# Phyre²

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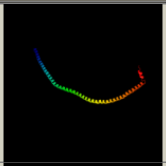
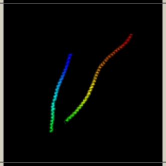
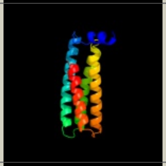
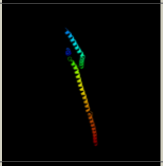
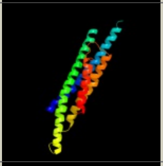
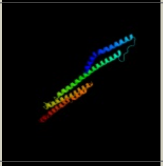
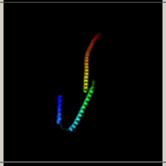
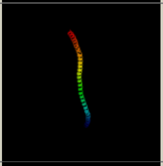
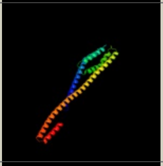
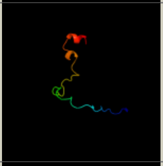
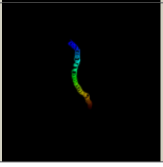
| Email | l.a.kelley@imperial.ac.uk |
| Description | P36682 |
| Date | Thu Jan 5 11:53:47 GMT 2012 |
| Unique Job ID | a3f7b54b27d8afa6 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2zv4O_ | Alignment |  | 96.7 | 11 | **PDB header:**structural protein<br>**Chain:** O: **PDB Molecule:**major vault protein;<br>**PDBTitle:** the structure of rat liver vault at 3.5 angstrom resolution |
| 2 | c2dfsA_ | Alignment |  | 96.4 | 6 | **PDB header:**contractile protein/transport protein<br>**Chain:** A: **PDB Molecule:**myosin-5a;<br>**PDBTitle:** 3-d structure of myosin-v inhibited state |
| 3 | c1y4cA_ | Alignment |  | 94.7 | 11 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**maltose binding protein fused with designed<br>**PDBTitle:** designed helical protein fusion mbp |
| 4 | c3ojaB_ | Alignment |  | 92.5 | 10 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein<br>**PDBTitle:** crystal structure of lrim1/apl1c complex |
| 5 | c1bf5A_ | Alignment |  | 89.6 | 6 | **PDB header:**gene regulation/dna<br>**Chain:** A: **PDB Molecule:**signal transducer and activator of transcription<br>**PDBTitle:** tyrosine phosphorylated stat-1/dna complex |
| 6 | c1g8xB_ | Alignment |  | 88.0 | 8 | **PDB header:**structural protein<br>**Chain:** B: **PDB Molecule:**myosin ii heavy chain fused to alpha-actinin 3;<br>**PDBTitle:** structure of a genetically engineered molecular motor |
| 7 | c3ojaA_ | Alignment |  | 87.7 | 8 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1;<br>**PDBTitle:** crystal structure of lrim1/apl1c complex |
| 8 | c1ei3E_ | Alignment |  | 78.1 | 7 | **PDB header:**<br>**PDB COMPND:** |
| 9 | c1f5nA_ | Alignment |  | 77.4 | 9 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**interferon-induced guanylate-binding protein 1;<br>**PDBTitle:** human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp. |
| 10 | d1wp1a_ | Alignment |  | 65.0 | 15 | **Fold:**Outer membrane efflux proteins (OEP)<br>**Superfamily:**Outer membrane efflux proteins (OEP)<br>**Family:**Outer membrane efflux proteins (OEP) |
| 11 | c3ghgK_ | Alignment |  | 63.3 | 6 | **PDB header:**blood clotting<br>**Chain:** K: **PDB Molecule:**fibrinogen beta chain;<br>**PDBTitle:** crystal structure of human fibrinogen |

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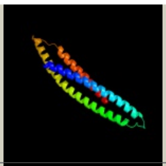
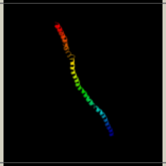
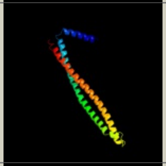
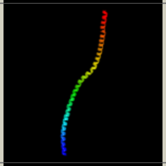
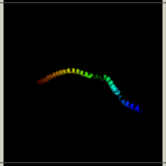
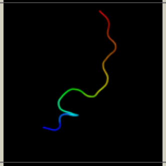
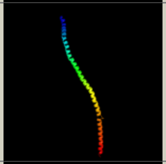
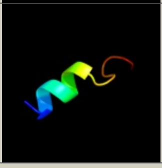
|---|---|---|---|---|---|---|
| 12 | c1bg1A_ | Alignment |  | 60.4 | 7 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**protein (transcription factor stat3b);<br>**PDBTitle:** transcription factor stat3b/dna complex |
| 13 | c1deqO_ | Alignment |  | 57.6 | 8 | **PDB header:**<br>**PDB COMPND:** |
| 14 | c1jchC_ | Alignment |  | 57.0 | 11 | **PDB header:**ribosome inhibitor, hydrolase<br>**Chain:** C: **PDB Molecule:**colicin e3;<br>**PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein |
| 15 | c3cwgA_ | Alignment |  | 55.2 | 11 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**signal transducer and activator of transcription<br>**PDBTitle:** unphosphorylated mouse stat3 core fragment |
| 16 | c1ei3C_ | Alignment |  | 54.8 | 8 | **PDB header:**<br>**PDB COMPND:** |
| 17 | c1deqF_ | Alignment |  | 47.4 | 9 | **PDB header:**<br>**PDB COMPND:** |
| 18 | c3r3sD_ | Alignment |  | 33.5 | 24 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**oxidoreductase;<br>**PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica |
| 19 | c3dtpA_ | Alignment |  | 33.5 | 7 | **PDB header:**contractile protein<br>**Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and<br>**PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map |
| 20 | c3fxeA_ | Alignment |  | 32.3 | 40 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**protein icmq;<br>**PDBTitle:** crystal structure of interacting domains of icmr and icmq (seleno-2 derivative) |
| 21 | d2au5a1 | Alignment | not modelled | 32.0 | 25 | **Fold:**EF2947-like<br>**Superfamily:**EF2947-like<br>**Family:**EF2947-like |
| 22 | c3g33D_ | Alignment | not modelled | 27.3 | 7 | **PDB header:**cell cycle<br>**Chain:** D: **PDB Molecule:**ccnd3 protein;<br>**PDBTitle:** crystal structure of cdk4/cyclin d3 |
| 23 | c3a9rA_ | Alignment | not modelled | 26.0 | 19 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**d-arabinose isomerase;<br>**PDBTitle:** x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol |
| 24 | c2rnmC_ | Alignment | not modelled | 24.5 | 25 | **PDB header:**protein fibril<br>**Chain:** C: **PDB Molecule:**small s protein;<br>**PDBTitle:** structure of the het-s(218-289) prion in its amyloid form2 obtained by solid-state nmr |
| 25 | c1h28B_ | Alignment | not modelled | 23.4 | 17 | **PDB header:**cell cycle/transferase substrate<br>**Chain:** B: **PDB Molecule:**cyclin a2;<br>**PDBTitle:** cdk2/cyclin a in complex with an 11-residue recruitment peptide from2 p107 |
| 26 | c3e0dA_ | Alignment | not modelled | 20.5 | 24 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha;<br>**PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit |
| 27 | c3na7A_ | Alignment | not modelled | 20.3 | 8 | **PDB header:**gene regulation, chaperone<br>**Chain:** A: **PDB Molecule:**hp0958;<br>**PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874 |
| 28 | d1epwa3 | Alignment | not modelled | 18.4 | 24 | **Fold:**Zincin-like<br>**Superfamily:**Metalloproteases ("zincins"), catalytic domain<br>**Family:**Clostridium neurotoxins, catalytic domain |

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| 29 | c3mlqE_ | Alignment | not modelled | 18.0 | 10 | **PDB header:**transferase/transcription<br>**Chain:** E: **PDB Molecule:**transcription-repair coupling factor;<br>**PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain |
| 30 | c3mlqH_ | Alignment | not modelled | 16.0 | 8 | **PDB header:**transferase/transcription<br>**Chain:** H: **PDB Molecule:**transcription-repair coupling factor;<br>**PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain |
| 31 | d2cchb2 | Alignment | not modelled | 13.9 | 15 | **Fold:**Cyclin-like<br>**Superfamily:**Cyclin-like<br>**Family:**Cyclin |
| 32 | c2l81A_ | Alignment | not modelled | 13.8 | 26 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**enhancer of filamentation 1;<br>**PDBTitle:** solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a |
| 33 | c1p8cD_ | Alignment | not modelled | 12.6 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**conserved hypothetical protein;<br>**PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima |
| 34 | d1k3ra1 | Alignment | not modelled | 12.2 | 50 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Hypothetical protein MTH1 (MT0001), insert domain |
| 35 | c2xu8B_ | Alignment | not modelled | 11.8 | 27 | **PDB header:**structural genomics<br>**Chain:** B: **PDB Molecule:**pa1645;<br>**PDBTitle:** structure of pa1645 |
| 36 | d1chka_ | Alignment | not modelled | 11.7 | 24 | **Fold:**Lysozyme-like<br>**Superfamily:**Lysozyme-like<br>**Family:**Chitosanase |
| 37 | c2j58G_ | Alignment | not modelled | 11.3 | 29 | **PDB header:**membrane protein<br>**Chain:** G: **PDB Molecule:**outer membrane lipoprotein wza;<br>**PDBTitle:** the structure of wza |
| 38 | c3sqgE_ | Alignment | not modelled | 11.0 | 17 | **PDB header:**transferase<br>**Chain:** E: **PDB Molecule:**methyl-coenzyme m reductase, beta subunit;<br>**PDBTitle:** crystal structure of a methyl-coenzyme m reductase purified from black2 sea mats |
| 39 | c3a0fA_ | Alignment | not modelled | 10.9 | 46 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**xyloglucanase;<br>**PDBTitle:** the crystal structure of geotrichum sp. m128 xyloglucanase |
| 40 | d1v3ya_ | Alignment | not modelled | 10.7 | 38 | **Fold:**Peptide deformylase<br>**Superfamily:**Peptide deformylase<br>**Family:**Peptide deformylase |
| 41 | d2fyuk1 | Alignment | not modelled | 10.5 | 33 | **Fold:**Single transmembrane helix<br>**Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br>**Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 42 | d1l0nk_ | Alignment | not modelled | 10.4 | 33 | **Fold:**Single transmembrane helix<br>**Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)<br>**Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 43 | c1g3nG_ | Alignment | not modelled | 10.4 | 15 | **PDB header:**cell cycle, signaling protein<br>**Chain:** G: **PDB Molecule:**v-cyclin;<br>**PDBTitle:** structure of a p18(ink4c)-cdk6-k-cyclin ternary complex |
| 44 | d1e6vb1 | Alignment | not modelled | 10.1 | 22 | **Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain<br>**Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain<br>**Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain |
| 45 | c3hizB_ | Alignment | not modelled | 9.9 | 10 | **PDB header:**transferase/oncoprotein<br>**Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit<br>**PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha |
| 46 | c2v6yA_ | Alignment | not modelled | 9.8 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aaa family atpase, p60 katanin;<br>**PDBTitle:** structure of the mit domain from a s. solfataricus vps4-2 like atpase |
| 47 | c1zy1B_ | Alignment | not modelled | 9.6 | 13 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**peptide deformylase, mitochondrial;<br>**PDBTitle:** x-ray structure of peptide deformylase from arabidopsis2 thaliana (atpdf1a) in complex with met-ala-ser |
| 48 | d1st6a6 | Alignment | not modelled | 9.4 | 17 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**alpha-catenin/vinculin-like<br>**Family:**alpha-catenin/vinculin |
| 49 | c2ebsB_ | Alignment | not modelled | 8.6 | 46 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**oligoxyloglucan reducing end-specific<br>**PDBTitle:** crystal structure anaalysis of oligoxyloglucan reducing-end-2 specific cellobiohydrolase (oxg-rcbh) d465n mutant3 complexed with a xyloglucan heptasaccharide |
| 50 | d3ddqb2 | Alignment | not modelled | 8.4 | 15 | **Fold:**Cyclin-like<br>**Superfamily:**Cyclin-like<br>**Family:**Cyclin |
| 51 | c1hbmE_ | Alignment | not modelled | 8.3 | 20 | **PDB header:**methanogenesis<br>**Chain:** E: **PDB Molecule:**methyl-coenzyme m reductase i beta subunit;<br>**PDBTitle:** methyl-coenzyme m reductase enzyme product complex |
| 52 | d1lmea_ | Alignment | not modelled | 8.1 | 17 | **Fold:**Peptide deformylase<br>**Superfamily:**Peptide deformylase<br>**Family:**Peptide deformylase |

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|---|---|---|---|---|---|---|
| 53 | c3oqvA_ | Alignment | not modelled | 7.9 | 21 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**albc;<br>**PDBTitle:** albc, a cyclodipeptide synthase from streptomyces noursei |
| 54 | c2w2uA_ | Alignment | not modelled | 7.7 | 26 | **PDB header:**hydrolase/transport<br>**Chain:** A: **PDB Molecule:**hypothetical p60 katanin;<br>**PDBTitle:** structural insight into the interaction between archaeal2 escrt-iii and aaa-atpase |
| 55 | c2kxhB_ | Alignment | not modelled | 7.7 | 50 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**peptide of far upstream element-binding protein 1;<br>**PDBTitle:** solution structure of the first two rrm domains of fir in the complex2 with fbp nbox peptide |
| 56 | d1hmca_ | Alignment | not modelled | 7.5 | 22 | **Fold:**4-helical cytokines<br>**Superfamily:**4-helical cytokines<br>**Family:**Short-chain cytokines |
| 57 | d1yzma1 | Alignment | not modelled | 7.4 | 17 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Rabenosyn-5 Rab-binding domain-like<br>**Family:**Rabenosyn-5 Rab-binding domain-like |
| 58 | c3fbvL_ | Alignment | not modelled | 7.3 | 15 | **PDB header:**transferase, hydrolase<br>**Chain:** L: **PDB Molecule:**serine/threonine-protein kinase/endoribonuclease ire1;<br>**PDBTitle:** crystal structure of the oligomer formed by the kinase-ribonuclease2 domain of ire1 |
| 59 | d2eyqa1 | Alignment | not modelled | 7.2 | 13 | **Fold:**SH3-like barrel<br>**Superfamily:**CarD-like<br>**Family:**CarD-like |
| 60 | d1dmta_ | Alignment | not modelled | 7.1 | 16 | **Fold:**Zincin-like<br>**Superfamily:**Metalloproteases ("zincins"), catalytic domain<br>**Family:**Neutral endopeptidase (neprilysin) |
| 61 | c2x9qA_ | Alignment | not modelled | 6.9 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**cyclodipeptide synthetase;<br>**PDBTitle:** structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases. |
| 62 | d1z0kb1 | Alignment | not modelled | 6.9 | 22 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Rabenosyn-5 Rab-binding domain-like<br>**Family:**Rabenosyn-5 Rab-binding domain-like |
| 63 | c2w8iG_ | Alignment | not modelled | 6.8 | 29 | **PDB header:**membrane protein<br>**Chain:** G: **PDB Molecule:**putative outer membrane lipoprotein wza;<br>**PDBTitle:** crystal structure of wza24-345. |
| 64 | c3dldA_ | Alignment | not modelled | 6.7 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptide deformylase;<br>**PDBTitle:** crystal structure of peptide deformylase, xoo1075, from2 xanthomonas oryzae pv. oryzae kacc10331 |
| 65 | d2djia3 | Alignment | not modelled | 6.6 | 10 | **Fold:**Thiamin diphosphate-binding fold (THDP-binding)<br>**Superfamily:**Thiamin diphosphate-binding fold (THDP-binding)<br>**Family:**Pyruvate oxidase and decarboxylase PP module |
| 66 | c3g6nA_ | Alignment | not modelled | 6.5 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptide deformylase;<br>**PDBTitle:** crystal structure of an efpdf complex with met-ala-ser |
| 67 | c2jvwA_ | Alignment | not modelled | 6.4 | 50 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution nmr structure of uncharacterized protein q5e7h1 from vibrio2 fischeri. northeast structural genomics target vfr117 |
| 68 | c2gu1A_ | Alignment | not modelled | 6.4 | 9 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**zinc peptidase;<br>**PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae |
| 69 | c1e6yE_ | Alignment | not modelled | 6.3 | 17 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**methyl-coenzyme m reductase i beta subunit;<br>**PDBTitle:** methyl-coenzyme m reductase from methanosarcina barkeri |
| 70 | c3dclC_ | Alignment | not modelled | 6.2 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**tm1086;<br>**PDBTitle:** crystal structure of tm1086 |
| 71 | d1hbnb1 | Alignment | not modelled | 6.2 | 20 | **Fold:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain<br>**Superfamily:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain<br>**Family:**Methyl-coenzyme M reductase alpha and beta chain C-terminal domain |
| 72 | c3lkxB_ | Alignment | not modelled | 6.2 | 33 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**nascent polypeptide-associated complex subunit alpha;<br>**PDBTitle:** human nac dimerization domain |
| 73 | d1pcla_ | Alignment | not modelled | 6.1 | 20 | **Fold:**Single-stranded right-handed beta-helix<br>**Superfamily:**Pectin lyase-like<br>**Family:**Pectate lyase-like |
| 74 | d3blhb1 | Alignment | not modelled | 6.1 | 30 | **Fold:**Cyclin-like<br>**Superfamily:**Cyclin-like<br>**Family:**Cyclin |
| 75 | c2f9jP_ | Alignment | not modelled | 6.0 | 18 | **PDB header:**rna binding protein<br>**Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1;<br>**PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155 |
| 76 | c3oqhB_ | Alignment | not modelled | 6.0 | 24 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein yvmc;<br>**PDBTitle:** crystal structure of b. licheniformis cdps yvmc-blic |
