# Phyre2

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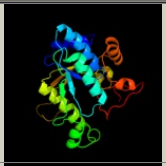
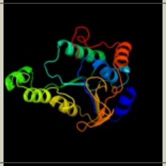
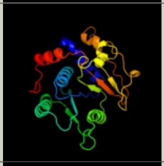
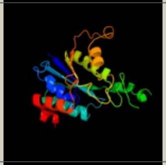
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77216 |
| Date | Thu Jan 5 12:26:29 GMT 2012 |
| Unique Job ID | fe8998a249eecf5a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2oq2B_ | Alignment |  | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase;<br>**PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex |
| 2 | c3g59A_ | Alignment |  | 100.0 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fmn adenylyltransferase;<br>**PDBTitle:** crystal structure of candida glabrata fmn2 adenylyltransferase in complex with atp |
| 3 | c2wsiA_ | Alignment |  | 100.0 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**fad synthetase;<br>**PDBTitle:** crystal structure of yeast fad synthetase (fad1) in complex2 with fad |
| 4 | c2o8vA_ | Alignment |  | 100.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase;<br>**PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a |
| 5 | c1zunA_ | Alignment |  | 100.0 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2;<br>**PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae |
| 6 | c2goyC_ | Alignment |  | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase;<br>**PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps |
| 7 | d1sura_ | Alignment |  | 100.0 | 20 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**PAPS reductase-like |
| 8 | d1zuna1 | Alignment |  | 100.0 | 20 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**PAPS reductase-like |
| 9 | c3bl5E_ | Alignment |  | 99.6 | 15 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec;<br>**PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis |
| 10 | c3a2kB_ | Alignment |  | 99.5 | 16 | **PDB header:**ligase/rna<br>**Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase;<br>**PDBTitle:** crystal structure of tils complexed with trna |
| 11 | d1wy5a1 | Alignment |  | 99.5 | 13 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**PP-loop ATPase |

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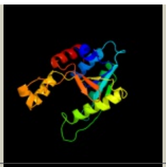
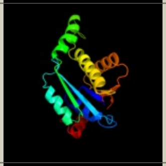
| 12 | d1ni5a1 | Alignment |  | 99.5 | 13 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**PP-loop ATPase |
| 13 | d1k92a1 | Alignment |  | 99.3 | 12 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 14 | c2e21A_ | Alignment |  | 99.3 | 12 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase;<br>**PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus. |
| 15 | c1ni5A_ | Alignment |  | 99.3 | 12 | **PDB header:**cell cycle<br>**Chain:** A: **PDB Molecule:**putative cell cycle protein mesj;<br>**PDBTitle:** structure of the mesj pp-atpase from escherichia coli |
| 16 | d1j20a1 | Alignment |  | 99.3 | 13 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 17 | c3p52B_ | Alignment |  | 99.2 | 13 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase;<br>**PDBTitle:** nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion |
| 18 | c2dplA_ | Alignment |  | 99.2 | 15 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b;<br>**PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3 |
| 19 | d1vl2a1 | Alignment |  | 99.1 | 11 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 20 | c2e18B_ | Alignment |  | 99.1 | 14 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase;<br>**PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3 |
| 21 | d1gpma1 | Alignment | not modelled | 99.1 | 18 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 22 | c1kh2D_ | Alignment | not modelled | 99.0 | 12 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**argininosuccinate synthetase;<br>**PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp |
| 23 | d2pg3a1 | Alignment | not modelled | 99.0 | 17 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 24 | d1xnga1 | Alignment | not modelled | 98.9 | 12 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 25 | c2nz2A_ | Alignment | not modelled | 98.9 | 13 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**argininosuccinate synthase;<br>**PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline |
| 26 | c1k97A_ | Alignment | not modelled | 98.9 | 12 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**argininosuccinate synthase;<br>**PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline |
| 27 | c1vl2C_ | Alignment | not modelled | 98.9 | 13 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**argininosuccinate synthase;<br>**PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution |
| 28 | d2c5sa1 | Alignment | not modelled | 98.8 | 16 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**ThiI-like |
| | | | | | | **PDB header:**ligase |

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| 29 | c3fiuD_ | Alignment | not modelled | 98.8 | 14 | **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase;<br>**PDBTitle:** structure of nmn synthetase from francisella tularensis |
| 30 | c3tqiB_ | Alignment | not modelled | 98.8 | 14 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing];<br>**PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii |
| 31 | c2ywcC_ | Alignment | not modelled | 98.6 | 13 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing];<br>**PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp |
| 32 | c1gpmD_ | Alignment | not modelled | 98.6 | 11 | **PDB header:**transferase (glutamine amidotransferase)<br>**Chain:** D: **PDB Molecule:**gmp synthetase;<br>**PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate |
| 33 | c2derA_ | Alignment | not modelled | 98.5 | 13 | **PDB header:**transferase/rna<br>**Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma;<br>**PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state |
| 34 | c3uowB_ | Alignment | not modelled | 98.5 | 16 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**gmp synthetase;<br>**PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum |
| 35 | c2vxoB_ | Alignment | not modelled | 98.4 | 13 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing];<br>**PDBTitle:** human gmp synthetase in complex with xmp |
| 36 | c2hmaA_ | Alignment | not modelled | 98.4 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)-<br>**PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae |
| 37 | d1kqpa_ | Alignment | not modelled | 98.2 | 14 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 38 | c2c5sA_ | Alignment | not modelled | 98.2 | 16 | **PDB header:**rna-binding protein<br>**Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii;<br>**PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain |
| 39 | c3k32D_ | Alignment | not modelled | 98.1 | 23 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**uncharacterized protein mj0690;<br>**PDBTitle:** the crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm |
| 40 | c3q4gA_ | Alignment | not modelled | 98.1 | 13 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase;<br>**PDBTitle:** structure of nad synthetase from vibrio cholerae |
| 41 | c3dpiA_ | Alignment | not modelled | 98.0 | 14 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**nad+ synthetase;<br>**PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei |
| 42 | d1vbka1 | Alignment | not modelled | 98.0 | 14 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**ThiI-like |
| 43 | d1ru8a_ | Alignment | not modelled | 97.9 | 15 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 44 | d1wxia1 | Alignment | not modelled | 97.7 | 12 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 45 | c3n05B_ | Alignment | not modelled | 97.2 | 12 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase;<br>**PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis |
| 46 | d2d13a1 | Alignment | not modelled | 96.9 | 41 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 47 | d1q15a1 | Alignment | not modelled | 95.2 | 22 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 48 | d1jgta1 | Alignment | not modelled | 95.1 | 16 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 49 | c1ct9D_ | Alignment | not modelled | 94.3 | 17 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**asparagine synthetase b;<br>**PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli |
| 50 | d1ct9a1 | Alignment | not modelled | 93.4 | 18 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**N-type ATP pyrophosphatases |
| 51 | c1q15A_ | Alignment | not modelled | 93.0 | 22 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**cara;<br>**PDBTitle:** carbapenam synthetase |
| 52 | c3dlaD_ | Alignment | not modelled | 93.0 | 21 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase;<br>**PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don |
| 53 | c1m1zB_ | Alignment | not modelled | 92.8 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**beta-lactam synthetase;<br>**PDBTitle:** beta-lactam synthetase apo enzyme |
| 54 | c3ilvA_ | Alignment | not modelled | 84.6 | 21 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase;<br>**PDBTitle:** crystal structure of a glutamine-dependent nad(+) |

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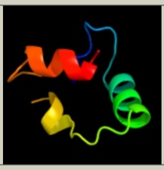
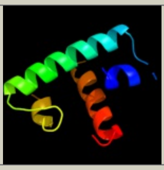
| | | | | | | synthetase2 from cytophaga hutchinsonii |
| 55 | c2pfsA_ | Alignment | not modelled | 83.4 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**universal stress protein;<br>**PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea |
| 56 | c2ghjD_ | Alignment |  | 77.1 | 19 | **PDB header:**structural protein<br>**Chain:** D: **PDB Molecule:**50s ribosomal protein l20;<br>**PDBTitle:** crystal structure of folded and partially unfolded forms of2 aquifex aeolicus ribosomal protein l20 |
| 57 | c1wozA_ | Alignment | not modelled | 75.3 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**177aa long conserved hypothetical protein (st1454);<br>**PDBTitle:** crystal structure of uncharacterized protein st1454 from sulfolobus2 tokodaii |
| 58 | d1gyza_ | Alignment |  | 73.2 | 18 | **Fold:**PABP domain-like<br>**Superfamily:**Ribosomal protein L20<br>**Family:**Ribosomal protein L20 |
| 59 | d2zjrn1 | Alignment | not modelled | 70.8 | 19 | **Fold:**PABP domain-like<br>**Superfamily:**Ribosomal protein L20<br>**Family:**Ribosomal protein L20 |
| 60 | c3bs7A_ | Alignment | not modelled | 69.3 | 26 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**protein aveugle;<br>**PDBTitle:** crystal structure of the sterile alpha motif (sam) domain2 of hyphen/aveugle |
| 61 | d2j01u1 | Alignment | not modelled | 66.9 | 21 | **Fold:**PABP domain-like<br>**Superfamily:**Ribosomal protein L20<br>**Family:**Ribosomal protein L20 |
| 62 | c2ftcL_ | Alignment | not modelled | 66.1 | 18 | **PDB header:**ribosome<br>**Chain:** L: **PDB Molecule:**mrpl20 protein;<br>**PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome |
| 63 | d1tq8a_ | Alignment | not modelled | 65.6 | 14 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**Universal stress protein-like |
| 64 | c2nt8A_ | Alignment | not modelled | 64.6 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase;<br>**PDBTitle:** atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri |
| 65 | c2ah6B_ | Alignment | not modelled | 63.5 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**bh1595, unknown conserved protein;<br>**PDBTitle:** crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution |
| 66 | c3bs5A_ | Alignment | not modelled | 61.2 | 26 | **PDB header:**signaling protein/membrane protein<br>**Chain:** A: **PDB Molecule:**protein aveugle;<br>**PDBTitle:** crystal structure of hcnk2-sam/dhyp-sam complex |
| 67 | d1a0pa1 | Alignment |  | 59.9 | 25 | **Fold:**SAM domain-like<br>**Superfamily:**lambda integrase-like, N-terminal domain<br>**Family:**lambda integrase-like, N-terminal domain |
| 68 | c3bq7A_ | Alignment | not modelled | 57.4 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**diacylglycerol kinase delta;<br>**PDBTitle:** sam domain of diacylglycerol kinase delta1 (e35g) |
| 69 | c3ci1A_ | Alignment | not modelled | 55.4 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase pduo-like protein;<br>**PDBTitle:** structure of the pduo-type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri complexed3 with four-coordinate cob(ii)alamin and atp |
| 70 | c1nogA_ | Alignment | not modelled | 53.9 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**conserved hypothetical protein ta0546;<br>**PDBTitle:** crystal structure of conserved protein 0546 from thermoplasma2 acidophilum |
| 71 | d1noga_ | Alignment | not modelled | 53.9 | 17 | **Fold:**Ferritin-like<br>**Superfamily:**Cobalamin adenosyltransferase-like<br>**Family:**Cobalamin adenosyltransferase |
| 72 | d1rtya_ | Alignment | not modelled | 53.5 | 18 | **Fold:**Ferritin-like<br>**Superfamily:**Cobalamin adenosyltransferase-like<br>**Family:**Cobalamin adenosyltransferase |
| 73 | c2zhzC_ | Alignment | not modelled | 53.4 | 19 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase, putative;<br>**PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis |
| 74 | c1vbkA_ | Alignment | not modelled | 52.9 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein ph1313;<br>**PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3 |
| 75 | d2z3va1 | Alignment | not modelled | 52.8 | 11 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**Universal stress protein-like |
| 76 | c3ke4B_ | Alignment | not modelled | 52.3 | 18 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hypothetical cytosolic protein;<br>**PDBTitle:** crystal structure of a pduo-type atp:cob(i)alamin adenosyltransferase2 from bacillus cereus |

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| 77 | c2idxA_ | Alignment | not modelled | 51.2 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**cob(i)yrinic acid a,c-diamide<br>**PDBTitle:** structure of human atp:cobalamin adenosyltransferase bound2 to atp. |
| 78 | c2g2dA_ | Alignment | not modelled | 51.1 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**atp:cobalamin adenosyltransferase;<br>**PDBTitle:** crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis |
| 79 | d1rtyb_ | Alignment | not modelled | 50.8 | 18 | **Fold:**Ferritin-like<br>**Superfamily:**Cobalamin adenosyltransferase-like<br>**Family:**Cobalamin adenosyltransferase |
| 80 | c1y89B_ | Alignment | not modelled | 49.6 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**devb protein;<br>**PDBTitle:** crystal structure of devb protein |
| 81 | d1pk1c1 | Alignment | not modelled | 47.9 | 25 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 82 | c1wvtA_ | Alignment | not modelled | 41.9 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein st2180;<br>**PDBTitle:** crystal structure of uncharacterized protein st2180 from sulfolobus2 tokodaii |
| 83 | c1pk1B_ | Alignment | not modelled | 41.5 | 12 | **PDB header:**transcription repression<br>**Chain:** B: **PDB Molecule:**sex comb on midleg cg9495-pa;<br>**PDBTitle:** hetero sam domain structure of ph and scm. |
| 84 | c3bboS_ | Alignment | not modelled | 41.4 | 11 | **PDB header:**ribosome<br>**Chain:** S: **PDB Molecule:**ribosomal protein l20;<br>**PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome |
| 85 | c2e7pC_ | Alignment | not modelled | 38.0 | 18 | **PDB header:**electron transport<br>**Chain:** C: **PDB Molecule:**glutaredoxin;<br>**PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides |
| 86 | c2j0eA_ | Alignment | not modelled | 35.3 | 11 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**6-phosphogluconolactonase;<br>**PDBTitle:** three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei |
| 87 | c2jrmA_ | Alignment | not modelled | 32.9 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ribosome modulation factor;<br>**PDBTitle:** solution nmr structure of ribosome modulation factor vp1593 from2 vibrio parahaemolyticus. northeast structural genomics target vpr55 |
| 88 | c1pk1A_ | Alignment | not modelled | 30.7 | 28 | **PDB header:**transcription repression<br>**Chain:** A: **PDB Molecule:**polyhomeotic-proximal chromatin protein;<br>**PDBTitle:** hetero sam domain structure of ph and scm. |
| 89 | d1wwva1 | Alignment | not modelled | 30.7 | 20 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 90 | c1tx2A_ | Alignment | not modelled | 30.6 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase;<br>**PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis |
| 91 | d1tx2a_ | Alignment | not modelled | 30.6 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Dihydropteroate synthetase-like<br>**Family:**Dihydropteroate synthetase |
| 92 | d2gyco1 | Alignment | not modelled | 29.3 | 12 | **Fold:**PABP domain-like<br>**Superfamily:**Ribosomal protein L20<br>**Family:**Ribosomal protein L20 |
| 93 | c3mt0A_ | Alignment | not modelled | 27.9 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein pa1789;<br>**PDBTitle:** the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1 |
| 94 | c1wy1B_ | Alignment | not modelled | 27.5 | 13 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**hypothetical protein ph0671;<br>**PDBTitle:** crystal structure of the ph0671 protein from pyrococcus horikoshii ot3 |
| 95 | c1v85A_ | Alignment | not modelled | 27.5 | 9 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**similar to ring finger protein 36;<br>**PDBTitle:** sterile alpha motif (sam) domain of mouse bifunctional2 apoptosis regulator |
| 96 | d1kw4a_ | Alignment | not modelled | 27.2 | 28 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**SAM (sterile alpha motif) domain |
| 97 | c1pbtA_ | Alignment | not modelled | 26.9 | 19 | **PDB header:**hydrolase, oxidoreductase<br>**Chain:** A: **PDB Molecule:**6-phosphogluconolactonase;<br>**PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima |
| 98 | c3oc6A_ | Alignment | not modelled | 26.8 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**6-phosphogluconolactonase;<br>**PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form |
| 99 | c3loqA_ | Alignment | not modelled | 26.7 | 10 | **PDB header:**structure genomics, unknown function<br>**Chain:** A: **PDB Molecule:**universal stress protein;<br>**PDBTitle:** the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304 |
| 100 | c3lhiA_ | Alignment | not modelled | 26.2 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase;<br>**PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution |
| 101 | d1vl1a_ | Alignment | not modelled | 25.8 | 19 | **Fold:**NagB/RpiA/CoA transferase-like<br>**Superfamily:**NagB/RpiA/CoA transferase-like<br>**Family:**NagB-like |
| 102 | c3lwdA_ | Alignment | not modelled | 24.9 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**6-phosphogluconolactonase;<br>**PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | 1.88 a resolution |
| 103 | c2dkzA_ | Alignment | not modelled | 24.7 | 0 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**hypothetical protein loc64762;<br>**PDBTitle:** solution structure of the sam_pnt-domain of the2 hypothetical protein loc64762 |
| 104 | c3olqA_ | Alignment | not modelled | 24.2 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**universal stress protein e;<br>**PDBTitle:** the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320 |
| 105 | c3bkhA_ | Alignment | not modelled | 24.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**lytic transglycosylase;<br>**PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144 |
| 106 | c2gleA_ | Alignment | not modelled | 23.4 | 9 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**neurabin-1;<br>**PDBTitle:** solution structure of neurabin sam domain |
| 107 | d1luaa2 | Alignment | not modelled | 23.3 | 16 | **Fold:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain<br>**Family:**Methylene-tetrahydromethanopterin dehydrogenase |
| 108 | d1fsfa_ | Alignment | not modelled | 22.9 | 14 | **Fold:**NagB/RpiA/CoA transferase-like<br>**Superfamily:**NagB/RpiA/CoA transferase-like<br>**Family:**NagB-like |
| 109 | d1sv0a_ | Alignment | not modelled | 22.2 | 14 | **Fold:**SAM domain-like<br>**Superfamily:**SAM/Pointed domain<br>**Family:**Pointed domain |
| 110 | c2d1fA_ | Alignment | not modelled | 21.4 | 10 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**threonine synthase;<br>**PDBTitle:** structure of mycobacterium tuberculosis threonine synthase |
| 111 | c2jacA_ | Alignment | not modelled | 20.9 | 11 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**glutaredoxin-1;<br>**PDBTitle:** glutaredoxin grx1p c30s mutant from yeast |
| 112 | c3hn6D_ | Alignment | not modelled | 20.5 | 14 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase;<br>**PDBTitle:** crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi |