGTKLTIVSRGTRRTVPMDHTFFPSYRKTLLGPEEILLSIEIPYSRE

>d1jroa4 d.145.1.3 (A:179-345) Xanthine dehydrogenase chain A, domain 3 {Rhodobacter capsulatus}

PAFLPETSDALADWYLAHPEATLIAGGTDVSLWVTKALRDLPEVAFLSHCKDLAQIRETPDGYGIGAGVTIAALRAFAEGPHPALAGLLRRFASEQVRQVATIGGNIANGSPIGDGPPALIAMGASLTLRRGQERRRMPLEDFFLEYRKQDRRPGEFVESVTLPKSA

>d1uxy\_2 d.146.1.1 (201-342) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Escherichia coli}

VTPQQVFNAVCHMRTTKLPDPKVNGNAGAFFKNPVVSAETAKALLSQFPTAPNYPQADGSVKLAAGWLIDQCQLKGMQIGGAAVHRQQALVLINEDNAKSEDVVQLAHHVRQKVGEKFNVWLEPEVRFIGASGEVSAVETIS

>d1hska2 d.146.1.1 (A:209-317) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Staphylococcus aureus}

GKMTEIQAKMDDLTERRESKQPLEYPSCGSVFQRPPGHFAGKLIQDSNLQGHRIGGVEVSTKHAGFMVNVDNGTATDYENLIHYVQKTVKEKFGIELNREVRIIGEHPK

>d1qr0a1 d.150.1.1 (A:1-101) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

MKIYGIYMDRPLSQEENERFMTFISPEKREKCRRFYHKEDAHRTLLGDVLVRSVISRQYQLDKSDIRFSTQEYGKPCIPDLPDAHFNISHSGRWVIGAFDS

>d1qr0a2 d.150.1.1 (A:102-228) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

QPIGIDIEKTKPISLEIAKRFFSKTEYSDLLAKDKDEQTDYFYHLWSMKESFIKQEGKGLSLPLDSFSVRLHQDGQVSIELPDSHSPCYIKTYEVDPGYKMAVCAAHPDFPEDITMVSYEELLRAAA

>d1ako\_\_ d.151.1.1 (-) DNA-repair enzyme exonuclease III {Escherichia coli}

MKFVSFNINGLRARPHQLEAIVEKHQPDVIGLQETKVHDDMFPLEEVAKLGYNVFYHGQKGHYGVALLTKETPIAVRRGFPGDDEEAQRRIIMAEIPSLLGNVTVINGYFPQGESRDHPIKFPAKAQFYQNLQNYLETELKRDNPVLIMGDMNISPTDLDIGIGEENRKRWLRTGKCSFLPEEREWMDRLMSWGLVDTFRHANPQTADRFSWFDYRSKGFDDNRGLRIDLLLASQPLAECCVETGIDYEIRSMEKPSDHAPVWATFRR

>d1hd7a\_ d.151.1.1 (A:) DNA repair endonuclease Hap1 {Human (Homo sapiens)}

LYEDPPDQKTSPSGKPATLKICSWNVDGLRAWIKKKGLDWVKEEAPDILCLQETKCSENKLPAELQELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGIGDEEHDQEGRVIVAEFDSFVLVTAYVPNAGRGLVRLEYRQRWDEAFRKFLKGLASRKPLVLCGDLNVAHEEIDLRNPKGNKKNAGFTPQERQGFGELLQAVPLADSFRHLYPNTPYAYTFWTYMMNARSKNVGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPITLYLAL

>d2dnja\_ d.151.1.1 (A:) Deoxyribonuclease I {Cow (Bos taurus)}

LKIAAFNIRTFGETKMSNATLASYIVRIVRRYDIVLIQEVRDSHLVAVGKLLDYLNQDDPNTYHYVVSEPLGRNSYKERYLFLFRPNKVSVLDTYQYDDGCESCGNDSFSREPAVVKFSSHSTKVKEFAIVALHSAPSDAVAEINSLYDVYLDVQQKWHLNDVMLMGDFNADCSYVTSSQWSSIRLRTSSTFQWLIPDSADTTATSTNCAYDRIVVAGSLLQSSVVPGSAAPFDFQAAYGLSNEMALAISDHYPVEVTLT

>d1gdoa\_ d.153.1.1 (A:) Glucosamine 6-phosphate synthase, N-terminal domain {Escherichia coli}

CGIVGAIAQRDVAEILLEGLRRLEYRGYDSAGLAVVDAEGHMTRLRRLGKVQMLAQAAEEHPLHGGTGIAHTRWATHGEPSEVNAHPHVSEHIVVVHNGIIENHEPLREELKARGYTFVSETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVIMDSRHPDTLLAARSGSPLVIGLGMGENFIASDQLALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRQDIESNL

>d1gph12 d.153.1.1 (1:1-234) Glutamine PRPP amidotransferase, N-terminal domain {Bacillus subtilis}

CGVFGIWGHEEAPQITYYGLHSLQHRGQEGAGIVATDGEKLTAHKGQGLITEVFQNGELSKVKGKGAIGHVRYATAGGGGYENVQPLLFRSQNNGSLALAHNGNLVNATQLKQQLENQGSIFQTSSDTEVLAHLIKRSGHFTLKDQIKNSLSMLKGAYAFLIMTETEMIVALDPNGLRPLSIGMMGDAYVVASETCAFDVVGATYLREVEPGEMLIINDEGMKSERFSMNINRS

>d1ecfa2 d.153.1.1 (A:1-249) Glutamine PRPP amidotransferase, N-terminal domain {Escherichia coli}

CGIVGIAGVMPVNQSIYDALTVLQHRGQDAAGIITIDANNCFRLRKANGLVSDVFEARHMQRLQGNMGIGHVRYPTAGSSSASEAQPFYVNSPYGITLAHNGNLTNAHELRKKLFEEKRRHINTTSDSEILLNIFASELDNFRHYPLEADNIFAAIAATNRLIRGAYACVAMIIGHGMVAFRDPNGIRPLVLGKRDIDENRTEYMVASESVALDTLGFDFLRDVAPGEAIYITEEGQLFTRQCADNPVS

>d1ct9a2 d.153.1.1 (A:1-192) Asparagine synthetase B, N-terminal domain {Escherichia coli}

ASIFGVFDIKTDAVELRKKALELSRLMRHRGPDWSGIYASDNAILAHERLSIVDVNAGAQPLYNQQKTHVLAVNGEIYNHQALRAEYGDRYQFQTGSDCEVILALYQEKGPEFLDDLQGMFAFALYDSEKDAYLIGRDHLGIIPLYMGYDEHGQLYVASEMKALVPVCRTIKEFPAGSYLWSQDGEIRSYYH

>d1jgta2 d.153.1.1 (A:4-209) beta-Lactam synthetase {Streptomyces clavuligerus}

PVLPAAFGFLASARTGGGRAPGPVFATRGSHTDIDTPQGERSLAATLVHAPSVAPDRAVARSLTGAPTTAVLAGEIYNRDELLSVLPAGPAPEGDAELVLRLLERYDLHAFRLVNGRFATVVRTGDRVLLATDHAGSVPLYTCVAPGEVRASTEAKALAAHRDPKGFPLADARRVAGLTGVYQVPAGAVMDIDLGSGTAVTHRTWT

>d1ea0a3 d.153.1.1 (A:1-422) Alpha subunit of glutamate synthase, N-terminal domain {Azospirillum brasilense}

CGVGFIAAIDGKPRRSVVEKGIEALKAVWHRGAVDADGKTGDGAGIHVAVPQKFFKDHVKVIGHRAPDNKLAVGQVFLPRISLDAQEACRCIVETEILAFGYYIYGWRQVPINVDIIGEKANATRPEIEQIIVGNNKGVSDEQFELDLYIIRRRIEKAVKGEQINDFYICSLSARSIIYKGMFLAEQLTTFYPDLLDERFESDFAIYHQRYSTNTFPTWPLAQPFRMLAHNGEINTVKGNVNWMKAHETRMEHPAFGTHMQDLKPVIGVGLSDSGSLDTVFEVMVRAGRTAPMVKMMLVPQALTSSQTTPDNHKALIQYCNSVMEPWDGPAALAMTDGRWVVGGMDRNGLRPMRYTITTDGLIIGGSETGMVKIDETQVIEKGRLGPGEMIAVDLQSGKLYRDRELKDHLATLKPWDKWVQN

>g1gk9.1 d.153.1.2 (A:,B:) Penicillin acylase {Escherichia coli}

QSSSEIKIVRDEYGMPHIYANDTWHLFYGYGYVVAQDRLFQMEMARRSTQGTVAEVLGKDFVKFDKDIRRNYWPDAIRAQIAALSPEDMSILQGYADGMNAWIDKVNTNPETLLPKQFNTFGFTPKRWEPFDVAMIFVGTMANRFSDSTSEIDNLALLTALKDKYGVSQGMAVFNQLKWLVNPSAPTTIAVQESNYPLKFNQQNSQTAXSNMWVIGKSKAQDAKAIMVNGPQFGWYAPAYTYGIGLHGAGYDVTGNTPFAYPGLVFGHNGVISWGSTAGFGDDVDIFAERLSAEKPGYYLHNGKWVKMLSREETITVKNGQAETFTVWRTVHGNILQTDQTTQTAYAKSRAWDGKEVASLLAWTHQMKAKNWQEWTQQAAKQALTINWYYADVNGNIGYVHTGAYPDRQSGHDPRLPVPGTGKWDWKGLLPFEMNPKVYNPQSGYIANWNNSPQKDYPASDLFAFLWGGADRVTEIDRLLEQKPRLTADQAWDVIRQTSRQDLNLRLFLPTLQAATSGLTQSDPRRQLVETLTRWDGINLLNDDGKTWQQPGSAILNVWLTSMLKRTVVAAVPMPFDKWYSASGYETTQDGPTGSLNISVGAKILYEAVQGDKSPIPQAVDLFAGKPQQEVVLAALEDTWETLSKRYGNNVSNWKTPAMALTFRANNFFGVPQAAAEETRHQAEYQNRGTENDMIVFSPTTSDRPVLAWDVVAPGQSGFIAPDGTVDKHYEDQLKMYENFGRKSLWLTKQDVEAHKESQEVLHVQR

>g1fm2.1 d.153.1.2 (A:,B:) Cephalosporin acylase {Brevundimonas diminuta}

QAPIAAYKPRSNEILWDGYGVPHIYGVDAPSAFYGYGWAQARSHGDNILRLYGEARGKGAEYWGPDYEQTTVWLLTNGVPERAQQWYAQQSPDFRANLDAFAAGINAYAQQNPDDISPEVRQVLPVSGADVVAHAHRLMNFLYVASPGRTLGXSNSWAVAPGKTANGNALLLQNPHLSWTTDYFTYYEAHLVTPDFEIYGATQIGLPVIRFAFNQRMGITNTVNGMVGATNYRLTLQDGGYLYDGQVRPFERRQASYRLRQADGSTVDKPLEIRSSVHGPVFERADGTAVAVRVAGLDRPGMLEQYFDMITAHSFDDYEAAMARMQVPTFNIVYADREGTINYSFNGVAPKRAEGDIAFWQGNVPGDSSRYLWTETHPLDDLPRVTNPPGGFVQNSNDPPWTPTWPVTYCPANHPSYLAPQTPHSLRAQQSVRLMSENDDLTLERFMALQFSHRAVMADRTLPDLIPAALIDPDPEVQAAARLLAAWDRDFTSDSRAALLFEEWARLFAGQNFAGQAAFATPWSLDKPVSTPYGVRDPKAAVDQLRTAIANTKRKYGAIDRPFGDASRMILNDVNVPGAAGYGNLGSFRVFTWSDPDENGIRTPVHGETWVAMIEFSTPVRAYGLMSYGNSRQPGTTHYSDQIERVSRADFRELLLRREQVEAAVQERTPFNF

>d1pma1\_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Archaeon Thermoplasma acidophilum}

TTTVGITLKDAVIMATERRVTMENFIMHKNGKKLFQIDTYTGMTIAGLVGDAQVLVRYMKAELELYRLQRRVNMPIEAVATLLSNMLNQVKYMPYMVQLLVGGIDTAPHVFSIDAAGGSVEDIYASTGSGSPFVYGVLESQYSEKMTVDEGVDLVIRAISAAKQRDSASGGMIDVAVITRKDGYVQLPTDQIESRIRKLGLIL

>d1ryp1\_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

QFNPYGDNGGTILGIAGEDFAVLAGDTRNITDYSINSRYEPKVFDCGDNIVMSANGFAADGDALVKRFKNSVKWYHFDHNDKKLSINSAARNIQHLLYGKRFFPYYVHTIIAGLDEDGKGAVYSFDPVGSYEREQCRAGGAAASLIMPFLDNQVNFKNQYEPGTNGKVKKPLKYLSVEEVIKLVRDSFTSATERHIQVGDGLEILIVTKDGVRKEFYELKRD

>d1ryp2\_ d.153.1.4 (2:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TQQPIVTGTSVISMKYDNGVIIAADNLGSYGSLLRFNGVERLIPVGDNTVVGISGDISDMQHIERLLKDLVTENAYDNPLADAEEALEPSYIFEYLATVMYQRRSKMNPLWNAIIVAGVQSNGDQFLRYVNLLGVTYSSPTLATGFGAHMANPLLRKVVDRESDIPKTTVQVAEEAIVNAMRVLYYRDARSSRNFSLAIIDKNTGLTFKKNLQVENMKWDFAKDIKGYGTQKI

>d1ryph\_ d.153.1.4 (H:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

LKKGEVSLGASIMAVTFKDGVILGADSRTTTGAYIANRVTDKLTRVHDKIWCCRSGSAADTQAIADIVQYHLELYTSQYGTPSTETAASVFKELCYENKDNLTAGIIVAGYDDKNKGEVYTIPLGGSVHKLPYAIAGSGSTFIYGYCDKNFRENMSKEETVDFIKHSLSQAIKWDGSSGGVIRMVVLTAAGVERLIFYPDEYEQL

>d1rypi\_ d.153.1.4 (I:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTIVGVKFNNGVVIAADTRSTQGPIVADKNCAKLHRISPKIWCAGAGTAADTEAVTQLIGSNIELHSLYTSREPRVVSALQMLKQHLFKYQGHIGAYLIVAGVDPTGSHLFSIHAHGSTDVGYYLSLGSGSLAAMAVLESHWKQDLTKEEAIKLASDAIQAGIWNDLGSGSNVDVCVMEIGKDAEYLRNYLTPNVREEKQKSYKFPRGTTAVLKESIVNICD

>d1rypj\_ d.153.1.4 (J:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

SDPSSINGGIVVAMTGKDCVAIACDLRLGSQSLGVSNKFEKIFHYGHVFLGITGLATDVTTLNEMFRYKTNLYKLKEERAIEPETFTQLVSSSLYERRFGPYFVGPVVAGINSKSGKPFIAGFDLIGCIDEAKDFIVSGTASDQLFGMCESLYEPNLEPEDLFETISQALLNAADRDALSGWGAVVYIIKKDEVVKRYLKMRQD

>d1rypk\_ d.153.1.4 (K:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MDIILGIRVQDSVILASSKAVTRGISVLKDSDDKTRQLSPHTLMSFAGEAGDTVQFAEYIQANIQLYSIREDYELSPQAVSSFVRQELAKSIRSRRPYQVNVLIGGYDKKKNKPELYQIDYLGTKVELPYGAHGYSGFYTFSLLDHHYRPDMTTEEGLDLLKLCVQELEKRMPMDFKGVIVKIVDKDGIRQVDDFQAQ

>d1rypl\_ d.153.1.4 (L:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTTLAFRFQGGIIVAVDSRATAGNWVASQTVKRVIEINPFLLGTMAGGAADCQFWETWLGSQCRLHELREKERISVAAASKILSNLVYQYKGAGLSMGTMICGYTRKEGPTIYYVDSDGTRLKGDIFCVGSGQTFAYGVLDSNYKWDLSVEDALYLGKRSILAAAHRDAYSGGSVNLYHVTEDGWIYHGNHDVGELFWKVKEEEGSFNNVIG

>d1rypa\_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

AGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVPDKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFRYKYGYDMPCDVLAKRMANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYYVGYKATATGPKQQEITTNLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVATKDKFFTLSAENIEERLVAIAEQD

>d1rypb\_ d.153.1.4 (B:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MTDRYSFSLTTFSPSGKLGQIDYALTAVKQGVTSLGIKATNGVVIATEKKSSSPLAMSETLSKVSLLTPDIGAVYSGMGPDYRVLVDKSRKVAHTSYKRIYGEYPPTKLLVSEVAKIMQEATQSGGVRPFGVSLLIAGHDEFNGFSLYQVDPSGSYFPWKATAIGKGSVAAKTFLEKRWNDELELEDAIHIALLTLKESVEGEFNGDTIELAIIGDENPDLLGYTGIPTDKGPRFRKLTSQEINDRLEAL

>d1rypc\_ d.153.1.4 (C:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GSRRYDSRTTIFSPEGRLYQVEYALESISHAGTAIGIMASDGIVLAAERKVTSTLLEQDTSTEKLYKLNDKIAVAVAGLTADAEILINTARIHAQNYLKTYNEDIPVEILVRRLSDIKQGYTQHGGLRPFGVSFIYAGYDDRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLLQMDYKDDMKVDDAIELALKTLSKTTDSSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILVKTGIT

>d1rypd\_ d.153.1.4 (D:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GYDRALSIFSPDGHIFQVEYALEAVKRGTCAVGVKGKNCVVLGCERRSTLKLQDTRITPSKVSKIDSHVVLSFSGLNADSRILIEKARVEAQSHRLTLEDPVTVEYLTRYVAGVQQRYTQSGGVRPFGVSTLIAGFDPRDDEPKLYQTEPSGIYSSWSAQTIGRNSKTVREFLEKNYDRKEPPATVEECVKLTVRSLLEVVQTGAKNIEITVVKPDSDIVALSSEEINQYVTQIEQEKQEQ

>d1rype\_ d.153.1.4 (E:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

DRGVSTFSPEGRLFQVEYSLEAIKLGSTAIGIATKEGVVLGVEKRATSPLLESDSIEKIVEIDRHIGCAMSGLTADARSMIEHARTAAVTHNLYYDEDINVESLTQSVCDLALRFGEGASGEERLMSRPFGVALLIAGHDADDGYQLFHAEPSGTFYRYNAKAIGSGSEGAQAELLNEWHSSLTLKEAELLVLKILKQVMEEKLDENNAQLSCITKQDGFKIYDNEKTAELIKELKEKEAAE

>d1rypf\_ d.153.1.4 (F:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

FRNNYDGDTVTFSPTGRLFQVEYALEAIKQGSVTVGLRSNTHAVLVALKRNADELSSYQKKIIKCDEHMGLSLAGLAPDARVLSNYLRQQCNYSSLVFNRKLAVERAGHLLCDKAQKNTQSYGGRPYGVGLLIIGYDKSGAHLLEFQPSGNVTELYGTAIGARSQGAKTYLERTLDTFIKIDGNPDELIKAGVEAISQSLRDESLTVDNLSIAIVGKDTPFTIYDGEAVAKYI

>d1rypg\_ d.153.1.4 (G:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GTGYDLSNSVFSPDGRNFQVEYAVKAVENGTTSIGIKCNDGVVFAVEKLITSKLLVPQKNVKIQVVDRHIGCVYSGLIPDGRHLVNRGREEAASFKKLYKTPIPIPAFADRLGQYVQAHTLYNSVRPFGVSTIFGGVDKNGAHLYMLEPSGSYWGYKGAATGKGRQSAKAELEKLVDHHPEGLSAREAVKQAAKIIYLAHEDNKEKDFELEISWCSLSETNGLHKFVKGDLLQEAIDFAQKEIN

>d1ht1a\_ d.153.1.4 (A:) HslV (ClpQ) protease {Escherichia coli}

TTIVSVRRNGHVVIAGDGQATLGNTVMKGNVKKVRRLYNDKVIAGFAGGTADAFTLFELFERKLEMHQGHLVKAAVELAKDWRTDRMLRKLEALLAVADETASLIITGNGDVVQPENDLIAIGSGGPYAQAAARALLENTELSAREIAEKALDIAGDICIYTNHFHTIEELSYK

>g1apy.1 d.153.1.5 (A:,B:) Glycosylasparaginase (aspartylglucosaminidase, AGA) {Human (Homo sapiens)}

SPLPLVVNTWPFKNATEAAWRALASGGSALDAVESGCAMCEREQCDGSVGFGGSPDELGETTLDAMIMDGTTMDVGAVGDLRRIKNAIGVARKVLEHTTHTLLVGESATTFAQSMGFINEDLSTSASQALHSDWLARNCQPNYWRNVIPDPSKYCGPYKPPXTIGMVVIHKTGHIAAGTSTNGIKFKIHGRVGDSPIPGAGAYADDTAGAAAATGNGDILMRFLPSYQAVEYMRRGEDPTIACQKVISRIQKHFPEFFGAVICANVTGSYGAACNKLSTFTQFSFMVYNSEKNQPTEEKVDCI

>g2gac.1 d.153.1.5 (A:,B:) Glycosylasparaginase (aspartylglucosaminidase, AGA) {Flavobacterium meningosepticum}

NKPIVLSTWNFGLHANVEAWKVLSKGGKALDAVEKGVRLVEDDPTERSVGYGGRPDRDGRVTLDACIMDENYNIGSVACMEHIKNPISVARAVMEKTPHVMLVGDGALEFALSQGFKKENLLTAESEKEWKEWLKTXCIGMIALDAQGNLSGACTTSGMAYKMHGRVGDSPIIGAGLFVDNEIGAATATGHGEEVIRTVGTHLVVELMNQGRTPQQACKEAVERIVKIVNRRGKNLKDIQVGFIALNKKGEYGAYCIQDGFNFAVHDQKGNRLETP

>d2bc2a\_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacillus cereus}

TVIKNETGTISISQLNKNVWVHTELGSFNGEAVPSNGLVLNTSKGLVLVDSSWDDKLTKELIEMVEKKFQKRVTDVIITHAHADRIGGIKTLKERGIKAHSTALTAELAKKNGYEEPLGDLQTVTNLKFGNMKVETFYPGKGHTEDNIVVWLPQYNILVGGALVKSTSAKDLGNVADAYVNEWSTSIENVLKRYRNINAVVPGHGEVGDKGLLLHTLDLLK

>d1a7ta\_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacteroides fragilis}

SVKISDDISITQLSDKVYTYVSLAEIEGWGMVPSNGMIVINNHQAALLDTPINDAQTEMLVNWVTDSLHAKVTTFIPNHWHGDCIGGLGYLQRKGVQSYANQMTIDLAKEKGLPVPEHGFTDSLTVSLDGMPLQCYYLGGGHATDNIVVWLPTENILFGGCMLKDNQTTSIGNISDADVTAWPKTLDKVKAKFPSARYVVPGHGNYGGTELIEHTKQIVNQYIESTS

>d1smla\_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Xanthomonas maltophilia}

EVPLPQLRAYTVDASWLQPMAPLQIADHTWQIGTEDLTALLVQTPDGAVLLDGGMPQMASHLLDNMKARGVTPRDLRLILLSHAHADHAGPVAELKRRTGAKVAANAESAVLLARGGSDDLHFGDGITYPPANADRIVMDGEVITVGGIVFTAHFMAGHTPGSTAWTWTDTRNGKPVRIAYADSLSAPGYQLQGNPRYPHLIEDYRRSFATVRALPCDVLLTPHPGASNWDYAAGARAGAKALTCKAYADAAEQKFDGQLAKETAG

>d1jjea\_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Pseudomonas aeruginosa, IMP-1}

SLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYASELTNELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKILFGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPSHSEVGDASLLKLTLEQAVKGLNESKK

>d4kbpa2 d.159.1.1 (A:121-432) Plant purple acid phosphatase, catalytic domain {Kidney bean (Phaseolus vulgaris)}

QTGLDVPYTFGLIGDLGQSFDSNTTLSHYELSPKKGQTVLFVGDLSYADRYPNHDNVRWDTWGRFTERSVAYQPWIWTAGNHEIEFAPEINETEPFKPFSYRYHVPYEASQSTSPFWYSIKRASAHIIVLSSYSAYGRGTPQYTWLKKELRKVKRSETPWLIVLMHSPLYNSYNHHFMEGEAMRTKFEAWFVKYKVDVVFAGHVHAYERSERVSNIAYKITDGLCTPVKDQSAPVYITIGDAGNYGVIDSNMIQPQPEYSAFREASFGHGMFDIKNRTHAHFSWNRNQDGVAVEADSVWFFNRHWYPVDDST

>d1utea\_ d.159.1.1 (A:) Mammalian purple acid phosphatase {Pig (Sus scrofa)}

PTPILRFVAVGDWGGVPNAPFHTAREMANAKAIATTVKTLGADFILSLGDNFYFTGVHDAKDKRFQETFEDVFSDPSLRNVPWHVLAGNHDHLGNVSAQIAYSKISKRWNFPSPYYRLRFKIPRSNVSVAIFMLDTVTLCGNSDDFVSQQPERPRNLALARTQLAWIKKQLAAAKEDYVLVAGHYPVWSIAEHGPTHCLVKQLLPLLTTHKVTAYLCGHDHNLQYLQDENGLGFVLSGAGNFMDPSKKHLRKVPNGYLRFHFGAENSLGGFAYVEITPKEMSVTYIEASGKSLFKTKLPRRA

>d1jk7a\_ d.159.1.3 (A:) Protein phosphatase-1 (PP-1) {Human (Homo sapiens)}

KLNIDSIIQRLLEVRGSKPGKNVQLQENEIRGLCLKSREIFLSQPILLELEAPLKICGDIHGQYYDLLRLFEYGGFPPESNYLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHECASINRIYGFYDECKRRYNIKLWKTFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQSMEQIRRIMRPTDVPDQGLLCDLLWSDPDKDVLGWGENDRGVSFTFGAEVVAKFLHKHDLDLICRAHQVVEDGYEFFAKRQLVTLFSAPNYCGEFDNAGAMMSVDETLMCSFQILKPA

>d1auia\_ d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Human (Homo sapiens)}

TDRVVKAVPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIITEGASILRQEKNLLDIDAPVTVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRGNHECRHLTEYFTFKQECKIKYSERVYDACMDAFDCLPLAALMNQQFLCVHGGLSPEINTLDDIRKLDRFKEPPAYGPMCDILWSDPLEDFGNEKTQEHFTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRAHEAQDAGYRMYRKSQTTGFPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPHPYWLPNFMDVFTWSLPFVGEKVTEMLVNVLNICSDDELGSEEDGFDGATAAARKEVIRNKIRAIGKMARVFSVLREESESVLTLKGLTPTGMLPSGVLSGGKQTLQSATVEAIEADEAIKGFSPQHKITSFEEAKGLDRINERMPPR

>d1g5ba\_ d.159.1.3 (A:) lambda ser/thr protein phosphatase {Bacteriophage lambda}

MRYYEKIDGSKYRNIWVVGDLHGCYTNLMNKLDTIGFDNKKDLLISVGDLVDRGAENVECLELITFPWFRAVRGNHEQMMIDGLSERGNVNHWLLNGGGWFFNLDYDKEILAKALAHKADELPLIIELVSKDKKYVICHADYPFDEYEFGKPVDHQQVIWNRERISNSQNGIVKEIKGADTFIFGHTPAVKPLKFANQMYIDTGAVFCGNLTLIQVQGA

>d1emsa2 d.160.1.1 (A:10-280) NIT-FHIT fusion protein, N-terminal domain {Nematode (Caenorhabditis elegans)}

MATGRHFIAVCQMTSDNDLEKNFQAAKNMIERAGEKKCEMVFLPECFDFIGLNKNEQIDLAMATDCEYMEKYRELARKHNIWLSLGGLHHKDPSDAAHPWNTHLIIDSDGVTRAEYNKLHLFDLEIPGKVRLMESEFSKAGTEMIPPVDTPIGRLGLSICYDVRFPELSLWNRKRGAQLLSFPSAFTLNTGLAHWETLLRARAIENQCYVVAAAQTGAHNPKRQSYGHSMVVDPWGAVVAQCSERVDMCFAEIDLSYVDTLREMQPVFSHR

>d1f89a\_ d.160.1.1 (A:) hypothetical protein yl85 {Baker's yeast (Saccharomyces cerevisiae)}

SASKILSQKIKVALVQLSGSSPDKMANLQRAATFIERAMKEQPDTKLVVLPECFNSPYSTDQFRKYSEVINPKEPSTSVQFLSNLANKFKIILVGGTIPELDPKTDKIYNTSIIFNEDGKLIDKHRKVHLFDVDIPNGISFHESETLSPGEKSTTIDTKYGKFGVGICYDMRFPELAMLSARKGAFAMIYPSAFNTVTGPLHWHLLARSRAVDNQVYVMLCSPARNLQSSYHAYGHSIVVDPRGKIVAEAGEGEEIIYAELDPEVIESFRQAVPLTKQRRF

>d1qdla\_ d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase subunit, TrpE {Archaeon Sulfolobus solfataricus}

AMEVHPISEFASPFEVFKCIERDFKVAGLLESIGGPQYKARYSVIAWSTNGYLKIHDDPVNILNGYLKDLKLADIPGLFKGGMIGYISYDAVRFWEKIRDLKPAAEDWPYAEFFTPDNIIIYDHNEGKVYVNADLSSVGGCGDIGEFKVSFYDESLNKNSYERIVSESLEYIRSGYIFQVVLSRFYRYIFSGDPLRIYYNLRRINPSPYMFYLKFDEKYLIGSSPELLFRVQDNIVETYPIAGTRPRGADQEEDLKLELELMNSEKDKAEHLMLVDLARNDLGKVCVPGTVKVPELMYVEKYSHVQHIVSKVIGTLKKKYNALNVLSATFPAGTVSGAPKPMAMNIIETLEEYKRGPYAGAVGFISADGNAEFAIAIRTAFLNKELLRIHAGAGIVYDSNPESEYFETEHKLKALKTAIGVR

>d1i7qa\_ d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase subunit, TrpE {Serratia marcescens}

TKPQLTLLKVQASYRGDPTTLFHQLCGARPATLLLESAEINDKQNLQSLLVIDSALRITALGHTVSVQALTANGPALLPLLDEALPPEVRNQARPNGRELTFPAIDAVQDEDARLRSLSVFDALRTILTLVDSPADEREAVMLGGLFAYDLVAGFENLPALRQDQRCPDFCFYLAETLLVLDHQRGSARLQASVFSEQASEAQRLQHRLEQLQAELQQPPQPIPHQKLENMQLSCNQSDEEYGAVVSELQEAIRQGEIFQVVPSRRFSLPCPAPLGPYQTLKDNNPSPYMFFMQDDDFTLFGASPESALKYDAGNRQIEIYPIAGTRPRGRRADGSLDLDLDSRIELEMRTDHKELAEHLMLVDLARNDLARICQAGSRYVADLTKVDRYSFVMHLVSRVVGTLRADLDVLHAYQACMNMGTLSGAPKVRAMQLIAALRSTRRGSYGGRVGYFTAVRNLDTCIVIRSAYVEDGHRTVQAGAGVVQDSIPEREADETRNKARAVLRAIATAHHAKEVF

>d1k0ga\_ d.161.1.1 (A:) P-aminobenzoate synthase component I {Escherichia coli}

MKTLSPAVITLLWRQDAAEFYFSRLSHLPWAMLLHSGYADHPYSRFDIVVAEPICTLTTFGKETVVSESEKRTTTTDDPLQVLQQVLDRADIRPTHNEDLPFQGGALGLFGYDLGRRFESLPEIAEQDIVLPDMAVGIYDWALIVDHQRHTVSLLSHNDVNARRAWLESQQFSPQEDFTLTSDWQSNMTREQYGEKFRQVQEYLHSGDCYQVNLAQRFHATYSGDEWQAFLQLNQANRAPFSAFLRLEQGAILSLSPERFILCDNSEIQTRPIKGTLPRLPDPQEDSKQAVKLANSAKDRAENLMIVDLMRNDIGRVAVAGSVKVPELFVVEPFPAVHHLVSTITAQLPEQLHASDLLRAAFPGGSITGAPKVRAMEIIDELEPQRRNAWCGSIGYLSFCGNMDTSITIRTLTAINGQIFCSAGGGIVADSQEEAEYQETFDKVNRILKQLEK

>d1mlda2 d.162.1.1 (A:145-313) Malate dehydrogenase {Pig (Sus scrofa)}

VTTLDIVRANAFVAELKGLDPARVSVPVIGGHAGKTIIPLISQCTPKVDFPQDQLSTLTGRIQEAGTEVVKAKAGAGSATLSMAYAGARFVFSLVDAMNGKEGVVECSFVKSQETDCPYFSTPLLLGKKGIEKNLGIGKISPFEEKMIAEAIPELKASIKKGEEFVKNM

>d1civa2 d.162.1.1 (A:194-385) Malate dehydrogenase {Flaveria bidentis, chloroplast}

TRLDENRAKCQLALKAGVFYDKVSNVTIWGNHSTTQVPDFLNAKIHGIPVTEVIRDRKWLEDEFTNMVQTRGGVLIKKWGRSSAASTAVSIVDAIRSLVTPTPEGDWFSTGVYTNGNPYGIAEDIVFSMPCRSKGDGDYEFVKDVIFDDYLSKKIKKSEDELLAEKKCVAHLTGEGIAVCDLPEDTMLPGEM

>d2hlpa2 d.162.1.1 (A:163-330) Malate dehydrogenase {Archaeon Haloarcula marismortui}

FGGRLDSARFRYVLSEEFDAPVQNVEGTILGEHGDAQVPVFSKVRVDGTDPEFSGDEKEQLLGDLQESAMDVIERKGATEWGPARGVAHMVEAILHDTGRVLPASVKLEGEFGHEDTAFGVPVRLGSNGVEEIVEWDLDDYEQDLMADAAEKLSDQYDKIS

>d1b8pa2 d.162.1.1 (A:159-329) Malate dehydrogenase {Aquaspirillum arcticum}

LRLDHNRALSQIAAKTGKPVSSIEKLFVWGNHSPTMYADYRYAQIDGASVKDMINDDAWNRDTFLPTVGKRGAAIIDARGVSSAASAANAAIDHIHDWVLGTAGKWTTMGIPSDGSYGIPEGVIFGFPVTTENGEYKIVQGLSIDAFSQERINVTLNELLEEQNGVQHLLG

>d1gv0a2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium tepidum}

AGVLDSARFRSFIAMELGVSMQDVTACVLGGHGDAMVPVVKYTTVAGIPVADLISAERIAELVERTRTGGAEIVNHLKQGSAFYSPATSVVEMVESIVLDRKRVLTCAVSLDGQYGIDGTFVGVPVKLGKNGVEHIYEIKLDQSDLDLLQKSAKIVDENCKML

>d1hyha2 d.162.1.1 (A:167-329) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus confusus}

GTLLDTARMQRAVGEAFDLDPRSVSGYNLGEHGNSQFVAWSTVRVMGQPIVTLADAGDIDLAAIEEEARKGGFTVLNGKGYTSYGVATSAIRIAKAVMADAHAELVVSNRRDDMGMYLSYPAIIGRDGVLAETTLDLTTDEQEKLLQSRDYIQQRFDEIVDTL

>d9ldta2 d.162.1.1 (A:163-331) Lactate dehydrogenase {Pig (Sus scrofa)}

SGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKNLHPELGTDADKEHWKAVHKEVVDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGIKENVFLSVPCILGQNGISDVVKVTLTPEEEAHLKKSADTLWGIQKELQF

>d1ceqa2 d.162.1.1 (A:164-329) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}

GGVLDTSRLKYYISQKLNVCPRDVNAHIVGAHGNKMVLLKRYITVGGIPLQEFINNKLISDAELEAIFDRTVNTALEIVNLHASPYVAPAAAIIEMAESYLKDLKKVLICSTLLEGQYGHSDIFGGTPVVLGANGVEQVIELQLNSEEKAKFDEAIAETKRMKALA

>d1llc\_2 d.162.1.1 (165-334) Lactate dehydrogenase {Lactobacillus casei}

TSLDTARFRQSIAEMVNVDARSVHAYIMGEHGDTEFPVWSHANIGGVTIAEWVKAHPEIKEDKLVKMFEDVRDAAYEIIKLKGATFYGIATALARISKAILNDENAVLPLSVYMDGQYGINDLYIGTPAVINRNGIQNILEIPLTDHEEESMQKSASQLKKVLTDAFAKNDI

>d1llda2 d.162.1.1 (A:150-319) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}

TNLDSARLRFLIAQQTGVNVKNVHAYIAGEHGDSEVPLWESATIGGVPMSDWTPLPGHDPLDADKREEIHQEVKNAAYKIINGKGATNYAIGMSGVDIIEAVLHDTNRILPVSSMLKDFHGISDICMSVPTLLNRQGVNNTINTPVSDKELAALKRSAETLKETAAQFGF

>d1hyea2 d.162.1.1 (A:146-313) MJ0490, lactate/malate dehydrogenase {Archaeon Methanococcus jannaschii}

LGTHLDSLRFKVAIAKFFGVHIDEVRTRIIGEHGDSMVPLLSATSIGGIPIQKFERFKELPIDEIIEDVKTKGEQIIRLKGGSEFGPAAAILNVVRCIVNNEKRLLTLSAYVDGEFDGIRDVCIGVPVKIGRDGIEEVVSIELDKDEIIAFRKSAEIIKKYCEEVKNL

>d1aiha\_ d.163.1.1 (A:) Integrase {Bacteriophage HP1}

ETELAFLYERDIYRLLAECDNSRNPDLGLIVRICLATGARWSEAETLTQSQVMPYKITFTNTKSKKNRTVPISDELFDMLPKKRGRLFNDAYESFENAVLRAEIELPKGQLTHVLRHTFASHFMMNGGNILVLKEILGHSTIEMTMRYAHFAPSHLESAVKFNPLSNPAQ

>d1ae9a\_ d.163.1.1 (A:) Integrase (Int) {Bacteriophage lambda}

RSRLTADEYLKIYQAAESSPCWLRLAMELAVVTGQRVGDLCEMKWSDIVDGYLYVEQSKTGVKIAIPTALHIDALGISMKETLDKCKEILGGETIIASTRREPLSSGTVSRYFMRARKASGLSFEGDPPTFHELRSLSARLYEKQISDKFAQHLLGHKSDTMASQFRDDRGREWDKIEI

>d1f44a2 d.163.1.1 (A:130-343) Cre recombinase {Bacteriophage P1}

RAKQALAFERTDFDQVRSLMENSDRCQDIRNLAFLGIAYNTLLRIAEIARIRVKDISRTDGGRMLIHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTRALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGGWTNVNIVMNFIRNLDSETGAMVRLLEDGD

>d1a0p\_2 d.163.1.1 (111-292) Recombinase XerD {Escherichia coli}

KDLSEAQVERLLQAPLIDQPLELRDKAMLEVLYATGLRVSELVGLTMSDISLRQGVVRVIGKGNKERLVPLGEEAVYWLETYLEHGRPWLLNGVSIDVLFPSQRAQQMTRQTFWHRIKHYAVLAGIDSEKLSPHVLRHAFATHLLNHGADLRVVQMLLGHSDLSTTQIYTHVATERLRQLHQ

>d1floa2 d.163.1.1 (A:135-423) Flp recombinase {Baker's yeast (Saccharomyces cerevisiae)}

KGNSHSKKMLKALLSEGESIWEITEKILNSFEYTSRFTKTKTLYQFLFLATFINCGRFSDIKNVDPKSFKLVQNKYLGVIIQCLVTETKTSVSRHIYFFSARGRIDPLVYLDEFLRNSEPVLKRVNRTGNSSSNKQEYQLLKDNLVRSYNKALKKNAPYSIFAIKNGPKSHIGRHLMTSFLSMKGLTELTNVVGNWSDKRASAVARTTYTHQITAIPDHYFALVSRYYAYDPISKEMIALKDETNPIEEWQHIEQLKGSAEGSIRYPAWNGIISQEVLDYLSSYINRRI

>d1a31a1 d.163.1.2 (A:431-626,A:720-765) Eukaryotic DNA topoisomerase I, catalytic core {Human (Homo sapiens)}

PSSRIKGEKDWQKYETARRLKKCVDKIRNQYREDWKSKEMKVRQRAVALYFIDKLALRAGNEKEEGETADTVGCCSLRVEHINLHPELDGQEYVVEFDFLGKDSIRYYNKVPVEKRVFKNLQLFMENKQPEDDLFDRLNTGILNKHLQDLMEGLTAKVFRTYNASITLQQQLKELTAPDENIPAKILSYNRANRAVXKLNYLDPRITVAWCKKWGVPIEKIYNKTQREKFAWAIDMADEDYEF

>d1a41\_\_ d.163.1.2 (-) Eukaryotic DNA topoisomerase I, catalytic core {Vaccinia virus}

NAKRDRIFVRVYNVMKRINCFINKNIKKSSTDSNYQLAVFMLMETMFFIRFGKMKYLKENETVGLLTLKNKHIEISPDEIVIKFVGKDKVSHEFVVHKSNRLYKPLLKLTDDSSPEEFLFNKLSERKVYECIKQFGIRIKDLRTYGVNYTFLYNFWTNVKSISPLPSPKKLIALTIKQTAEVVGHTPSISKRAYMATTILEMVKDKNFLDVVSKTTFDEFLSIVVDHVKS

>d1cf5a\_ d.165.1.1 (A:) Beta-momorcharin {Bitter gourd (Momordica charantia)}

DVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTLFYYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVATNFKPNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPTGQRFQVTNVDSDVVKGNIKLLLNSRASTADEN

>d1ce7a\_ d.165.1.1 (A:) Mistletoe lectin I A-chain {European mistletoe (Viscum album)}

YERGDLDVTAQTTGAGYFSFITLLRDYVSSGSFSNAIPLLSQSGGGGEAGRFVLVELTNSGGDGITVAIDVTNLYVVAYQAGSQSYFLSGPGGRHGFTGTTRSSLPFNGSYPDLEQYGGQRKQIPLGIDQLIQSVTALKFPGSTRTGARSILILIQMISEAARFNPILWRARQYINSGASFLPDVYMLELETSWGQQSTQVQHSTDGVFNNPIALADPGGGVTLTNVRDVIASLAIMLFVC

>d1d6aa\_ d.165.1.1 (A:) Pokeweed antiviral protein alpha {Pokeweed (Phytolacca americana)}

VNTIIYNVGSTTISKYATFLNDLRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPFETNKCRYHIFNDISGTERQDVETTLCPNANSRVSKNINFDSRYPTLESKAGVKSRSQVQLGIQILDSNIGKISGVMSFTEKTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFNPNPKVLNLQETWGKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEIKPDVALLNYVGGSCQTT

>d1qi7a\_ d.165.1.1 (A:) Saporin So6 {Common soapwort (Saponaria officinalis)}

VTSITLDLVNPTAGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGPPSKEKFLRINFQSSRGTVSLGLKRDNLYVVAYLAMDNTNVNRAYYFKSEITSAELTALFPEATTANQKALEYTEDYQSIEKNAQITQGDKSRKELGLGIDLLLTFMEAVNKKARVVKNEARFLLIAIQMTAEVARFRYIQNLVTKNFPNKFDSDNKVIQFEVSWRKISTAIYGDAKNGVFNKDYDFGFGKVRQVKDLQMGLLMYLGKPK

>d1ift\_\_ d.165.1.1 (-) Ricin A-chain {Castor bean (Ricinus communis)}

YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPP

>d1hwma\_ d.165.1.1 (A:) Ebulin A-chain {Sambucus ebulus}

IDYPSVSFNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNYNGDTVTSAVDVTNLYLVAFSANGNSYFFKDATELQKSNLFLGTTQHTLSFTGNYDNLETAAGTRRESIELGPNPLDGAITSLWYDGGVARSLLVLIQMVPEAARFRYIEQEVRRSLQQLTSFTPNALMLSMENNWSSMSLEVQLSGDNVSPFSGTVQLQNYDHTPRLVDNFEELYKITGIAILLFRCVA

>d1f0la2 d.166.1.1 (A:1-187) Diphtheria toxin, N-terminal domain {Corynebacterium diphtheriae}

GADDVVDSSKSFVMENFSSYHGTKPGYVDSIQKGIQKPKSGTQGNYDDDWKGFYSTDNKYDAAGYSVDNENPLSGKAGGVVKVTYPGLTKVLALKVDNAETIKKELGLSLTEPLMEQVGTEEFIKRFGDGASRVVLSLPFAEGSSSVEYINNWEQAKALSVELEINFETRGKRGQDAMYEYMAQACA

>d1ikpa2 d.166.1.1 (A:395-606) Exotoxin A, C-terminal domain {Pseudomonas aeruginosa}

PTGAEFLGDGGDVSFSTRGTQNWTVERLLQAHRQLEERGYVFVGYHGTFLEAAQSIVFGGVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYRTSLTLAAPEAAGEVERLIGHPLPLRLDAITGPEEEGGRLETILGWPLAERTVVIPSAIPTDPRNVGGDLDPSSIPDKEQAISALPDYASQPGK

>d1prta\_ d.166.1.1 (A:) Pertussis toxin, S1 subunit {Bordetella pertussis}

DPPATVYRYDSRPPEDVFQNGFTAWGNNDNVLEHLTGRSCQVGSSNSAFVSTSSSRRYTEVYLEHRMQEAVEAERAGRGTGHFIGYIYEVRADNNFYGAASSYFEYVDTYGDNAGRILAGALATYQSEYLAHRRIPPENIRRVTRVYHNGITGETTTTEYSNARYVSQQTRANPNPYTSRRSVASIVGTLVRMAPVVGACMARQAESSEAMAAWSERAGEAMVLVYYESIAYSF

>g1xtc.1 d.166.1.1 (A:,C:) Cholera toxin {Vibrio cholerae}

NDDKLYRADSRPPDEIKQSGGLMPRGQSEYFDRGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHSTYYLYVLATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHFGVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRXSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL

>d1qs1a1 d.166.1.1 (A:60-264) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

TDKVEDFKEDKEKAKEWGKEKEKEWKLTATEKGKMNNFLDNKNDIKTNYKEITFSMAGSFEDEIKDLKEIDKMFDKTNLSNSIITYKNVEPTTIGFNKSLTEGNTINSDAMAQFKEQFLDRDIKFDSYLDTHLTAQQVSSKERVILKVTVPSGKGSTTPTKAGVILNNSEYKMLIDNGYMVHVDKVSKVVKKGVECLQIEGTLKK

>d1qs1a2 d.166.1.1 (A:265-461) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

SLDFKNDINAEAHSWGMKNYEEWAKDLTDSQREALDGYARQDYKEINNYLRNQGGSGNEKLDAQIKNISDALGKKPIPENITVYRWCGMPEFGYQISDPLPSLKDFEEQFLNTIKEDKGYMSTSLSSERLAAFGSRKIILRLQVPKGSTGAYLSAIGGFASEKEILLDKDSKYHIDKVTEVIIKGVKRYVVDATLLT

>d1g24a\_ d.166.1.1 (A:) Exoenzyme c3 {Clostridium botulinum}

AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNLIKQVELLDKSFNKMKTPENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAKAKFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLPRHSTYHIDDMRLSSDGKQIIITATMMGTAINPK

>d1j7na3 d.166.1.1 (A:264-550) Anthrax toxin lethal factor, middle domain {Bacillus anthracis}

MLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKLQIPIEPKKDDIIHSLSQEEKELLKRIQIDSSDFLSTEEKEFLKKLQIDIRDSLSEEEKELLNRIQVDSSNPLSEKEKEFLKKLKLDIQPYDINQRLQDTGGLIDSPSINLDVRKQYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATLGADLVDSTDNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDNERLKWRIQLSPDTRAGYLENGKLILQRNIGLEIKDVQIIKQSEKEYIRIDAKVV

>d1chua3 d.168.1.1 (A:238-353) L-aspartate oxidase {Escherichia coli}

LEFNQFHPTALYHPQARNFLLTEALRGEGAYLKRPDGTRFMPDFDERGELAPRDIVARAIDHEMKRLGADCMFLDISHKPADFIRQHFPMIYEKLLGLGIDLTQEPVPIVPAAHYT

>d1fuma3 d.168.1.1 (A:226-357) Fumarate reductase flavoprotein subunit {Escherichia coli}

MEFVQYHPTGLPGSGILMTEGCRGEGGILVNKNGYRYLQDYGMGPETPLGEPKNKYMELGPRDKVSQAFWHEWRKGNTISTPRGDVVYLDLRHLGEKKLHERLPFICELAKAYVGVDPVKEPIPVRPTAHYT

>d1e39a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

QYIQAAPTLSVKGGVMVTEAVRGNGAILVNREGKRFVNEITTRDKASAAILAQTGKSAYLIFDDSVRKSLSKIDKYIGLGVAPTADSLVKLGKMEGIDGKALTETVARYNSLVSSGKDTDFERPNLPRALNEGNYYAIEVTPGVHH

>d1jnra3 d.168.1.1 (A:257-401) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

FEHRFIPFRFKDGYGPVGAWFLFFKCKAKNAYGEEYIKTRAAELEKYKPYGAAQPIPTPLRNHQVMLEIMDGNQPIYMHTEEALAELAGGDKKKLKHIYEEAFEDFLDMTVSQALLWACQNIDPQEQPSEAAPAEPYIMGSHSGE

>d1qdda\_ d.169.1.1 (A:) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}

QEAQTELPQARISCPEGTNAYRSYCYYFNEDRETWVDADLYCQNMNSGNLVSVLTQAEGAFVASLIKESGTDDFNVWIGLHDPKKNRAWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWKDVPCEDKFSFVCKFKN

>d1b6e\_\_ d.169.1.1 (-) CD94 {Human (Homo sapiens)}

CSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSSSQQFYWIGLSYSEEHTAWLWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQLI

>d1e87a\_ d.169.1.1 (A:) CD69 {Human (Homo sapiens)}

SSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVGLKKEPGHPWKWSNGKEFNNWFNVTGSDKCVFLKNTEVSSMECEKNLYWICNKPYK

>d1hyra\_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Human (Homo sapiens)}

ESYCGPCPKNWICYKNNCYQFFDESKNWYESQASCMSQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIPTNGSWQWEDGSILSPNLLTIIEMQKGDCALYASSFKGYIENCSTPNTYICMQRTV

>d1egia\_ d.169.1.1 (A:) Macrophage mannose receptor, CRD4 {Human (Homo sapiens)}

CPEDWGASSRTSLCFKLYAKGKHEKKTWFESRDFCRALGGDLASINNKEEQQTIWRLITASGSYHKLFWLGLTYGSPSEGFTWSDGSPVSYENWAYGEPNNYQNVEYCGELKGDPTMSWNDINCEHLNNWICQIQ

>d1c3aa\_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis), flavocetin-A}

DFDCIPGWSAYDRYCYQAFSKPKNWEDAESFCEEGVKTSHLVSIESSGEGDFVAQLVAEKIKTSFQYVWIGLRIQNKEQQCRSEWSDASSVNYENLVKQFSKKCYALKKGTELRTWFNVYCGTENPEVCKYTPEC

>d1c3ab\_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis), flavocetin-A}

GFCCPLGWSSYDEHCYQVFQQKMNWEDAEKFCTQQHKGSHLVSFHSSEEVDFVTSKTFPILKYDFVWIGLSNVWNECTKEWSDGTKLDYKAWSGGSDCIVSKTTDNQWLSMDCSSKYYVVCKFQA

>d2afpa\_ d.169.1.1 (A:) Type II antifreeze protein {Sea raven (Hemitripterus americanus)}

QRAGPNCPAGWQPLGDRCIYYETTAMTWALAETNCMKLGGHLASIHSQEEHSFIQTLNAGVVWIGGSACLQAGAWTWSDGTPMNFRSWCSTKPDDVLAACCMQMTAAADQCWDDLPCPASHKSVCAMTF

>d1h8ua\_ d.169.1.1 (A:) Eosinophil major basic protein {Human (Homo sapiens)}

RYLLVRSLQTFSQAWFTCRRCYRGNLVSIHNFNINYRIQCSVSALNQGQVWIGGRITGSGRCRRFQWVDGSRWNFAYWAAHQPWSRGGHCVALCTRGGYWRRAHCLRRLPFICSY

>d1qo3c\_ d.169.1.1 (C:) NK cell receptor ly49a {Mouse (Mus musculus)}

STVLDSLQHTGRGDKVYWFCYGMKCYYFVMDRKTWSGCKQTCQSSSLSLLKIDDEDELKFLQLVVPSDSCWVGLSYDNKKKDWAWIDNRPSKLALNTRKYNIRDGGCMLLSKTRLDNGNCDQVFICICGKRLD

>d1dv8a\_ d.169.1.1 (A:) H1 subunit of the asialoglycoprotein receptor {Human (Homo sapiens)}

CPVNWVEHERSCYWFSRSGKAWADADNYCRLEDAHLVVVTSWEEQKFVQHHIGPVNTWMGLHDQNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGEDCAHFTDDGRWNDDVCQRPYRWVCETEL

>d1k9ja\_ d.169.1.1 (A:) DC-SIGNR (DC-SIGN related receptor) {Human (Homo sapiens)}

CRHCPKDWTFFQGNCYFMSNSQRNWHDSVTACQEVRAQLVVIKTAEEQNFLQLQTSRSNRFSWMGLSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPNNSGNEDCAEFSGSGWNDNRCDVDNYWICKKPAA

>d1g1sa1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}

WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPYYSSYYWIGIRKNNKTWTWVGTKKALTNEAENWADNEPNNKRNNEDCVEIYIKSPSAPGKWNDEHCLKKKHALCY

>d1fifa1 d.169.1.1 (A:105-226) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}

KKSGKKFFVTNHERMPFSKVKALCSELRGTVAIPRNAEENKAIQEVAKTSAFLGITDEVTEGQFMYVTGGRLTYSNWKKDQPDDWYGHGLGGGEDCVHIVDNGLWNDDSCQRPYTAVCEFPA

>d1byfa\_ d.169.1.1 (A:) Lectin TC14 {Tunicate (Polyandrocarpa misakiensis)}

DYEILFSDETMNYADAGTYCQSRGMALVSSAMRDSTMVKAILAFTEVKGHDYWVGADNLQDGAYNFLWNDGVSLPTDSDLWSPNEPSNPQSWQLCVQIWSKYNLLDDVGCGGARRVICEKELD

>d1tn3\_\_ d.169.1.1 (-) Tetranectin {Human (Homo sapiens)}

ALQTVCLKGTKVHMKCFLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWLGLNDMAAEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPYICQFGIV

>d1prtb2 d.169.1.2 (B:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}

GIVIPPQEQITQHGSPYGRCANKTRALTVAELRGSGDLQEYLRHVTRGWSIFALYDGTYLGGEYGGVIKDGTPGGAFDLKTTFCIM

>d1prea1 d.169.1.2 (A:2-84) Proaerolysin, N-terminal domain {Aeromonas hydrophila}

EPVYPDQLRLFSLGQGVCGDKYRPVNREEAQSVKSNIVGMMGQWQISGLANGWVIMGPGYNGEIKPGTASNTWCYPTNPVTGE

>d1f00i3 d.169.1.3 (I:842-939) Intimin {Escherichia coli}

LIVPNMSKRVTYNDAVNTCKNFGGKLPSSQNELENVFKAWGAANKYEYYKSSQTIISWVQQTAQDAKSGVASTYDLVKQNPLNNIKASESNAYATCVK

>d1cwva5 d.169.1.3 (A:887-986) Invasin {Yersinia pseudotuberculosis}

NRWIYDGGRSLVSSLEASRQCQGSDMSAVLESSRATNGTRAPDGTLWGEWGSLTAYSSDWQSGEYWVKKTSTDFETMNMDTGALQPGPAYLAFPLCALSI

>d1jfeb1 d.171.1.1 (B:200-464) Fibrinogen C-terminal domains {Chicken (Gallus gallus), beta}

SPCVASCNIPVVSGRECEDIYRKGGETSEMYIIQPDPFTTPYRVYCDMETDNGGWTLIQNRQDGSVNFGRAWDEYKRGFGNIAKSGGKKYCDTPGEYWLGNDKISQLTKIGPTKVLIEMEDWNGDKVSALYGGFTIHNEGNKYQLSVSNYKGNAGNALMEGASQLYGENRTMTIHNGMYFSTYDRDNDGWLTTDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGGTYSWDMAKHGTDDGIVWMNWKGSWYSMKKMSMKIKPYFPD

>d1jc9a\_ d.171.1.1 (A:) Tachylectin 5a {Japanese horseshoe crab (Tachypleus tridentatus)}

DPTDCADILLNGYRSSGGYRIWPKSWMTVGTLNVYCDMETDGGGWTVIQRRGNYGNPSDYFYKPWKNYKLGFGNIEKDFWLGNDRIFALTNQRNYMIRFDLKDKENDTRYAIYQDFWIENEDYLYCLHIGNYSGDAGNSFGRHNGHNFSTIDKDHDTHETHCAQTYKGGWWYDRCHESNLNGLYLNGEHNSYADGIEWRAWKGYHYSLPQVEMKIRPVEF

>d1hyoa2 d.177.1.1 (A:119-416) Fumarylacetoacetate hydrolase, FAH, C-terminal domain {Mouse (Mus musculus)}

ATIGDYTDFYSSRQHATNVGIMFRGKENALLPNWLHLPVGYHGRASSIVVSGTPIRRPMGQMRPDNSKPPVYGACRLLDMELEMAFFVGPGNRFGEPIPISKAHEHIFGMVLMNDWSARDIQQWEYVPLGPFLGKSFGTTISPWVVPMDALMPFVVPNPKQDPKPLPYLCHSQPYTFDINLSVSLKGEGMSQAATICRSNFKHMYWTMLQQLTHHSVNGCNLRPGDLLASGTISGSDPESFGSMLELSWKGTKAIDVGQGQTRTFLLDGDEVIITGHCQGDGYRVGFGQCAGKVLPAL

>d1i7oa1 d.177.1.1 (A:1-213) 4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpcE {Escherichia coli}

MKGTIFAVALNHRSQLDAWQEAFQQSPYKAPPKTAVWFIKPRNTVIGCGEPIPFPQGEKVLSGATVALIVGKTATKVREEDAAEYIAGYALANDVSLPEESFYRPAIKAKCRDGFCPIGETVALSNVDNLTIYTEINGRPADHWNTADLQRNAAQLLSALSEFATLNPGDAILLGTPQARVEIQPGDRVRVLAEGFPPLENPVVDEREVTTRK

>d1i7oa2 d.177.1.1 (A:214-429) 4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpcE {Escherichia coli}

SFPTLPHPHGTLFALGLNYADHASELEFKPPEEPLVFLKAPNTLTGDNQTSVRPNNIEYMHYEAELVVVIGKQARNVSEADAMDYVAGYTVCNDYAIRDYLENYYRPNLRVKSRDGLTPMLSTIVPKEAIPDPHNLTLRTFVNGELRQQGTTADLIFSVPFLIAYLSEFMTLNPGDMIATGTPKGLSDVVPGDEVVVEVEGVGRLVNRIVSEETAK

>d1hw8a2 d.179.1.1 (A:441-586,A:704-861) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

EPRPNEECLQILGNAEKGAKFLSDAEIIQLVNAKHIPAYKLETLIETHERGVSIRRQLLSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAGH

>d1qaxa2 d.179.1.1 (A:4-110,A:221-428) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLLANAGALPMDIANGMIENVIGTFELPYAVASNFQINGRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPXRLARAQVRITPQQLETAEFSGEAVIEGILDAYAFAAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLTTWEKDNNGHLVGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALAEIAVAVGLAQNLGAMRALATEGIQRGHMALHARNIAVVAGARGDEVDWVARQLVEYHDVRADRAVALLKQKRGQ

>d1bdfa2 d.181.1.1 (A:53-178) RNA polymerase alpha subunit {Escherichia coli}

GCAVTEVEIDGVLHEYSTKEGVQEDILEILLNLKGLAVRVQGKDEVILTLNKSGIGPVTAADITHDGDVEIVKPQHVICHLTDENASISMRIKVQRGRGYVPASTRIHSEEDERPIGRLLVDACYS

>d1i50c2 d.181.1.1 (C:42-172) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

PTLAIDSVEVETNTTVLADEFIAHRLGLIPLQSMDIEQLEYSRDCFCEDHCDKCSVVLTLQAFGESESTTNVYSKDLVIVSNLMGRNIGHPIIQDKEGNGVLICKLRKGQELKLTCVAKKGIAKEHAKWGP

>d1ovaa\_ e.1.1.1 (A:) Ovalbumin {Hen (Gallus gallus)}

GSIGAASMEFCFDVFKELKVHHANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRFDKLPGFGDSIEAQCGTSVNVHSSLRDILNQITKPNDVYSFSLASRLYAEERYPILPEYLQCVKELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQPSSVDSQTAMVLVNAIVFKGLWEKAFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPFASGTMSMLVLLPDEVSGLEQLESIINFEKLTEWTSSNVMEERKIKVYLPRMKMEEKYNLTSVLMAMGITDVFSSSANLSGISSAESLKISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFRADHPFLFCIKHIATNAVLFFGRCVSP

>d1qlpa\_ e.1.1.1 (A:) Antitrypsin, alpha-1 {Human (Homo sapiens)}

FNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK

>d1e05i\_ e.1.1.1 (I:) Antithrombin {Human (Homo sapiens)}

SPVDICTAKPRDIPMNPMCIYRSPEKKATEDEGSEQKIPEATNRRVWELSKANSRFATTFYQHLADSKNDNDNIFLSPLSISTAFAMTKLGACNDTLQQLMEVFKFDTISEKTSDQIHFFFAKLNCRLYRKANKSSKLVSANRLFGDKSLTFNETYQDISELVYGAKLQPLDFKENAEQSRAAINKWVSNKTEGRITDVIPSEAINELTVLVLVNTIYFKGLWKSKFSPENTRKELFYKADGESCSASMMYQEGKFRYRRVAEGTQVLELPFKGDDITMVLILPKPEKSLAKVEKELTPEVLQEWLDELEEMMLVVHMPRFRIEDGFSLKEQLQDMGLVDLFSPEKSKLPGIVAEGRDDLYVSDAFHKAFLEVNEEGSEAAASTAVVIAGRSLNPNRVTFKANRPFLVFIREVPLNTIIFMGRVANPCV

>d1a7ca\_ e.1.1.1 (A:) Plasminogen activator inhibitor-1 {Human (Homo sapiens)}

HHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVESSSTAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP

>d1by7a\_ e.1.1.1 (A:) Plasminogen activator inhibitor-2 {Human (Homo sapiens)}

EDLCVANTLFALNLFKHLAKASPTQNLFLSPWSISSTMAMVYMGSRGSTEDQMAKVLQFNEVGAAADKIHSSFRSLSSAINASTGNYLLESVNKLFGEKSASFREEYIRLCQKYYSSEPQAVDFLECAEEARKKINSWVKTQTKGKIPNLLPEGSVDGDTRMVLVNAVYFKGKWKTPFEKKLNGLYPFRVNSAQRTPVQMMYLREKLNIGYIEDLKAQILELPYAGDVSMFLLLPDEIADVSTGLELLESEITYDKLNKWTSKDKMAEDEVEVYIPQFKLEEHYELRSILRSMGMEDAFNKGRANFSGMSERNDLFLSEVFHQAMVDVNEEGTEAAAGTGGVMTGRTGHGGPQFVADHPFLFLIMHKITNCILFFGRFSSP

>g1jjo.1 e.1.1.1 (A:,C:,E:) Neuroserpin {Mouse (Mus musculus)}

TITEWSVNMYNHLRGTGEDENILFSPLSIALAMGMMELGAXENQYVMKLANSLFVQNGFHVNEEFLQMLKMYFNAEVNHVDFSQNVAVANSINKWVENYTNSLLKDLVSPEDFDGVTNLALINAVYFKGNWKSQFRPENTRTFSFTKDDESEVQIPMMYQQGEFYYGEFSDGSNEAGGIYQVLEIPYEGDEISMMLALSRQEVPLATLEPLLKAQLIEEWANSVKKQKVEVYLPRFTVEQEIDLKDILKALGVTEIFIKDANLTAMSDKKELFLSKAVHKSCIEVNEEGSEAAAASGMIAISXYPQVIVDHPFLYLIRNRKSGIILFMGRVMNPHH

>d1sek\_\_ e.1.1.1 (-) Serpin K {Tobacco hawkmoth (Manduca sexta)}

GETDLQKILRESNDQFTAQMFSEVVKANPGQNVVLSAFSVLPPLGQLALASVGESHDELLRALALPNDNVTKDVFADLNRGVRAVKGVDLKMASKIYVAKGLELNDDFAAVSRDVFGSEVQNVDFVKSVEAAGAINKWVEDQTNNRIKNLVDPDALDETTRSVLVNAIYFKGSWKDKFNKERTMDRDFHVSKDKTIKVPTMIGKKDVRYADVPELDAKMIEMSYEGDQASMIIILPNQVDGITALEQKLKDPKALSRAEERLYNTEVEIYLPKFKIETTTDLKEVLSNMNIKKLFTPGAARLENLLKTKESLYVDAAIQKAFIEVNEEGAEAAAANAFKITTYSFHFVPKVEINKPFFFSLKYNRNSMFSGVCVQP

>g1f0c.1 e.1.1.1 (A:,B:) Viral serpin crmA (cytokine response modifier protein) {Cowpox virus}

MDIFREIASSMKGENVFISPPSISSVLTILYYGANGSTAEQLSKYVEKEADKNKDDISFKSMNKVYGRYSAVFKDSFLRKIGDNFQTVDFTDCRTVDAINKCVDIFTEGKINPLLDEPLSPDTCLLAISAVYFKAKWLMPFEKEFTSDYPFYVSPTEMVDVSMMSMYGEAFNHASVKESFGNFSIIELPYVGDTSMVVILPDNIDGLESIEQNLTDTNFKKWCDSMDAMFIDVHIPKFKVTGSYNLVDALVKLGLTEVFGSTGDYSNMCNSDVSVDAMIHKTYIDVNEEYTEAAAATCALVADCAXSTVTNEFCADHPFIYVIRHVDGKILFVGRYCSPTTN

>d1imva\_ e.1.1.1 (A:) Rigment epithelium-derived factor, PEDF {Human (Homo sapiens)}

TGALVEEEDPFFKVPVNKLAAAVSNFGYDLYRVRSSMSPTTNVLLSPLSVATALSALSLGADERTESIIHRALYYDLISSPDIHGTYKELLDTVTAPQKNLKSASRIVFEKKLRIKSSFVAPLEKSYGTRPRVLTGNPRLDLQEINNWVQAQMKGKLARSTKEIPDEISILLLGVAHFKGQWVTKFDSRKTSLEDFYLDEERTVRVPMMSDPKAVLRYGLDSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSEFIHDIDRELKTVQAVLTVPKLKLSYEGEVTKSLQEMKLQSLFDSPDFSKITGKPIKLTQVEHRAGFEWNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFIGKILDPRGP

>d1es5a\_ e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., K15}

KPTIAAVGGYAMNNGTGTTLYTKAADTRRSTGSTTKIMTAKVVLAQSNLNLDAKVTIQKAYSDYVVANNASQAHLIVGDKVTVRQLLYGLMLPSGCDAAYALADKYGSGSTRAARVKSFIGKMNTAATNLGLHNTHFDSFDGIGNGANYSTPRDLTKIASSAMKNSTFRTVVKTKAYTAKTVTKTGSIRTMDTWKNTNGLLSSYSGAIGVKTGAGPEAKYCLVFAATRGGKTVIGTVLASTSIPARESDATKIMNYGFAL

>d1hvba\_ e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., R61}

DLPAPDDTGLQAVLHTALSQGAPGAMVRVDDNGTIHQLSEGVADRATGRAITTTDRFRVGSVTKSFSAVVLLQLVDEGKLDLDASVNTYLPGLLPDDRITVRQVMSHRSGLYDYTNDMFAQTVPGFESVRNKVFSYQDLITLSLKHGVTNAPGAAYSYSNTNFVVAGMLIEKLTGHSVATEYQNRIFTPLNLTDTFYVHPDTVIPGTHANGYLTPDEAGGALVDSTEQTVSWAQSAGAVISSTQDLDTFFSALMSGQLMSAAQLAQMQQWTTVNSTQGYGLGLRRRDLSCGISVYGHTGTVQGYYTYAFASKDGKRSVTALANTSNNVNVLNTMARTLESAFCGKP

>d1ci9a\_ e.3.1.1 (A:) Esterase EstB {Burkholderia gladioli}

AASLAARLDAVFDQALRERRLVGAVAIVARHGEILYRRAQGLADREAGRPMREDTLFRLASVTKPIVALAVLRLVARGELALDAPVTRWLPEFRPRLADGSEPLVTIHHLLTHTSGLGYWLLEGAGSVYDRLGISDGIDLRDFDLDENLRRLASAPLSFAPGSGWQYSLALDVLGAVVERATGQPLAAAVDALVAQPLGMRDCGFVSAEPERFAVPYHDGQPEPVRMRDGIEVPLPEGHGAAVRFAPSRVFEPGAYPSGGAGMYGSADDVLRALEAIRANPGFLPETLADAARRDQAGVGAETRGPGWGFGYLSAVLDDPAAAGTPQHAGTLQWGGVYGHSWFVDRALGLSVLLLTNTAYEGMSGPLTIALRDAVYA

>d1g6aa\_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PSE-4 carbenicillinase}

SKFQQVEQDVKAIEVSLSARIGVSVLDTQNGEYWDYNGNQRFPLTSTFKTIACAKLLYDAEQGKVNPNSTVEIKKADLVTYSPVIEKQVGQAITLDDACFATMTTSDNTAANIILSAVGGPKGVTDFLRQIGDKETRLDRIEPDLNEGKLGDLRDTTTPKAIASTLNKFLFGSALSEMNQKKLESWMVNNQVTGNLLRSVLPAGWNIADKSGAGGFGARSITAVVWSEHQAPIIVSIYLAQTQASMEERNDAIVKIGHSIFDVYTS

>d1alq\_\_ e.3.1.1 (-) beta-Lactamase, class A {Staphylococcus aureus}

SEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEFAAGSKNAAKELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVAYSPILEKYVGKDITLKALIEASMTYSDNTANNKIIKEIGGIKKVKQRLKELGDKVTNPVRYEIELNYYSPKSKKDTSTPAAFGKTLNKLIANGKLSKENKKFLLDLMLNNKSGDTLIKDGVPKDYKVADKSGQAITYASRNDVAFVYPK

>d1mfoa\_ e.3.1.1 (A:) beta-Lactamase, class A {Mycobacterium fortuitum}

APIDDQLAELERRDNVLIGLYAANLQSGRRITHRPDEMFAMCSTFKGYVAARVLQMAEHGEISLDNRVFVDADALVPNSPVTEARAGAEMTLAELCQAALQRSDNTAANLLLKTIGGPAAVTAFARSVGDERTRLDRWEVELNSAIPGDPRDTSTPAALAVGYRAILAGDALSPPQRGLLEDWMRANQTSSMRAGLPEGWTTADKTGSGDYGSTNDAGIAFGPDGQRLLLVMMTRSQAHDPKAENLRPLIGELTALVLPSLL

>d1e25a\_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PER-1}

SPLLKEQIESIVIGKKATVGVAVWGPDDLEPLLINPFEKFPMQSVFKLHLAMLVLHQVDQGKLDLNQTVIVNRAKVLQNTWAPIMKAYQGDEFSVPVQQLLQYSVSHSDNVACDLLFELVGGPAALHDYIQSMGIKETAVVANEAQMHADDQVQYQNWTSMKGAAEILKKFEQKTQLSETSQALLWKWMVETTTGPERLKGLLPAGTVVAHKTGTSQIKAGKTAATNDLGIILLPDGRPLLVAVFVKDSAESSRTNEAIIAQVAQTAYQFELKKLSAL

>d1dy6a\_ e.3.1.1 (A:) beta-Lactamase, class A {Serratia marcescens, Sme-1}

NKSDAAAKQIKKLEEDFDGRIGVFAIDTGSGNTFGYRSDERFPLCSSFKGFLAAAVLERVQQKKLDINQKVKYESRDLEYHSPITTKYKGSGMTLGDMASAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGDNEFRLDRWELELNTAIPGDKRDTSTPKAVANSLNKLALGNVLNAKVKAIYQNWLKGNTTGDARIRASVPADWVVGDKTGSCGAYGTANDYAVIWPKNRAPLIVSIYTTRKSKDDKHSDKTIAEASRIAIQAID

>d1ga0a\_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Enterobacter cloacae, P99, cephalosporinase}

PVSEKQLAEVVANTVTPLMKAQSVPGMAVAVIYQGKPHYYTFGKADIAANKPVTPQTLFELGSISKTFTGVLGGDAIARGEISLDDPVTRYWPQLTGKQWQGIRMLDLATYTAGGLPLQVPDEVTDNASLLRFYQNWQPQWKPGTTRLYANASIGLFGALAVKPSGMPYEQAMTTRVLKPLKLDHTWINVPKAEEAHYAWGYRDGKAVRAVRVSPGMLDAQAYGVKTNVQDMANWVMANMAPENVADASLKQGIALAQSRYWRIGSMYQGLGWEMLNWPVEANTVVEGSDSKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIVMLANTSYPNPARVEAAYHILEALQ

>d1k55a\_ e.3.1.1 (A:) Class D beta-lactamase {Pseudomonas aeruginosa, OXA-10}

SITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLESLYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGIIG

>d1k25a4 e.3.1.1 (A:264-631) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {Streptococcus pneumoniae}

TLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSELKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASTTRNHMILVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVT

>d1hd8a2 e.3.1.1 (A:3-262) Penicillin-binding protein 5, N-terminal domain {Escherichia coli}

LNIKTMIPGVPQIDAESYILIDYNSGKVLAEQNADVRRDPASLTKMMTSYVIGQAMKAGKFKETDLVTIGNDAWATGNPVFKGSSLMFLKPGMQVPVSQLIRDINLQSGNDACVAMADFAAGSQDAFVGLMNSYVNALGLKNTHFQTVHGLDADGQYSSARDMALIGQALIRDVPNEYSIYKEKEFTFNGIRQLNRNGLLWDNSLNVDGIKTGHTDKAGYNLVASATEGQMRLISAVMGGRTFKGREAESKKLLTWGFRF

>d1ei5a3 e.3.1.1 (A:3-335) D-aminopeptidase, N-terminal domain {Ochrobactrum anthropi}

KFDTSALEAFVRHIPQNYKGPGGVVAVVKDGEVVLQHAWGFADLRTRTPMTLDTRMPICSVSKQFTCAVLLDAVGEPELLDDALEAYLDKFEDERPAVRDLCNNQSGLRDYWALSVLCGADPEGVFLPAQAQSLLRRLKTTHFEPGSHYSYCNGNFRILADLIEAHTGRTLVDILSERIFAPAGMKRAELISDTALFDECTGYEGDTVRGFLPATNRIQWMGDAGICASLNDMIAWEQFIDATRDDESGLYRRLSGPQTFKDGVAAPYGFGLNLHETGGKRLTGHGGALRGWRCQRWHCADERLSTIAMFNFEGGASEVAFKLMNIALGVSSS

>d1hbza\_ e.5.1.1 (A:) Catalase I {Micrococcus lysodeikticus}

TTPHATGSTRQNGAPAVSDRQSLTVGSEGPIVLHDTHLLETHQHFNRMNIPERRPHAKGSGAFGEFEVTEDVSKYTKALVFQPGTKTETLLRFSTVAGELGSPDTWRDVRGFALRFYTEEGNYDLVGNNTPIFFLRDPMKFTHFIRSQKRLPDSGLRDATMQWDFWTNNPESAHQVTYLMGPRGLPRTWREMNGYGSHTYLWVNAQGEKHWVKYHFISQQGVHNLSNDEATKIAGENADFHRQDLFESIAKGDHPKWDLYIQAIPYEEGKTYRFNPFDLTKTISQKDYPRIKVGTLTLNRNPKNHFAQIESAAFSPSNTVPGIGLSPDRMLLGRAFAYHDAQLYRVGAHVNQLPVNRPKNAVHNYAFEGQMWYDHTGDRSTYVPNSNGDSWSDETGPVDDGWEADGTLTREAQALRADDDDFGQAGTLVREVFSDQERDDFVETVAGALKGVRQDVQARAFEYWKNVDATIGQRIEDEVKRHEGDGIPGVEAGGEARI

>d1cf9a2 e.5.1.1 (A:27-597) Catalase II {Escherichia coli, HPII}

DSLAPEDGSHRPAAEPTPPGAQPTAPGSLKAPDTRNEKLNSLEDVRKGSENYALTTNQGVRIADDQNSLRAGSRGPTLLEDFILREKITHFDHERIPERIVHARGSAAHGYFQPYKSLSDITKADFLSDPNKITPVFVRFSTCQGGAGSADTVRDIRGFATKFYTEEGIFDLVGNNTPIFFIQDAHKFPDFVHAVKPEPHWAIPQGQSAHDTFWDYVSLQPETLHNVMWAMSDRGIPRSYRTMEGFGIHTFRLINAEGKATFVRFHWKPLAGKASLVWDEAQKLTGRDPDFHRRELWEAIEAGDFPEYELGFQLIPEEDEFKFDFDLLDPTKLIPEELVPVQRVGKMVLNRNPDNFFAENEQAAFHPGHIVPGLDFTNDPLLQGRLFSYTDTQISRLGGPNFHEIPINRPTCPYHNFQRDGMHRMGIDTNPANYEPNSINDNWPRETPPGPKRGGFESYQERVEGNKVRERSPSFGEYYSHPRLFWLSQTPFEQRHIVDGFSFELSKVVRPYIRERVVDQLAHIDLTLAQAVAKNLGIELTDDQLNITPPPDVNGLKKDPSLSLYAIPDGD

>d1buca2 e.6.1.1 (A:1-232) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}

MDFNLTDIQQDFLKLAHDFGEKKLAPTVTERDHKGIYDKELIDELLSLGITGAYFEEKYGGSGDDGGDVLSYILAVEELAKYDAGVAITLSATVSLCANPIWQFGTEAQKEKFLVPLVEGTKLGAFGLTEPNAGTDASGQQTIATKNDDGTYTLNGSKIFITNGGAADIYIVFAMTDKSKGNHGITAFILEDGTPGFTYGKKEDKMGIHTSQTMELVFQDVKVPAENMLGEE

>d1jqia2 e.6.1.1 (A:4-234) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}

VYQSVELPETHQMLRQTCRDFAEKELVPIAAQLDKEHLFPTSQVKKMGELGLLAMDVPEELSGAGLDYLAYSIALEEISRGCASTGVIMSVNNSLYLGPILKFGSSQQKQQWITPFTNGDKIGCFALSEPGNGSDAGAASTTAREEGDSWVLNGTKAWITNSWEASATVVFASTDRSRQNKGISAFLVPMPTPGLTLGKKEDKLGIRASSTANLIFEDCRIPKENLLGEPG

>d1egda2 e.6.1.1 (A:10-241) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}

LGFSFEFTEQQKEFQATARKFAREEIIPVAAEYDKTGEYPVPLIRRAWELGLMNTHIPENCGGLGLGTFDACLISEELAYGCTGVQTAIEGNSLGQMPIIIAGNDQQKKKYLGRMTEEPLMCAYCVTEPGAGSDVAGIKTKAEKKGDEYIINGQKMWITNGGKANWYFLLARSDPDPKAPANKAFTGFIVEADTPGIQIGRKELNMGQRCSDTRGIVFEDVKVPKENVLIGD

>d1ivha2 e.6.1.1 (A:6-241) Isovaleryl-coa dehydrogenase {Human (Homo sapiens)}

VDDAINGLSEEQRQLRQTMAKFLQEHLAPKAQEIDRSNEFKNLREFWKQLGNLGVLGITAPVQYGGSGLGYLEHVLVMEEISRASGAVGLSYGAHSNLCINQLVRNGNEAQKEKYLPKLISGEYIGALAMSEPNAGSDVVSMKLKAEKKGNHYILNGNKFWITNGPDADVLIVYAKTDLAAVPASRGITAFIVEKGMPGFSTSKKLDKLGMRGSNTCELIFEDCKIPAANILGHEN

>d1spia\_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Spinach (Spinacia oleracea)}

AATQTKARTRSKYEIETLTGWLLKQPMAGVIDAELTIVLSSISLACKQIASLVQRAGISNLTGIQGAVNIQGEDQKKLDVVSNEVFSSCLRSSGRTGIIASEEEDVPVAVEESYSGNYIVVFDPLDGSSNIDAAVSTGSIFGIYSPNDECIVDSDHDDESQLSAEEQRCVVNVCQPGDNLLAAGYCMYSSSVIFVLTIGKGVYAFTLDPMYGEFVLTSEKIQIPKAGKIYSFNEGNYKMWPDKLKKYMDDLKEPGESQKPYSSRYIGSLVGDFHRTLLYGGIYGYPRDAKSKNGKLRLLYECAPMSFIVEQAGGKGSDGHQRILDIQPTEIHQRVPLYIGSVEEVEKLEKYLA

>d2hhma\_ e.7.1.1 (A:) Inositol monophosphatase {Human (Homo sapiens)}

WQECMDYAVTLARQAGEVVCEAIKNEMNVMLKSSPVDLVTATDQKVEKMLISSIKEKYPSHSFIGEESVAAGEKSILTDNPTWIIDPIDGTTNFVHRFPFVAVSIGFAVNKKIEFGVVYSCVEGKMYTARKGKGAFCNGQKLQVSQQEDITKSLLVTELGSSRTPETVRMVLSNMEKLFCIPVHGIRSVGTAAVNMCLVATGGADAYYEMGIHCWDVAGAGIIVTEAGGVLMDVTGGPFDLMSRRVIAANNRILAERIAKEIQVIPLQRDDE

>d1g0ha\_ e.7.1.1 (A:) Archaeal inositol monophosphatase/fructose-1,6-bisphosphatase {Archaeon Methanococcus jannaschii, MJ0109}

MKWDEIGKNIAKEIEKEILPYFGRKDKSYVVGTSPSGDETEIFDKISEDIALKYLKSLNVNIVSEELGVIDNSSEWTVVIDPIDGSFNFINGIPFFAFCFGVFKNNEPYYGLTYEFLTKSFYEAYKGKGAYLNGRKIKVKDFNPNNIVISYYPSKKIDLEKLRNKVKRVRIFGAFGLEMCYVAKGTLDAVFDVRPKVRAVDIASSYIICKEAGALITDENGDELKFDLNATDRLNIIVANSKEMLDIILDLL

>d1inp\_\_ e.7.1.1 (-) Inositol polyphosphate 1-phosphatase {Cow (Bos taurus), brain}

MSDILQELLRVSEKAANIARACRQQETLFQLLIEEKKEGEKNKKFAVDFKTLADVLVQEVIKENMENKFPGLGKKIFGEESNELTNDLGEKIIMRLGPTEEETVALLSKVLNGNKLASEALAKVVHQDVFFSDPALDSVEINIPQDILGIWVDPIDSTYQYIKGSADITPNQGIFPSGLQCVTVLIGVYDIQTGVPLMGVINQPFVSQDLHTRRWKGQCYWGLSYLGTNIHSLLPPVSTRSNSEAQSQGTQNPSSEGSCRFSVVISTSEKETIKGALSHVCGERIFRAAGAGYKSLCVILGLADIYIFSEDTTFKWDSCAAHAILRAMGGGMVDLKECLERNPDTGLDLPQLVYHVGNEGAAGVDQWANKGGLIAYRSEKQLETFLSRLLQHLAPVATHT

>d1ka1a\_ e.7.1.1 (A:) 3';5'-adenosine bisphosphatase, PAP phosphatase {Baker's yeast (Saccharomyces cerevisiae)}

ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIKSNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDVRQIIDFGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLSSYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGHSSHDEQTAIKNKLNISKSLHLDSQAKYCLLALGLADVYLRLPIKLSYQEKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSR

>d1jp4a\_ e.7.1.1 (A:) PIPase {Rat (Rattus norvegicus)}

HNVLMRLVASAYSIAQKAGTIVRCVIAEGDLGIVQKTSATDLQTKADRMVQMSICSSLSRKFPKLTIIGEEDLPPGEVDQELIEDGQSEEILKQPCPSQYSAIKEEDLVVWVDPVDGTKEYTEGLLDNVTVLIGIAYEGKAIAGIINQPYYNYQAGPDAVLGRTIWGVLGLGAFGFQLKEAPAGKHIITTTRSHSNKLVTDCIAAMNPDNVLRVGGAGNKIIQLIEGKASAYVFASPGCKKWDTCAPEVILHAVGGKLTDIHGNPLQYDKEVKHMNSAGVLAALRNYEYYASRVPESVKSALIP

>d1kfsa2 e.8.1.1 (A:519-928) DNA polymerase I (Klenow fragment) {Escherichia coli}

HKGPLNVFENIEMPLVPVLSRIERNGVKIDPKVLHNHSEELTLRLAELEKKAHEIAGEEFNLSSTKQLQTILFEKQGIKPLKKTPGGAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKLPLMINPKTGRVHTSYHQAVTATGRLSSTDPNLQNIPVRNEEGRRIRQAFIAPEDYVIVSADYSQIELRIMAHLSRDKGLLTAFAEGKDIHRATAAEVFGLPLETVTSEQRRSAKAINFGLIYGMSAFGLARQLNIPRKEAQKYMDLYFERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLPDIKSSNGARRAAAERAAINAPMQGTAADIIKRAMIAVDAWLQAEQPRVRMIMQVHDELVFEVHKDDVDAVAKQIHQLMENCTRLDVPLLVEVGSGENWDQAH

>d1t7pa2 e.8.1.1 (A:211-704) T7 phage DNA polymerase {Bacteriophage T7}

LEAVDIEHRAAWLLAKQERNGFPFDTKAIEELYVELAARRSELLRKLTETFGSWYQPKGGTEMFCHPRTGKPLPKYPRIKTPKVGGIFKKPKNKAQREGREPCELDTREYVAGAPYTPVEHVVFNPSSRDHIQKKLQEAGWVPTKYTDKGAPVVDDEVLEGVRVDDPEKQAAIDLIKEYLMIQKRIGQSAEGDKAWLRYVAEDGKIHGSVNPNGAVTGRATHAFPNLAQIPGVRSPYGEQCRAAFGAEHHLDGITGKPWVQAGIDASGLELRCLAHFMARFDNGEYAHEILNGDIHTKNQIAAELPTRDNAKTFIYGFLYGAGDEKIGQIVGAGKERGKELKKKFLENTPAIAALRESIQQTLVESSQWVAGEQQVKWKRRWIKGLDGRKVHVRSPHAALNTLLQSAGALICKLWIIKTEEMLVEKGLKHGWDGDFAYMAWVHDEIQVGCRTEEIAQVVIETAQEAMRWVGDHWNFRCLLDTEGKMGPNWAICH

>d1ih7a2 e.8.1.1 (A:376-903) T4-like DNA polymerase {Bacteriophage RB69}

QNKVIPQGRSHPVQPYPGAFVKEPIPNRYKYVMSFDLTSLYPSIIRQVNISPETIAGTFKVAPLHDYINAVAERPSDVYSCSPNGMMYYKDRDGVVPTEITKVFNQRKEHKGYMLAAQRNGEIIKEALHNPNLSVDEPLDVDYRFDFSDEIKEKIKKLSAKSLNEMLFRAQRTEVAGMTAQINRKLLINSLYGALGNVWFRYYDLRNATAITTFGQMALQWIERKVNEYLNEVCGTEGEAFVLYGDTDSIYVSADKIIDKVGESKFRDTNHWVDFLDKFARERMEPAIDRGFREMCEYMNNKQHLMFMDREAIAGPPLGSKGIGGFWTGKKRYALNVWDMEGTRYAEPKLKIMGLETQKSSTPKAVQKALKECIRRMLQEGEESLQEYFKEFEKEFRQLNYISIASVSSANNIAKYDVGGFPGPKCPFHIRGILTYNRAIKGNIDAPQVVEGEKVYVLPLREGNPFGDKCIAWPSGTEITDLIKDDVLHWMDYTVLLEKTFIKPLEGFTSAAKLDYEKKASLFDMFDF

>d1tgoa2 e.8.1.1 (A:348-773) T4-like DNA polymerase {Archaeon Thermococcus gorgonarius}

STGNLVEWFLLRKAYERNELAPNKPDERELARRRESYAGGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQKVKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYADTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKT

>d1k1sa\_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}

MIVIFVDFDYFFAQVEEVLNPQYKGKPLVVSVYSGRTKTSGAVATANYEARKLGVKAGMPIIKAMQIAPSAIYVPMRKPIYEAFSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENGIELARKIKQEILEKEKITVTVGVAPNKILAKIIADKSKPNGLGVIRPTEVQDFLNELDIDEIPGIGSVLARRLNELGIQKLRDILSKNYNELEKITGKAKALYLLKLAQNKYSEPVENKSKIPHGRYLTLPYNTRDVKVILPYLKKAINEAYNKVNGIPMRITVIAIMEDLDILSKGKKFKHGISIDNAYKVAEDLLRELLVRDKRRNVRRIGVKLDNIIIN

>d1jiha\_ e.8.1.5 (A:) DNA polymerase eta {Baker's yeast (Saccharomyces cerevisiae)}

MSKFTWKELIQLGSPSKAYESSLACIAHIDMNAFFAQVEQMRCGLSKEDPVVCVQWNSIIAVSYAARKYGISRMDTIQEALKKCSNLIPIHTAVFKKGEDFWQYHDGCGSWVQDPAKQISVEDHKVSLEPYRRESRKALKIFKSACDLVERASIDEVFLDLGRICFNMLMFDNEYELTGDLKLKDALSNIREAFIGGNYDINSHLPLIPEKIKSLKFEGDVFNPEGRDLITDWDDVILALGSQVCKGIRDSIKDILGYTTSCGLSSTKNVCKLASNYKKPDAQTIVKNDCLLDFLDCGKFEITSFWTLGGVLGKELIDVLDLPHENSIKHIRETWPDNAGQLKEFLDAKVKQSDYDRSTSNIDPLKTADLAEKLFKLSRGRYGLPLSSRPVVKSMMSNKNLRGKSCNSIVDCISWLEVFCAELTSRIQDLEQEYNKIVIPRTVSISLKTKSYEVYRKSGPVAYKGINFQSHELLKVGIKFVTDLDIKGKNKSYYPLTKLSMTITNFDII

>d1mml\_\_ e.8.1.2 (-) MMLV reverse transcriptase {Moloney murine leukemia virus}

TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLK

>d1c9rb1 e.8.1.2 (B:) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLAPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEAALGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFKAQNPDIVIYQYIDDLYVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWAAAAAAAAAAAAATVNDIQKLVGKLNWAAQIYPGIAAAALSAALAGTKALTAAAPLTAAAALELAANRAAAAAAAAGVYYDPSKDLIAEIQKQGQGQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWWTEYWQATWIPEWEFVNTPPLVALWYALE

>d1rdr\_\_ e.8.1.4 (-) Viral RNA-dependent RNA-polymerase {Poliovirus type 1, strain Mahoney}

VGYPIINAPSKTKLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALLLPEYSTLYRRWLDSF

>d1c2pa\_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Hepatitis C virus}

HHSYTWTGALITPCAAEESKLPINALSNSLLRHHNMVYATTSRSAGLRQKKVTFDRLQVLDDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIHSVWKDLLEDTVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTLPQVVMGSSYGFQYSPGQRVEFLVNTWKSKKNPMGFSYDTRCFDSTVTENDIRVEESIYQCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKASAACRAAKLQDCTMLVNGDDLVVICESAGVQEDAASLRAFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRARLLSQGGRAATCGKYLFNWAVKTKLKLTPIPAASQLDLSGWFVAGYSGGDIYHS

>d1khva\_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Rabbit hemorrhagic disease virus}

FCGEPIDYRGITAHRLVGAEPRPPVSGTRYAKVPGVPDEYKTGYRPANLGRSDPDSDKSLMNIAVKNLQVYQQEPKLDKVDEFIERAAADVLGYLRFLTKGERQANLNFKAAFNTLDLSTSCGPFVPGKKIDHVKDGVMDQVLAKHLYKCWSVANSGKALHHIYACGLKDELRPLDKVKEGKKRLLWGCDVGVAVCAAAVFHNICYKLKMVARFGPIAVGVDMTSRDVDVIINNLTSKASDFLCLDYSKWDSTMSPCVVRLAIDILADCCEQTELTKSVVLTLKSHPMTILDAMIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSCAEIGLHCSNLYEDAPFYTYGDDGVYAMTPMMVSLLPAIIENLRDYGLSPTAADKTEFIDVCPLNKISFLKRTFELTDIGWVSKLDKSSILRQLEWSKTTSRHMVIEETYDLAKEERGVQLEELQVAAAAHGQEFFNFVCRELERQQAYTQFSVYSYDAARKILADRKR

