Email	l.a.kelley@imperial.ac.uk
Description	Q46832
Date	Thu Jan 5 12:34:56 GMT 2012
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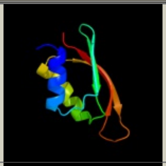
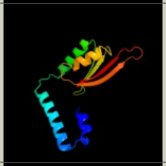
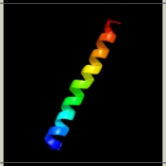
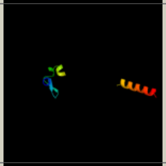
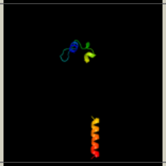
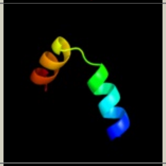
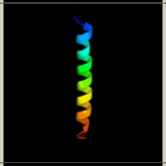
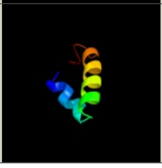
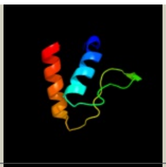
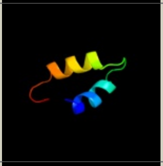
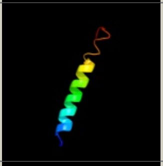
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1uv7A_	Alignment		99.9	36	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
2	d1uv7a_	Alignment		99.9	36	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
3	c2rjzA_	Alignment		97.7	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pilo protein; **PDBTitle:** crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
4	c2rddB_	Alignment		60.1	23	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
5	d1v54d_	Alignment		53.7	24	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit IV **Family:**Mitochondrial cytochrome c oxidase subunit IV
6	c2y69Q_	Alignment		49.0	24	**PDB header:**electron transport **Chain:** Q: **PDB Molecule:**cytochrome c oxidase subunit 4 isoform 1; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
7	d1yioa1	Alignment		44.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
8	d1ppjc2	Alignment		24.0	3	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
9	d1t9ma_	Alignment		23.4	9	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
10	c2y9kG_	Alignment		20.3	15	**PDB header:**protein transport **Chain:** G: **PDB Molecule:**protein invg; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
11	d1gt0d_	Alignment		19.2	22	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box

12	d1bjna_	Alignment		18.9	6	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
13	d1x4pa1	Alignment		18.3	36	**Fold:**Surp module (SWAP domain) **Superfamily:**Surp module (SWAP domain) **Family:**Surp module (SWAP domain)
14	d1ulra_	Alignment		17.4	17	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
15	d1k99a_	Alignment		17.0	13	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
16	c2co9A_	Alignment		16.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox; **PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
17	d1ty9a_	Alignment		16.1	11	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
18	d1bccc3	Alignment		15.0	6	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
19	c2jsxA_	Alignment		14.0	7	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
20	c2yulA_	Alignment		13.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor sox-17; **PDBTitle:** solution structure of the hmg box of human transcription2 factor sox-17
21	c2eefA_	Alignment	not modelled	12.2	24	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**protein phosphatase 1, regulatory (inhibitor) **PDBTitle:** solution structure of the cbm_21 domain from human protein2 phosphatase 1, regulatory (inhibitor) subunit 3b
22	d1hywa_	Alignment	not modelled	11.4	16	**Fold:**gpW/XkdW-like **Superfamily:**Head-to-tail joining protein W, gpW **Family:**Head-to-tail joining protein W, gpW
23	c2rnjA_	Alignment	not modelled	11.3	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
24	c2cs1A_	Alignment	not modelled	11.2	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pms1 protein homolog 1; **PDBTitle:** solution structure of the hmg domain of human dna mismatch2 repair protein
25	c3cwbC_	Alignment	not modelled	11.1	6	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**cytochrome b; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
26	c2kncA_	Alignment	not modelled	11.1	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
27	c3mn7S_	Alignment	not modelled	10.7	50	**PDB header:**contractile protein/protein binding **Chain:** S: **PDB Molecule:**spire ddd; **PDBTitle:** structures of actin-bound wh2 domains of spire and the implication for2 filament nucleation
28	c3mn5S_	Alignment	not modelled	10.4	50	**PDB header:**contractile protein/protein binding **Chain:** S: **PDB Molecule:**protein spire; **PDBTitle:** structures of actin-bound wh2 domains of spire and the implication for2 filament nucleation

29	d1wgfa_	Alignment	not modelled	10.3	22	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
30	c1x3uA_	Alignment	not modelled	10.2	35	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
31	c3gr5A_	Alignment	not modelled	10.1	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**escc; **PDBTitle:** periplasmic domain of the outer membrane secretin escc from2 enteropathogenic e.coli (epec)
32	c2k4yA_	Alignment	not modelled	9.9	6	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**feoa-like protein; **PDBTitle:** nmr structure of feoa-like protein from clostridium2 acetobutylicum: northeast structural genomics consortium3 target car178
33	c1wz6A_	Alignment	not modelled	9.8	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hmg-box transcription factor bbx; **PDBTitle:** solution structure of the hmg_box domain of murine bobby2 sox homolog
34	d1w2ia_	Alignment	not modelled	9.8	13	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
35	d1b7yb4	Alignment	not modelled	9.8	13	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
36	d2c0ra1	Alignment	not modelled	9.0	6	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
37	c2w7vB_	Alignment	not modelled	7.7	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general secretion pathway protein l; **PDBTitle:** periplasmic domain of epsl from vibrio parahaemolyticus
38	c1peiA_	Alignment	not modelled	7.7	36	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**pepc22; **PDBTitle:** nmr structure of the membrane-binding domain of ctp2 phosphocholine cytidylyltransferase, 10 structures
39	d1j46a_	Alignment	not modelled	7.7	24	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
40	c3br8A_	Alignment	not modelled	7.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis
41	d2af7a1	Alignment	not modelled	7.5	13	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
42	d1j3da_	Alignment	not modelled	7.4	16	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
43	d1l3la1	Alignment	not modelled	7.2	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
44	c2lhjA_	Alignment	not modelled	7.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**high mobility group protein homolog nhp1; **PDBTitle:** nmr structure of the high mobility group protein-like protein nhp12 from babesia bovis t2bo (baboa.00841.a)
45	c2xlkB_	Alignment	not modelled	6.8	24	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**csy4 endoribonuclease; **PDBTitle:** crystal structure of the csy4-crrna complex, orthorhombic form
46	c2gv1A_	Alignment	not modelled	6.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** nmr solution structure of the acylphosphatase from2 eschaerichia coli
47	c3qm2A_	Alignment	not modelled	6.6	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** 2.25 angstrom crystal structure of phosphoserine aminotransferase2 (serc) from salmonella enterica subsp. enterica serovar typhimurium
48	c2bjeA_	Alignment	not modelled	6.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylphosphatase; **PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
49	d1dwka2	Alignment	not modelled	6.5	24	**Fold:**Cyanase C-terminal domain **Superfamily:**Cyanase C-terminal domain **Family:**Cyanase C-terminal domain
50	c2k1aA_	Alignment	not modelled	6.4	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
51	c2iv1J_	Alignment	not modelled	6.3	16	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
52	d1j5wa_	Alignment	not modelled	6.1	25	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
53	d1jjcb4	Alignment	not modelled	6.1	13	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
54	c2crjA_	Alignment	not modelled	6.0	24	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the hmg domain of mouse hmg

						domain2 protein hmgx2
55	c2d88A_	Alignment	not modelled	6.0	27	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**protein mical-3; **PDBTitle:** solution structure of the ch domain from human mical-32 protein
56	d1hsma_	Alignment	not modelled	6.0	13	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
57	c2d89A_	Alignment	not modelled	5.6	23	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**ehbp1 protein; **PDBTitle:** solution structure of the ch domain from human eh domain2 binding protein 1
58	d2lefa_	Alignment	not modelled	5.5	19	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
59	d2h3ja1	Alignment	not modelled	5.4	13	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
60	c2kncB_	Alignment	not modelled	5.3	19	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
61	c1wylA_	Alignment	not modelled	5.1	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** solution structure of the ch domain of human nedd92 interacting protein with calponin homology and lim domains
62	c2e6oA_	Alignment	not modelled	5.1	13	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** solution structure of the hmg box domain from human hmg-box2 transcription factor 1