| 77 | d2k0bx1 | Alignment | not modelled | 5.8 | 15 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**UBA-like<br>**Family:**UBA domain |
| | | | | | | **PDB header:**translation/rna |

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|---|---|---|---|---|---|---|
| 78 | c2pjpA_ | Alignment | not modelled | 5.8 | 21 | **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor;<br>**PDBTitle:** structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna |
| 79 | d1bgfa_ | Alignment | not modelled | 5.7 | 19 | **Fold:**Transcription factor STAT-4 N-domain<br>**Superfamily:**Transcription factor STAT-4 N-domain<br>**Family:**Transcription factor STAT-4 N-domain |
| 80 | c2xqoA_ | Alignment | not modelled | 5.7 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cellulosome enzyme, dockerin type i;<br>**PDBTitle:** ctcel124: a cellulase from clostridium thermocellum |
| 81 | c3pbqA_ | Alignment | not modelled | 5.6 | 9 | **PDB header:**hydrolase/antibiotic<br>**Chain:** A: **PDB Molecule:**penicillin-binding protein 3;<br>**PDBTitle:** crystal structure of pbp3 complexed with imipenem |
| 82 | c1z23A_ | Alignment | not modelled | 5.6 | 23 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**crk-associated substrate;<br>**PDBTitle:** the serine-rich domain from crk-associated substrate2 (p130cas) |
| 83 | d1pvda3 | Alignment | not modelled | 5.6 | 13 | **Fold:**Thiamin diphosphate-binding fold (THDP-binding)<br>**Superfamily:**Thiamin diphosphate-binding fold (THDP-binding)<br>**Family:**Pyruvate oxidase and decarboxylase PP module |
| 84 | d1zpda3 | Alignment | not modelled | 5.5 | 19 | **Fold:**Thiamin diphosphate-binding fold (THDP-binding)<br>**Superfamily:**Thiamin diphosphate-binding fold (THDP-binding)<br>**Family:**Pyruvate oxidase and decarboxylase PP module |
| 85 | c3nb0A_ | Alignment | not modelled | 5.5 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**glycogen [starch] synthase isoform 2;<br>**PDBTitle:** glucose-6-phosphate activated form of yeast glycogen synthase |
| 86 | c3qz6A_ | Alignment | not modelled | 5.4 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**hpch/hpai aldolase;<br>**PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2 |
| 87 | d1nmla1 | Alignment | not modelled | 5.4 | 23 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**Di-heme cytochrome c peroxidase |
| 88 | d1iq0a1 | Alignment | not modelled | 5.3 | 18 | **Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases<br>**Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases |
| 89 | c3fo5A_ | Alignment | not modelled | 5.3 | 20 | **PDB header:**lipid transport<br>**Chain:** A: **PDB Molecule:**thioesterase, adipose associated, isoform bfit2;<br>**PDBTitle:** human start domain of acyl-coenzyme a thioesterase 11 (acot11) |
| 90 | c3e3uA_ | Alignment | not modelled | 5.2 | 33 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptide deformylase;<br>**PDBTitle:** crystal structure of mycobacterium tuberculosis peptide2 deformylase in complex with inhibitor |
| 91 | c2knjA_ | Alignment | not modelled | 5.2 | 17 | **PDB header:**antimicrobial protein<br>**Chain:** A: **PDB Molecule:**microplusin preprotein;<br>**PDBTitle:** nmr structure of microplusin a antimicrobial peptide from2 rhipicephalus (boophilus) microplus |
| 92 | d1lm6a_ | Alignment | not modelled | 5.1 | 13 | **Fold:**Peptide deformylase<br>**Superfamily:**Peptide deformylase<br>**Family:**Peptide deformylase |
| 93 | c2rd0B_ | Alignment | not modelled | 5.1 | 11 | **PDB header:**transferase/oncoprotein<br>**Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit alpha;<br>**PDBTitle:** structure of a human p110alpha/p85alpha complex |
| 94 | c3qu1B_ | Alignment | not modelled | 5.1 | 33 | **PDB header:**hydrolase, metal binding protein<br>**Chain:** B: **PDB Molecule:**peptide deformylase 2;<br>**PDBTitle:** peptide deformylase from vibrio cholerae |
| 95 | d2i53a2 | Alignment | not modelled | 5.1 | 13 | **Fold:**Cyclin-like<br>**Superfamily:**Cyclin-like<br>**Family:**Cyclin |