# Phyre$^2$

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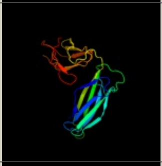
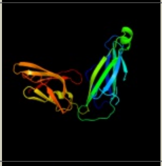
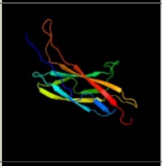
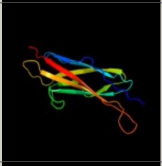
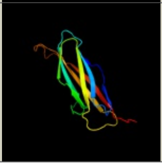
| Description | P28722 |
| Date | Thu Jan 5 11:45:14 GMT 2012 |
| Unique Job ID | d166b8b34544e516 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c1z9sA_ | Alignment |  | 100.0 | 23 | **PDB header:**chaperone/immune system<br>**Chain:** A: **PDB Molecule:**chaperone protein caf1m;<br>**PDBTitle:** crystal structure of the native chaperone:subunit:subunit2 caf1m:caf1:caf1 complex |
| 2 | c2co7B_ | Alignment |  | 100.0 | 18 | **PDB header:**fibril protein<br>**Chain:** B: **PDB Molecule:**putative fimbriae assembly chaperone;<br>**PDBTitle:** salmonella enterica safa pilin in complex with the safb2 chaperone (type ii) |
| 3 | c1qunA_ | Alignment |  | 100.0 | 17 | **PDB header:**chaperone/structural protein<br>**Chain:** A: **PDB Molecule:**papd-like chaperone fimc;<br>**PDBTitle:** x-ray structure of the fimc-fimh chaperone adhesin complex2 from uropathogenic e.coli |
| 4 | c1qpxA_ | Alignment |  | 100.0 | 19 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**papd chaperone;<br>**PDBTitle:** crystal structures of self-capping papd chaperone homodimers |
| 5 | c1l4iA_ | Alignment |  | 100.0 | 18 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**sfae protein;<br>**PDBTitle:** crystal structure of the periplasmic chaperone sfae |
| 6 | c3q48B_ | Alignment |  | 100.0 | 20 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**chaperone cupb2;<br>**PDBTitle:** crystal structure of pseudomonas aeruginosa cupb2 chaperone |
| 7 | c3f6iB_ | Alignment |  | 100.0 | 16 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**chaperone protein faee;<br>**PDBTitle:** structure of the semet labeled f4 fibrial chaperone faee |
| 8 | d1p5va1 | Alignment |  | 100.0 | 27 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**Pilus chaperone |
| 9 | d2co7b1 | Alignment |  | 100.0 | 19 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**Pilus chaperone |
| 10 | d2j2za1 | Alignment |  | 100.0 | 20 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**Pilus chaperone |
| 11 | d3bwuc1 | Alignment |  | 100.0 | 19 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**Pilus chaperone |

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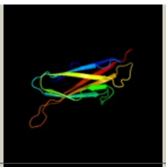
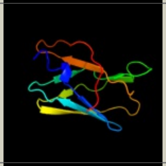
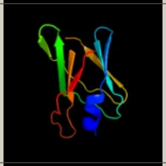
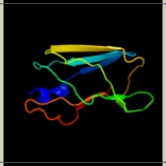
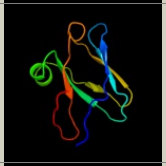
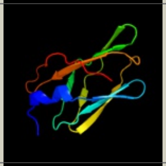
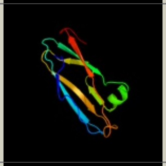
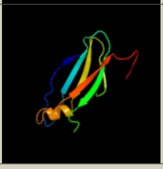
|---|---|---|---|---|---|---|
| 12 | d1l4ia1 | Alignment |  | 100.0 | 21 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**Pilus chaperone |
| 13 | d3bwuc2 | Alignment |  | 99.8 | 15 | **Fold:**C2 domain-like<br>**Superfamily:**Periplasmic chaperone C-domain<br>**Family:**Periplasmic chaperone C-domain |
| 14 | d1p5va2 | Alignment |  | 99.8 | 18 | **Fold:**C2 domain-like<br>**Superfamily:**Periplasmic chaperone C-domain<br>**Family:**Periplasmic chaperone C-domain |
| 15 | d2co7b2 | Alignment |  | 99.7 | 17 | **Fold:**C2 domain-like<br>**Superfamily:**Periplasmic chaperone C-domain<br>**Family:**Periplasmic chaperone C-domain |
| 16 | d2j2za2 | Alignment |  | 99.7 | 21 | **Fold:**C2 domain-like<br>**Superfamily:**Periplasmic chaperone C-domain<br>**Family:**Periplasmic chaperone C-domain |
| 17 | d1l4ia2 | Alignment |  | 99.7 | 16 | **Fold:**C2 domain-like<br>**Superfamily:**Periplasmic chaperone C-domain<br>**Family:**Periplasmic chaperone C-domain |
| 18 | d1m1sa_ | Alignment |  | 97.5 | 11 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**MSP-like |
| 19 | d1grwa_ | Alignment |  | 97.2 | 14 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**MSP-like |
| 20 | d1rowa_ | Alignment |  | 97.0 | 13 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**MSP-like |
| 21 | d1mspa_ | Alignment | not modelled | 96.1 | 11 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**MSP-like |
| 22 | c2e6jA_ | Alignment | not modelled | 96.0 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hydin protein;<br>**PDBTitle:** solution structure of the c-terminal papd-like domain from2 human hydin protein |
| 23 | c2qsvA_ | Alignment | not modelled | 96.0 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of protein of unknown function from porphyromonas2 gingivalis w83 |
| 24 | c3qisA_ | Alignment | not modelled | 96.0 | 7 | **PDB header:**hydrolase/protein binding<br>**Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1;<br>**PDBTitle:** recognition of the f&h motif by the lowe syndrome protein ocrl |
| 25 | c2ys4A_ | Alignment | not modelled | 95.6 | 6 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hydrocephalus-inducing protein homolog;<br>**PDBTitle:** solution structure of the n-terminal papd-like domain of2 hydin protein from human |
| 26 | c1z9oB_ | Alignment | not modelled | 95.1 | 18 | **PDB header:**protein binding/lipid binding protein<br>**Chain:** B: **PDB Molecule:**vesicle-associated membrane protein-associated protein a;<br>**PDBTitle:** 1.9 angstrom crystal structure of the rat vap-a msp homology domain in2 complex with the rat orp1 ffat motif |
| 27 | c3qbtH_ | Alignment | not modelled | 94.5 | 8 | **PDB header:**protein transport/hydrolase<br>**Chain:** H: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1;<br>**PDBTitle:** crystal structure of ocrl1 540-678 in complex with rab8a:gppnhp |

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| 28 | d1wica_ | Alignment | not modelled | 94.3 | 7 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**PapD-like<br>**Family:**MSP-like |
| 29 | c3o0lB_ | Alignment | not modelled | 89.5 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a pfam duf1425 family member (shew_1734) from2 shewanella sp. pv-4 at 1.81 a resolution |
| 30 | d1ejxb_ | Alignment | not modelled | 87.2 | 21 | **Fold:**beta-clip<br>**Superfamily:**Urease, beta-subunit<br>**Family:**Urease, beta-subunit |
| 31 | d4ubpb_ | Alignment | not modelled | 86.6 | 23 | **Fold:**beta-clip<br>**Superfamily:**Urease, beta-subunit<br>**Family:**Urease, beta-subunit |
| 32 | d1e9ya1 | Alignment | not modelled | 83.4 | 20 | **Fold:**beta-clip<br>**Superfamily:**Urease, beta-subunit<br>**Family:**Urease, beta-subunit |
| 33 | d1ufga_ | Alignment | not modelled | 82.7 | 14 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Lamin A/C globular tail domain<br>**Family:**Lamin A/C globular tail domain |
| 34 | c2lllA_ | Alignment | not modelled | 81.9 | 18 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**lamin-b2;<br>**PDBTitle:** solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a |
| 35 | c3qgaD_ | Alignment | not modelled | 81.2 | 16 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits;<br>**PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae |
| 36 | d1e42a1 | Alignment | not modelled | 80.6 | 14 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Clathrin adaptor appendage domain<br>**Family:**Alpha-adaptin ear subdomain-like |
| 37 | d2vzsa2 | Alignment | not modelled | 79.3 | 10 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**beta-Galactosidase/glucuronidase domain<br>**Family:**beta-Galactosidase/glucuronidase domain |
| 38 | c1e9zA_ | Alignment | not modelled | 79.2 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**urease subunit alpha;<br>**PDBTitle:** crystal structure of helicobacter pylori urease |
| 39 | c3jt0B_ | Alignment | not modelled | 72.2 | 16 | **PDB header:**structural protein<br>**Chain:** B: **PDB Molecule:**lamin-b1;<br>**PDBTitle:** crystal structure of the c-terminal fragment (426-558)2 lamin-b1 from homo sapiens, northeast structural genomics3 consortium target hr5546a |
| 40 | d1ifra_ | Alignment | not modelled | 72.1 | 12 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Lamin A/C globular tail domain<br>**Family:**Lamin A/C globular tail domain |
| 41 | c1yycA_ | Alignment | not modelled | 60.9 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative late embryogenesis abundant protein;<br>**PDBTitle:** solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1 |
| 42 | d1aoza2 | Alignment | not modelled | 60.6 | 14 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Multidomain cupredoxins |
| 43 | c2qvkA_ | Alignment | not modelled | 59.9 | 10 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**sodium/calcium exchanger 1;<br>**PDBTitle:** the second ca2+-binding domain of the na+-ca2+ exchanger is2 essential for regulation: crystal structures and3 mutational analysis |
| 44 | c1e42A_ | Alignment | not modelled | 56.7 | 14 | **PDB header:**endocytosis<br>**Chain:** A: **PDB Molecule:**ap-2 complex subunit beta;<br>**PDBTitle:** beta2-adaptin appendage domain, from clathrin adaptor ap2 |
| 45 | d1hfua2 | Alignment | not modelled | 54.6 | 14 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Multidomain cupredoxins |
| 46 | c3eujB_ | Alignment | not modelled | 51.8 | 9 | **PDB header:**cell cycle<br>**Chain:** B: **PDB Molecule:**chromosome partition protein mukf;<br>**PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, symmetric dimer |
| 47 | c3ginB_ | Alignment | not modelled | 49.2 | 12 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**sodium/calcium exchanger 1;<br>**PDBTitle:** crystal structure of e454k-cbd1 |
| 48 | d1xo8a_ | Alignment | not modelled | 46.1 | 11 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**LEA14-like<br>**Family:**LEA14-like |
| 49 | d1gyca2 | Alignment | not modelled | 44.5 | 17 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Multidomain cupredoxins |
| 50 | d1ivta_ | Alignment | not modelled | 42.2 | 13 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Lamin A/C globular tail domain<br>**Family:**Lamin A/C globular tail domain |
| 51 | d1v10a2 | Alignment | not modelled | 40.8 | 13 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Multidomain cupredoxins |
| 52 | d2q9oa2 | Alignment | not modelled | 38.8 | 17 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Multidomain cupredoxins |
| 53 | d1kyaa2 | Alignment | not modelled | 37.1 | 13 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Multidomain cupredoxins |

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| 54 | c3butA_ | Alignment | not modelled | 36.8 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein af_0446;<br>**PDBTitle:** crystal structure of protein af_0446 from archaeoglobus fulgidus |
| 55 | c3h6aB_ | Alignment | not modelled | 34.8 | 10 | **PDB header:**cell adhesion<br>**Chain:** B: **PDB Molecule:**integrin beta-4;<br>**PDBTitle:** structure of the calx-beta domain of integrin beta42 crystallized in the presence of calcium |
| 56 | d2fwua1 | Alignment | not modelled | 32.7 | 10 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**CalX-like<br>**Family:**CalX-beta domain |
| 57 | d1k3ra1 | Alignment | not modelled | 30.6 | 11 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Hypothetical protein MTH1 (MT0001), insert domain |
| 58 | c1v10A_ | Alignment | not modelled | 29.7 | 10 | **PDB header:**oxidase<br>**Chain:** A: **PDB Molecule:**laccase;<br>**PDBTitle:** structure of rigidoporus lignosus laccase from hemihedrally2 twinned crystals |
| 59 | c3isyA_ | Alignment | not modelled | 28.9 | 15 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor;<br>**PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution |
| 60 | d2phla2 | Alignment | not modelled | 28.3 | 14 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**Germin/Seed storage 7S protein |
| 61 | d1khua_ | Alignment | not modelled | 26.6 | 10 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**SMAD domain |
| 62 | c3ac0B_ | Alignment | not modelled | 26.4 | 21 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**beta-glucosidase i;<br>**PDBTitle:** crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose |
| 63 | c3hs8A_ | Alignment | not modelled | 25.0 | 14 | **PDB header:**endocytosis<br>**Chain:** A: **PDB Molecule:**adaptor protein complex ap-2, alpha 2 subunit;<br>**PDBTitle:** intersectin 1-peptide-ap2 alpha ear complex |
| 64 | c3rb7E_ | Alignment | not modelled | 24.1 | 13 | **PDB header:**metal binding protein<br>**Chain:** E: **PDB Molecule:**na/ca exchange protein;<br>**PDBTitle:** crystal structure of cbd12 from calx1.2 |
| 65 | c3fcsA_ | Alignment | not modelled | 24.1 | 15 | **PDB header:**cell adhesion/blood clotting<br>**Chain:** A: **PDB Molecule:**integrin, alpha 2b;<br>**PDBTitle:** structure of complete ectodomain of integrin aiibb3 |
| 66 | c1zpuE_ | Alignment | not modelled | 19.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**iron transport multicopper oxidase fet3;<br>**PDBTitle:** crystal structure of fet3p, a multicopper oxidase that functions in2 iron import |
| 67 | c2x41A_ | Alignment | not modelled | 18.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-glucosidase;<br>**PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose |
| 68 | d2dpka1 | Alignment | not modelled | 18.0 | 13 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**CalX-like<br>**Family:**CalX-beta domain |
| 69 | d1ygsa_ | Alignment | not modelled | 16.2 | 13 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**SMAD domain |
| 70 | d1dd1a_ | Alignment | not modelled | 15.1 | 13 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**SMAD domain |
| 71 | c3ppsD_ | Alignment | not modelled | 15.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**laccase;<br>**PDBTitle:** crystal structure of an ascomycete fungal laccase from thielavia2 arenaria |
| 72 | d1khxa_ | Alignment | not modelled | 14.9 | 10 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**SMAD domain |
| 73 | c1khxA_ | Alignment | not modelled | 14.9 | 10 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**smad2;<br>**PDBTitle:** crystal structure of a phosphorylated smad2 |
| 74 | d1jz8a2 | Alignment | not modelled | 14.6 | 11 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**beta-Galactosidase/glucuronidase domain<br>**Family:**beta-Galactosidase/glucuronidase domain |
| 75 | c3tqzA_ | Alignment | not modelled | 13.7 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**deoxyuridine 5'-triphosphate nucleotidohydrolase;<br>**PDBTitle:** structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii |
| 76 | d1w8oa1 | Alignment | not modelled | 13.5 | 11 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**E set domains<br>**Family:**E-set domains of sugar-utilizing enzymes |
| 77 | d1exha_ | Alignment | not modelled | 13.5 | 20 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**Carbohydrate-binding domain<br>**Family:**Cellulose-binding domain family II |
| 78 | c2q9oA_ | Alignment | not modelled | 12.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**laccase-1;<br>**PDBTitle:** near-atomic resolution structure of a melanocarpus albomyces laccase |
| 79 | c1wkwB_ | Alignment | not modelled | 11.7 | 22 | **PDB header:**translation/protein binding<br>**Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 4e<br>**PDBTitle:** crystal structure of the ternary complex of eif4e-m7gpppa-2 4ebp1 peptide |
|  |  |  |  |  |  | **PDB header:**lipoprotein<br>**Chain:** A: **PDB Molecule:**uncharacterized lipoprotein yaji; |

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| 80 | c2jwyA_ | Alignment | not modelled | 10.8 | 12 | **PDBTitle:** solution nmr structure of uncharacterized lipoprotein yaji from2 escherichia coli. northeast structural genomics target er540 |
| 81 | c1l9mB_ | Alignment | not modelled | 10.2 | 8 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**protein-glutamine glutamyltransferase e3;<br>**PDBTitle:** three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation |
| 82 | c3e9tD_ | Alignment | not modelled | 10.1 | 14 | **PDB header:**membrane protein<br>**Chain:** D: **PDB Molecule:**na/ca exchange protein;<br>**PDBTitle:** crystal structure of apo-form calx cbd1 domain |
| 83 | d1mjsa_ | Alignment | not modelled | 9.6 | 11 | **Fold:**SMAD/FHA domain<br>**Superfamily:**SMAD/FHA domain<br>**Family:**SMAD domain |
| 84 | c2ii8F_ | Alignment | not modelled | 9.4 | 14 | **PDB header:**signaling protein<br>**Chain:** F: **PDB Molecule:**anabaena sensory rhodopsin transducer protein;<br>**PDBTitle:** anabaena sensory rhodopsin transducer |
| 85 | c3e9uA_ | Alignment | not modelled | 9.0 | 8 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**na/ca exchange protein;<br>**PDBTitle:** crystal structure of calx cbd2 domain |
| 86 | c1l5gA_ | Alignment | not modelled | 8.9 | 13 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha v;<br>**PDBTitle:** crystal structure of the extracellular segment of integrin avb3 in2 complex with an arg-gly-asp ligand |
| 87 | c1a65A_ | Alignment | not modelled | 8.5 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**laccase;<br>**PDBTitle:** type-2 cu-depleted laccase from coprinus cinereus |
| 88 | c2qziA_ | Alignment | not modelled | 7.7 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the crystal structure of a conserved protein of unknown function from2 streptococcus thermophilus lmg 18311. |
| 89 | d1ex0a2 | Alignment | not modelled | 7.6 | 9 | **Fold:**Immunoglobulin-like beta-sandwich<br>**Superfamily:**Transglutaminase, two C-terminal domains<br>**Family:**Transglutaminase, two C-terminal domains |
| 90 | d1euwa_ | Alignment | not modelled | 7.6 | 24 | **Fold:**beta-clip<br>**Superfamily:**dUTPase-like<br>**Family:**dUTPase-like |
| 91 | c2r39A_ | Alignment | not modelled | 7.3 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**fixg-related protein;<br>**PDBTitle:** crystal structure of fixg-related protein from vibrio parahaemolyticus |
| 92 | d1plca_ | Alignment | not modelled | 7.1 | 16 | **Fold:**Cupredoxin-like<br>**Superfamily:**Cupredoxins<br>**Family:**Plastocyanin/azurin-like |
| 93 | c2l02B_ | Alignment | not modelled | 6.7 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375 |
| 94 | c3rfrI_ | Alignment | not modelled | 6.3 | 16 | **PDB header:**oxidoreductase<br>**Chain:** I: **PDB Molecule:**pmob;<br>**PDBTitle:** crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m |
| 95 | c1gycA_ | Alignment | not modelled | 6.2 | 15 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**laccase 2;<br>**PDBTitle:** crystal structure determination at room temperature of a2 laccase from trametes versicolor in its oxidised form3 containing a full complement of copper ions |
| 96 | c2phgB_ | Alignment | not modelled | 6.1 | 33 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**alpha trans-inducing protein;<br>**PDBTitle:** model for vp16 binding to tfiib |
| 97 | c2pheC_ | Alignment | not modelled | 6.1 | 33 | **PDB header:**transcription<br>**Chain:** C: **PDB Molecule:**alpha trans-inducing protein;<br>**PDBTitle:** model for vp16 binding to pc4 |
| 98 | c2frgP_ | Alignment | not modelled | 5.9 | 12 | **PDB header:**immune system<br>**Chain:** P: **PDB Molecule:**trem-like transcript-1;<br>**PDBTitle:** structure of the immunoglobulin-like domain of human tlt-1 |
| 99 | c2qv2A_ | Alignment | not modelled | 5.9 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**inositol polyphosphate 5-phosphatase ocrl-1;<br>**PDBTitle:** a role of the lowe syndrome protein ocrl in early steps of2 the endocytic pathway |