# Phyre$^2$

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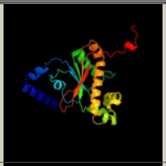
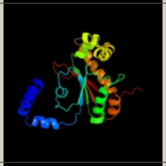
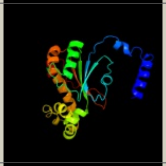
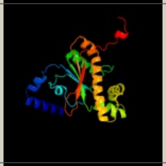
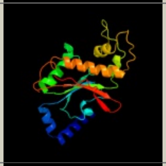
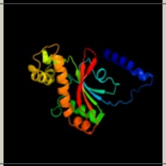
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ABE9 |
| Date | Wed Jan 25 15:20:22 GMT 2012 |
| Unique Job ID | 5e81d5c98bfb2ec0 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1ddza1 | Alignment |  | 100.0 | 25 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 2 | d1ekja_ | Alignment |  | 100.0 | 33 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 3 | d1ddza2 | Alignment |  | 100.0 | 24 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 4 | d1i6pa_ | Alignment |  | 100.0 | 29 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 5 | c1ddzA_ | Alignment |  | 100.0 | 25 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1 |
| 6 | c3ucoB_ | Alignment |  | 100.0 | 28 | **PDB header:**lyase/lyase inhibitor<br>**Chain:** B: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide |
| 7 | c2a8cE_ | Alignment |  | 100.0 | 31 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**carbonic anhydrase 2;<br>**PDBTitle:** haemophilus influenzae beta-carbonic anhydrase |
| 8 | c2w3nA_ | Alignment |  | 100.0 | 26 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbonic anhydrase 2;<br>**PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans |
| 9 | c2a5vB_ | Alignment |  | 100.0 | 25 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**carbonic anhydrase (carbonate dehydratase) (carbonic<br>**PDBTitle:** crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form |
| 10 | c3eyxB_ | Alignment |  | 100.0 | 27 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae |
| 11 | c3lasA_ | Alignment |  | 100.0 | 25 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative carbonic anhydrase;<br>**PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution |

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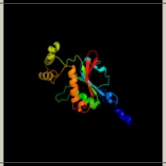
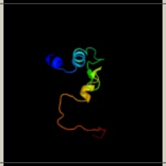
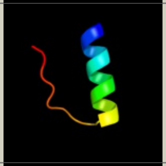
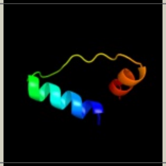
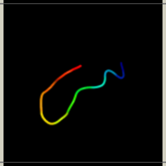
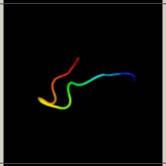
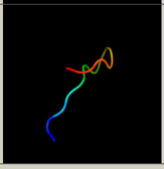
|---|---|---|---|---|---|---|
| 12 | c1ylkA_ | Alignment |  | 100.0 | 22 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein rv1284/mt1322;<br>**PDBTitle:** crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate |
| 13 | d1g5ca_ | Alignment |  | 100.0 | 33 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 14 | c2hwkA_ | Alignment |  | 61.5 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**helicase nsp2;<br>**PDBTitle:** crystal structure of venezuelan equine encephalitis2 alphavirus nsp2 protease domain |
| 15 | d1hlga_ | Alignment |  | 40.0 | 18 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Gastric lipase |
| 16 | d1zo0a1 | Alignment |  | 40.0 | 32 | **Fold:**Acyl-CoA N-acyltransferases (Nat)<br>**Superfamily:**Acyl-CoA N-acyltransferases (Nat)<br>**Family:**Ornithine decarboxylase antizyme-like |
| 17 | d1k8qa_ | Alignment |  | 39.9 | 15 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Gastric lipase |
| 18 | c3d89A_ | Alignment |  | 37.2 | 17 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**rieske domain-containing protein;<br>**PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus |
| 19 | d1fqta_ | Alignment |  | 34.0 | 15 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 20 | c2de7E_ | Alignment |  | 33.2 | 31 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**ferredoxin component of carbazole;<br>**PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase |
| 21 | d2jo6a1 | Alignment | not modelled | 32.4 | 8 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**NirD-like |
| 22 | d1z01a1 | Alignment | not modelled | 32.1 | 38 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 23 | d2de6a1 | Alignment | not modelled | 32.1 | 38 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 24 | c3gceA_ | Alignment | not modelled | 30.4 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ferredoxin component of carbazole 1,9a-<br>**PDBTitle:** ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177 |
| 25 | c3i8sC_ | Alignment | not modelled | 29.4 | 36 | **PDB header:**transport protein<br>**Chain:** C: **PDB Molecule:**ferrous iron transport protein b;<br>**PDBTitle:** structure of the cytosolic domain of e. coli feob, nucleotide-free2 form |