>d1i50a\_ e.29.1.1 (A:) RBP1 {Baker's yeast (Saccharomyces cerevisiae)}

VGQQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTRAKIGGLNDPRLGSIDRNLKCQTCQEGMNECPGHFGHIDLAKPVFHVGFIAKIKKVCECVCMHCGKLLLDEHNELMRQALAIKDSKKRFAAIWTLCKTKMVCETDVPSEDDPTQLVSRGGCGNTQPTIRKDGLKLVGSWKKDRATGDADEPELRVLSTEEILNIFKHISVKDFTSLGFNEVFSRPEWMILTCLPVPPPPVRPSISFNESQRGEDDLTFKLADILKANISLETLEHNGAPHHAIEEAESLLQFHVATYMDNDIAGQPQALQKSGRPVKSIRARLKGKEGRIRGNLMGKRVDFSARTVISGDPNLELDQVGVPKSIAKTLTYPEVVTPYNIDRLTQLVRNGPNEHPGAKYVIRDSGDRIDLRYSKRAGDIQLQYGWKVERHIMDNDPVLFNRQPSLHKMSMMAHRVKVIPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQSNKPCMGIVQDTLCGIRKLTLRDTFIELDQVLNMLYWVPDWDGVIPTPAIIKPKPLWSGKQILSVAIPNGIHLQRFDEGTTLLSPKDNGMLIIDGQIIFGVVEKKTVGSSNGGLIHVVTREKGPQVCAKLFGNIQKVVNFWLLHNGFSTGIGDTIADGPTMREITETIAEAKKKVLDVTKEAQANLLTAKHGMTLRESFEDNVVRFLNEARDKAGRLAEVNLKDLNNVKQMVMAGSKGSFINIAQMSACVGQQSVEGKRIAFGFVDRTLPHFSKDDYSPESKGFVENSYLRGLTPQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDNTTRNSLGNVIQFIYGEDGMDAAHIEKQSLDTIGGSDAAFEKRYRVDLLNTDHTLDPSLLESGSEILGDLKLQVLLDEEYKQLVKDRKFLREVFVDGEANWPLPVNIRRIIQNAQQTFHIDHTKPSDLTIKDIVLGVKDLQENLLVLRGKNEIIQNAQRDAVTLFCCLLRSRLATRRVLQEYRLTKQAFDWVLSNIEAQFLRSVVHPGEMVGVLAAQSIGEPATQMTLNTFHFAGVASKKVTSGVPRLKEILNVAKNMKTPSLTVYLEPGHAADQEQAKLIRSAIEHTTLKSVTIASEIYYDPDPRSTVIPEDEEIIQLHFSLLDEEAEQSFDQQSPWLLRLELDRAAMNDKDLTMGQVGERIKQTFKNDLFVIWSEDNDEKLIIRCRVVRPKSLDAETEAEEDHMLKKIENTMLENITLRGVENIERVVMMKYDRKVPSPTGEYVKEPEWVLETDGVNLSEVMTVPGIDPTRIYTNSFIDIMEVLGIEAGRAALYKEVYNVIASDGSYVNYRHMALLVDVMTTQGGLTSVTRHGFNRSNTGALMRCSFEETVEILFEAGASAELDDCRGVSENVILGQMAPIGTGAFDVMIDEESL

>d1i6vc\_ e.29.1.1 (C:) RNA-polymerase beta {Thermus aquaticus}

KIKRFGRIREVIPLPPLTEIQVESYKKALQADVPPEKRENVGIQAAFKETFPIEEGDKGKGGLVLDFLEYRIGDPPFSQDECREKDLTYQAPLYARLQLIHKDTGLIKEDEVFLGHLPLMTEDGSFIINGADRVIVSQIHRSPGVYFTPDPARPGRYIASIIPLPKRGPWIDLEVEASGVVTMKVNKRKFPLVLLLRVLGYDQETLVRELSAYGDLVQGLLDEAVLAMRPEEAMVRLFTLLRPGDPPKKDKALAYLFGLLADPKRYDLGEAGRYKAEEKLGVGLSGRTLVRFEDGEFKDEVFLPTLRYLFALTAGVPGHEVDDIDHLGNRRIRTVGELMADQFRVGLARLARGVRERMVMGSPDTLTPAKLVNSRPLEAALREFFSRSQLSQFKDETNPLSSLRHKRRISALGPGGLTRERAGFDVRDVHRTHYGRICPVETPEGANIGLITSLAAYARVDALGFIRTPYRRVKNGVVTEEVVYMTASEEDRYTIAQANTPLEGDRIATDRVVARRRGEPVIVAPEEVEFMDVSPKQVFSLNTNLIPFLEHDDANRALMGSNMQTQAVPLIRAQAPVVMTGLEERVVRDSLAALYAEEDGEVVKVDGTRIAVRYEDGRLVHPLRRYARSNQGTAFDQRPRVRVGQRVKKGDLLADGPASEEGFLALGQNVLVAIMPFDGYNFEDAIVISEELLKRDFYTSIHIERYEIEARDTKLGPERITRDIPHLSEAALRDLDEEGIVRIGAEVKPGDILVGRTSFKGEQEPSPEERLLRSIFGEKARDVKDTSLRVPPGEGGIVVGRLRLRRGDPGVELKPGVREVVRVFVAQKRKLQVGDKLANRHGNKGVVAKILPVEDMPHLPDGTPVDVILNPLGVPSRMNLGQILETHLGLAGYFLGQRYISPVFDGATEPEIKELLAEAFNLYFGKRQGEGFGVDKREKEVLARAEKLGLVSPGKSPEEQLKELFDLGKVVLYDGRTGEPFEGPIVVGQMFIMKLYHMVEDKMHARSTGPYSLITQQPLGGKAQFGGQRFGEMEVWALEAYGAAHTLQEMLTIKSDDIEGRNAAYQAIIKGEDVPEPSVPESFRVLVKELQALALDVQTLDEKDNPVDVFEGL

>d1i50b\_ e.29.1.2 (B:) RBP2 {Baker's yeast (Saccharomyces cerevisiae)}

FEDESAPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQDIICEDSTLILEQLAQHTTESDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLRNLTYSSGLFVDVKKRTYEAIDVPGRELKYELIAEESEDDSESGKVFIGRLPIMLRSKNCYLSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEIRSALEKGSRFISTLQVKLYGREGSSARTIKATLPYIKQDIPIVIIFRALGIIPDGEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKDILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLAQLFKTLFKKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPARLMETLRTLRRKGDINPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDESLGHKELKVRKGHIAKLMATEYQDIEGGFEDVEEYTWSSLLNEGLVEYIDAEEEESILIAMQPEDLEPAEANEENDLDVDPAKRIRVSHHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMANILYYPQKPLGTTRAMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQEKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDVIIGKTTPISPDEEELGQRTAYHSKRDASTPLRSTENGIVDQVLVTTNQDGLKFVKVRVRTTKIPQIGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTDITVEGISKLLREHGYQSRGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQFECKGCDNKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF

>d1i6vd\_ e.29.1.2 (D:) RNA-polymerase beta-prime {Thermus aquaticus}

KEVRKVRIALASPEKIRSWSYGEVEKPETINYRTLKPERDGLFDERIFGPIKDYECACGKYKRQRFEAKVCERCAVEVTRSIVRRYRMAHIELATPAAHIWFVKDVPSKIATLLDLSATELEQVLYFNKYIVLDPKAAVLDAVPVEKRQLLTDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIDARMGAEAIQELLKELDLEKLERELLEEMKHPSRARRAKARKRLEVVRAFLDSGNRPEWMILEAVPVLPPDLRPMVQVDGGRFATSDLNDLYRRLINRNNRLKKLLAQGAPEIIIRNEKRMLQEAVDAVIDNGRRGSPVTNPGSERPLRSLTDILSGKQGRFRQNLLGKRVDYSGRSVIVVGPQLKLHQCGLPKRMALELFKPFLLKKMEEKAFAPNVKAARRMLERQRDIKDEVWDALEEVIHGKVVLLNRAPTLHRLGIQAFQPVLVEGQSIQLHPLVCEAFNADFDGDQMAVHVPLSSFAQAEARIQMLSAHNLLSPASGEPLAKPSRDIILGLYYITQVRKEKKGAGMAFATPEEALAAYERGEVALNAPIVVAGRETSVGRLKFVFANPDEALLAVAHGLLDLQDTVTTRYLGRRLETSPGRILFARIVGEAVGDEKVAQELIQMDVPQEKNSLKDLVYQAFLRLGMEKTARLLDALKYYGFTLSTTSGITIGIDDAVIPEEKQRYLEEADRKLRQIEQAYEMGFLTDRERYDQVIQLWTETTEKVTQAVFNNFEENYPFNPLYVMAQSGARGNPQQIRQLCGMRGLMQKPSGETFEVPVRSSFREGLTVLEYFISSHGARKGGADTALRTADSGYLTRKLVDVAHEIVVREADCGTTNYISVPLFQMDEVTRTLRLRKRSDIESGLYGRVLAREVEALGRRLEEGRYLSLEDVHFLIKAAEAGEVREVPVRSPLTCQTRYGVCQKCYGYDLSMARPVSIGEAVGVVAAESIGEPGTQLTMRTFHTGGVAVGTDITQGLPRVIELFEARRPKAKAVISEIDGVVRIEEGEDRLSVFVESEGFSKEYKLPKDARLLVKDGDYVEAGQPLTRGAIDPHQLLEAKGPEAVERYLVDEIQKVYRAQGVKLHDKHIEIVVRQMLKYVEVTDPGDSRLLEGQVLEKWDVEALNERLIAEGKVPVAWKPLLMGVTKSALSTKSWLSAASFQNTTHVLTEAAIAGKKDELIGLKENVILGRLIPAGTGSDFVRFTQVVDQRTLKAIE

>d1jn3a\_ e.9.1.1 (A:) DNA polymerase beta, catalytic (31 kD) fragment {Rat (Rattus norvegicus)}

DDTSSSINFLTRVTGIGPSAARKLVDEGIKTLEDLRKNEDKLNHHQRIGLKYFEDFEKRIPREEMLQMQDIVLNEVKKLDPEYIATVCGSFRRGAESSGDMDVLLTHPNFTSESSKQPKLLHRVVEQLQKVRFITDTLSKGETKFMGVCQLPSENDENEYPHRRIDIRLIPKDQYYCGVLYFTGSDIFNKNLRAHALEKGFTINEYTIRPLGVTGVAGEPLPVDSEQDIFDYIQWRYREPKDRSE

>d1jmsa2 e.9.1.1 (A:243-510) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}

DERYKSFKLFTSVFGVGLKTAEKWFRMGFRTLSKIQSDKSLRFTQMQKAGFLYYEDLVSCVNRPEAEAVSMLVKEAVVTFLPDALVTMTGGFRRGKMTGHDVDFLITSPEATEDEEQQLLHKVTDFWKQQGLLLYCDILESTFEKFKQPSRKVDALDHFQKCFLILKLDHGRVHSEKSGQQEGKGWKAIRVDLVMCPYDRRAFALLGWTGSRQFERDLRRYATHERKMMLDNHALYDRTKRVFLEAESEEEIFAHLGLDYIEPWERNA

>d1jaja\_ e.9.1.1 (A:) DNA polymerase X {African swine fever virus}

MLTLIQGKKIVNHLRSRLAFEYNGQLIKILSKNIVAVGSLRREEKMLNDVDLLIIVPEKKLLKHVLPNIRIKGLSFSVKVCGERKCVLFIEWEKKTYQLDLFTALAEEKPYAIFHFTGPVSYLIRIRAALKKKNYKLNQYGLFKNQTLVPLKITTEKELIKELGFTYRIPKKRL

>d1ecl\_\_ e.10.1.1 (-) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}

GKALVIVESPAKAKTINKYLGSDYVVKSSVGHIRDLTSGSAAKKSADSTSTKTAKKPKKPDERGALVNRMGVDPWHNWEAHYEVLPGKEKVVSELKQLAEKADHIYLATDLDREGEAIAWHLREVIGGDDARYSRVVFNEITKNAIRQAFNKPGELNIDRVNAQQARRFMDRVVGYMVSPLLWKKIARGLSAGRVQSVAVRLVVEREREIKAFVPEEFWEVDASTTTPSGEALALQVTHQNDKPFRPVNKEQTQAAVSLLEKARYSVLEREDKPTTSKPGAPFITSTLQQAASTRLGFGVKKTMMMAQRLYEAGYITYMRTDSTNLSQDAVNMVRGYISDNFGKKYLPESPNQYASKGNSQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMTPAKYDSTTLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQHFTKPPARFSEASLVKELEKRGIGRPSTYASIISTIQDRGYVRVENRRFYAEKMGEIVTDRLEENFRELMNYDFTAQMENSLDQVANHEAEWKAVLDHFFSDFTQQLDKAEKDPEEGGMRPN

>d1i7da\_ e.10.1.1 (A:) DNA topoisomerase III {Escherichia coli}

MRLFIAEKPSLARAIADVLPKPHRKGDGFIECGNGQVVTWCIGHLLEQAQPDAYDSRYARWNLADLPIVPEKWQLQPRPSVTKQLNVIKRFLHEASEIVHAGDPDREGQLLVDEVLDYLQLAPEKRQQVQRCLINDLNPQAVERAIDRLRSNSEFVPLCVSALARARADWLYGINMTRAYTILGRNAGYQGVLSVGRVQTPVLGLVVRRDEEIENFVAKDFFEVKAHIVTPADERFTAIWQPSEACEPYQDEEGRLLHRPLAEHVVNRISGQPAIVTSYNDKRESESAPLPFSLSALQIEAAKRFGLSAQNVLDICQKLYETHKLITFPRSDCRYLPEEHFAGRHAVMNAISVHAPDLLPQPVVDPDIRNRCWDDKKVDAHHAIIPTARSSAINLTENEAKVYNLIARQYLMQFCPDAVFRKCVIELDIAKGKFVAKARFLAEAGWRTLLGSKERDEENDGTPLPVVAKGDELLCEKGEVVERQTQPPRHFTDATLLSAMTGIARFVQDKDLKKILRATDGLGTEATRAGIIELLFKRGFLTKKGRYIHSTDAGKALFHSLPEMATRPDMTAHWESVLTQISEKQCRYQDFMQPLVGTLYQLIDQAKRTPVRQFRGIVAP

>d1gkub3 e.10.1.1 (B:499-1054) Topoisomerase "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

QEFDLIKPALFIVESPTKARQISRFFGKPSVKVLDGAVVYEIPMQKYVLMVTASIGHVVDLITNRGFHGVLVNGRFVPVYASIKRCRDCGYQFTEDRESCPKCGSENVDNSRSRIEALRKLAHDAEFVIVGTDPDTEGEKIAWDLKNLLSGCGAVKRAEFHEVTRRAILEALESLRDVDENLVKAQVVRRIEDRWIGFVLSQKLWERFNNRNLSAGRAQTLVLGWIIDRFQESRERRKIAIVRDFDLVLEHDEEEFDLTIKLVEEREELRTPLPPYTTETMLSDANRILKFSVKQTMQIAQELFENGLITYHRTDSTRVSDVGQRIAKEYLGDDFVGREWGESGAHECIRPTRPLTRDDVQRLIQEGVLVVEGLRWEHFALYDLIFRRFMASQCRPFKVVVKKYSIEFDGKTAEEERIVRAEGRAYELYRAVWVKNELPTGTFRVKAEVKSVPKVLPFTQSEIIQMMKERGIGRPSTYATIVDRLFMRNYVVEKYGRMIPTKLGIDVFRFLVRRYAKFVSEDRTRDLESRMDAIERGELDYLKALEDMYAEIKSID

>d1bjt\_\_ e.11.1.1 (-) DNA topoisomerase II, C-terminal fragment (residues 410-1202) {Baker's yeast (Saccharomyces cerevisiae)}

RKSRITNYPKLEDANKAGTKEGYKCTLVLTEGDSALSLAVAGLAVVGRDYYGCYPLRGKMLNVREASADQILKNAEIQAIKKIMGLQHRKKYEDTKSLRYGHLMIMTDQDHDGSHIKGLIINFLESSFLGLLDIQGFLLEFITPIIKVSITKPTKNTIAFYNMPDYEKWREEESHKFTWKQKYYKGLGTSLAQEVREYFSNLDRHLKIFHSLQGNDKDYIDLAFSKKKADDRKEWLRQYEPGTVLDPTLKEIPISDFINKELILFSLADNIRSIPNVLDGFKPGQRKVLYGCFKKNLKSELKVAQLAPYVSECTAYHHGEQSLAQTIIGLAQNFVGSNNIYLLLPNGAFGTRATGGKDAAAARYIYTELNKLTRKIFHPADDPLYKYIQEDEKTVEPEWYLPILPMILVNGAEGIGTGWSTYIPPFNPLEIIKNIRHLMNDEELEQMHPWFRGWTGTIEEIEPLRYRMYGRIEQIGDNVLEITELPARTWTSTIKEYLLLGLSGNDKIKPWIKDMEEQHDDNIKFIITLSPEEMAKTRKIGFYERFKLISPISLMNMVAFDPHGKIKKYNSVNEILSEFYYVRLEYYQKRKDHMSERLQWEVEKYSFQVKFIKMIIEKELTVTNKPRNAIIQELENLGFPRFNKEGKPYYGSPNDEIAEQINDVKGATSDEEDEESSHEDTENVINGPEELYGTYEYLLGMRIWSLTKERYQKLLKQKQEKETELENLLKLSAKDIWNTDLKAFEVGYQEFLQRDAEARG

>d1ab4\_\_ e.11.1.1 (-) DNA Gyrase A {Escherichia coli}

VGRALPDVRDGLKPVHRRVLYAMNVLGNDWNKAYKKSARVVGDVIGKYHPHGDSAVYDTIVRMAQPFSLRYMLVDGQGNFGSIDGDSAAAMRYTEIRLAKIAHELMADLEKETVDFVDNYDGTEKIPDVMPTKIPNLLVNGSSGIAVGMATNIPPHNLTEVINGCLAYIDDEDISIEGLMEHIPGPDFPTAAIINGRRGIEEAYRTGRGKVYIRARAEVEVETIIVHEIPYQVNKARLIEKIAELVKEKRVEGISALRDESDKDGMRIVIEGEVVLNNLYSQTQLQVSFGINMVALHHGQPKIMNLKDIIAAFVRHRREVVTRRTIFELRKARDRAHILEALAVALANIDPIIELIRHAPTPAEAKTALVANPWQLGNVAAMLEDAARPEWLEPEFGVRDGLYYLTEQQAQAILDLRLQKLTGLEHEKLLDEYKELLDQIAELLRILGSADRLMEVIREELELVREQFGDKRRTEIT

>d1daaa\_ e.17.1.1 (A:) D-amino acid aminotransferase {Bacillus sp., strain YM-1}

GYTLWNDQIVKDEEVKIDKEDRGYQFGDGVYEVVKVYNGEMFTVNEHIDRLYASAEKIRITIPYTKDKFHQLLHELVEKNELNTGHIYFQVTRGTSPRAHQFPENTVKPVIIGYTKENPRPLENLEKGVKATFVEDIRWLRCDIKSLNLLGAVLAKQEAHEKGCYEAILHRNNTVTEGSSSNVFGIKDGILYTHPANNMILKGITRDVVIACANEINMPVKEIPFTTHEALKMDELFVTSTTSEITPVIEIDGKLIRDGKVGEWTRKLQKQFETKIP

>d1i1ka\_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Escherichia coli}

KADYIWFNGEMVRWEDAKVHVMSHALHYGTSVFEGIRCYDSHKGPVVFRHREHMQRLHDSAKIYRFPVSQSIDELMEACRDVIRKNNLTSAYIRPLIFVGDVGMGVNPPAGYSTDVIIAAFPWGAYLGAEALEQGIDAMVSSWNRAAPNTIPTAAKAGGNYLSSLLVGSEARRHGYQEGIALDVNGYISEGAGENLFEVKDGVLFTPPFTSSALPGITRDAIIKLAKELGIEVREQVLSRESLYLADEVFMSGTAAEITPVRSVDGIQVGEGRCGPVTKRIQQAFFGLFTGETEDKWGWLDQVNQ

>d1ekfa\_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Human (Homo sapiens), mitochondrial}

ASSSFKAADLQLEMTQKPHKKPGPGEPLVFGKTFTDHMLMVEWNDKGWGQPRIQPFQNLTLHPASSSLHYSLQLFEGMKAFKGKDQQVRLFRPWLNMDRMLRSAMRLCLPSFDKLELLECIRRLIEVDKDWVPDAAGTSLYVRPVLIGNEPSLGVSQPRRALLFVILCPVGAYFPGGSVTPVSLLADPAFIRAWVGGVGNYKLGGNYGPTVLVQQEALKRGCEQVLWLYGPDHQLTEVGTMNIFVYWTHEDGVLELVTPPLNGVILPGVVRQSLLDMAQTWGEFRVVERTITMKQLLRALEEGRVREVFGSGTACQVCPVHRILYKDRNLHIPTMENGPELILRFQKELKEIQYGIRAHEWMFPV

>d1et0a\_ e.17.1.1 (A:) Aminodeoxychorismate lyase {Escherichia coli}

MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGKVSLLSAHIQRLQDACQRLMISCDFWPQLEQEMKTLAAEQQNGVLKVVISRGSGGRGYSTLNSGPATRILSVTAYPAHYDRLRNEGITLALSPVRLGRNPHLAGIKHLNRLEQVLIRSHLEQTNADEALVLDSEGWVTECCAANLFWRKGNVVYTPRLDQAGVNGIMRQFCIRLLAQSSYQLVEVQASLEESLQADEMVICNALMPVMPVCACGDVSFSSATLYEYLAPLCE

>d1frfl\_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio fructosovorans}

TPQSTFTGPIVVDPITRIEGHLRIMVEVENGKVKDAWSSSQLFRGLEIILKGRDPRDAQHFTQRACGVCTYVHALASSRCVDDAVKVSIPANARMMRNLVMASQYLHDHLVHFYHLHALDWVDVTAALKADPNKAAKLAASIDTARTGNSEKALKAVQDKLKAFVESGQLGIFTNAYFLGGHKAYYLPPEVNLIATAHYLEALHMQVKAASAMAILGGKNPHTQFTVVGGCSNYQGLTKDPLANYLALSKEVCQFVNECYIPDLLAVAGFYKDWGGIGGTSNYLAFGEFATDDSSPEKHLATSQFPSGVITGRDLGKVDNVDLGAIYEDVKYSWYAPGGDGKHPYDGVTDPKYTKLDDKDHYSWMKAPRYKGKAMEVGPLARTFIAYAKGQPDFKKVVDMVLGKLSVPATALHSTLGRTAARGIETAIVCANMEKWIKEMADSGAKDNTLCAKWEMPEESKGVGLADAPRGSLSHWIRIKGKKIDNFQLVVPSTWNLGPRGPQGDKSPVEEALIGTPIADPKRPVEILRTVHAFDPCIACGVH

>d1cc1l\_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfomicrobium baculatum}

