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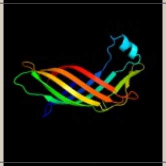
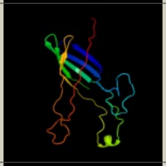
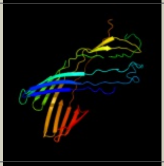
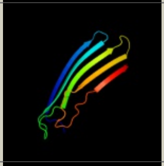
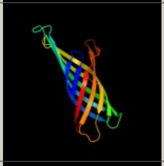
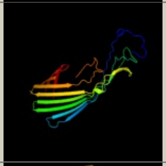
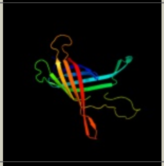
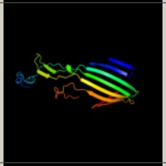
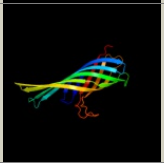
| Email | l.a.kelley@imperial.ac.uk |
| Description | P32689 |
| Date | Thu Jan 5 11:50:13 GMT 2012 |
| Unique Job ID | e9c80fe6158140ce |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2k0lA_ | Alignment |  | 95.5 | 21 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein a;<br>**PDBTitle:** nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles. |
| 2 | d1p4ta_ | Alignment |  | 88.3 | 18 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 3 | d1g90a_ | Alignment |  | 85.6 | 19 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |
| 4 | c3bryB_ | Alignment |  | 79.6 | 17 | **PDB header:**transport protein<br>**Chain:** B: **PDB Molecule:**tbux;<br>**PDBTitle:** crystal structure of the ralstonia pickettii toluene2 transporter tbux |
| 5 | d1phoa_ | Alignment |  | 75.0 | 14 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 6 | c3nb3C_ | Alignment |  | 62.8 | 26 | **PDB header:**virus<br>**Chain:** C: **PDB Molecule:**outer membrane protein a;<br>**PDBTitle:** the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components |
| 7 | c3dwoX_ | Alignment |  | 60.9 | 12 | **PDB header:**membrane protein<br>**Chain:** X: **PDB Molecule:**probable outer membrane protein;<br>**PDBTitle:** crystal structure of a pseudomonas aeruginosa fadl homologue |
| 8 | c3qraA_ | Alignment |  | 55.2 | 24 | **PDB header:**cell invasion<br>**Chain:** A: **PDB Molecule:**attachment invasion locus protein;<br>**PDBTitle:** the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis |
| 9 | c2jmmA_ | Alignment |  | 52.0 | 16 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein a;<br>**PDBTitle:** nmr solution structure of a minimal transmembrane beta-2 barrel platform protein |
| 10 | d1t16a_ | Alignment |  | 50.4 | 13 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Outer membrane protein transport protein |
| 11 | d1qjpa_ | Alignment |  | 47.7 | 22 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**OMPA-like<br>**Family:**Outer membrane protein |

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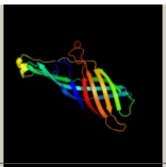
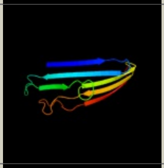
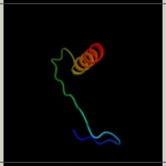
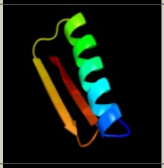
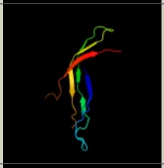
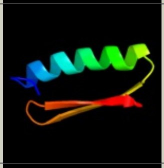
|---|---|---|---|---|---|---|
| 12 | c2f1tB_ | Alignment |  | 46.3 | 19 | **PDB header:**membrane protein<br>**Chain:** B: **PDB Molecule:**outer membrane protein w;<br>**PDBTitle:** outer membrane protein ompw |
| 13 | d2zfga1 | Alignment |  | 40.5 | 16 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 14 | c2x27X_ | Alignment |  | 37.5 | 14 | **PDB header:**membrane protein<br>**Chain:** X: **PDB Molecule:**outer membrane protein oprg;<br>**PDBTitle:** crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa |
| 15 | d1ynja1 | Alignment |  | 37.3 | 18 | **Fold:**DCoH-like<br>**Superfamily:**RBP11-like subunits of RNA polymerase<br>**Family:**RNA polymerase alpha subunit dimerisation domain |
| 16 | c2jvfA_ | Alignment |  | 36.4 | 12 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**de novo protein m7;<br>**PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein |
| 17 | c2lhfA_ | Alignment |  | 33.6 | 20 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein h1;<br>**PDBTitle:** solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles |
| 18 | c1qysA_ | Alignment |  | 29.3 | 22 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**top7;<br>**PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold |
| 19 | c3brzA_ | Alignment |  | 28.0 | 13 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**todx;<br>**PDBTitle:** crystal structure of the pseudomonas putida toluene2 transporter todx |
| 20 | c2e0gA_ | Alignment |  | 25.9 | 11 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa;<br>**PDBTitle:** dnaa n-terminal domain |
| 21 | c3a2rX_ | Alignment | not modelled | 25.5 | 14 | **PDB header:**membrane protein<br>**Chain:** X: **PDB Molecule:**outer membrane protein ii;<br>**PDBTitle:** crystal structure of outer membrane protein porb from neisseria2 meningitidis |
| 22 | d2fgqx1 | Alignment | not modelled | 21.5 | 16 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 23 | c2i9zB_ | Alignment | not modelled | 20.2 | 22 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative septation protein spovg;<br>**PDBTitle:** structural genomics, the crystal structure of full-length spovg from2 staphylococcus epidermidis atcc 12228 |
| 24 | d2i9xa1 | Alignment | not modelled | 20.2 | 22 | **Fold:**SpoVG-like<br>**Superfamily:**SpoVG-like<br>**Family:**SpoVG-like |
| 25 | d1uynx_ | Alignment | not modelled | 15.9 | 11 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Autotransporter<br>**Family:**Autotransporter |
| 26 | d1bdfa1 | Alignment | not modelled | 14.0 | 33 | **Fold:**DCoH-like<br>**Superfamily:**RBP11-like subunits of RNA polymerase<br>**Family:**RNA polymerase alpha subunit dimerisation domain |
| 27 | d1umha_ | Alignment | not modelled | 10.3 | 25 | **Fold:**Galactose-binding domain-like<br>**Superfamily:**Galactose-binding domain-like<br>**Family:**F-box associated region, FBA |
| 28 | d1u69a_ | Alignment | not modelled | 10.3 | 23 | **Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase<br>**Family:**3-demethylubiquinone-9 3-methyltransferase |

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| 29 | d1kpta_ | Alignment | not modelled | 9.5 | 35 | **Fold:**Yeast killer toxins<br>**Superfamily:**Yeast killer toxins<br>**Family:**Virally encoded KP4 toxin |
| 30 | c2gjhA_ | Alignment | not modelled | 9.1 | 30 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**designed protein;<br>**PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7) |
| 31 | d2gufa1 | Alignment | not modelled | 9.0 | 18 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Ligand-gated protein channel |
| 32 | c2x4mD_ | Alignment | not modelled | 8.6 | 19 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**coagulase/fibrinolysin;<br>**PDBTitle:** yersinia pestis plasminogen activator pla |
| 33 | c3qwnC_ | Alignment | not modelled | 8.5 | 23 | **PDB header:**antitoxin<br>**Chain:** C: **PDB Molecule:**hypothetical nigd-like protein;<br>**PDBTitle:** crystal structure of a hypothetical nigd-like protein (baccac_03262)2 from bacteroides caccae at 2.42 a resolution |
| 34 | d1tdha3 | Alignment | not modelled | 8.0 | 20 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins |
| 35 | c2djmA_ | Alignment | not modelled | 7.7 | 16 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**glucoamylase a;<br>**PDBTitle:** solution structure of n-terminal starch-binding domain of2 glucoamylase from rhizopus oryzae |
| 36 | c3qv0A_ | Alignment | not modelled | 7.7 | 16 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**mitochondrial acidic protein mam33;<br>**PDBTitle:** crystal structure of saccharomyces cerevisiae mam33 |
| 37 | d1smya1 | Alignment | not modelled | 7.7 | 20 | **Fold:**DCoH-like<br>**Superfamily:**RBP11-like subunits of RNA polymerase<br>**Family:**RNA polymerase alpha subunit dimerisation domain |
| 38 | d1f2va_ | Alignment | not modelled | 7.6 | 18 | **Fold:**Flavodoxin-like<br>**Superfamily:**Precorrin-8X methylmutase CbiC/CobH<br>**Family:**Precorrin-8X methylmutase CbiC/CobH |
| 39 | d1txka2 | Alignment | not modelled | 7.0 | 18 | **Fold:**Supersandwich<br>**Superfamily:**Galactose mutarotase-like<br>**Family:**MdoG-like |
| 40 | d1kkea2 | Alignment | not modelled | 7.0 | 20 | **Fold:**Virus attachment protein globular domain<br>**Superfamily:**Virus attachment protein globular domain<br>**Family:**Reovirus attachment protein sigma 1 head domain |
| 41 | d1smyc_ | Alignment | not modelled | 6.9 | 32 | **Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase<br>**Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase<br>**Family:**RNA-polymerase beta |
| 42 | c3e7dC_ | Alignment | not modelled | 6.9 | 18 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**cobh, precorrin-8x methylmutase;<br>**PDBTitle:** crystal structure of precorrin-8x methyl mutase cbic/cobh from2 brucella melitensis |
| 43 | c2r28D_ | Alignment | not modelled | 6.9 | 18 | **PDB header:**metal binding protein/hydrolase<br>**Chain:** D: **PDB Molecule:**serine/threonine-protein phosphatase 2b<br>**PDBTitle:** the complex structure of calmodulin bound to a calcineurin2 peptide |
| 44 | c1txkA_ | Alignment | not modelled | 6.7 | 18 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**glucans biosynthesis protein g;<br>**PDBTitle:** crystal structure of escherichia coli opgg |
| 45 | c2jziB_ | Alignment | not modelled | 6.7 | 20 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase 2b<br>**PDBTitle:** structure of calmodulin complexed with the calmodulin2 binding domain of calcineurin |
| 46 | c3cjtP_ | Alignment | not modelled | 6.5 | 23 | **PDB header:**transferase/ribosomal protein<br>**Chain:** P: **PDB Molecule:**50s ribosomal protein l11;<br>**PDBTitle:** ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11 |
| 47 | d1kk1a2 | Alignment | not modelled | 6.5 | 25 | **Fold:**Elongation factor/aminomethyltransferase common domain<br>**Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain<br>**Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain |
| 48 | c2rqeA_ | Alignment | not modelled | 6.4 | 75 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**beta-1,3-glucan-binding protein;<br>**PDBTitle:** solution structure of the silkworm bgrp/gnbp3 n-terminal2 domain reveals the mechanism for b-1,3-glucan specific3 recognition |
| 49 | c3fhhA_ | Alignment | not modelled | 6.4 | 6 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane heme receptor shua;<br>**PDBTitle:** crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae |
| 50 | c2afvB_ | Alignment | not modelled | 6.3 | 24 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**cobalamin biosynthesis precorrin isomerase;<br>**PDBTitle:** the crystal structure of putative precorrin isomerase cbic2 in cobalamin biosynthesis |
| 51 | c1uv7A_ | Alignment | not modelled | 6.2 | 10 | **PDB header:**transport<br>**Chain:** A: **PDB Molecule:**general secretion pathway protein m;<br>**PDBTitle:** periplasmic domain of epsm from vibrio cholerae |
| 52 | d1uv7a_ | Alignment | not modelled | 6.2 | 10 | **Fold:**RRF/tRNA synthetase additional domain-like<br>**Superfamily:**General secretion pathway protein M, EpsM<br>**Family:**General secretion pathway protein M, EpsM |
| 53 | d2cura2 | Alignment | not modelled | 6.2 | 55 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |
| 54 | c3ie4A_ | Alignment | not modelled | 6.2 | 63 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**gram-negative binding protein 3;<br>**PDBTitle:** b-glucan binding domain of drosophila gnbp3 defines a novel2 family of pattern recognition receptor |

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| 55 | d2jnaa1 | Alignment | not modelled | 6.0 | 24 | **Fold:**Dodecin subunit-like<br>**Superfamily:**YdgH-like<br>**Family:**YdgH-like |
| 56 | c3iydC_ | Alignment | not modelled | 5.7 | 27 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**dna-directed rna polymerase subunit beta;<br>**PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex |
| 57 | c2khaA_ | Alignment | not modelled | 5.5 | 44 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**beta-1,3-glucan-binding protein;<br>**PDBTitle:** solution structure of a pathogen recognition domain from a2 lepidopteran insect, plodia interpunctella |
| 58 | c1kkeA_ | Alignment | not modelled | 5.4 | 20 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**sigma 1 protein;<br>**PDBTitle:** crystal structure of reovirus attachment protein sigma12 trimer |
| 59 | d2d8za1 | Alignment | not modelled | 5.4 | 55 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**LIM domain |
| 60 | d2cnaa_ | Alignment | not modelled | 5.4 | 19 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Legume lectins |
| 61 | d2gr8a1 | Alignment | not modelled | 5.4 | 18 | **Fold:**Pili subunits<br>**Superfamily:**Pili subunits<br>**Family:**YadA C-terminal domain-like |
| 62 | c3jsrA_ | Alignment | not modelled | 5.4 | 33 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**all0216 protein;<br>**PDBTitle:** x-ray structure of all0216 protein from nostoc sp. pcc 7120 at the2 resolution 1.8a. northeast structural genomics consortium target3 nsr236 |
| 63 | d2pwwa1 | Alignment | not modelled | 5.3 | 21 | **Fold:**TBP-like<br>**Superfamily:**YugN-like<br>**Family:**YugN-like |
| 64 | c3e8vA_ | Alignment | not modelled | 5.2 | 35 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**possible transglutaminase-family protein;<br>**PDBTitle:** crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis |
| 65 | d1ou0a_ | Alignment | not modelled | 5.2 | 35 | **Fold:**Flavodoxin-like<br>**Superfamily:**Precorrin-8X methylmutase CbiC/CobH<br>**Family:**Precorrin-8X methylmutase CbiC/CobH |
| 66 | c3nsgA_ | Alignment | not modelled | 5.2 | 15 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**outer membrane protein f;<br>**PDBTitle:** crystal structure of ompf, an outer membrane protein from salmonella2 typhi |
| 67 | c3o27B_ | Alignment | not modelled | 5.2 | 17 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein;<br>**PDBTitle:** the crystal structure of c68 from the hybrid virus-plasmid pssvx |
| 68 | c3qq2C_ | Alignment | not modelled | 5.2 | 15 | **PDB header:**membrane protein/protein transport<br>**Chain:** C: **PDB Molecule:**brka autotransporter;<br>**PDBTitle:** crystal structure of the beta domain of the bordetella autotransporter2 brka |
| 69 | d3prna_ | Alignment | not modelled | 5.1 | 11 | **Fold:**Transmembrane beta-barrels<br>**Superfamily:**Porins<br>**Family:**Porin |
| 70 | d3cjsb1 | Alignment | not modelled | 5.1 | 27 | **Fold:**Ribosomal L11/L12e N-terminal domain<br>**Superfamily:**Ribosomal L11/L12e N-terminal domain<br>**Family:**Ribosomal L11/L12e N-terminal domain |
| 71 | d1h9wa_ | Alignment | not modelled | 5.0 | 19 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Legume lectins |
| 72 | d2okga1 | Alignment | not modelled | 5.0 | 13 | **Fold:**NagB/RpiA/CoA transferase-like<br>**Superfamily:**NagB/RpiA/CoA transferase-like<br>**Family:**SorC sugar-binding domain-like |