# Phyre2

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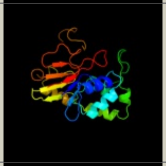
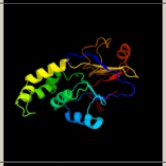
| Email | l.a.kelley@imperial.ac.uk |
| Description | P55798 |
| Date | Thu Jan 5 12:06:12 GMT 2012 |
| Unique Job ID | 32b59543aa4563ed |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1g5ba_ | Alignment |  | 100.0 | 48 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Protein serine/threonine phosphatase |
| 2 | c2qjcA_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**diadenosine tetraphosphatase, putative;<br>**PDBTitle:** crystal structure of a putative diadenosine tetraphosphatase |
| 3 | c2dfjA_ | Alignment |  | 100.0 | 28 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase;<br>**PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a |
| 4 | c2zbmA_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**protein-tyrosine-phosphatase;<br>**PDBTitle:** crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase |
| 5 | d1jk7a_ | Alignment |  | 100.0 | 24 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Protein serine/threonine phosphatase |
| 6 | d3c5wc1 | Alignment |  | 100.0 | 20 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Protein serine/threonine phosphatase |
| 7 | d1s95a_ | Alignment |  | 100.0 | 20 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Protein serine/threonine phosphatase |
| 8 | d1s70a_ | Alignment |  | 100.0 | 24 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Protein serine/threonine phosphatase |
| 9 | c2jogA_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha<br>**PDBTitle:** structure of the calcineurin-nfat complex |
| 10 | c3icfB_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase t;<br>**PDBTitle:** structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5 |
| 11 | d1auia_ | Alignment |  | 100.0 | 17 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Protein serine/threonine phosphatase |

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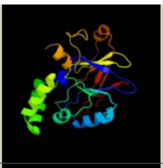
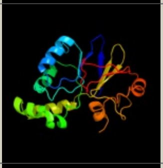
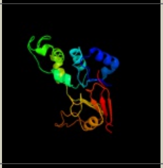
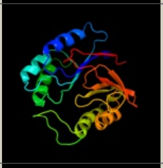
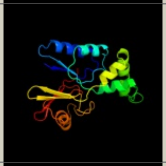
| 12 | c1auiA_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**serine/threonine phosphatase 2b;<br>**PDBTitle:** human calcineurin heterodimer |
| 13 | d1nnwa_ | Alignment |  | 99.9 | 11 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Phosphoesterase-related |
| 14 | c1wao4_ | Alignment |  | 99.9 | 19 | **PDB header:**hydrolase<br>**Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5;<br>**PDBTitle:** pp5 structure |
| 15 | c2p6bC_ | Alignment |  | 99.9 | 19 | **PDB header:**hydrolase/hydrolase regulator<br>**Chain:** C: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha<br>**PDBTitle:** crystal structure of human calcineurin in complex with2 pvivit peptide |
| 16 | d2p6ba1 | Alignment |  | 99.9 | 19 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Protein serine/threonine phosphatase |
| 17 | c3rqzC_ | Alignment |  | 99.9 | 21 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**metallophosphoesterase;<br>**PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus |
| 18 | d1uf3a_ | Alignment |  | 99.9 | 16 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**TT1561-like |
| 19 | c3qfnA_ | Alignment |  | 99.9 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate |
| 20 | c1su1A_ | Alignment |  | 99.9 | 25 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein yfce;<br>**PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli |
| 21 | d1su1a_ | Alignment | not modelled | 99.9 | 25 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**YfcE-like |
| 22 | d3ck2a1 | Alignment | not modelled | 99.9 | 20 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**YfcE-like |
| 23 | c2kknA_ | Alignment | not modelled | 99.8 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57 |
| 24 | d2a22a1 | Alignment | not modelled | 99.8 | 19 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**YfcE-like |
| 25 | c1s3mA_ | Alignment | not modelled | 99.8 | 21 | **PDB header:**phosphodiesterase<br>**Chain:** A: **PDB Molecule:**hypothetical protein mj0936;<br>**PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase |
| 26 | d1s3la_ | Alignment | not modelled | 99.8 | 21 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**YfcE-like |
| 27 | d2yvta1 | Alignment | not modelled | 99.8 | 14 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**TT1561-like |
| 28 | d1z2wa1 | Alignment | not modelled | 99.7 | 22 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**YfcE-like |
| 29 | d1xm7a_ | Alignment | not modelled | 99.5 | 14 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases |

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| | | | | | | **Family:**Hypothetical protein aq 1666 |
| 30 | c3av0A_ | Alignment | not modelled | 99.5 | 15 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11;<br>**PDBTitle:** crystal structure of mre11-rad50 bound to atp s |
| 31 | c3auzA_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11;<br>**PDBTitle:** crystal structure of mre11 with manganese |
| 32 | d1ii7a_ | Alignment | not modelled | 99.4 | 19 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**DNA double-strand break repair nuclease |
| 33 | c3rl4A_ | Alignment | not modelled | 99.4 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2;<br>**PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant |
| 34 | c3ib7A_ | Alignment | not modelled | 99.4 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**icc protein;<br>**PDBTitle:** crystal structure of full length rv0805 |
| 35 | d2hy1a1 | Alignment | not modelled | 99.3 | 16 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**GpdQ-like |
| 36 | c2hy1A_ | Alignment | not modelled | 99.3 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**rv0805;<br>**PDBTitle:** crystal structure of rv0805 |
| 37 | d3d03a1 | Alignment | not modelled | 99.2 | 10 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**GpdQ-like |
| 38 | c2xmoB_ | Alignment | not modelled | 99.1 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**lmo2642 protein;<br>**PDBTitle:** the crystal structure of lmo2642 |
| 39 | c2q8uA_ | Alignment | not modelled | 99.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**exonuclease, putative;<br>**PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution |
| 40 | d2nxfa1 | Alignment | not modelled | 99.0 | 16 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**ADPRibase-Mn-like |
| 41 | c1oidA_ | Alignment | not modelled | 98.8 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**protein usha;<br>**PDBTitle:** 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c) |
| 42 | c3qfkA_ | Alignment | not modelled | 98.8 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate |
| 43 | d1xzwa2 | Alignment | not modelled | 98.8 | 15 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Purple acid phosphatase-like |
| 44 | c3ivdA_ | Alignment | not modelled | 98.7 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nucleotidase;<br>**PDBTitle:** putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine |
| 45 | d2qfra2 | Alignment | not modelled | 98.7 | 12 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Purple acid phosphatase-like |
| 46 | d1usha2 | Alignment | not modelled | 98.6 | 16 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain |
| 47 | c3qg5D_ | Alignment | not modelled | 98.6 | 27 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**mre11;<br>**PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair |
| 48 | d1qhwa_ | Alignment | not modelled | 98.5 | 15 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Purple acid phosphatase-like |
| 49 | c1qhwA_ | Alignment | not modelled | 98.5 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**protein (purple acid phosphatase);<br>**PDBTitle:** purple acid phosphatase from rat bone |
| 50 | c2z1aA_ | Alignment | not modelled | 98.5 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**5'-nucleotidase;<br>**PDBTitle:** crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8 |
| 51 | d1utea_ | Alignment | not modelled | 98.4 | 17 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**Purple acid phosphatase-like |
| 52 | d2z1aa2 | Alignment | not modelled | 98.4 | 16 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain |
| 53 | c3jyfB_ | Alignment | not modelled | 98.3 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-<br>**PDBTitle:** the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578 |
| 54 | c3t1iC_ | Alignment | not modelled | 98.3 | 30 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a;<br>**PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations |
| | | | | | | **PDB header:**structural genomics, unknown function |

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| 55 | c3gveB_ | Alignment | not modelled | 98.3 | 16 | **Chain:** B: **PDB Molecule:**yfkn protein;<br>**PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis |
| 56 | c3zu0A_ | Alignment | not modelled | 98.2 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nad nucleotidase;<br>**PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn) |
| 57 | c2wdfA_ | Alignment | not modelled | 98.1 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb;<br>**PDBTitle:** termus thermophilus sulfate thiohydrolase soxb |
| 58 | d3c9fa2 | Alignment | not modelled | 97.0 | 23 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain |
| 59 | c1xzwB_ | Alignment | not modelled | 96.7 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**purple acid phosphatase;<br>**PDBTitle:** sweet potato purple acid phosphatase/phosphate complex |
| 60 | c1kbpB_ | Alignment | not modelled | 96.6 | 17 | **PDB header:**hydrolase (phosphoric monoester)<br>**Chain:** B: **PDB Molecule:**purple acid phosphatase;<br>**PDBTitle:** kidney bean purple acid phosphatase |
| 61 | c3c9fB_ | Alignment | not modelled | 96.2 | 23 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**5'-nucleotidase;<br>**PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314 |
| 62 | d2z06a1 | Alignment | not modelled | 95.6 | 31 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**TTHA0625-like |
| 63 | c3e0jG_ | Alignment | not modelled | 95.2 | 15 | **PDB header:**transferase<br>**Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2;<br>**PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta |
| 64 | d1t71a_ | Alignment | not modelled | 95.1 | 22 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**DR1281-like |
| 65 | d1t70a_ | Alignment | not modelled | 95.0 | 21 | **Fold:**Metallo-dependent phosphatases<br>**Superfamily:**Metallo-dependent phosphatases<br>**Family:**DR1281-like |
| 66 | c3floG_ | Alignment | not modelled | 91.7 | 20 | **PDB header:**transferase<br>**Chain:** G: **PDB Molecule:**dna polymerase alpha subunit b;<br>**PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit |
| 67 | d1gg4a1 | Alignment | not modelled | 63.8 | 15 | **Fold:**MurD-like peptide ligases, peptide-binding domain<br>**Superfamily:**MurD-like peptide ligases, peptide-binding domain<br>**Family:**MurCDEF C-terminal domain |
| 68 | c3nh8A_ | Alignment | not modelled | 47.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aspartoacylase-2;<br>**PDBTitle:** crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine |
| 69 | d1ylea1 | Alignment | not modelled | 35.0 | 29 | **Fold:**Acyl-CoA N-acyltransferases (Nat)<br>**Superfamily:**Acyl-CoA N-acyltransferases (Nat)<br>**Family:**AstA-like |
| 70 | c2issF_ | Alignment | not modelled | 29.4 | 21 | **PDB header:**lyase, transferase<br>**Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt;<br>**PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima |
| 71 | c2qj8B_ | Alignment | not modelled | 23.3 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**mlr6093 protein;<br>**PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution |
| 72 | c1z9bA_ | Alignment | not modelled | 22.6 | 19 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**translation initiation factor if-2;<br>**PDBTitle:** solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2 |
| 73 | c3cdxB_ | Alignment | not modelled | 19.9 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase;<br>**PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides |
| 74 | c3na6A_ | Alignment | not modelled | 19.0 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase;<br>**PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution |
| 75 | c2dlcX_ | Alignment | not modelled | 17.8 | 13 | **PDB header:**ligase/trna<br>**Chain:** X: **PDB Molecule:**tyrosyl-trna synthetase, cytoplasmic;<br>**PDBTitle:** crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase |
| 76 | d3beda1 | Alignment | not modelled | 15.2 | 11 | **Fold:**PTS system fructose IIA component-like<br>**Superfamily:**PTS system fructose IIA component-like<br>**Family:**EIIA-man component-like |
| 77 | c3n9iA_ | Alignment | not modelled | 14.6 | 20 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase;<br>**PDBTitle:** crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92 |
| 78 | c3prhB_ | Alignment | not modelled | 13.9 | 10 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase;<br>**PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis |
| 79 | d1q7ra_ | Alignment | not modelled | 13.3 | 21 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |
| 80 | c2el7A_ | Alignment | not modelled | 13.0 | 22 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase;<br>**PDBTitle:** crystal structure of tryptophanyl-trna synthetase from |

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| | | | | | | thermus2 thermophilus |
| 81 | c2cybA_ | Alignment | not modelled | 12.9 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase;<br>**PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus |
| 82 | d1j1ua_ | Alignment | not modelled | 12.2 | 27 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain |
| 83 | d1i6la_ | Alignment | not modelled | 12.1 | 17 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Nucleotidylyl transferase<br>**Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain |
| 84 | d1otha2 | Alignment | not modelled | 12.0 | 12 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/ornithine carbamoyltransferase<br>**Family:**Aspartate/ornithine carbamoyltransferase |
| 85 | c3hp7A_ | Alignment | not modelled | 10.5 | 43 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hemolysin, putative;<br>**PDBTitle:** putative hemolysin from streptococcus thermophilus. |
| 86 | d1ux6a1 | Alignment | not modelled | 10.1 | 33 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Thrombospondin C-terminal domain |
| 87 | c2vdwA_ | Alignment | not modelled | 10.0 | 13 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**vaccinia virus capping enzyme d1 subunit;<br>**PDBTitle:** guanosine n7 methyl-transferase sub-complex (d1-d12) of the2 vaccinia virus mrna capping enzyme |
| 88 | d2at2a2 | Alignment | not modelled | 9.3 | 27 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/ornithine carbamoyltransferase<br>**Family:**Aspartate/ornithine carbamoyltransferase |
| 89 | d2z1ca1 | Alignment | not modelled | 8.6 | 40 | **Fold:**OB-fold<br>**Superfamily:**HupF/HypC-like<br>**Family:**HupF/HypC-like |
| 90 | c3ujcA_ | Alignment | not modelled | 8.5 | 36 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphoethanolamine n-methyltransferase;<br>**PDBTitle:** phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine |
| 91 | d2o57a1 | Alignment | not modelled | 8.4 | 36 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**Mycolic acid cyclopropane synthase |
| 92 | d3d3ra1 | Alignment | not modelled | 7.8 | 30 | **Fold:**OB-fold<br>**Superfamily:**HupF/HypC-like<br>**Family:**HupF/HypC-like |
| 93 | c1gg4A_ | Alignment | not modelled | 7.8 | 14 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylmuramoylalanyl-d-glutamyl-2,6-<br>**PDBTitle:** crystal structure of escherichia coli udpmurnac-tripeptide2 d-alanyl-d-alanine-adding enzyme (murf) at 2.3 angstrom3 resolution |
| 94 | c3fmcC_ | Alignment | not modelled | 7.6 | 11 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase;<br>**PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution |
| 95 | d1dxha2 | Alignment | not modelled | 7.5 | 12 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/ornithine carbamoyltransferase<br>**Family:**Aspartate/ornithine carbamoyltransferase |
| 96 | c3d3rA_ | Alignment | not modelled | 7.4 | 30 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf;<br>**PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1 |
| 97 | d2i3ca1 | Alignment | not modelled | 7.2 | 16 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Zn-dependent exopeptidases<br>**Family:**AstE/AspA-like |
| 98 | c3m5wB_ | Alignment | not modelled | 7.0 | 13 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase;<br>**PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni |
| 99 | d2ot2a1 | Alignment | not modelled | 7.0 | 30 | **Fold:**OB-fold<br>**Superfamily:**HupF/HypC-like<br>**Family:**HupF/HypC-like |