VKISIDPLTRVEGHLKIEVEVKDGKVVDAKCSGGMFRGFEQILRGRDPRDSSQIVQRICGVCPTAHCTASVMAQDDAFGVKVTTNGRITRNLIFGANYLQSHILHFYHLAALDYVKGPDVSPFVPRYANADLLTDRIKDGAKADATNTYGLNQYLKALEIRRICHEMVAMFGGRMPHVQGMVVGGATEIPTADKVAEYAARFKEVQKFVIEEYLPLIYTLGSVYTDLFETGIGWKNVIAFGVFPEDDDYKTFLLKPGVYIDGKDEEFDSKLVKEYVGHSFFDHSAPGGLHYSVGETNPNPDKPGAYSFVKAPRYKDKPCEVGPLARMWVQNPELSPVGQKLLKELYGIEAKKFRDLGDKAFSIMGRHVLRAEETWLTAVAVEKWLKQVQPGAETYVKSEIPDAAEGTGFTEAPRGALLHYLKIKDKKIENYQIVSATLWNANPRDDMGQRGPIEEALIGVPVPDIKNPVNVGRLVRSYDPXLGCAVH

>d1cc1s\_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfomicrobium baculatum}

KKAPVIWVQGQGCTGCSVSLLNAVHPRIKEILLDVISLEFHPTVMASEGEMALAHMYEIAEKFNGNFFLLVEGAIPTAKEGRYCIVGETLDAKAHHHEVTMMELIRDLAPKSLATVAVGTCSAYGGIPAAEGNVTGSKSVRDFFADEKIEKLLVNVPGCPPHPDWMVGTLVAAWSHVLNPTEHPLPELDDDGRPLLFFGDNIHENCPYLDKYDNSEFAETFTKPGCKAELGCKGPSTYADCAKRRWNNGINWCVENAVCIGCVEPDFPDGKSPFYVAE

>d1e3da\_ e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio desulfuricans}

SRPSVVYLHAAECTGCSEALLRTYQPFIDTLILDTISLDYHETIMAAAGEAAEEALQAAVNGPDGFICLVEGAIPTGMDNKYGYIAGHTMYDICKNILPKAKAVVSIGTCACYGGIQAAKPNPTAAKGINDCYADLGVKAINVPGCPPNPLNMVGTLVAFLKGQKIELDEVGRPVMFFGQSVHDLCERRKHFDAGEFAPSFNSEEARKGWCLYDVGCKGPETYNNCPKVLFNETNWPVAAGHPCIGCSEPNFWDDMTPFYQN

>d1lci\_\_ e.23.1.1 (-) Luciferase {Firefly (Photinus pyralis)}

AKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVNITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQFFMPVLGALFIGVAVAPANDIYNERELLNSMNISQPTVVFVSKKGLQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVLMYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTGKLDARKIREILIKAKK

>d1amua\_ e.23.1.1 (A:) Phenylalanine activating domain of gramicidin synthetase 1 {Bacillus brevis}

GTHEEEQYLFAVNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVCENEQLTYHELNVKANQLARIFIEKGIGKDTLVGIMMEKSIDLFIGILAVLKAGGAYVPIDIEYPKERIQYILDDSQARMLLTQKHLVHLIHNIQFNGQVEIFEEDTIKIREGTNLHVPSKSTDLAYVIYTSGTTGNPKGTMLEHKGISNLKVFFENSLNVTEKDRIGQFASISFDASVWEMFMALLTGASLYIILKDTINDFVKFEQYINQKEITVITLPPTYVVHLDPERILSIQTLITAGSATSPSLVNKWKEKVTYINAYGPTETTICATTWVATKETIGHSVPIGAPIQNTQIYIVDENLQLKSVGEAGELCIGGEGLARGYWKRPELTSQKFVDNPFVPGEKLYKTGDQARWLSDGNIEYLGRIDNQVKIRGHRVELEEVESILLKHMYISETAVSVHKDHQEQPYLCAYFVSEKHIPLEQLRQFSSEELPTYMIPSYFIQLDKMPLTSNGKIDRKQLPEPDLTF

>d1ad2\_\_ e.24.1.1 (-) Ribosomal protein L1 {Thermus thermophilus}

KRYRALLEKVDPNKIYTIDEAAHLVKELATAKFDETVEVHAKLGIDPRRSDQNVRGTVSLPHGLGKQVRVLAIAKGEKIKEAEEAGADYVGGEEIIQKILDGWMDFDAVVATPDVMGAVGSKLGRILGPRGLLPNPKAGTVGFNIGEIIREIKAGRIEFRNDKTGAIHAPVGKACFPPEKLADNIRAFIRALEAHKPEGAKGTFLRSVYVTTTMGPSVRINPHS

>d1cjsa\_ e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus jannaschii}

MDREALLQAVKEARELAKPRNFTQSFEFIATLKEIDMRKPENRIKTEVVLPHGRGKEAKIAVIGTGDLAKQAEELGLTVIRKEEIEELGKNKRKLRKIAKAHDFFIAQADLMPLIGRYMGVILGPRGKMPKPVPANANIKPLVERLKKTVVINTRDKPYFQVLVGNEKMTDEQIVDNIEAVLNVVAKKYEKGLYHIKDAYVKLTMGPAVKVKK

>d1a87\_\_ f.1.1.1 (-) Colicin N {Escherichia coli}

SAKVGEITITPDNSKPGRYISSNPEYSLLAKLIDAESIKGTEVYTFHTRKGQYVKVTVPDSNIDKMRVDYVNWKGPKYNNKLVKRFVSQFLLFRKEEKEKNEKEALLKASELVSGMGDKLGEYLGVKYKNVAKEVANDIKNFHGRNIRSYNEAMASLNKVLANPKMKVNKSDKDAIVNAWKQVNAKDMANKIGNLGKAFKVADLAIKVEKIREKSIEGYNTGNWGPLLLEVESWIIGGVVAGVAISLFGAVLSFLPISGLAVTALGVIGIMTISYLSSFIDANRVSNINNIISSVIR

>d1cii\_1 f.1.1.1 (451-624) Colicin Ia {Escherichia coli}

DAINFTTEFLKSVSEKYGAKAEQLAREMAGQAKGKKIRNVEEALKTYEKYRADINKKINAKDRAAIAAALESVKLSDISSNLNRFSRGLGYAGKFTSLADWITEFGKAVRTENWRPLFVKTETIIAGNAATALVALVFSILTGSALGIIGYGLLMAVTGALIDESLVEKANKFW

>d1dlc\_3 f.1.3.1 (61-289) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}

TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR

>d1ciy\_3 f.1.3.1 (33-255) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis, CRYIA (A)}

YTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTVLDIVALFSNYDSRRY

>d1i5pa3 f.1.3.1 (A:1-263) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

MNNVLNSGRTTICDAYNVVAHDPFSFEHKSLDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLLKKVGSLIGKRILSELWGIIFPSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELIGLQANIREFNQQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHDMLEFRTYMFLNVFEYVSIWSLFK

>d1lxl\_\_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERLEHHHHHH

>d2bida\_ f.1.4.1 (A:) Proapoptotic molecule Bid {Human (Homo sapiens)}

GSMDCEVNNGSSLRDECITNLLVFGFLQSCSDNSFRRELDALGHELPVLAPQWEGYDELQTDGNRSSHSRLGRIEADSESQEDIIRNIARHLAQVGDSMDRSIPPGLVNGLALQLRNTSRSEEDRNRDLATALEQLLQAYPRDMEKEKTMLVLALLLAKKVASHTPSLLRDVFHTTVNFINQNLRTYVRSLARNGMD

>d1f16a\_ f.1.4.1 (A:) Proapoptotic molecule Bax {Human (Homo sapiens)}

MDGSGEQPRGGGPTSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKRIGDELDSNMELQRMIAAVDTDSPREVFFRVAADMFSDGNFNWGRVVALFYFASKLVLKALCTKVPELIRTIMGWTLDFLRERLLGWIQDQGGWDGLLSYFGTPTWQTVTIFVAGVLTASLTIWKKMG

>d1c3wa\_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPIYWARYADWLFTTPLLLLDLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFSMRPEVASTFKVLRNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGLILLRSRAIFG

>d1e12a\_ f.2.1.1 (A:) Halorhodopsin {Halobacterium salinarum}

RENALLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRLIWGATLMIPLVSISSYLGLLSGLTVGMIEMPAGHALAGEMVRSQWGRYLTWALSTPMILLALGLLADVDLGSLFTVIAADIGMCVTGLAAAMTTSALLFRWAFYAISCAFFVVVLSALVTDWAASASSAGTAEIFDTLRVLTVVLWLGYPIVWAVGVEGLALVQSVGATSWAYSVLDVFAKYVFAFILLRWVANNERTVAV

>d1h68a\_ f.2.1.1 (A:) Sensory rhodopsin II {Natronobacterium pharaonis}

VGLTTLFWLGAIGMLVGTLAFAWAGRDAGSGERRYYVTLVGISGIAAVAYVVMALGVGWVPVAERTVFAPRYIDWILTTPLIVYFLGLLAGLDSREFGIVITLNTVVMLAGFAGAMVPGIERYALFGMGAVAFLGLVYYLVGPMTESASQRSSGIKSLYVRLRNLTVILWAIYPFIWLLGPPGVALLTPTVDVALIVYLDLVTKVGFGFIALDAAATL

>d1hzxa\_ f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}

MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLLIMLGFPINFLTLYVTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVHFIIPLIVIFFCYGQLVFTVKEAAAQQQESATTQKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRNCMVTTLCCGKNPLGDDEASTTVSKTETSQVAPA

>d1dxrh2 f.2.1.2 (H:1-36) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

MYHGALAQHLDIAQLVWYAQWLVIWTVVLLYLRRED

>d1dxrm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

ADYQTIYTQIQARGPHITVSGEWGDNDRVGKPFYSYWLGKIGDAQIGPIYLGASGIAAFAFGSTAILIILFNMAAEVHFDPLQFFRQFFWLGLYPPKAQYGMGIPPLHDGGWWLMAGLFMTLSLGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVPFGIWPHIDWLTAFSIRYGNFYYCPWHGFSIGFAYGCGLLFAAHGATILAVARFGGDREIEQITDRGTAVERAALFWRWTIGFNATIESVHRWGWFFSLMVMVSASVGILLTGTFVDNWYLWCVKHGAAPDYPAYLPATPDPASLPGAPK

>d1qovl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

ALLSFERKYRVPGGTLVGGNLFDFWVGPFYVGFFGVATFFFAALGIILIAWSAVLQGTWNPQLISVYPPALEYGLGGAPLAKGGLWQIITICATGAFVSWALREVEICRKLGIGYHIPFAFAFAILAYLTLVLFRPVMMGAWGYAFPYGIWTHLDWVSNTGYTYGNFHYNPAHMIAISFFFTNALALALHGALVLSAANPEKGKEMRTPDHEDTFFRDLVGYSIGTLGIHRLGLLLSLSAVFFSALCMIITGTIWFDQWVDWWQWWVKLPWWANIPGGING

>d1eysh2 f.2.1.2 (H:7-43) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

HYIDAAQITIWAFWLFFFGLIIYLRREDKREGYPLDS

>d1ocrb2 f.2.1.3 (B:1-90) Cytochrome c oxidase {Cow (Bos taurus)}

MAYPMQLGFQDATSPIMEELLHFHDHTLMIVFLISSLVLYIISLMLTTKLTHTSTMDAQEVETIWTILPAIILILIALPSLRILYMMDEI

>d1ocrd1 f.2.1.3 (D:) Cytochrome c oxidase {Cow (Bos taurus)}

SVVKSEDYALPSYVDRRDYPLPDVAHVKNLSASQKALKEKEKASWSSLSIDEKVELYRLKFKESFAEMNRSTNEWKTVVGAAMFFIGFTALLLIWEKHYVYGPIPHTFEEEWVAKQTKRMLDMKVAPIQGFSAKWDYDKNEWKK

>d1ocrg1 f.2.1.3 (G:) Cytochrome c oxidase {Cow (Bos taurus)}

ASAAKGDHGGTGARTWRFLTFGLALPSVALCTLNSWLHSGHRERPAFIPYHHLRIRTKPFSWGDGNHTFFHNPRVNPLPTGYEK

>d1ocri1 f.2.1.3 (I:) Cytochrome c oxidase {Cow (Bos taurus)}

STALAKPQMRGLLARRLRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFYRNYDSMKDFEEMRKAGIFQSAK

>d1ocrj1 f.2.1.3 (J:) Cytochrome c oxidase {Cow (Bos taurus)}

FENRVAEKQKLFQEDNGLPVHLKGGATDNILYRVTMTLCLGGTLYSLYCLGWASFPHK

>d1ocrl1 f.2.1.3 (L:) Cytochrome c oxidase {Cow (Bos taurus)}

SHYEEGPGKNIPFSVENKWRLLAMMTLFFGSGFAAPFFIVRHQLLKK

>d1ocrm1 f.2.1.3 (M:) Cytochrome c oxidase {Cow (Bos taurus)}

ITAKPAKTPTSPKEQAIGLSVTFLSFLLPAGWVLYHLDNYKKS

>d1ar1a1 f.2.1.3 (A:) Cytochrome c oxidase {Paracoccus denitrificans}

GFFTRWFMSTNHKDIGILYLFTAGIVGLISVCFTVYMRMELQHPGVQYMCLEGARLIADASAECTPNGHLWNVMITYHGVLMMFFVVIPALFGGFGNYFMPLHIGAPDMAFPRLNNLSYWMYVCGVALGVASLLAPGGNDQMGSGVGWVLYPPLSTTEAGYSMDLAIFAVHVSGASSILGAINIITTFLNMRAPGMTLFKVPLFAWSVFITAWLILLSLPVLAGAITMLLMDRNFGTQFFDPAGGGDPVLYQHILWFFGHPEVYIIILPGFGIISHVISTFAKKPIFGYLPMVLAMAAIGILGFVVWAHHMYTAGMSLTQQAYFMLATMTIAVPTGIKVFSWIATMWGGSIEFKTPMLWAFGFLFLFTVGGVTGVVLSQAPLDRVYHDTYYVVAHFHYVMSLGAVFGIFAGVYYWIGKMSGRQYPEWAGQLHFWMMFIGSNLIFFPQHFLGRQGMPRRYIDYPVEFAYWNNISSIGAYISFASFLFFIGIVFYTLFAGKRVNVPNYWNEHADTLEWTLPSPPPEHTFET

>d1ar1b2 f.2.1.3 (B:1-107) Cytochrome c oxidase {Paracoccus denitrificans}

QDVLGDLPVIGKPVNGGMNFQPASSPLAHDQQWLDHFVLYIITAVTIFVCLLLLICIVRFNRRANPVPARFTHNTPIEVIWTLVPVLILVAIGAFSLPILFRSQEMP

>d1qlec1 f.2.1.3 (C:) Cytochrome c oxidase {Paracoccus denitrificans}

AHVKNHDYQILPPSIWPFFGAIGAFVMLTGAVAWMKGITFFGLPVEGPWMFLIGLVGVLYVMFGWWADVVNEGETGEHTPVVRIGLQYGFILFIMSEVMFFVAWFWAFIKNALYPMGPDSPIKDGVWPPEGIVTFDPWHLPLINTLILLLSGVAVTWAHHAFVLEGDRKTTINGLIVAVILGVCFTGLQAYEYSHAAFGLADTVYAGAFYMATGFHGAHVIIGTIFLFVCLIRLLKGQMTQKQHVGFEAAAWYWHFVDVVWLFLFVVIYIWGR

>d1ehka1 f.2.1.3 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYPEKKATLYFLVLGFLALIVGSLFGPFQALNYGNVDAYPLLKRLLPFVQSYYQGLTLHGVLNAIVFTQLFAQAIMVYLPARELNMRPNMGLMWLSWWMAFIGLVVAALPLLANEATVLYTFYPPLKGHWAFYLGASVFVLSTWVSIYIVLDLWRRWKAANPGKVTPLVTYMAVVFWLMWFLASLGLVLEAVLFLLPWSFGLVEGVDPLVARTLFWWTGHPIVYFWLLPAYAIIYTILPKQAGGKLVSDPMARLAFLLFLLLSTPVGFHHQFADPGIDPTWKMIHSVLTLFVAVPSLMTAFTVAASLEFAGRLRGGRGLFGWIRALPWDNPAFVAPVLGLLGFIPGGAGGIVNASFTLDYVVHNTAWVPGHFHLQVASLVTLTAMGSLYWLLPNLTGKPISDAQRRLGLAVVWLWFLGMMIMAVGLHWAGLLNVPRRAYIAQVPDAYPHAAVPMVFNVLAGIVLLVALLLFIYGLFSVLLSRERKPELAEAPLPFAEVISGPEDRRLVLAMDRIGFWFAVAAILVVLAYGPTLVQLFGHLNPVPGWRLW

>d1ehkb2 f.2.1.3 (B:3-40) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

DEHKAHKAILAYEKGWLAFSLAMLFVFIALIAYTLATH

>d1ffta1 f.2.1.3 (A:) Ubiquinol oxidase {Escherichia coli}

VDHKRLGIMYIIVAIVMLLRGFADAIMMRSQQALASAGEAGFLPPHHYDQIFTAHGVIMIFFVAMPFVIGLMNLVVPLQIGARDVAFPFLNNLSFWFTVVGVILVNVSLGVGEFAQTGWLAYPPLSGIEYSPGVGVDYWIWSLQLSGIGTTLTGINFFVTILKMRAPGMTMFKMPVFTWASLCANVLIIASFPILTVTVALLTLDRYLGTHFFTNDMGGNMMMYINLIWAWGHPEVYILILPVFGVFSEIAATFSRKRLFGYTSLVWATVCITVLSFIVWLHHFFTMGAGANVNAFFGITTMIIAIPTGVKIFNWLFTMYQGRIVFHSAMLWTIGFIVTFSVGGMTGVLLAVPGADFVLHNSLFLIAHFHNVIIGGVVFGCFAGMTYWWPKAFGFKLNETWGKRAFWFWIIGFFVAFMPLYALGFMGMTRRLSQQIDPQFHTMLMIAASGAVLIALGILCLVIQMYVSIRDRDQNRDLTGDPWGGRTLEWATSSPPPFYNF

>d1fftb2 f.2.1.3 (B:27-117) Ubiquinol oxidase {Escherichia coli}

SALLDPKGQIGLEQRSLILTAFGLMLIVVIPAILMAVGFAWKYRASNKDAKYSPNWSHSNKVEAVVWTVPILIIIFLAVLTWKTTHALEPS

>d1fftc1 f.2.1.3 (C:) Ubiquinol oxidase {Escherichia coli}

HDAGGTKIFGFWIYLMSDCILFSILFATYAVLVNGTAGGPTGKDIFELPFVLVETFLLLFSSITYGMAAIAMYKNNKSQVISWLALTWLFGAGFIGMEIYEFHHLIVNGMGPDRSGFLSAFFALVGTHGLHVTSGLIWMAVLMVQIARRGLTSTNRTRIMCLSLFWHFLDVVWICVFTVVYLMGA

>d1c0va\_ f.2.1.4 (A:) Subunit C {Escherichia coli}

MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLVDAIPMIAVGLGLYVMFAVA

>d1c17m\_ f.2.1.4 (M:) Subunit A {Escherichia coli}

HGKSKLIAPLALTIFVWVFLMNLMDLLPIDLLPYIAEHVLGLPALRVVPSADVNVTLSMALGVFILILFYSIKMKGIGGFTKELTLQPFNHWAFIPVNLILEGVSLLSKPVSLGLRLFGNMYAGELIFILIAGLLPWWSQWILNVPWAIFHILIITLQAFIFMVLTIVYLS

>d1h6ia\_ f.2.1.5 (A:) Aquaporin-1 {Human (Homo sapiens)}

LFWRAVVAEFLATTLFVFISIGSALGFKYPVGNNQTAVQDNVKVSLAFGLSIATLAQSVGHISGAHLNPAVTLGLLLSCQISIFRALMYIIAQCVGAIVATAILSGITSSLTGNSLGRNDLADGVNSGQGLGIEIIGTLQLVLCVLATTDRRRRDLGGSAPLAIGLSVALGHLLAIDYTGCGINPARSFGSAVITHNFSNHWIFWVGPFIGGALAVLIYDFILAP

>d1fx8a\_ f.2.1.5 (A:) Glycerol uptake facilitator protein GlpF {Escherichia coli}

TLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAILMGLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHL

>d1f6ga\_ f.2.1.11 (A:) Potassium chanel protein {Streptomyces lividans}

MPPMLSGLLARLVKLLLGRHGSALHWAAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPAALWWSVETATTVGYGDLYPVTLWGRCVAVVVMVAGITSFGLVTAALATWFVGREQERRGHFVRHSEKAAEEAYTRTTRALHERFDRLERMLDDNRR

>d1kkda\_ f.2.1.11 (A:) Small conductance potassium channel {Rat (Rattus norvegicus)}

RKLELTKAEKHVHNFMMDTQLTKRVKNAAANVLRETWLIYKNTKLVKKIDHAKVRKHQRKFLQAIHQLRSVKMEQRKLNDQANTLVDLAKTQ

>d1msla\_ f.2.1.11 (A:) Gated mechanosensitive channel {Mycobacterium tuberculosis}

ARGNIVDLAVAVVIGTAFTALVTKFTDSIITPLINRIGVNAQSDVGILRIGIGGGQTIDLNVLLSAAINFFLIAFAVYFLVVLPYNTLRKKGEVEQPGDTQVVLLTEIR

>d1be3e2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

SHTDIKVPDFSDYRRPEVLDSTKSSKESSEARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSASADVL

>d1be3f1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

AVSASSRWLEGIRKWYYNAAGFNKLGLMRDDTIHENDDVKEAIRRLPENLYDDRVFRIKRALDLSMRQQILPKEQWTKYEEDKSYLEPYLKEVIRERKEREEWAKK

>d1be3g1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRRTRACILRVAPPFVAFYLVYTWGTQEFEKSKRKNPAAYENDR

>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

>d1bcch1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

LVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSQTEEDCTEELFDFLHARDHCVAHKLFNSLK

>d1bccj1 f.2.1.8 (J:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

TLTARLYSLLFRRTSTFALTIVVGALLFERAFDQGADAIYEHINEGKLWKHIKHKYENK

>d1ezvc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

MAFRKSNVYLSLVNSYIIDSPQPSSINYWWNMGSLLGLCLVIQIVTGIFMAMHYSSNIELAFSSVEHIMRDVHNGYILRYLHANGASFFFMVMFMHMAKGLYYGSYRSPRVTLWNVGVIIFTLTIATAFLGYCCVYGQMSHWGATVITNLFSAIPFVGNDIVSWLWGGFSVSNPTIQRFFALHYLVPFIIAAMVIMHLMALHIHGSSNPLGITGNLDRIPMHSYFIFKDLVTVFLFMLILALFVFYSPNTLGHPDNYIPGNPLVTPASIVPEWYLLPFYAILRSIPDKLLGVITMFAAILVLLVLPFTDRSVVRGNTFKVLSKFFFFIFVFNFVLLGQIGACHVEVPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIGRVNK

>d1ezve2 f.2.1.8 (E:31-86) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

KSTYRTPNFDDVLKENNDADKGRSYAYFMVGAMGLLSSAGAKSTVETFISSMTATA

>d1ezvf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

QSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRRLPEDESYARAYRIIRAHQTELTHHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIEVSK

>d1ezvg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

GPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVFNSFRRFKSQFLYVLIPAGIYWYWWKNGNEYNEFLYSKAGREELERVNV

>d1ezvh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

VTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHKEDCVEEFFHLQHYLDTATAPRLFDKLK

>d1ezvi1 f.2.1.8 (I:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

SSLYKTFFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAA

>d1fumc\_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Escherichia coli}

TTKRKPYVRPMTSTWWKKLPFYRFYMLREGTAVPAVWFSIELIFGLFALKNGPEAWAGFVDFLQNPVIVIINLITLAAALLHTKTWFELAPKAANIIVKDEKMGPEPIIKSLWAVTVVATIVILFVALYW

>d1fumd\_ f.2.1.9 (D:) Fumarate reductase respiratory complex transmembrane subunits {Escherichia coli}

INPNPKRSDEPVFWGLFGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLAFAQSFIGRVFLFLMIVLPLWCGLHRMHHAMHDLKIHVPAGKWVFYGLAAILTVVTLIGVVTI

>d1qlac\_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Wolinella succinogenes}

MTNESILESYSGVTPERKKSRMPAKLDWWQSATGLFLGLFMIGHMFFVSTILLGDNVMLWVTKKFELDFIFEGGKPIVVSFLAAFVFAVFIAHAFLAMRKFPINYRQYLTFKTHKDLMRHGDTTLWWIQAMTGFAMFFLGSVHLYIMMTQPQTIGPVSSSFRMVSEWMWPLYLVLLFAVELHGSVGLYRLAVKWGWFDGETPDKTRANLKKLKTLMSAFLIVLGLLTFGAYVKKGLEQTDPNIDYKYFDYKRTH

>d1jb0a\_ f.2.1.12 (A:) Photosystem I {Synechococcus elongatus}

RVVVDNDPVPTSFEKWAKPGHFDRTLARGPQTTTWIWNLHALAHDFDTHTSDLEDISRKIFSAHFGHLAVVFIWLSGMYFHGAKFSNYEAWLADPTGIKPSAQVVWPIVGQGILNGDVGGGFHGIQITSGLFQLWRASGITNEFQLYCTAIGGLVMAGLMLFAGWFHYHKRAPKLEWFQNVESMLNHHLAGLLGLGSLAWAGHQIHVSLPINKLLDAGVAAKDIPLPHEFILNPSLMAELYPKVDWGFFSGVIPFFTFNWAAYSDFLTFNGGLNPVTGGLWLSDTAHHHLAIAVLFIIAGHMYRTNWGIGHSLKEILEAHKGPFTGAGHKGLYEVLTTSWHAQLAINLAMMGSLSIIVAQHMYAMPPYPYLATDYPTQLSLFTHHMWIGGFLVVGGAAHGAIFMVRDYDPAMNQNNVLDRVLRHRDAIISHLNWVCIFLGFHSFGLYVHNDTMRAFGRPQDMFSDTGIQLQPVFAQWVQNLHTLAPGGTAPNAAATASVAFGGDVVAVGGKVAMMPIVLGTADFMVHHIHAFTIHVTVLILLKGVLFARSSRLIPDKANLGFRFPCDGPGRGGTCQVSGWDHVFLGLFWMYNCISVVIFHFSWKMQSDVWGTVAPDGTVSHITGGNFAQSAITINGWLRDFLWAQASQVIGSYGSALSAYGLLFLGAHFIWAFSLMFLFSGRGYWQELIESIVWAHNKLKVAPAIQPRALSIIQGRAVGVAHYLLGGIATTWAFFLARIISVG

>d1jb0f\_ f.2.1.12 (F:) Photosystem I {Synechococcus elongatus}

DVAGLVPCKDSPAFQKRAAAAVNTTADPASGQKRFERYSQALCGEDGLPHLVVDGRLSRAGDFLIPSVLFLYIAGWIGWVGRAYLIAVRNSGEANEKEIIIDVPLAIKCMLTGFAWPLAALKELASGELTAKDNEITVSPR

>d1jb0i\_ f.2.1.12 (I:) Photosystem I {Synechococcus elongatus}

MMGSYAASFLPWIFIPVVCWLMPTVVMGLLFLYIEGEA

>d1jb0k\_ f.2.1.12 (K:) Photosystem I {Synechococcus elongatus}

ILCNLFAIALGRYAIQSRGKGPGLPIALPALFEGFGLPELLATTSFGHLLAAGVVSGL

>d1jb0l\_ f.2.1.12 (L:) Photosystem I {Synechococcus elongatus}

LVKPYNGDPFVGHLSTPISDSGLVKTFIGNLPAYRQGLSPILRGLEVGMAHGYFLIGPWVKLGPLRDSDVANLGGLISGIALILVATACLAAYGLVSFQKGGSSSDPLKTSEGWSQFTAGFFVGAMGSAFVAFFLLENFLVVDGIMTGLFN

>d1kzua\_ f.3.1.1 (A:) Light-harvesting complex subunits {Purple bacterium (Rhodopseudomonas acidophila)}

MNQGKIWTVVNPAIGIPALLGSVTVIAILVHLAILSHTTWFPAYWQGGV

>d1lgha\_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodospirillum molischianum}

SNPKDDYKIWLVINPSTWLPVIWIVATVVAIAVHAAVLAAPGFNWIALGAAKSAAK

>d1lghb\_ f.3.1.1 (B:) Light-harvesting complex subunits {Rhodospirillum molischianum}

RSLSGLTEEEAIAVHDQFKTTFSAFIILAAVAHVLVWVWKPWF

>d1jo5a\_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodobacter sphaeroides}

ADKSDLGYTGLTDEQAQELHSVYMSGLWLFSAVAIVAHLAVYIWRPWF

>d1g90a\_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}

APKDNTWYTGAKLGFSQYHDTGFINNNGPTHENQLGAGAFGGYQVNPYVGFEMGYDFLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVFRADTKSNVYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQFTNNIGDAHTIGTRPDNGMLSLGVSYRFGQGEAA

>d1qj8a\_ f.4.1.1 (A:) Outer membrane protein X (OMPX) {Escherichia coli}

ATSTVTGGYAQSDAQGQMNKMGGFNLKYRYEEDNSPLGVIGSFTYTEKSRTASSGDYNKNQYYGITAGPAYRINDWASIYGVVGVGYGKFQTTEYPTYKNDTSDYGFSYGAGLQFNPMENVALDFSYEQSRIRSVDVGTWIAGVGYRF

>d2por\_\_ f.4.3.1 (-) Porin {Rhodobacter capsulatus}

EVKLSGDARMGVMYNGDDWNFSSRSRVLFTMSGTTDSGLEFGASFKAHESVGAETGEDGTVFLSGAFGKIEMGDALGASEALFGDLYEVGYTDLDDRGGNDIPYLTGDERLTAEDNPVLLYTYSAGAFSVAASMSDGKVGETSEDDAQEMAVAAAYTFGNYTVGLGYEKIDSPDTALMADMEQLELAAIAKFGATNVKAYYADGELDRDFARAVFDLTPVAAAATAVDHKAYGLSVDSTFGATTVGGYVQVLDIDTIDDVTYYGLGASYDLGGGASIVGGIADNDLPNSDMVADLGVKFKF

>d3prn\_\_ f.4.3.1 (-) Porin {Rhodopseudomonas blastica, strain DSM2131}

MISLNGYGRFGLQYVEDRGVGLEDTIISSRLRINIVGTTETDQGVTFGAKLRMQWDDGDAFAGTAGNAAQFWTSYNGVTVSVGNVDTAFDSVALTYDSEMGYEWSSFGDAQSSFFAYNSKYDASGALDNYNGIAVTYSISGVNLYLSYVDPDQTVDSSLVTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGATTVRAYVSDIDRAGADTAYGIGADYQFAEGVKVSGSVQSGFANETVADVGVRFDF

>d1osma\_ f.4.3.1 (A:) Porin {Klebsiella pneumoniae}

AEIYNKDGNKLDLYGKIDGLHYFSDDKDVDGDQTYMRLGVKGETQINDQLTGYGQWEYNVQANNTESSSDQAWTRLAFAGLKFGDAGSFDYGRNYGVVYDVTSWTDVLPEFGGDTYGSDNFLQSRANGVATYRNSDFFGLVDGLNFALQYQGKNGSVSGEGATNNGRGALKQNGDGFGTSVTYDIFDGISAGFAYANSKRTDDQNQLLLGEGDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSLGFANKAQNFEVAAQYQFDFGLRPSVAYLQSKGKDLNGYGDQDILKYVDVGATYYFNKNMSTYVDYKINLLDDNSFTRSAGISTDDVVALGLVYQF

>d1e54a\_ f.4.3.1 (A:) Porin {Comamonas acidovorans}

ESSVTLFGIVDTNVAYVNKDAAGDSRYGLGTSGASTSRLGLRGTEDLGGGLKAGFWLEGEIFGDDGNASGFNFKRRSTVSLSGNFGEVRLGRDLVPTSQKLTSYDLFSATGIGPFMGFRNWAAGQGADDNGIRANNLISYYTPNFGGFNAGFGYAFDEKQTIGTADSVGRYIGGYVAYDNGPLSASLGLAQQKTAVGGLATDRDEITLGASYNFGVAKLSGLLQQTKFKRDIGGDIKTNSYMLGASAPVGGVGEVKLQYALYDQKAIDSKAHQITLGYVHNLSKRTALYGNLAFLKNKDASTLGLQAKGVYAGGVQAGESQTGVQVGIRHAF

>d1af6a\_ f.4.3.2 (A:) Maltoporin (also LamB protein) {Escherichia coli}

VDFHGYARSGIGWTGSGGEQQCFQTTGAQSKYRLGNECETYAELKLGQEVWKEGDKSFYFDTNVAYSVAQQNDWEATDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYYWDISGPGAGLENIDVGFGKLSLAATRSSEAGGSSSFASNNIYDYTNETANDVFDVRLAQMEINPGGTLELGVDYGRANLRDNYRLVDGASKDGWLFTAEHTQSVLKGFNKFVVQYATDSMTSQGKGLSQGSGVAFDNEKFAYNINNNGHMLRILDHGAISMGDNWDMMYVGMYQDINWDNDNGTKWWTVGIRPMYKWTPIMSTVMEIGYDNVESQRTGDKNNQYKITLAQQWQAGDSIWSRPAIRVFATYAKWDEKWGYDYTGNADNNANFGKAVPADFNGGSFGRGDSDEWTFGAQMEIWW

>d1a0tp\_ f.4.3.2 (P:) Sucrose-specific porin {Enterobacterium (Salmonella typhimurium)}

SGFEFHGYARSGVIMNDSGASTKSGAYITPAGETGGAIGRLGNQADTYVEMNLEHKQTLDNGATTRFKVMVADGQTSYNDWTASTSDLNVRQAFVELGNLPTFAGPFKGSTLWAGKRFDRDNFDIHWIDSDVVFLAGTGGGIYDVKWNDGLRSNFSLYGRNFGDIDDSSNSVQNYILTMNHFAGPLQMMVSGLRAKDNDERKDSNGNLAKGDAANTGVHALLGLHNDSFYGLRDGSSKTALLYGHGLGAEVKGIGSDGALRPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQWATFNLRLIQAINQNFALAYEGSYQYMDLKPEGYNDRQAVNGSFYKLTFAPTFKVGSIGDFFSRPEIRFYTSWMDWSKKLNNYASDDALGSDGFNSGGEWSFGVQMETWF

>d1by5a\_ f.4.3.3 (A:) Ferric hydroxamate uptake receptor FhuA {Escherichia coli}

QESAWGPAATIAARQSATGTKTDTPIQKVPQSISVVTAEEMALHQPKSVKEALSYTPGVSVGTRGASNTYDHLIIRGFAAEGQSQNNYLNGLKLQGNFYNDAVIDPYMLERAEIMRGPVSVLYGKSSPGGLLNMVSKRPTTEPLKEVQFKAGTDSLFQTGFDFSDSLDDDGVYSYRLTGLARSANAQQKGSEEQRYAIAPAFTWRPDDKTNFTFLSYFQNEPETGYYGWLPKEGTVEPLPNGKRLPTDFNEGAKNNTYSRNEKMVGYSFDHEFNDTFTVRQNLRFAENKTSQNSVYGYGVCSDPANAYSKQCAALAPADKGHYLARKYVVDDEKLQNFSVDTQLQSKFATGDIDHTLLTGVDFMRMRNDINAWFGYDDSVPLLNLYNPVNTDFDFNAKDPANSGPYRILNKQKQTGVYVQDQAQWDKVLVTLGGRYDWADQESLNRVAGTTDKRDDKQFTWRGGVNYLFDNGVTPYFSYSESFEPSSQVGKDGNIFAPSKGKQYEVGVKYVPEDRPIVVTGAVYNLTKTNNLMADPEGSFFSVEGGEIRARGVEIEAKRPLSASVNVVGSYTYTDAEYTTDTTYKGNTPAQVPKHMASLWADYTFFDGPLSGLTLGTGGRYTGSSYGDPANSFKVGSYTVVDALVRYDLARVGMAGSNVALHVNNLFDREYVASCFNTYGCFWGAERQVVATATFRF

>d1fepa\_ f.4.3.3 (A:) Ferric enterobactin receptor FepA {Escherichia coli}

DDTIVVTAAEQNLQAPGVSTITADEIRKNPVARDVSKIIRTMPGVNLTGNSTSGQRGNNRQIDIRGMGPENTLILIDGKPVSSRNSVRQGWRGERDTRGDTSWVPPEMIERIEVLRGPAAARYGNGAAGGVVNIITKKGSGEWHGSWDAYFNAPEHKEEGATKRTNFSLTGPLGDEFSFRLYGNLDKTQADAWDINQGHQSARAGTYATTLPAGREGVINKDINGVVRWDFAPLQSLELEAGYSRQGNLYAGDTQNTNSDSYTRSKYGDETNRLYRQNYALTWNGGWDNGVTTSNWVQYEHTRNSRIPEGLAGGTEGKFNEKATQDFVDIDLDDVMLHSEVNLPIDFLVNQTLTLGTEWNQQRMKDLSSNTQALTGTNTGGAIDGVSTTDRSPYSKAEIFSLFAENNMELTDSTIVTPGLRFDHHSIVGNNWSPALNISQGLGDDFTLKMGIARAYKAPSLYQTNPNYILYSKGQGCYASAGGCYLQGNDDLKAETSINKEIGLEFKRDGWLAGVTWFRNDYRNKIEAGYVAVGQNAVGTDLYQWDNVPKAVVEGLEGSLNVPVSETVMWTNNITYMLKSENKTTGDRLSIIPEYTLNSTLSWQAREDLSMQTTFTWYGKQQPKKYNYKGQPAVGPETKEISPYSIVGLSATWDVTKNVSLTGGVDNLFDKRLWRAGNAQTTGDLAGANYIAGAGAYTYNEPGRTWYMSVNTHF

>d7ahla\_ f.6.1.1 (A:) Alpha-hemolysin {Staphylococcus aureus}

ADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFIDDKNHNKKLLVIRTKGTIAGQYRVYSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMSTLTYGFNGNVTGDDTGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWGPYDRDSWNPVYGNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFSPDFATVITMDRKASKQQTNIDVIYERVRDDYQLHWTSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN

>d1pvl\_\_ f.6.1.1 (-) Leucocidin K component LukF-PV {Staphylococcus aureus}

AQHITPVSEKKVDDKITLYKTTATSDSDKLKISQILTFNFIKDKSYDKDTLILKAAGNIYSGYTKPNPKDTISSQFYWGSKYNISINSDSNDSVNVVDYAPKNQNEEFQVQQTVGYSYGGDINISNGLSGGGNGSKSFSETINYKQESYRTSLDKRTNFKKIGWDVEAHKIMNNGWGPYGRDSYHSTYGNEMFLGSRQSNLNAGQNFLEYHKMPVLSRGNFNPEFIGVLSRKQNAAKKSKITVTYQREMDRYTNFWNQLHWIGNNYKDENRATHTSIYEVDWENHTVKLIDTQSKEKNPMS

>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)}

MFPAMPLSSLFVNGPRTLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRACQTGIVDECCFRSCDLRRLEMYCAPLKPAKSA

>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)}

LFECSFSCEIEKEGDKPCKKKKCKGGWKCKFNMCVKV

>d1jzaa\_ g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing, variant 2}

KEGYLVNKSTGCKYGCLKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSCS

>d1bcg\_\_ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthotus judaicus), BJXTR-IT}

MKKNGYPLDRNGKTTECSGVNAIAPHYCNSECTKVYYAESGYCCWGACYCFGLEDDKPIGPMKDITKKYCDVQI

>d1bmr\_\_ g.3.7.1 (-) LQH III alpha-like toxin, LQH {Hebraei scorpion (Leiurus quinquestriatus hebraeus)}

VRDGYIAQPENCVYHCFPGSSGCDTLCKEKGGTSGHCGFKVGHGLACWCNALPDNVGIIVEGEKCHS

>d1cmr\_\_ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}

CTTSKECWSVCQRLHNTSKGWCDHRGCICES

>d1chl\_\_ g.3.7.2 (-) Chlorootoxin {Scorpion (Leiurus quinquestriatus), venom}

MCMPCFTTDHQMARKCDDCCGGKGRGKCYGPQCLCR

>d1c55a\_ g.3.7.2 (A:) Butantoxin {Brazilian scorpion (Tityus serrulatus)}

WCSTCLDLACGASRECYDPCFKAFGRAHGKCMNNKCRCYT

>d1pnh\_\_ g.3.7.2 (-) Toxin analog {Scorpion (Androctonus mauretanicus mauretanicus)}

TVCNLRRCQLSCRSLGLLGKCIGVKCECVKH

>d1gpt\_\_ g.3.7.5 (-) gamma-Thionin {Barley (Hordeum vulgare)}

RICRRRSAGFKGPCVSNKNCAQVCMQEGWGGGNCDGPLRRCKCMRRC

>d1ayj\_\_ g.3.7.5 (-) Antifungal protein 1 (RS-AFP1) {Radish (Raphanus sativus)}

EKLCERPSGTWSGVCGNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC

>d1brz\_\_ g.3.7.5 (-) Brazzein {J'oublie (Pentadiplandra brazzeana)}

EDKCKKVYENYPVSKCQLANQCNYDCKLDKHARSGECFYDEKRNLQCICDYCEY

>d1boea\_ g.3.9.1 (A:) Insulin-like growth factor-binding protein-5 (IGFBP-5) {Human (Homo sapiens)}

ALAEGQSCGVYTERCAQGLRCLPRQDEEKPLHALLHGRGVCLNEKS

>d1igra3 g.3.9.1 (A:150-299) Cys-rich domain of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

DLCPGTMEEKPMCEKTTINNEYNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVACRHYYYAGVCVPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCEGPCP

>d1lpba2 g.3.10.1 (A:45-90) (Pro)colipase {Pig (Sus scrofa)}

ENSECSAFTLYGVYYKCPCERGLTCEGDKSLVGSITNTNFGICHNV

>d1pco\_1 g.3.10.1 (1-44) (Pro)colipase {Pig (Sus scrofa)}

VPDPRGIIINLDEGELCLNSAQCKSNCCQHDTILSLSRCALKAR

>d1imt\_1 g.3.10.1 (1-36) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}

AVITGACERDLQCGKGTCCAVSLWIKSVRVCTPVGT

>d1imt\_2 g.3.10.1 (37-80) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}

SGEDCHPASHKIPFSGQRMHHTCPCAPNLACVQTSPKKFKCLSK

>d1pfxl2 g.3.11.1 (L:87-146) Factor IX (IXa) {Pig (Sus scrofa)}

TCNIKNGRCKQFCKTGADSKVLCSCTTGYRLAPDQKSCKPAVPFPCGRVSVSHSPTTLTR

>d1danl2 g.3.11.1 (L:87-142) Coagulation factor VIIa {Human (Homo sapiens)}

DQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPILE

>d1f7ea\_ g.3.11.1 (A:) Coagulation factor VIIa {Human (Homo sapiens)}

SDGDQCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDGSA

>d1g1sa2 g.3.11.1 (A:119-158) E-selectin, EGF-domain {Human (Homo sapiens)}

TASCQDMSCSKQGECLETIGNYTCSCYPGFYGPECEYVRD

>d1autl1 g.3.11.1 (L:49-96) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}

QCLVLPLEHPCASLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFL

>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)}

NSYPGCPSSYDGYCLNGGVCMHIESLDSYTCNCVIGYSGDRCQTRDLRWWELR

>d3tgf\_\_ g.3.11.1 (-) Transforming growth factor alpha {Human (Homo sapiens)}

VVSHFNDCPDSHTQFCFHGTCRFLVQEDKPACVCHSGYVGARCEHADLLA

>d1urk\_1 g.3.11.1 (6-49) Plasminogen activator (urokinase-type) {Human (Homo sapiens)}

QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKT

>d1hae\_\_ g.3.11.1 (-) Heregulin-alpha, EGF-like domain {Human (Homo sapiens)}

SHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKVQNQEKAEELY

>d1zaq\_\_ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}

EPVDPCFRANCEYQCQPLNQTSYLCVCAEGFAPIPHEPHRCQMF

>d1apq\_\_ 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)}

VNWCERTTLSNGGCQYLCLPAPQINPHSPKFTCACPDGMLLARDMRSCLT

>d1klo\_1 g.3.11.2 (11-65) Laminin gamma1 chain {Mouse (Mus musculus)}

CPCPGGSSCAIVPKTKEVVCTHCPTGTAGKRCELCDDGYFGDPLGSNGPVRLCRP

>d1klo\_2 g.3.11.2 (66-121) Laminin gamma1 chain {Mouse (Mus musculus)}

CQCNDNIDPNAVGNCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKA

>d1klo\_3 g.3.11.2 (122-172) Laminin gamma1 chain {Mouse (Mus musculus)}

CACNPYGTVQQQSSCNPVTGQCQCLPHVSGRDCGTCDPGYYNLQSGQGCER

>d1b9wa1 g.3.11.4 (A:1-45) Merozoite surface protein 1 (MSP-1) {Plasmodium cynomolgi}

MSSEHRCIDTNVPENAACYRYLDGTEEWRCLLYFKEDAGKCVPAP

>d1ceja2 g.3.11.4 (A:46-96) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}

NPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN

>d1df9c\_ g.3.13.1 (C:) Bowman-Birk inhibitor, BBI {Mung bean (Vigna radiata)}

SHDEPSESSEPCCDSCDCTKSIPPQCHCANIRLNSCHSACKSCICTRSMPGKCRCLDTDDFCYKPCESMDKD

>d1c2aa1 g.3.13.1 (A:4-64) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}

KRPWKCCDEAVCTRSIPPICTCMDEVFECPKTCKSCGPSMGDPSRRICQDQYVGDPGPICR

>d1ejab\_ g.3.15.1 (B:) Bdellastasin {Medicinal leech (Hirudo medicinalis)}

TTPCGPVTCSGAQMCEVDKCVCSDLHCKVKCEHGFKKDDNGCEYACICADAPQ

>d1skz\_1 g.3.15.1 (7-58) Factor Xa inhibitor antistasin {Mexican leech (Haementeria officinalis)}

GCEEAGCPEGSACNIITDRCTCSGVRCRVHCPHGFQRSRYGCEFCKCRLEPM

>d1hrti\_ g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}

VVYTDCTESGQNLCLCEGSNVCGQGNKCILGSDGEKNQCVTGEGTPKPQSHNDGDFEEIPEEYLQ

>d1e0fi\_ g.3.15.2 (I:) Haemadin {Indian leech (Haemadipsa sylvestris)}

IRFGMGKVPCPDGEVGYTCDCGEKICLYGQSCNDGQCSGDPKPSSEFEEFEIDEEEK

>d1fas\_\_ g.7.1.1 (-) Fasciculin {Green mamba (Dendroaspis angusticeps)}

TMCYSHTTTSRAILTNCGENSCYRKSRRHPPKMVLGRGCGCPPGDDYLEVKCCTSPDKCNY

>d1hc9a\_ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), Alpha-bungarotoxin}

IVCHTTATSPISAVTCPPGENLCYRKMWCDVFCSSRGKVVELGCAATCPSKKPYEEVTCCSTDKCNPHPKQRPG

>d1f94a\_ g.7.1.1 (A:) Bucandin {Malayan krait (Bungarus candidus)}

MECYRCGVSGCHLKITCSAEETFCYKWLNKISNERWLGCAKTCTEIDTWNVYNKCCTTNLCNT

>d1jgka\_ g.7.1.1 (A:) Candoxin {Malayan krait (Bungarus candidus)}

MKCKICNFDTCRAGELKVCASGEKYCFKESWREARGTRIERGCAATCPKGSVYGLYVLCCTTDDCN

>d1erh\_\_ g.7.1.3 (-) CD59 {Human (Homo sapiens)}

LQCYNCPNPTADCKTAVNCSSDFDACLITKAGLQVYNKCWKFEHCNFNDVTTRLRENELTYYCCKKDLCN

>d1btea\_ g.7.1.3 (A:) Type II activin receptor {Mouse (Mus musculus)}

ETQECLFFNANWERDRTNQTGVEPCYGDKDKRRHCFATWKNISGSIEIVKQGCWLDDINCYDRTDCIEKKDSPEVYFCCCEGNMCNEKFSYFPEME

>d1es7b\_ g.7.1.3 (B:) BMP receptor Ia ectodomain {Human (Homo sapiens)}

TLPFLKCYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYLQPTLPP

>d1ktzb\_ g.7.1.3 (B:) TGF-beta type II receptor extracellular domain {Human (Homo sapiens)}

PQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSCSSDECNDNIIFSEEY

>d1adz\_\_ g.8.1.1 (-) Tissue factor pathway inhibitor {Human (Homo sapiens)}

DYKDDDDKLKPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDGPNGF

>d1irha\_ g.8.1.1 (A:) Tissue factor pathway inhibitor {Human (Homo sapiens)}

EFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGCGGNENNFTSKQECLRACKKG

>d1bunb\_ g.8.1.1 (B:) beta2-bungarotoxin, neurotoxin chain {Many-banded krait (elapid) (Bungarus multicinctus)}

RKRHPDCDKPPDTKICQTVVRAFYYKPSAKRCVQFRYGGCNGNGNHFKSDHLCRCECLEYR

>d1bf0\_\_ g.8.1.1 (-) Calcicludine (cac) {Green mamba (Dendroaspis angusticeps)}

WQPPWYCKEPVRIGSCKKQFSSFYFKWTAKKCLPFLFSGCGGNANRFQTIGECRKKCLGK

>d1tocr1 g.8.1.2 (R:1A-56) Ornithodorin {Soft tick (Ornithodoros moubata)}

SLNVLCNNPHTADCNNDAQVDRYFREGTTCLMSPACTSEGYASQHECQQACFVGGED

>d1tocr2 g.8.1.2 (R:57-119) Ornithodorin {Soft tick (Ornithodoros moubata)}

HSSEMHSSCLGDPPTSCAEGTDITYYDSDSKTCKVLAASCPSGENTFESEVECQVACGAPIEG

>d1d0da\_ g.8.1.2 (A:) Anticoagulant protein, factor Xa inhibitor {Soft tick (Ornithodoros moubata)}

YNRLCIKPRDWIDECDSNEGGERAYFRNGKGGCDSFWICPEDHTGADYYSSYRDCFNACI

>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)}

AACKCDDEGPDIRTAPLTGTVDLGSCNAGWEKCASYYTIIADCCRKKK

>d1ahl\_\_ g.9.1.1 (-) Anthopleurin-A {Giant green sea anemone (Anthopleura xanthogrammica)}

GVSCLCDSDGPSVRGNTLSGTLWLYPSGCPSGWHNCKAHGPTIGWCCKQ

>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)}

AVGDRCERNEFQCQDGKCISYKWVCDGSAECQDGSDESQETCLSVT

>d1k7ba\_ g.12.1.1 (A:) soluble Tva ectodomain, sTva47 {Quail (Coturnix coturnix)}

SCPPGQFRCSEPPGAHGECYPQDWLCDGHPDCDDGRDEWGCG

>d1ejga\_ g.13.1.1 (A:) Crambin {Abyssinian cabbage (Crambe abyssinica)}

TTCCPSIVARSNFNVCRLPGTPEALCATYTGCIIIPGATCPGDYAN

>d1bhp\_\_ g.13.1.1 (-) beta-Purothionin {Wheat (Triticum aestivum)}

KSCCKSTLGRNCYNLCRARGAQKLCANVCRCKLTSGLSCPKDFPK

>d1pmla\_ g.14.1.1 (A:) Plasminogen kringles {Human (Homo sapiens)}

SDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCST

>d2pf1\_1 g.14.1.1 (66-156) Prothrombin kringle domain {Cow (Bos taurus)}

CAEGVGMNYRGNVSVTRSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSITGPWCYTTSPTLRREECSVPVCGQDRVTVEVIPR

>d1a0ha1 g.14.1.1 (A:164-270) Meizothrombin kringle domain {Cow (Bos taurus)}

SPLLETCVPDRGREYRGRLAVTTHGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVADQPGDFEYCDLNYCEEPVDGDLGDRLGEDPDPDAAIEG

>d1tbrr1 g.15.1.1 (R:1-51) Rhodniin {Bug (Rhodnius prolixus)}

EGGEPCACPHALHRVCGSDGETYSNPCTLNCAKFNGKPELVKVHDGPCEPD

>d1tbrr2 g.15.1.1 (R:52-103) Rhodniin {Bug (Rhodnius prolixus)}

EDEDVCQECDGDEYKPVCGSDDITYDNNCRLECASISSSPGVELKHEGPCRT

>d1nuba3 g.15.1.1 (A:78-135) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}

CQDPTSCPAPIGEFEKVCSNDNKTFDSSCHFFATKCTLEGTKKGHKLHLDYIGPCKYI

>d2bus\_\_ g.15.1.1 (-) Seminal plasma inhibitor IIa {Cow (Bos taurus)}

EGAQVDCAEFKDPKVYCTRESNPHCGSNGETYGNKCAFCKAVMKSGGKINLKHRGKC

>d1pce\_\_ g.15.1.1 (-) PEC-60 peptide {Pig (Sus scrofa)}

EKQVFSRMPICEHMTESPDCSRIYDPVCGTDGVTYESECKLCLARIENKQDIQIVKDGEC

>d1pdga\_ g.17.1.1 (A:) Platelet-derived growth factor BB {Human (Homo sapiens)}

EPAMIAECKTRTEVFEISRRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQCRPTQVQLRPVQVRKIEIVRKKPIFKKATVTLEDHLACKCETVAA

>d1fzva\_ g.17.1.1 (A:) Placenta growth factor-1, PLGF-1 {Human (Homo sapiens)}

SSEVEVVPFQEVWGRSYCRALERLVDVVSEYPSEVEHMFSPSCVSLLRCTGCCGDENLHCVPVETANVTMQLLKIRSGDRPSYVELTFSQHVRCECRPLR

>d1tgj\_\_ g.17.1.2 (-) TGF-beta3 {Human (Homo sapiens)}

ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS

>d1bmp\_\_ g.17.1.2 (-) Bone morphogenetic protein-7 (BMP-7) {Human (Homo sapiens)}

QACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGCH

>d1agqa\_ g.17.1.2 (A:) Glial cell-derived neurotrophic factor, GDNF {Rat (Rattus norvegicus)}

NRGCVLTAIHLNVTDLGLGYETKEELIFRYCSGSCEAAETMYDKILKNLSRSRRLTSDKVGQACCRPVAFDDDLSFLDDSLVYHILRKHSAKRCGCI

>d1hcna\_ g.17.1.4 (A:) Glycoprotein hormones alpha chain (Gonadotropin A, Follitropin alpha) {Human (Homo sapiens)}

QDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYY

>d1hcnb\_ g.17.1.4 (B:) Gonadotropin B chain {Human (Homo sapiens)}

KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD

>d1fl7b\_ g.17.1.4 (B:) Follicle stimulating hormone, follitropin, beta chain {Human (Homo sapiens)}

CELTNITIAIEKEECRFCISINTAWCAGYCYTRDLVYKDPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTYPVATQCHCGKCDSDSTDCTVRGLGPSYCSFGEM

>d1hcc\_\_ g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}

EGLPCKSPPEISHGVVAHMSDSYQYGEEVTYKCFEGFGIDGPAIAKCLGEKWSHPPSCI

>d1hfi\_\_ g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}

EKIPCSQPPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKWSSPPQCE

>d1g40a1 g.18.1.1 (A:1-64) Complement control protein {Vaccinia virus}

CCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFNQCIK

>d1g40a3 g.18.1.1 (A:127-184) Complement control protein {Vaccinia virus}

VKCQSPPSISNGRHNGYEDFYTDGSVVTYSCNSGYSLIGNSGVLCSGGEWSDPPTCQI

>d1g40a4 g.18.1.1 (A:185-243) Complement control protein {Vaccinia virus}

VKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKCV

>d1ckla1 g.18.1.1 (A:1-62) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}

CEEPPTFEAMELIGKPKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYR

>d1ckla2 g.18.1.1 (A:63-126) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}

ETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKV

>d1c1za5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}

SCKLPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEHSSLAFWKTDASDVKPC

>d1quba1 g.18.1.1 (A:1-62) beta2-glycoprotein I {Human (Homo sapiens)}

GRTCPKPDDLPFSTVVPLKTFYEPGEEITYSCKPGYVSRGGMRKFICPLTGLWPINTLKCTP

>d1quba2 g.18.1.1 (A:63-120) beta2-glycoprotein I {Human (Homo sapiens)}

RVCPFAGILENGAVRYTTFEYPNTISFSCNTGFYLNGADSAKCTEEGKWSPELPVCAP

>d1quba3 g.18.1.1 (A:121-183) beta2-glycoprotein I {Human (Homo sapiens)}

IICPPPSIPTFATLRVYKPSAGNNSLYRDTAVFECLPQHAMFGNDTITCTTHGNWTKLPECRE

>d1quba4 g.18.1.1 (A:184-243) beta2-glycoprotein I {Human (Homo sapiens)}

VKCPFPSRPDNGFVNYPAKPTLYYKDKATFGCHDGYSLDGPEEIECTKLGNWSAMPSCKA

>d1ghqb1 g.18.1.1 (B:1-66) Complement receptor 2, cr2 {Human (Homo sapiens)}

AISCGSPPPILNGRISYYSTPIAVGTVIRYSCSGTFRLIGEKSLLCITKDKVDGTWDKPAPKCEYF

>d1ghqb2 g.18.1.1 (B:67-129) Complement receptor 2, cr2 {Human (Homo sapiens)}

NKYSSCPEPIVPGGYKIRGSTPYRHGDSVTFACKTNFSMNGNKSVWCQANNMWGPTRLPTCVS

>d1elva2 g.18.1.1 (A:342-409) Complement C1S protease domain {Human (Homo sapiens)}

LDCGIPESIENGKVEDPESTLFGSVIRYTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPKCVPV

>d1atb\_\_ g.22.1.1 (-) Ascaris trypsin inhibitor, ATI {Pig roundworm (Ascaris Lumbricoides), variant suum}

EAEKCTKPNEQWTKCGGCEGTCAQKIVPCTRECKPPRCECIASAGFVRDAQGNCIKFEDCPK

>d1coua\_ g.22.1.1 (A:) Anticoagulant protein {Dog hookworm (Ancylostoma caninum)}

KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNKDDKCVSAEDCELDNMDFIYPGTRNP

>d1exta1 g.24.1.1 (A:13-71) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL

>d1exta2 g.24.1.1 (A:72-115) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCF

>d1exta3 g.24.1.1 (A:116-172) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

NCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN

>d1d4va1 g.24.1.1 (A:69-114) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}

PQQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCL

>d1jmab1 g.24.1.1 (B:4-59) Cellular receptor HveA {Human (Homo sapiens)}

CKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQ

>d1e88a3 g.27.1.1 (A:1-41) Fibronectin {Human (Homo sapiens)}

YGHCVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGVSCQET

>d1fbr\_2 g.27.1.1 (47-93) Fibronectin {Human (Homo sapiens)}

NRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCERHTS

>d1qgba1 g.27.1.1 (A:17-60) Fibronectin {Human (Homo sapiens)}

SKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESKP

>d1qgba2 g.27.1.1 (A:61-109) Fibronectin {Human (Homo sapiens)}

EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANR

>d1tpg\_2 g.27.1.1 (1-50) Tissue-type plasminogen activator, t-PA {Human (Homo sapiens)}

SYQVICRDEKTQMIYQQHQSWLRPVLRSNRVEYCWCNSGRAQCHSVPVKS

>d1isua\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Rhodocyclus tenuis}

GTNAAMRKAFNYQDTAKNGKKCSGCAQFVPGASPTAAGGCKVIPGDNQIAPGGYCDAFIVKK

>d1js2a\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum, (formerly Chromatium vinosum)}

MEFMSAPANAVAADDATAIALKYNQDATKSERVAAARPGLPPEEQHCANCQFMQADAAGATDEWKGCQLFPGKLINVNGWSASWTLKAG

>d2hipa\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Ectothiorhodospira halophila}

EPRAEDGHAHDYVNEAADASGHPRYQEGQLCENCAFWGEAVQDGWGRCTHPDFDEVLVKAEGWCSVYAPAS

>d1hpi\_\_ g.35.1.1 (-) HIPIP (high potential iron protein) {Ectothiorhodospira vacuolata}

MERLSEDDPAAQALEYRHDASSVQHPAYEEGQTCLNCLLYTDASAQDWGPCSVFPGKLVSANGWCTAWVAR

>d1f2ig1 g.37.1.1 (G:1093-1131) ZIF268 {Mouse (Mus musculus)}

NLLNYVVPKMRPYACPVESCDRRFSRSDELTRHIRIHTG

>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)}

GSLLKPARFMCLPCGIAFSSPSTLEAHQAYYCSHRI

>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)}

RKRNRIPLRCTICRKRKVKCDKLRPHCQQCTKTGVAHLCHYME

>d2alca\_ g.38.1.1 (A:) Ethanol regulon transcriptional activator ALCR DNA-binding domain {Aspergillus nidulans and Emericella nidulans}

GSMADTRRRQNHSCDPCRKGKRRCDAPENRNEANENGWVSCSNCKRWNKDCTFNWLSSQRSKNSS

>d2nllb\_ g.39.1.2 (B:) Thyroid hormone receptor (TR-beta) DNA-binding domain {Human (Homo sapiens)}

DELCVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLHPSYSCKYEGKCVIDKVTRNQCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRRREELEK

>d1glua\_ g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain {Rat (Rattus norvegicus)}

MKPARPCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEARKTKK

>d1b8ta2 g.39.1.3 (A:36-100) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

LCMVCKKNLDSTTVAVHGDEIYCKSCYGKKYGPKGKGKGMGAGTLSTDKGESLGIKYEEGQSHRP

>d1b8ta3 g.39.1.3 (A:101-143) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

TNPNASRMAQKVGGSDGCPRCGQAVYAAEKVIGAGKSWHKSCF

>d1tfi\_\_ g.41.3.1 (-) Transcriptional factor SII, C-terminal domain {Human (Homo sapiens)}

KTGGTQTDLFTCGKCKKKNCTYTQVQTRSADEPMTTFVVCNECGNRWKFC

>d1pft\_\_ g.41.3.1 (-) Transcription inititiation factor TFIIB, N-terminal domain {Archaeon Pyrococcus furiosus}

MVNKQKVCPACESAELIYDPERGEIVCAKCGYVIEENIIDMGPEWRAFDA

>d1dl6a\_ g.41.3.1 (A:) Transcription inititiation factor TFIIB, N-terminal domain {Human (Homo sapiens)}

ASTSRLDALPRVTCPNHPDAILVEDYRAGDMICPECGLVVGDRVIDVGSEWRTFSNDK

>d1yua\_1 g.41.3.3 (1-65) Prokariotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}

MNGEVAPPKEDPVPLPELPCEKSDAYFVLRDGAAGVFLAANTFPKSRETRAPLVEELYRFRDRLP

>d1yua\_2 g.41.3.3 (66-122) Prokariotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}

EKLRYLADAPQQDPEGNKTMVRFSRKTKQQYVSSEKDGKATGWSAFYVDGKWVEGKK

>d1qcva\_ g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}

AKWVLKITGYIYDEDAGDPDNGISPGTKFEELPDDWVAPITGAPKSEFEKLED

>d1dx8a\_ g.41.5.1 (A:) Rubredoxin {Guillardia theta}

MEIDEGKYECEACGYIYEPEKGDKFAGIPPGTPFVDLSDSFMCPACRSPKNQFKSIKKVIAGFAENQKYG

>d1qyp\_\_ g.41.9.1 (-) RBP9 subunit of RNA polymerase II {Archaeon Thermococcus celer}

GSHMEQDLKTLPTTKITCPKCGNDTAYWWEMQTRAGDEPSTIFYKCTKCGHTWRSYE

>d1i50i1 g.41.9.1 (I:1-49) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}

MTTFRFCRDCNNMLYPREDKENNRLLFECRTCSYVEEAGSPLVYRHELI

>d1i50i2 g.41.9.1 (I:50-122) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}

TNIGETAGVVQDIGSDPTLPRSDRECPKCHSRENVFFQSQQRRKDTSMVLFFVCLSCSHIFTSDQKNKRTQFS

>d1fbva4 g.44.1.1 (A:356-434) CBL {Human (Homo sapiens)}

TPQDHIKVTQEQYELYCEMGSTFQLCKICAENDKDVKIEPCGHLMCTSCLTSWQESEGQGCPFCRCEIKGTEPIVVDPF

>d1rmd\_2 g.44.1.1 (1-86) V(D)J recombination activating protein 1 (RAG1), dimerization domain {Mouse (Mus musculus)}

NCSKIHLSTKLLAVDFPAHFVKSISCQICEHILADPVETSCKHLFCRICILRCLKVMGSYCPSCRYPCFPTDLESPVKSFLNILNS

>d1chc\_\_ g.44.1.1 (-) Immediate early protein, IEEHV {Equine herpes virus type 1}

MATVAERCPICLEDPSNYSMALPCLHAFCYVCITRWIRQNPTCPLCKVPVESVVHTIESDSEFGDQLI

>d1bor\_\_ g.44.1.1 (-) Acute promyelocytic leukaemia proto-onkoprotein PML {Human (Homo sapiens)}

EEEFQFLRCQQCQAEAKCPKLLPCLHTLCSGCLEASGMQCPICQAPWPLGADTPAL

>d1g25a\_ g.44.1.1 (A:) TFIIH Mat1 subunit {Human (Homo sapiens)}

MDDQGCPRCKTTKYRNPSLKLMVNVCGHTLCESCVDLLFVRGAGNCPECGTPLRKSNFRVQLFED

>d1e4ua\_ g.44.1.1 (A:) Not-4 N-terminal RING finger domain {Human (Homo sapiens)}

MSRSPDAKEDPVECPLCMEPLEIDDINFFPCTCGYQICRFCWHRIRTDENGLCPACRKPYPEDPAVYKPLSQEELQRI

>d1jm7a\_ g.44.1.1 (A:) brca1 RING domain {Human (Homo sapiens)}

MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQESTRFSQLVEELLKIICAFQLDTGLEYAN

>d1jm7b\_ g.44.1.1 (B:) bard1 RING domain {Human (Homo sapiens)}

MEPDGRGAWAHSRAALDRLEKLLRCSRCTNILREPVCLGGCEHIFCSNCVSDCIGTGCPVCYTPAWIQDLKINRQLDSMIQLCSKLRNLLHDNELSD

>d4mt2\_\_ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}

MDPNCSCATDGSCSCAGSCKCKQCKCTSCKKSCCSCCPVGCAKCSQGCICKEASDKCSCCA

>d1qjka\_ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus purpuratus)}

PDVKCVCCTEGKECACFGQDCCVTGECCKDGTCCGI

>d1faq\_\_ g.49.1.1 (-) RAF-1 {Human (Homo sapiens)}

LTTHNFARKTFLKLAFCDICQKFLLNGFRCQTCGYKFHEHCSTKVPTMCVDW

>d1tbo\_\_ g.49.1.1 (-) Protein kinase c-gamma {Rat (Rattus rattus)}

QTDDPRNKHKFRLHSYSSPTFCDHCGSLLYGLVHQGMKCSCCEMNVHRRCVRSVPSLCGVDHTERR

>d1kbea\_ g.49.1.1 (A:) Kinase suppressor of Ras, Ksr {Mouse (Mus musculus)}

GSVTHRFSTKSWLSQVCNVCQKSMIFGVKCKHCRLKCHNKCTKEAPACR

>d1dvpa2 g.50.1.1 (A:149-220) Hrs {Fruit fly (Drosophila melanogaster)}

MFTADTAPNWADGRVCHRCRVEFTFTNRKHHCRNCGQVFCGQCTAKQCPLPKYGIEKEVRVCDGCFAALQRG

>d1zbdb\_ g.50.1.1 (B:) Effector domain of rabphilin-3a {Rat (Rattus norvegicus)}

EELTDEEKEIINRVIARAEKMETMEQERIGRLVDRLETMRKNVAGDGVNRCILCGEQLGMLGSASVVCEDCKKNVCTKCGVETSNNRPHPVWLCKICLEQREVWKRSGAWFFKGFPKQVLPQPM

>d1adt\_2 g.51.1.1 (266-385) First Zn-domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}

TGCALWLHRCAEIEGELKCLHGSIMINKEHVIEMDVTSENGQRALKEQSSKAKIVKNRWGRNVVQISNTDARCCVHDAACPANQFSGKSCGMFFSEGAKAQVAFKQIKAFMQALYPNAQT

>d1adt\_3 g.51.1.1 (386-529) Second Zn-domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}

GHGHLLMPLRCECNSKPGHAPFLGRQLPKLTPFALSNAEDLDADLISDKSVLASVHHPALIVFQCCNPVYRNSRAQGGGPNCDFKISAPDLLNALVMVRSLWSENFTELPRMVVPQFKWSTKHQYRNVSLPVAHSDARQNPFDF

>d1f9xa\_ g.52.1.1 (A:) BIR domains of XIAP {Human (Homo sapiens)}

MSDAVSSDRNFPNSTNLPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTT

>d1i3oe\_ g.52.1.1 (E:) BIR domains of XIAP {Human (Homo sapiens)}

FALDRPSETHADYLLRTGQVVDISDTIYPRNPAMYSEEARLKSFQNWPDYAHLTPRELASAGLYYTGIGDQVQCFACGGKLKNWEPGDRAWSEHRRHFPNCFFVLGRNLNI

>d1e31a\_ g.52.1.1 (A:) Anti-apoptotic protein survivin {Human (Homo sapiens)}

TLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAA