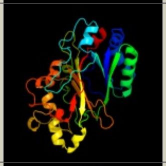
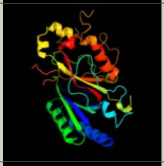
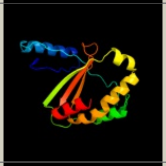
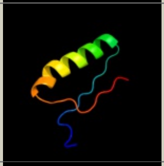
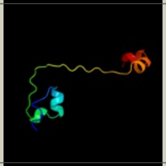
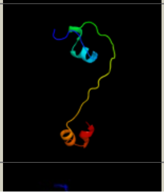
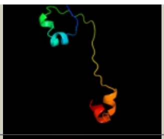
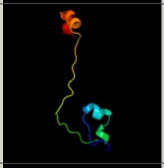
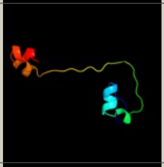
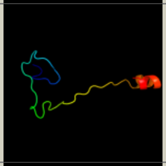
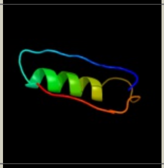
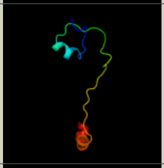
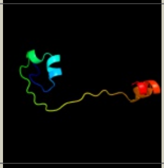
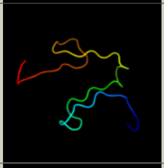
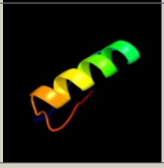
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76536
Date	Thu Jan 5 12:24:05 GMT 2012
Unique Job ID	bf1d669316f34b13

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2iiza1	Alignment		100.0	37	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Dyp-type peroxidase-like
2	c3qnsA_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dyp peroxidase; **PDBTitle:** dypb from rhodococcus jostii rha1, crystal form 2
3	d2gvka1	Alignment		100.0	33	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Dyp-type peroxidase-like
4	c2wx6B_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxidase ycdb; **PDBTitle:** x-ray crystallographic structure of e. coli apo-efeb
5	d2d3qa1	Alignment		100.0	24	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Dyp-type peroxidase-like
6	c3nn4C_	Alignment		81.8	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**chlorite dismutase; **PDBTitle:** structure of chlorite dismutase from candidatus nitrospira defluvii2 r173k mutant
7	c2vxhF_	Alignment		81.1	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**chlorite dismutase; **PDBTitle:** the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
8	c3dtzB_	Alignment		62.2	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative chlorite dismutase ta0507; **PDBTitle:** crystal structure of putative chlorite dismutase ta0507
9	d1t0tv_	Alignment		47.8	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
10	c2hpgB_	Alignment		40.3	13	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding **PDBTitle:** the crystal structure of a thermophilic trap periplasmic2 binding protein
11	c2pfyA_	Alignment		29.7	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid

12	c3b50A_	Alignment		28.6	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sialic acid-binding periplasmic protein siap; **PDBTitle:** structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
13	c3gyyC_	Alignment		24.6	22	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
14	c3fxbB_	Alignment		23.4	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of the ectoine-binding protein ueha
15	c2zzxD_	Alignment		20.7	16	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc transporter, solute-binding protein; **PDBTitle:** crystal structure of a periplasmic substrate binding protein in2 complex with lactate
16	d1vdha_	Alignment		20.1	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
17	c2hzkB_	Alignment		19.5	11	**PDB header:**ligand binding, transport protein **Chain:** B: **PDB Molecule:**trap-t family sorbitol/mannitol transporter, periplasmic **PDBTitle:** crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
18	c2pfzA_	Alignment		17.5	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
19	d2piea1	Alignment		9.5	18	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
20	c3b0vD_	Alignment		9.5	10	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
21	d1uoua3	Alignment	not modelled	9.0	12	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
22	d1sfea2	Alignment	not modelled	8.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain
23	d2cg4a2	Alignment	not modelled	8.1	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
24	d1vjja1	Alignment	not modelled	7.9	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
25	d2q3za1	Alignment	not modelled	7.6	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
26	d1g0da1	Alignment	not modelled	7.4	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
27	c2e1aD_	Alignment	not modelled	7.1	8	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
28	d1s6na_	Alignment	not modelled	6.5	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
29	c2vpnB_	Alignment	not modelled	6.3	26	**PDB header:**transport **Chain:** B: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** high-resolution structure of the periplasmic ectoine-2

						binding protein from teaabc trap-transporter of halomonas3 elongata
30	c2qdrA_	Alignment	not modelled	6.3	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution
31	d2i7pa2	Alignment	not modelled	6.2	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
32	d4tsva_	Alignment	not modelled	6.1	7	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
33	c1ohfB_	Alignment	not modelled	5.7	39	**PDB header:**virus **Chain:** B: **PDB Molecule:**nudaurelia capensis omega virus capsid protein; **PDBTitle:** the refined structure of nudaurelia capensis omega virus
34	c2h0pA_	Alignment	not modelled	5.7	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein; **PDBTitle:** nmr structure of the dengue-4 virus envelope protein domain2 iii
35	d1ok8a1	Alignment	not modelled	5.7	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
36	d1ex0a1	Alignment	not modelled	5.3	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
37	c1fuiB_	Alignment	not modelled	5.1	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli