Phyre$^2$

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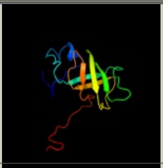
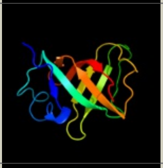
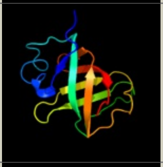
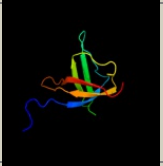
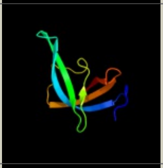
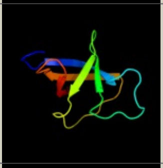
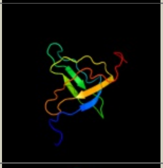
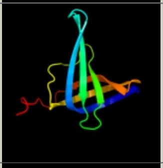
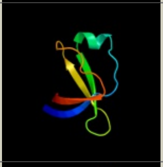
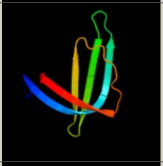
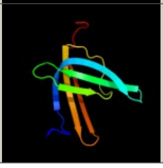
| Email | l.a.kelley@imperial.ac.uk |
| Description | P69490 |
| Date | Thu Jan 5 12:11:44 GMT 2012 |
| Unique Job ID | 1d8c6b616f6b42b5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1sr3a_ | Alignment |  | 100.0 | 100 | **Fold:**OB-fold<br>**Superfamily:**Heme chaperone CcmE<br>**Family:**Heme chaperone CcmE |
| 2 | d1j6qa_ | Alignment |  | 100.0 | 59 | **Fold:**OB-fold<br>**Superfamily:**Heme chaperone CcmE<br>**Family:**Heme chaperone CcmE |
| 3 | c1j6qA_ | Alignment |  | 100.0 | 59 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**cytochrome c maturation protein e;<br>**PDBTitle:** solution structure and characterization of the heme2 chaperone ccme |
| 4 | c2kctA_ | Alignment |  | 99.9 | 25 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccme;<br>**PDBTitle:** solution nmr structure of the ob-fold domain of heme2 chaperone ccme from desulfovibrio vulgaris. northeast3 structural genomics target dvr115g. |
| 5 | c3e0jG_ | Alignment |  | 92.6 | 11 | **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 |
| 6 | c3floG_ | Alignment |  | 90.6 | 16 | **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 |
| 7 | c1asyA_ | Alignment |  | 86.1 | 11 | **PDB header:**complex (aminoacyl-trna synthase/trna)<br>**Chain:** A: **PDB Molecule:**aspartyl-trna synthetase;<br>**PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp |
| 8 | c1eqrC_ | Alignment |  | 85.0 | 26 | **PDB header:**ligase<br>**Chain:** C: **PDB Molecule:**aspartyl-trna synthetase;<br>**PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli |
| 9 | c2pi2A_ | Alignment |  | 83.4 | 17 | **PDB header:**replication, dna binding protein<br>**Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit;<br>**PDBTitle:** full-length replication protein a subunits rpa14 and rpa32 |
| 10 | d1c0aa1 | Alignment |  | 83.0 | 25 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 11 | c1wydB_ | Alignment |  | 82.2 | 16 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase;<br>**PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii |

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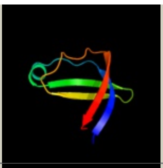
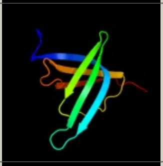
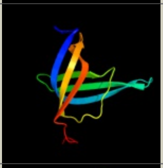
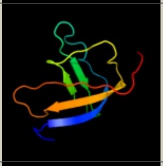
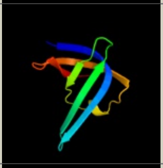
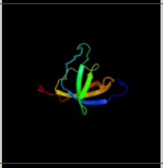
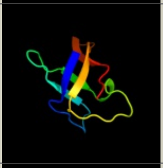
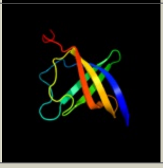
| 12 | d2pi2a1 | Alignment |  | 82.1 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 13 | d1b8aa1 | Alignment |  | 81.3 | 22 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 14 | c3i7fA_ | Alignment |  | 81.1 | 13 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**aspartyl-trna synthetase;<br>**PDBTitle:** aspartyl trna synthetase from entamoeba histolytica |
| 15 | d1l0wa1 | Alignment |  | 80.6 | 22 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 16 | c3m4qA_ | Alignment |  | 80.3 | 18 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative;<br>**PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs) |
| 17 | c3kf6A_ | Alignment |  | 80.1 | 17 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**protein stn1;<br>**PDBTitle:** crystal structure of s. pombe stn1-ten1 complex |
| 18 | c3bjuB_ | Alignment |  | 72.6 | 18 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**lysyl-trna synthetase;<br>**PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase |
| 19 | d1c9oa_ | Alignment |  | 72.3 | 23 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 20 | d1n9wa1 | Alignment |  | 71.0 | 25 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 21 | d1gm5a2 | Alignment | not modelled | 69.9 | 16 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**RecG "wedge" domain |
| 22 | c2xgtB_ | Alignment | not modelled | 65.1 | 21 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic;<br>**PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate |
| 23 | c3e0dA_ | Alignment | not modelled | 63.2 | 30 | **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 |
| 24 | c3e0eA_ | Alignment | not modelled | 59.7 | 18 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**replication protein a;<br>**PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b |
| 25 | c1efwA_ | Alignment | not modelled | 57.0 | 21 | **PDB header:**ligase/rna<br>**Chain:** A: **PDB Molecule:**aspartyl-trna synthetase;<br>**PDBTitle:** crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli |
| 26 | c1b8aB_ | Alignment | not modelled | 56.8 | 24 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase);<br>**PDBTitle:** aspartyl-trna synthetase |
| 27 | c1z9fA_ | Alignment | not modelled | 56.7 | 21 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**single-strand binding protein;<br>**PDBTitle:** crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution |
| | | | | | | **Fold:**OB-fold |

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| 28 | d1eova1 | Alignment | not modelled | 55.2 | 11 | **Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 29 | c1x55A_ | Alignment | not modelled | 43.9 | 24 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase;<br>**PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue |
| 30 | d1bbua1 | Alignment | not modelled | 43.7 | 21 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 31 | d2es2a1 | Alignment | not modelled | 40.4 | 22 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 32 | d1o7ia_ | Alignment | not modelled | 40.0 | 20 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 33 | d2pi2e1 | Alignment | not modelled | 40.0 | 13 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 34 | c1n9wA_ | Alignment | not modelled | 38.9 | 25 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2;<br>**PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus |
| 35 | c3najA_ | Alignment | not modelled | 37.8 | 24 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**galectin-8;<br>**PDBTitle:** crystal structure of a protease-resistant mutant form of human2 galectin-8 |
| 36 | c3a0jB_ | Alignment | not modelled | 37.3 | 23 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**cold shock protein;<br>**PDBTitle:** crystal structure of cold shock protein 1 from thermus2 thermophilus hb8 |
| 37 | d2hqsa2 | Alignment | not modelled | 31.9 | 25 | **Fold:**Anticodon-binding domain-like<br>**Superfamily:**TolB, N-terminal domain<br>**Family:**TolB, N-terminal domain |
| 38 | c3dm3A_ | Alignment | not modelled | 27.5 | 24 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**replication factor a;<br>**PDBTitle:** crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e |
| 39 | d1llca1 | Alignment | not modelled | 25.3 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 40 | c2kcmA_ | Alignment | not modelled | 24.8 | 20 | **PDB header:**nucleic acid binding protein<br>**Chain:** A: **PDB Molecule:**cold shock domain family protein;<br>**PDBTitle:** solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a. |
| 41 | c3o0rC_ | Alignment | not modelled | 23.8 | 10 | **PDB header:**immune system/oxidoreductase<br>**Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c;<br>**PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment |
| 42 | c2dycA_ | Alignment | not modelled | 23.7 | 21 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**galectin-4;<br>**PDBTitle:** crystal structure of the n-terminal domain of mouse galectin-4 |
| 43 | c3b9cB_ | Alignment | not modelled | 23.0 | 25 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**hspc159;<br>**PDBTitle:** crystal structure of human grp crd |
| 44 | c3nv4A_ | Alignment | not modelled | 22.4 | 4 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**galectin 9 short isoform variant;<br>**PDBTitle:** crystal structure of human galectin-9 c-terminal crd in complex with2 sialyllactose |
| 45 | c1n10A_ | Alignment | not modelled | 21.8 | 15 | **PDB header:**allergen<br>**Chain:** A: **PDB Molecule:**pollen allergen phl p 1;<br>**PDBTitle:** crystal structure of phl p 1, a major timothy grass pollen allergen |
| 46 | c2pqaB_ | Alignment | not modelled | 21.8 | 13 | **PDB header:**replication<br>**Chain:** B: **PDB Molecule:**replication protein a 14 kda subunit;<br>**PDBTitle:** crystal structure of full-length human rpa 14/32 heterodimer |
| 47 | c3mxnB_ | Alignment | not modelled | 21.6 | 19 | **PDB header:**replication<br>**Chain:** B: **PDB Molecule:**recq-mediated genome instability protein 2;<br>**PDBTitle:** crystal structure of the rmi core complex |
| 48 | c2yroA_ | Alignment | not modelled | 20.7 | 21 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**galectin-8;<br>**PDBTitle:** solution structure of the c-terminal gal-bind lectin2 protein from human galectin-8 |
| 49 | c1fguA_ | Alignment | not modelled | 19.1 | 12 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**replication protein a 70 kda dna-binding subunit;<br>**PDBTitle:** ssdna-binding domain of the large subunit of replication2 protein a |
| 50 | d2gala_ | Alignment | not modelled | 19.0 | 21 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Galectin (animal S-lectin) |
| 51 | c2yxsA_ | Alignment | not modelled | 18.4 | 29 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**galectin-8 variant;<br>**PDBTitle:** crystal sturcture of n-terminal domain of human galectin-8 with d-2 lactose |
| 52 | d2nn8a1 | Alignment | not modelled | 18.2 | 17 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Galectin (animal S-lectin) |
| 53 | c2k5nA_ | Alignment | not modelled | 17.6 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative cold-shock protein;<br>**PDBTitle:** solution nmr structure of the n-terminal domain of |

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| | | | | | | protein2 eca1580 from erwinia carotovora, northeast structural3 genomics consortium target ewr156a |
| 54 | c1gm5A_ | Alignment | not modelled | 17.5 | 15 | **PDB header:**helicase<br>**Chain:** A: **PDB Molecule:**recg;<br>**PDBTitle:** structure of recg bound to three-way dna junction |
| 55 | c2yf3F_ | Alignment | not modelled | 16.1 | 27 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**mazg-like nucleoside triphosphate pyrophosphohydrolase;<br>**PDBTitle:** crystal structure of dr2231, the mazg-like protein from2 deinococcus radiodurans, complex with manganese |
| 56 | d1h95a_ | Alignment | not modelled | 16.0 | 19 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 57 | d1g6pa_ | Alignment | not modelled | 15.8 | 26 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 58 | c3e9hB_ | Alignment | not modelled | 15.7 | 21 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**lysyl-trna synthetase;<br>**PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine |
| 59 | c3kojA_ | Alignment | not modelled | 15.5 | 16 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**uncharacterized protein ycf41;<br>**PDBTitle:** crystal structure of the ssb domain of q5n255_synp6 protein2 from synechococcus sp. northeast structural genomics3 consortium target snr59a. |
| 60 | d1lr0a_ | Alignment | not modelled | 15.5 | 18 | **Fold:**TolA/TonB C-terminal domain<br>**Superfamily:**TolA/TonB C-terminal domain<br>**Family:**TolA |
| 61 | c2d6lX_ | Alignment | not modelled | 14.9 | 25 | **PDB header:**sugar binding protein<br>**Chain:** X: **PDB Molecule:**lectin, galactose binding, soluble 9;<br>**PDBTitle:** crystal structure of mouse galectin-9 n-terminal crd2 (crystal form 2) |
| 62 | d1n10a1 | Alignment | not modelled | 14.2 | 11 | **Fold:**C2 domain-like<br>**Superfamily:**PHL pollen allergen<br>**Family:**PHL pollen allergen |
| 63 | c2ealB_ | Alignment | not modelled | 13.8 | 21 | **PDB header:**sugar binding protein<br>**Chain:** B: **PDB Molecule:**galectin-9;<br>**PDBTitle:** crystal structure of human galectin-9 n-terminal crd in complex with2 forssman pentasaccharide |
| 64 | c2wsuB_ | Alignment | not modelled | 13.1 | 16 | **PDB header:**viral protein<br>**Chain:** B: **PDB Molecule:**putative fiber protein;<br>**PDBTitle:** galectin domain of porcine adenovirus type 4 nadc-1 isolate2 fibre |
| 65 | d1whoa_ | Alignment | not modelled | 12.8 | 19 | **Fold:**C2 domain-like<br>**Superfamily:**PHL pollen allergen<br>**Family:**PHL pollen allergen |
| 66 | d1okja1 | Alignment | not modelled | 12.2 | 10 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Actin-like ATPase domain<br>**Family:**YeaZ-like |
| 67 | c2hczX_ | Alignment | not modelled | 12.1 | 9 | **PDB header:**allergen<br>**Chain:** X: **PDB Molecule:**beta-expansin 1a;<br>**PDBTitle:** crystal structure of expb1 (zea m 1), a beta-expansin and group-12 pollen allergen from maize |
| 68 | d1l4ia2 | Alignment | not modelled | 11.9 | 17 | **Fold:**C2 domain-like<br>**Superfamily:**Periplasmic chaperone C-domain<br>**Family:**Periplasmic chaperone C-domain |
| 69 | d1ldna1 | Alignment | not modelled | 11.2 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 70 | d1jmca1 | Alignment | not modelled | 10.9 | 10 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 71 | d2a6aa1 | Alignment | not modelled | 10.9 | 12 | **Fold:**Ribonuclease H-like motif<br>**Superfamily:**Actin-like ATPase domain<br>**Family:**YeaZ-like |
| 72 | d1k8wa3 | Alignment | not modelled | 10.8 | 10 | **Fold:**PUA domain-like<br>**Superfamily:**PUA domain-like<br>**Family:**PUA domain |
| 73 | c3lhnB_ | Alignment | not modelled | 10.8 | 29 | **PDB header:**lipid binding protein<br>**Chain:** B: **PDB Molecule:**lipoprotein;<br>**PDBTitle:** crystal structure of putative lipoprotein (np_718719.1) from2 shewanella oneidensis at 1.42 a resolution |
| 74 | c3k6oA_ | Alignment | not modelled | 10.7 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein duf1344;<br>**PDBTitle:** crystal structure of protein of unknown function duf13442 (yp_001299214.1) from bacteroides vulgatus atcc 8482 at 2.00 a3 resolution |
| 75 | c2qneA_ | Alignment | not modelled | 10.6 | 22 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative methyltransferase;<br>**PDBTitle:** crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution |
| 76 | c1ynxA_ | Alignment | not modelled | 10.5 | 10 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**replication factor-a protein 1;<br>**PDBTitle:** solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa) |
| 77 | d1krta_ | Alignment | not modelled | 10.2 | 20 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 78 | d1txya_ | Alignment | not modelled | 9.9 | 15 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| | | | | | | **Fold:**OB-fold |

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|---|---|---|---|---|---|---|
| 79 | d1nnxa_ | Alignment | not modelled | 9.4 | 19 | **Superfamily:**Hypothetical protein YgiW<br>**Family:**Hypothetical protein YgiW |
| 80 | d1jnya1 | Alignment | not modelled | 9.2 | 16 | **Fold:**Reductase/isomerase/elongation factor common domain<br>**Superfamily:**Translation proteins<br>**Family:**Elongation factors |
| 81 | d1c0pa1 | Alignment | not modelled | 9.1 | 15 | **Fold:**Nucleotide-binding domain<br>**Superfamily:**Nucleotide-binding domain<br>**Family:**D-aminoacid oxidase, N-terminal domain |
| 82 | c1e22A_ | Alignment | not modelled | 9.1 | 24 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**lysyl-trna synthetase;<br>**PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp |
| 83 | c3eoeC_ | Alignment | not modelled | 9.1 | 18 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007 |
| 84 | d1e1oa1 | Alignment | not modelled | 8.8 | 24 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 85 | c2jnzA_ | Alignment | not modelled | 8.7 | 26 | **PDB header:**allergen<br>**Chain:** A: **PDB Molecule:**phl p 3 allergen;<br>**PDBTitle:** solution structure of phl p 3, a major allergen from2 timothy grass pollen |
| 86 | c1llcA_ | Alignment | not modelled | 8.2 | 11 | **PDB header:**oxidoreductase(choh(d)-nad(a))<br>**Chain:** A: **PDB Molecule:**l-lactate dehydrogenase;<br>**PDBTitle:** structure determination of the allosteric l-lactate dehydrogenase from2 lactobacillus casei at 3.0 angstroms resolution |
| 87 | d1mjca_ | Alignment | not modelled | 8.1 | 26 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Cold shock DNA-binding domain-like |
| 88 | c1x50A_ | Alignment | not modelled | 8.0 | 17 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**galectin-4;<br>**PDBTitle:** solution structure of the c-terminal gal-bind lectin domain2 from human galectin-4 |
| 89 | c2z4hB_ | Alignment | not modelled | 7.6 | 29 | **PDB header:**signaling protein activator<br>**Chain:** B: **PDB Molecule:**copper homeostasis protein cutf;<br>**PDBTitle:** crystal structure of the cpx pathway activator nlpe from2 escherichia coli |
| 90 | c2kncA_ | Alignment | not modelled | 7.6 | 17 | **PDB header:**cell adhesion<br>**Chain:** A: **PDB Molecule:**integrin alpha-iib;<br>**PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex |
| 91 | d1jmca2 | Alignment | not modelled | 7.5 | 18 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Single strand DNA-binding domain, SSB |
| 92 | d1rmda1 | Alignment | not modelled | 6.9 | 13 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 93 | c3e8gB_ | Alignment | not modelled | 6.8 | 0 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**potassium channel protein;<br>**PDBTitle:** crystal structure of the the open nak channel-na+/ca2+ complex |
| 94 | c2j7aC_ | Alignment | not modelled | 6.6 | 19 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**cytochrome c quinol dehydrogenase nrfh;<br>**PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris |
| 95 | c2eqmA_ | Alignment | not modelled | 6.6 | 14 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**phd finger protein 20-like 1;<br>**PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens] |
| 96 | d1o65a_ | Alignment | not modelled | 6.5 | 25 | **Fold:**PK beta-barrel domain-like<br>**Superfamily:**PK beta-barrel domain-like<br>**Family:**MOSC (MOCO sulphurase C-terminal) domain |
| 97 | c3e1rB_ | Alignment | not modelled | 6.5 | 20 | **PDB header:**cell cycle/transport protein<br>**Chain:** B: **PDB Molecule:**centrosomal protein of 55 kda;<br>**PDBTitle:** midbody targeting of the escrt machinery by a non-canonical2 coiled-coil in cep55 |
| 98 | d1ldma1 | Alignment | not modelled | 6.5 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**LDH N-terminal domain-like |
| 99 | c1jpeA_ | Alignment | not modelled | 6.4 | 21 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**dsbd-alpha;<br>**PDBTitle:** crystal structure of dsbd-alpha; the n-terminal domain of2 dsbd |