# Phyre2

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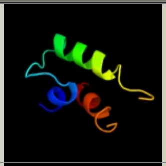
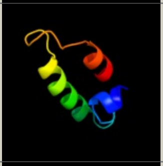
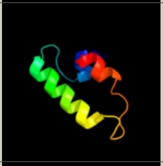
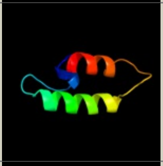
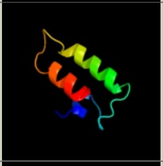
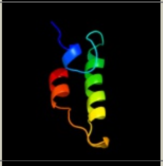
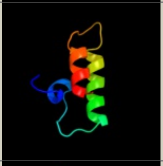
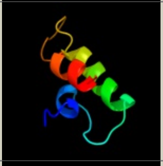
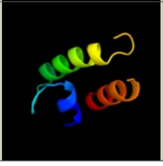
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77359 |
| Date | Thu Jan 5 12:28:09 GMT 2012 |
| Unique Job ID | a807daf83dbeae6e |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2pf4E_ | Alignment |  | 98.8 | 27 | **PDB header:**hydrolase regulator/viral protein<br>**Chain:** E: **PDB Molecule:**small t antigen;<br>**PDBTitle:** crystal structure of the full-length simian virus 40 small t antigen2 complexed with the protein phosphatase 2a aalpha subunit |
| 2 | d1gh6a_ | Alignment |  | 98.6 | 24 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |
| 3 | c1fpoA_ | Alignment |  | 98.5 | 11 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**chaperone protein hscb;<br>**PDBTitle:** hsc20 (hscb), a j-type co-chaperone from e. coli |
| 4 | c3hhoA_ | Alignment |  | 98.5 | 11 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**co-chaperone protein hscb homolog;<br>**PDBTitle:** chaperone hscb from vibrio cholerae |
| 5 | c3apqB_ | Alignment |  | 98.5 | 30 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10;<br>**PDBTitle:** crystal structure of j-trx1 fragment of erdj5 |
| 6 | c2ctqA_ | Alignment |  | 98.5 | 26 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 12;<br>**PDBTitle:** solution structure of j-domain from human dnaj subfamily c2 menber 12 |
| 7 | c3bvoA_ | Alignment |  | 98.5 | 13 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor;<br>**PDBTitle:** crystal structure of human co-chaperone protein hscb |
| 8 | c2lgwA_ | Alignment |  | 98.5 | 32 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 2;<br>**PDBTitle:** solution structure of the j domain of hsj1a |
| 9 | c2ys8A_ | Alignment |  | 98.4 | 30 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**rab-related gtp-binding protein rabj;<br>**PDBTitle:** solution structure of the dnaj-like domain from human ras-2 associated protein rap1 |
| 10 | c2kqxA_ | Alignment |  | 98.4 | 26 | **PDB header:**chaperone binding protein<br>**Chain:** A: **PDB Molecule:**curved dna-binding protein;<br>**PDBTitle:** nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa |
| 11 | d1fafa_ | Alignment |  | 98.4 | 17 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |

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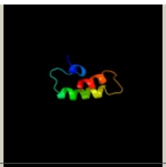
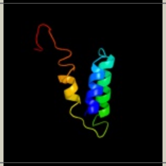
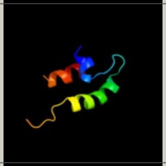
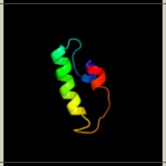
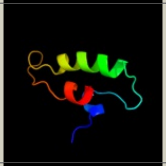
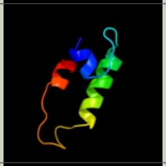
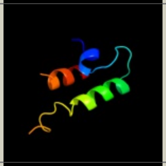
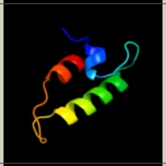
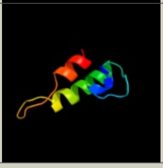
|---|---|---|---|---|---|---|
| 12 | c2ctwA_ | Alignment |  | 98.4 | 23 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 5;<br>**PDBTitle:** solution structure of j-domain from mouse dnaj subfamily c2 menber 5 |
| 13 | d1iura_ | Alignment |  | 98.3 | 16 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |
| 14 | c2l6lA_ | Alignment |  | 98.3 | 28 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24;<br>**PDBTitle:** solution structure of human j-protein co-chaperone, dph4 |
| 15 | c2ctrA_ | Alignment |  | 98.3 | 22 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 9;<br>**PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 member 9 |
| 16 | c2dmxA_ | Alignment |  | 98.3 | 28 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 8;<br>**PDBTitle:** solution structure of the j domain of dnaj homolog2 subfamily b member 8 |
| 17 | c2yuaA_ | Alignment |  | 98.2 | 28 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**williams-beuren syndrome chromosome region 18<br>**PDBTitle:** solution structure of the dnaj domain from human williams-2 beuren syndrome chromosome region 18 protein |
| 18 | d1wjza_ | Alignment |  | 98.2 | 28 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |
| 19 | c2qsaA_ | Alignment |  | 98.2 | 26 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog dnj-2;<br>**PDBTitle:** crystal structure of j-domain of dnaj homolog dnj-2 precursor from2 c.elegans. |
| 20 | d1xbla_ | Alignment |  | 98.2 | 30 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |
| 21 | c2ctpA_ | Alignment | not modelled | 98.2 | 26 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 12;<br>**PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 member 12 |
| 22 | d1hdja_ | Alignment | not modelled | 98.2 | 28 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |
| 23 | c2o37A_ | Alignment | not modelled | 98.2 | 17 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**protein sis1;<br>**PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae. |
| 24 | c2ochA_ | Alignment | not modelled | 98.2 | 28 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**hypothetical protein dnj-12;<br>**PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans |
| 25 | c2guzO_ | Alignment | not modelled | 98.1 | 16 | **PDB header:**chaperone, protein transport<br>**Chain:** O: **PDB Molecule:**mitochondrial import inner membrane translocase<br>**PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor |
| 26 | c2dn9A_ | Alignment | not modelled | 98.1 | 30 | **PDB header:**apoptosis, chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3;<br>**PDBTitle:** solution structure of j-domain from the dnaj homolog, human2 tid1 protein |
| 27 | c2cugA_ | Alignment | not modelled | 98.1 | 26 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**mkiaa0962 protein;<br>**PDBTitle:** solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962 |
| 28 | c3ag7A_ | Alignment | not modelled | 98.0 | 23 | **PDB header:**plant protein<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein f9e10.5;<br>**PDBTitle:** an auxilin-like j-domain containing protein, jac1 j-domain |

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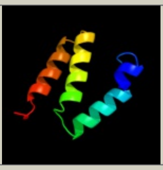
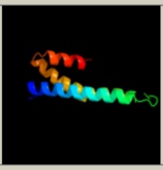
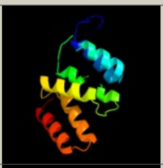
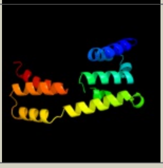
| 29 | c1bq0A_ | Alignment | not modelled | 97.8 | 30 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj;<br>**PDBTitle:** j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures |
| 30 | d1fpoa1 | Alignment | not modelled | 97.8 | 11 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |
| 31 | d1nz6a_ | Alignment | not modelled | 97.7 | 16 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |
| 32 | c2guzD_ | Alignment | not modelled | 97.7 | 20 | **PDB header:**chaperone, protein transport<br>**Chain:** D: **PDB Molecule:**mitochondrial import inner membrane translocase<br>**PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor |
| 33 | d1n4ca_ | Alignment | not modelled | 95.7 | 13 | **Fold:**Long alpha-hairpin<br>**Superfamily:**Chaperone J-domain<br>**Family:**Chaperone J-domain |
| 34 | c3uo2A_ | Alignment | not modelled | 90.1 | 20 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**j-type co-chaperone jac1, mitochondrial;<br>**PDBTitle:** jac1 co-chaperone from saccharomyces cerevisiae |
| 35 | c2y4tA_ | Alignment | not modelled | 90.1 | 20 | **PDB header:**chaperone<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3;<br>**PDBTitle:** crystal structure of the human co-chaperone p58(ipk) |
| 36 | c3beeB_ | Alignment |  | 87.0 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative yfre protein;<br>**PDBTitle:** crystal structure of putative yfre protein from vibrio2 parahaemolyticus |
| 37 | c3apoA_ | Alignment | not modelled | 83.0 | 37 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10;<br>**PDBTitle:** crystal structure of full-length erdj5 |
| 38 | c3urzB_ | Alignment |  | 75.4 | 17 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of a hypothetical protein (bacova_03105) from2 bacteroides ovatus atcc 8483 at 2.19 a resolution |
| 39 | c2katA_ | Alignment | not modelled | 67.0 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** solution structure of protein bpp2914 from bordetella2 parapertussis. northeast structural genomics consortium3 target bpr206 |
| 40 | c2e2eA_ | Alignment |  | 57.3 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**formate-dependent nitrite reductase complex nrfg subunit;<br>**PDBTitle:** tpr domain of nrfg mediates the complex formation between heme lyase2 and formate-dependent nitrite reductase in escherichia coli o157:h7 |
| 41 | c2r5sB_ | Alignment |  | 57.0 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein vp0806;<br>**PDBTitle:** the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633 |
| 42 | c1na3A_ | Alignment | not modelled | 51.3 | 19 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**designed protein ctpr2;<br>**PDBTitle:** design of stable alpha-helical arrays from an idealized tpr2 motif |
| 43 | c2ho1B_ | Alignment | not modelled | 50.7 | 3 | **PDB header:**protein binding<br>**Chain:** B: **PDB Molecule:**type 4 fimbrial biogenesis protein pilf;<br>**PDBTitle:** functional characterization of pseudomonas aeruginosa pilf |
| 44 | c3gyzB_ | Alignment | not modelled | 48.9 | 4 | **PDB header:**chaperone<br>**Chain:** B: **PDB Molecule:**chaperone protein ipgc;<br>**PDBTitle:** crystal structure of ipgc from shigella flexneri |
| 45 | c2vsnB_ | Alignment | not modelled | 48.9 | 20 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**xcogt;<br>**PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation |
| 46 | c3m1gC_ | Alignment | not modelled | 48.8 | 22 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**putative glutathione s-transferase;<br>**PDBTitle:** the structure of a putative glutathione s-transferase from2 corynebacterium glutamicum |
| 47 | d2pqrb1 | Alignment | not modelled | 46.2 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 48 | c1kt0A_ | Alignment | not modelled | 42.2 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**51 kda fk506-binding protein;<br>**PDBTitle:** structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes |
| 49 | c3qdnA_ | Alignment | not modelled | 40.2 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative thioredoxin protein;<br>**PDBTitle:** putative thioredoxin protein from salmonella typhimurium |
| 50 | d2axta1 | Alignment | not modelled | 38.4 | 14 | **Fold:**Bacterial photosystem II reaction centre, L and M subunits<br>**Superfamily:**Bacterial photosystem II reaction centre, L and M |

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|---|---|---|---|---|---|---|
| 50 | d2axta1 | Alignment | not modelled | 38.4 | 14 | subunits<br>**Family:**Bacterial photosystem II reaction centre, L and M subunits |
| 51 | c3q49B_ | Alignment | not modelled | 37.6 | 13 | **PDB header:**ligase/chaperone<br>**Chain:** B: **PDB Molecule:**stip1 homology and u box-containing protein 1;<br>**PDBTitle:** crystal structure of the tpr domain of chip complexed with hsp70-c2 peptide |
| 52 | d1wtya_ | Alignment | not modelled | 37.4 | 20 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Nucleotidyltransferase substrate binding subunit/domain<br>**Family:**Family 1 bi-partite nucleotidyltransferase subunit |
| 53 | d1wh7a_ | Alignment | not modelled | 35.6 | 32 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Homeodomain |
| 54 | c3lyiA_ | Alignment | not modelled | 35.6 | 28 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**bromodomain-containing protein 1;<br>**PDBTitle:** pwwp domain of human bromodomain-containing protein 1 |
| 55 | d1nzna_ | Alignment | not modelled | 35.3 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 56 | c3k9iA_ | Alignment | not modelled | 31.6 | 13 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**bh0479 protein;<br>**PDBTitle:** crystal structure of putative protein binding protein (np_241345.1)2 from bacillus halodurans at 2.71 a resolution |
| 57 | c2xcbA_ | Alignment | not modelled | 30.9 | 10 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**regulatory protein pcrh;<br>**PDBTitle:** crystal structure of pcrh in complex with the chaperone2 binding region of popd |
| 58 | d1l9bm_ | Alignment | not modelled | 30.4 | 21 | **Fold:**Bacterial photosystem II reaction centre, L and M subunits<br>**Superfamily:**Bacterial photosystem II reaction centre, L and M subunits<br>**Family:**Bacterial photosystem II reaction centre, L and M subunits |
| 59 | c2kcvA_ | Alignment | not modelled | 30.1 | 9 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**tetratricopeptide repeat domain protein;<br>**PDBTitle:** solution nmr structure of tetratricopeptide repeat domain2 protein sru_0103 from salinibacter ruber, northeast3 structural genomics consortium (nesg) target srr115c |
| 60 | c2wukD_ | Alignment | not modelled | 28.8 | 35 | **PDB header:**cell cycle<br>**Chain:** D: **PDB Molecule:**septum site-determining protein diviva;<br>**PDBTitle:** diviva n-terminal domain, f17a mutant |
| 61 | d1h2vc2 | Alignment | not modelled | 28.6 | 20 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**ARM repeat<br>**Family:**MIF4G domain-like |
| 62 | d1y8ma1 | Alignment | not modelled | 28.5 | 11 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 63 | c3pfsA_ | Alignment | not modelled | 28.1 | 25 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**bromodomain and phd finger-containing protein 3;<br>**PDBTitle:** pwwp domain of human bromodomain and phd finger-containing protein 3 |
| 64 | c3pe3D_ | Alignment | not modelled | 25.9 | 13 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n-<br>**PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate |
| 65 | c2x35A_ | Alignment | not modelled | 24.8 | 38 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**peregrin;<br>**PDBTitle:** molecular basis of histone h3k36me3 recognition by the pwwp2 domain of brpf1. |
| 66 | d2ooea1 | Alignment | not modelled | 24.4 | 8 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**HAT/Suf repeat |
| 67 | d2i5nl1 | Alignment | not modelled | 23.1 | 14 | **Fold:**Bacterial photosystem II reaction centre, L and M subunits<br>**Superfamily:**Bacterial photosystem II reaction centre, L and M subunits<br>**Family:**Bacterial photosystem II reaction centre, L and M subunits |
| 68 | d1i4aa_ | Alignment | not modelled | 21.3 | 16 | **Fold:**Annexin<br>**Superfamily:**Annexin<br>**Family:**Annexin |
| 69 | c3ly8A_ | Alignment | not modelled | 21.2 | 10 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**transcriptional activator cadc;<br>**PDBTitle:** crystal structure of mutant d471e of the periplasmic domain of cadc |
| 70 | c3myxA_ | Alignment | not modelled | 20.9 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein pspto_0244;<br>**PDBTitle:** crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution |
| 71 | c3rkvA_ | Alignment | not modelled | 20.3 | 12 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative peptidylprolyl isomerase;<br>**PDBTitle:** c-terminal domain of protein c56c10.10, a putative peptidylprolyl2 isomerase, from caenorhabditis elegans |
| 72 | d1ffvc1 | Alignment | not modelled | 19.6 | 29 | **Fold:**CO dehydrogenase flavoprotein C-domain-like<br>**Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like<br>**Family:**CO dehydrogenase flavoprotein C-terminal domain-like |
| 73 | c1wao4_ | Alignment | not modelled | 19.6 | 13 | **PDB header:**hydrolase<br>**Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5;<br>**PDBTitle:** pp5 structure |
| 74 | d2g7oa1 | Alignment | not modelled | 19.2 | 25 | **Fold:**TraM-like<br>**Superfamily:**TraM-like<br>**Family:**TraM-like |
| 75 | c3o3nA_ | Alignment | not modelled | 18.6 | 18 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**alpha-subunit 2-hydroxyisocaproyl-coa dehydratase;<br>**PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | its substrate2 (r)-2-hydroxyisocaproyl-coa |
| 76 | d2v7fa1 | Alignment | not modelled | 18.3 | 34 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**Rps19E-like |
| 77 | c2ph5A_ | Alignment | not modelled | 18.2 | 28 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**homospermidine synthase;<br>**PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54 |
| 78 | d1dxxa2 | Alignment | not modelled | 18.1 | 25 | **Fold:**CH domain-like<br>**Superfamily:**Calponin-homology domain, CH-domain<br>**Family:**Calponin-homology domain, CH-domain |
| 79 | c3hymB_ | Alignment | not modelled | 17.4 | 7 | **PDB header:**cell cycle, ligase<br>**Chain:** B: **PDB Molecule:**cell division cycle protein 16 homolog;<br>**PDBTitle:** insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure |
| 80 | d1omwa2 | Alignment | not modelled | 16.7 | 32 | **Fold:**PH domain-like barrel<br>**Superfamily:**PH domain-like<br>**Family:**Pleckstrin-homology domain (PH domain) |
| 81 | c1slyA_ | Alignment | not modelled | 15.6 | 16 | **PDB header:**glycosyltransferase<br>**Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase;<br>**PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a |
| 82 | d2i5nm1 | Alignment | not modelled | 14.8 | 5 | **Fold:**Bacterial photosystem II reaction centre, L and M subunits<br>**Superfamily:**Bacterial photosystem II reaction centre, L and M subunits<br>**Family:**Bacterial photosystem II reaction centre, L and M subunits |
| 83 | c3mv3B_ | Alignment | not modelled | 14.7 | 6 | **PDB header:**protein transport<br>**Chain:** B: **PDB Molecule:**coatomer subunit epsilon;<br>**PDBTitle:** crystal structure of a-cop in complex with e-cop |
| 84 | c2i3fA_ | Alignment | not modelled | 13.8 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**glycolipid transfer-like protein;<br>**PDBTitle:** crystal structure of a glycolipid transfer-like protein2 from galdieria sulphuraria |
| 85 | c2vq2A_ | Alignment | not modelled | 13.7 | 12 | **PDB header:**structural protein<br>**Chain:** A: **PDB Molecule:**putative fimbrial biogenesis and twitching<br>**PDBTitle:** crystal structure of pilw, widely conserved type iv pilus2 biogenesis factor |
| 86 | d2pyta1 | Alignment | not modelled | 13.6 | 20 | **Fold:**Double-stranded beta-helix<br>**Superfamily:**RmlC-like cupins<br>**Family:**EutQ-like |
| 87 | c2jqqA_ | Alignment | not modelled | 13.2 | 21 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**conserved oligomeric golgi complex subunit 2;<br>**PDBTitle:** solution structure of saccharomyces cerevisiae conserved2 oligomeric golgi subunit 2 protein (cog2p) |
| 88 | c2yicC_ | Alignment | not modelled | 13.1 | 14 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**2-oxoglutarate decarboxylase;<br>**PDBTitle:** crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form) |
| 89 | d1vk9a_ | Alignment | not modelled | 12.9 | 31 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Hypothetical protein TM1506 |
| 90 | d1pc2a_ | Alignment | not modelled | 12.8 | 12 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 91 | d1o1ya_ | Alignment | not modelled | 12.6 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Class I glutamine amidotransferase-like<br>**Family:**Class I glutamine amidotransferases (GAT) |
| 92 | c1aoaA_ | Alignment | not modelled | 12.5 | 31 | **PDB header:**actin-binding protein<br>**Chain:** A: **PDB Molecule:**t-fimbrin;<br>**PDBTitle:** n-terminal actin-crosslinking domain from human fimbrin |
| 93 | c2if4A_ | Alignment | not modelled | 12.5 | 16 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**atfkbp42;<br>**PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana |
| 94 | c3abqA_ | Alignment | not modelled | 12.4 | 16 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ethanolamine ammonia-lyase heavy chain;<br>**PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and 2-amino-1-propanol |
| 95 | d1hxia_ | Alignment | not modelled | 12.3 | 15 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 96 | c3o7kA_ | Alignment | not modelled | 12.3 | 21 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**ohcu decarboxylase;<br>**PDBTitle:** crystal structure of 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline2 decarboxylase from klebsiella pneumoniae |
| 97 | d2buga1 | Alignment | not modelled | 12.2 | 13 | **Fold:**alpha-alpha superhelix<br>**Superfamily:**TPR-like<br>**Family:**Tetratricopeptide repeat (TPR) |
| 98 | d1eysl_ | Alignment | not modelled | 11.8 | 24 | **Fold:**Bacterial photosystem II reaction centre, L and M subunits<br>**Superfamily:**Bacterial photosystem II reaction centre, L and M subunits<br>**Family:**Bacterial photosystem II reaction centre, L and M subunits |
| 99 | d1n62c1 | Alignment | not modelled | 11.6 | 23 | **Fold:**CO dehydrogenase flavoprotein C-domain-like<br>**Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like<br>**Family:**CO dehydrogenase flavoprotein C-terminal domain-like |