Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0ADS6
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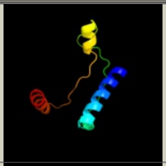
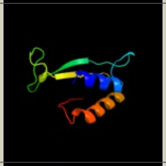
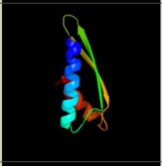
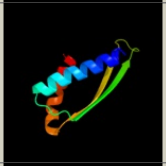
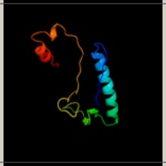
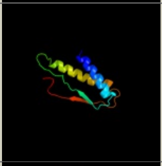
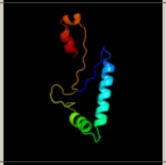
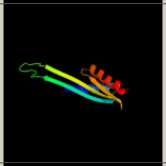
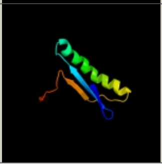
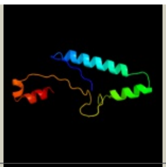
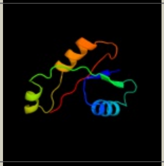
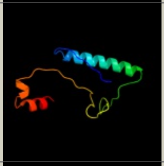
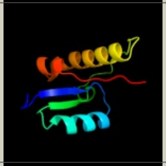
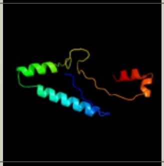
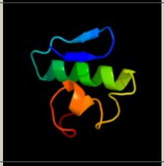
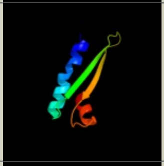
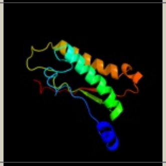
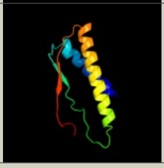
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cyqM_	Alignment		29.1	19	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
2	c3tquD_	Alignment		26.4	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**non-canonical purine ntp pyrophosphatase; **PDBTitle:** structure of a ham1 protein from coxiella burnetii
3	d2cz4a1	Alignment		23.0	7	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
4	d1nyed_	Alignment		22.4	23	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
5	d2onfa1	Alignment		21.7	10	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
6	d1u6ra2	Alignment		20.7	11	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
7	d1muwa_	Alignment		20.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
8	d1a0ea_	Alignment		20.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
9	d1crka2	Alignment		20.4	9	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
10	c3qtdC_	Alignment		19.9	21	**PDB header:**gene regulation **Chain:** C: **PDB Molecule:**pmba protein; **PDBTitle:** crystal structure of putative modulator of gyrase (pmba) from2 pseudomonas aeruginosa pao1
11	c2rrlA_	Alignment		19.2	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar hook-length control protein; **PDBTitle:** solution structure of the c-terminal domain of the flik

12	d1qk1a2	Alignment		18.9	7	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
13	d1b78a_	Alignment		18.2	12	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
14	d1vrpa2	Alignment		18.1	9	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
15	d1k7ka_	Alignment		17.8	19	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
16	d1qh4a2	Alignment		17.8	11	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
17	c2x48B_	Alignment		15.8	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
18	d1ukka_	Alignment		14.5	16	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
19	d1xlma_	Alignment		14.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
20	d1a0ca_	Alignment		14.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
21	d1a0da_	Alignment	not modelled	13.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
22	c1i0eD_	Alignment	not modelled	13.7	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**creatine kinase,m chain; **PDBTitle:** crystal structure of creatine kinase from human muscle
23	d2opla1	Alignment	not modelled	13.4	10	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
24	c2kxhB_	Alignment	not modelled	13.1	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**peptide of far upstream element-binding protein 1; **PDBTitle:** solution structure of the first two rrm domains of fir in the complex2 with fbp nbox peptide
25	d2cara1	Alignment	not modelled	12.9	10	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
26	c3k1dA_	Alignment	not modelled	12.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme; **PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
27	d1lqla_	Alignment	not modelled	12.5	14	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
28	c1lqlE_	Alignment	not modelled	12.5	14	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**osmotical inducible protein c like family; **PDBTitle:** crystal structure of osmc like protein from mycoplasma2 pneumoniae

29	d1qt1a_	Alignment	not modelled	12.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
30	c3amlA_	Alignment	not modelled	12.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l
31	c2zf8A_	Alignment	not modelled	11.3	7	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
32	d1xima_	Alignment	not modelled	10.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
33	d1qwia_	Alignment	not modelled	10.6	25	**Fold:**OsmC-like **Superfamily:**OsmC-like **Family:**Ohr/OsmC resistance proteins
34	d1h3ga3	Alignment	not modelled	10.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
35	c1m7xC_	Alignment	not modelled	10.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**1,4-alpha-glucan branching enzyme; **PDBTitle:** the x-ray crystallographic structure of branching enzyme
36	c1zb8B_	Alignment	not modelled	9.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**organic hydroperoxide resistance protein; **PDBTitle:** crystal structure of xylella fastidiosa organic peroxide resistance2 protein
37	c1jd7A_	Alignment	not modelled	9.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
38	d1g0wa2	Alignment	not modelled	8.7	12	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
39	d1r3na2	Alignment	not modelled	8.6	14	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
40	d1xp8a2	Alignment	not modelled	8.6	16	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
41	d1jjcb4	Alignment	not modelled	8.3	12	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
42	c1qk1H_	Alignment	not modelled	7.6	8	**PDB header:**transferase (creatine kinase) **Chain:** H: **PDB Molecule:**creatine kinase, ubiquitous mitochondrial; **PDBTitle:** crystal structure of human ubiquitous mitochondrial2 creatine kinase
43	c1ceuA_	Alignment	not modelled	7.3	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hiv-1 regulatory protein n-terminal **PDBTitle:** nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
44	c3eerA_	Alignment	not modelled	7.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**organic hydroperoxide resistance protein, putative; **PDBTitle:** high resolution structure of putative organic hydroperoxide resistance2 protein from vibrio cholerae o1 biovar eltor str. n16961
45	c1mg1A_	Alignment	not modelled	6.8	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (htlv-1 gp21 ectodomain/maltose-binding protein **PDBTitle:** htlv-1 gp21 ectodomain/maltose-binding protein chimera
46	c3l2eB_	Alignment	not modelled	6.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycocyamine kinase beta chain; **PDBTitle:** glycocyamine kinase, alpha-beta heterodimer from marine worm2 namalycastis sp.
47	c3onrI_	Alignment	not modelled	6.7	21	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
48	d1m7xa3	Alignment	not modelled	6.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
49	c3k8kB_	Alignment	not modelled	6.5	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
50	c1bf2A_	Alignment	not modelled	6.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isoamylase; **PDBTitle:** structure of pseudomonas isoamylase
51	c3mgjA_	Alignment	not modelled	6.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1480; **PDBTitle:** crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
52	d2aizp1	Alignment	not modelled	6.0	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
53	d1g94a2	Alignment	not modelled	5.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

54	c3jq3A_	Alignment	not modelled	5.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lombricine kinase; **PDBTitle:** crystal structure of lombricine kinase, complexed with substrate adp
55	d1y2ia_	Alignment	not modelled	5.7	17	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
56	c2kfsA_	Alignment	not modelled	5.5	16	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
57	c3amkA_	Alignment	not modelled	5.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**os06g0726400 protein; **PDBTitle:** structure of the starch branching enzyme i (bei) from oryza sativa l