| 26 | c3ibyA_ | Alignment | not modelled | 27.9 | 33 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**ferrous iron transport protein b;<br>**PDBTitle:** structure of cytosolic domain of l. pneumophila feob |
| 27 | d1nrjb_ | Alignment | not modelled | 27.8 | 42 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 28 | c3degC_ | Alignment | not modelled | 27.4 | 21 | **PDB header:**ribosome<br>**Chain:** C: **PDB Molecule:**gtp-binding protein lepa;<br>**PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp |
| | | | | | | **Fold:**P-loop containing nucleoside triphosphate hydrolases |

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|---|---|---|---|---|---|---|
| 29 | d1rkba_ | Alignment | not modelled | 26.9 | 20 | **Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**Nucleotide and nucleoside kinases |
| 30 | c2h5eB_ | Alignment | not modelled | 26.7 | 21 | **PDB header:**translation<br>**Chain:** B: **PDB Molecule:**peptide chain release factor rf-3;<br>**PDBTitle:** crystal structure of e.coli polypeptide release factor rf3 |
| 31 | d1w2ia_ | Alignment | not modelled | 26.4 | 26 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 32 | c1d2eA_ | Alignment | not modelled | 26.0 | 27 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**elongation factor tu (ef-tu);<br>**PDBTitle:** crystal structure of mitochondrial ef-tu in complex with gdp |
| 33 | c3melC_ | Alignment | not modelled | 25.6 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase family protein;<br>**PDBTitle:** crystal structure of thiamin pyrophosphokinase family protein from2 enterococcus faecalis, northeast structural genomics consortium3 target efr150 |
| 34 | d2fh5b1 | Alignment | not modelled | 25.6 | 17 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 35 | c3ihkC_ | Alignment | not modelled | 25.2 | 6 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**thiamin pyrophosphokinase;<br>**PDBTitle:** crystal structure of thiamin pyrophosphokinase from2 s.mutans, northeast structural genomics consortium target3 smr83 |
| 36 | d1j2ra_ | Alignment | not modelled | 24.8 | 21 | **Fold:**Isochorismatase-like hydrolases<br>**Superfamily:**Isochorismatase-like hydrolases<br>**Family:**Isochorismatase-like hydrolases |
| 37 | d1apsa_ | Alignment | not modelled | 24.7 | 26 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 38 | c2qpzA_ | Alignment | not modelled | 24.7 | 23 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase system ferredoxin<br>**PDBTitle:** naphthalene 1,2-dioxygenase rieske ferredoxin |
| 39 | c2i7fB_ | Alignment | not modelled | 24.7 | 42 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase;<br>**PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin |
| 40 | c2rauA_ | Alignment | not modelled | 24.5 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative esterase;<br>**PDBTitle:** crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution |
| 41 | d1s0ua3 | Alignment | not modelled | 24.3 | 36 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 42 | d2jzaa1 | Alignment | not modelled | 23.7 | 8 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**NirD-like |
| 43 | c1z01D_ | Alignment | not modelled | 23.6 | 36 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**2-oxo-1,2-dihydroquinoline 8-monooxygenase,<br>**PDBTitle:** 2-oxoquinoline 8-monooxygenase component: active site2 modulation by rieske-[2fe-2s] center oxidation/reduction |
| 44 | d2acya_ | Alignment | not modelled | 23.5 | 26 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 45 | c1mj1A_ | Alignment | not modelled | 23.3 | 27 | **PDB header:**ribosome<br>**Chain:** A: **PDB Molecule:**elongation factor tu;<br>**PDBTitle:** fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 13 a cryo-em map of the coli 70s ribosome |
| 46 | d1vm9a_ | Alignment | not modelled | 23.2 | 25 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 47 | d1n0ua2 | Alignment | not modelled | 23.0 | 23 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 48 | c2qagC_ | Alignment | not modelled | 22.8 | 27 | **PDB header:**cell cycle, structural protein<br>**Chain:** C: **PDB Molecule:**septin-7;<br>**PDBTitle:** crystal structure of human septin trimer 2/6/7 |
| 49 | c2ywfA_ | Alignment | not modelled | 22.6 | 29 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**gtp-binding protein lepa;<br>**PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus |
| 50 | c2qu8A_ | Alignment | not modelled | 22.5 | 29 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative nucleolar gtp-binding protein 1;<br>**PDBTitle:** crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum |
| 51 | d1e8ca1 | Alignment | not modelled | 22.5 | 57 | **Fold:**MurF and HprK N-domain-like<br>**Superfamily:**MurE/MurF N-terminal domain<br>**Family:**MurE/MurF N-terminal domain |
| 52 | d3c0da1 | Alignment | not modelled | 22.4 | 18 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**NirD-like |
| 53 | c1zunB_ | Alignment | not modelled | 22.4 | 27 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**sulfate adenylate transferase, subunit<br>**PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae |
| 54 | c2zxrA_ | Alignment | not modelled | 22.3 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**single-stranded dna specific exonuclease recj;<br>**PDBTitle:** crystal structure of recj in complex with mg2+ from |

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|---|---|---|---|---|---|---|
| | | | | | | thermus2 thermophilus hb8 |
| 55 | d1ex9a_ | Alignment | not modelled | 22.0 | 28 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Bacterial lipase |
| 56 | d1efca3 | Alignment | not modelled | 21.4 | 27 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 57 | c2bvnB_ | Alignment | not modelled | 21.3 | 27 | **PDB header:**elongation factor<br>**Chain:** B: **PDB Molecule:**elongation factor tu;<br>**PDBTitle:** e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia |
| 58 | c3izyP_ | Alignment | not modelled | 20.7 | 36 | **PDB header:**rna, ribosomal protein<br>**Chain:** P: **PDB Molecule:**translation initiation factor if-2, mitochondrial;<br>**PDBTitle:** mammalian mitochondrial translation initiation factor 2 |
| 59 | c2dy1A_ | Alignment | not modelled | 20.6 | 21 | **PDB header:**signaling protein, translation<br>**Chain:** A: **PDB Molecule:**elongation factor g;<br>**PDBTitle:** crystal structure of ef-g-2 from thermus thermophilus |
| 60 | c3hynA_ | Alignment | not modelled | 20.4 | 27 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**putative signal transduction protein;<br>**PDBTitle:** crystal structure of a putative signal transduction protein2 (eubrec_0645) from eubacterium rectale atcc 33656 at 1.20 a3 resolution |
| 61 | c3tr5C_ | Alignment | not modelled | 20.3 | 21 | **PDB header:**translation<br>**Chain:** C: **PDB Molecule:**peptide chain release factor 3;<br>**PDBTitle:** structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii |
| 62 | c3gkqB_ | Alignment | not modelled | 20.2 | 42 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a-<br>**PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 novosphingobium sp. ka1 |
| 63 | c3br8A_ | Alignment | not modelled | 20.1 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable acylphosphatase;<br>**PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis |
| 64 | c3cq9C_ | Alignment | not modelled | 20.0 | 6 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**uncharacterized protein lp_1622;<br>**PDBTitle:** crystal structure of the lp_1622 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr114 |
| 65 | c3t5dC_ | Alignment | not modelled | 19.7 | 27 | **PDB header:**signaling protein<br>**Chain:** C: **PDB Molecule:**septin-7;<br>**PDBTitle:** crystal structure of septin 7 in complex with gdp |
| 66 | c3k53B_ | Alignment | not modelled | 19.7 | 23 | **PDB header:**metal transport<br>**Chain:** B: **PDB Molecule:**ferrous iron transport protein b;<br>**PDBTitle:** crystal structure of nfeob from p. furiosus |
| 67 | d1r5ba3 | Alignment | not modelled | 19.3 | 45 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 68 | d1ulra_ | Alignment | not modelled | 19.3 | 10 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 69 | d1egaa1 | Alignment | not modelled | 18.7 | 50 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 70 | c2zyiB_ | Alignment | not modelled | 18.2 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**lipase, putative;<br>**PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium |
| 71 | c2wjjB_ | Alignment | not modelled | 18.2 | 40 | **PDB header:**metal transport<br>**Chain:** B: **PDB Molecule:**ferrous iron transport protein b homolog;<br>**PDBTitle:** structure and function of the feob g-domain from2 methanococcus jannaschii |
| 72 | c2bjeA_ | Alignment | not modelled | 18.1 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**acylphosphatase;<br>**PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group |
| 73 | c1r5nA_ | Alignment | not modelled | 17.6 | 45 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp-<br>**PDBTitle:** crystal structure analysis of sup35 complexed with gdp |
| 74 | c2de7B_ | Alignment | not modelled | 17.4 | 42 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole;<br>**PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase |
| 75 | d1g7sa4 | Alignment | not modelled | 17.3 | 27 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 76 | c1qgeD_ | Alignment | not modelled | 17.3 | 24 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase);<br>**PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase |
| 77 | d1svia_ | Alignment | not modelled | 16.9 | 36 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 78 | d1udxa2 | Alignment | not modelled | 16.9 | 31 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 79 | d1riea_ | Alignment | not modelled | 16.9 | 58 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |

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|---|---|---|---|---|---|---|
| 80 | d1gg4a3 | Alignment | not modelled | 16.7 | 50 | **Fold:**MurF and HprK N-domain-like<br>**Superfamily:**MurE/MurF N-terminal domain<br>**Family:**MurE/MurF N-terminal domain |
| 81 | d2ih2a2 | Alignment | not modelled | 16.5 | 12 | **Fold:**DNA methylase specificity domain<br>**Superfamily:**DNA methylase specificity domain<br>**Family:**TaqI C-terminal domain-like |
| 82 | c1s0uA_ | Alignment | not modelled | 16.5 | 36 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit;<br>**PDBTitle:** eif2gamma apo |
| 83 | c3hb7G_ | Alignment | not modelled | 16.3 | 8 | **PDB header:**hydrolase<br>**Chain:** G: **PDB Molecule:**isochorismatase hydrolase;<br>**PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a |
| 84 | c2xexA_ | Alignment | not modelled | 16.3 | 29 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**elongation factor g;<br>**PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g |
| 85 | c3pqcA_ | Alignment | not modelled | 16.2 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable gtp-binding protein engb;<br>**PDBTitle:** crystal structure of thermotoga maritima ribosome biogenesis gtp-2 binding protein engb (ysxc/yiha) in complex with gdp |
| 86 | c1wb1C_ | Alignment | not modelled | 15.8 | 36 | **PDB header:**protein synthesis<br>**Chain:** C: **PDB Molecule:**translation elongation factor selb;<br>**PDBTitle:** crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp |
| 87 | d2bv3a2 | Alignment | not modelled | 15.7 | 36 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**G proteins |
| 88 | c3p27A_ | Alignment | not modelled | 15.5 | 29 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**elongation factor 1 alpha-like protein;<br>**PDBTitle:** crystal structure of a translational gtpase (gdp form) |
| 89 | d2bmoa1 | Alignment | not modelled | 15.5 | 42 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 90 | c2r8bA_ | Alignment | not modelled | 15.2 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein atu2452;<br>**PDBTitle:** the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58 |
| 91 | c3a1vB_ | Alignment | not modelled | 15.1 | 27 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**iron(ii) transport protein b;<br>**PDBTitle:** crystal structue of the cytosolic domain of t. maritima feob2 iron iransporter in apo form |
| 92 | c1zo1I_ | Alignment | not modelled | 15.1 | 36 | **PDB header:**translation/rna<br>**Chain:** I: **PDB Molecule:**translation initiation factor 2;<br>**PDBTitle:** if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex |
| 93 | d2gmha2 | Alignment | not modelled | 14.4 | 27 | **Fold:**FAD-linked reductases, C-terminal domain<br>**Superfamily:**FAD-linked reductases, C-terminal domain<br>**Family:**Electron transfer flavoprotein-ubiquinone oxidoreductase-like |
| 94 | d1urra_ | Alignment | not modelled | 14.3 | 15 | **Fold:**Ferredoxin-like<br>**Superfamily:**Acylphosphatase/BLUF domain-like<br>**Family:**Acylphosphatase-like |
| 95 | c2d2rA_ | Alignment | not modelled | 14.3 | 30 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase;<br>**PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase |
| 96 | c3bwdD_ | Alignment | not modelled | 14.3 | 30 | **PDB header:**plant protein<br>**Chain:** D: **PDB Molecule:**rac-like gtp-binding protein arac6;<br>**PDBTitle:** crystal structure of the plant rho protein rop5 |
| 97 | c1g7cA_ | Alignment | not modelled | 14.3 | 36 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**elongation factor 1-alpha;<br>**PDBTitle:** yeast eef1a:eef1ba in complex with gdpnp |
| 98 | d2r8ba1 | Alignment | not modelled | 14.2 | 13 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carboxylesterase/thioesterase 1 |
| 99 | c2plfA_ | Alignment | not modelled | 14.1 | 36 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit;<br>**PDBTitle:** the structure of aif2gamma subunit from the archaeon2 sulfolobus solfataricus in the nucleotide-free form. |