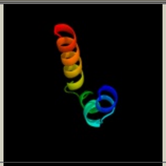
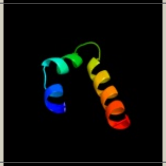
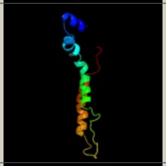
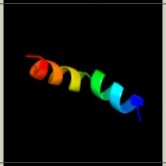
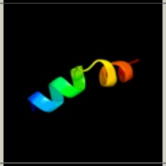
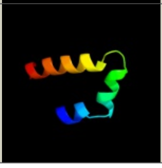
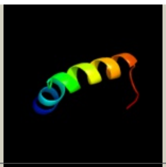
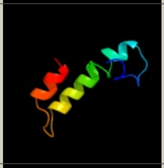
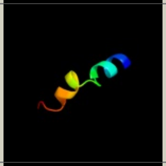
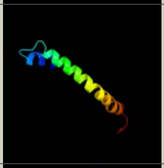
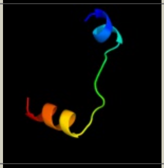
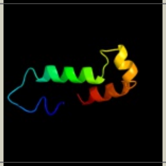
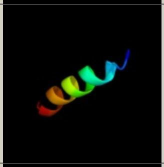
Email	l.a.kelley@imperial.ac.uk
Description	P0AF54
Date	Thu Jan 5 11:25:15 GMT 2012
Unique Job ID	979c06f115f3f880

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dqbB_	Alignment		51.4	29	**PDB header:**hydrolase, dna binding protein **Chain:** B: **PDB Molecule:**deoxyguanosinetriphosphate triphosphohydrolase, putative; **PDBTitle:** crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
2	c2pgsA_	Alignment		19.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyguanosinetriphosphate triphosphohydrolase; **PDBTitle:** crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
3	c3lo3E_	Alignment		17.7	9	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
4	c3fh6F_	Alignment		16.3	12	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**maltose transport system permease protein malf; **PDBTitle:** crystal structure of the resting state maltose transporter from e.2 coli
5	d2fiua1	Alignment		13.5	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Atu0297-like
6	d2o6ia1	Alignment		12.6	11	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
7	c2o6iA_	Alignment		12.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hd domain protein; **PDBTitle:** structure of an enterococcus faecalis hd domain phosphohydrolase
8	c2q14A_	Alignment		12.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase; **PDBTitle:** crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
9	d2heka1	Alignment		11.7	25	**Fold:**HD-domain/PDEase-like **Superfamily:**HD-domain/PDEase-like **Family:**HD domain
10	c2kjgA_	Alignment		11.3	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**archaeal protein sso6904; **PDBTitle:** solution structure of an archaeal protein sso6904 from2 hyperthermophilic sulfolobus solfataricus
11	c3bg2A_	Alignment		10.1	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dgtp triphosphohydrolase; **PDBTitle:** crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217

12	d1tu7a1	Alignment		9.6	26	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
13	c3sjbC_	Alignment		9.0	31	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
14	d1q59a_	Alignment		8.6	2	**Fold:**Toxins' membrane translocation domains **Superfamily:**Bcl-2 inhibitors of programmed cell death **Family:**Bcl-2 inhibitors of programmed cell death
15	c3u1nC_	Alignment		8.3	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sam domain and hd domain-containing protein 1; **PDBTitle:** structure of the catalytic core of human samhd1
16	c3qnqD_	Alignment		7.8	9	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
17	d1w6ka2	Alignment		7.5	21	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpene synthases
18	c2o2fA_	Alignment		7.5	13	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis regulator bcl-2; **PDBTitle:** solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand
19	c3sjaG_	Alignment		7.4	28	**PDB header:**hydrolase/transport protein **Chain:** G: **PDB Molecule:**golgi to er traffic protein 1; **PDBTitle:** crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
20	d1pv7a_	Alignment		6.5	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
21	c1sseB_	Alignment	not modelled	6.4	23	**PDB header:**transcription activator **Chain:** B: **PDB Molecule:**ap-1 like transcription factor yap1; **PDBTitle:** solution structure of the oxidized form of the yap1 redox2 domain
22	d1vpua_	Alignment	not modelled	6.1	25	**Fold:**HIV-1 VPU cytoplasmic domain **Superfamily:**HIV-1 VPU cytoplasmic domain **Family:**HIV-1 VPU cytoplasmic domain
23	d2gw6a1	Alignment	not modelled	5.5	17	**Fold:**Restriction endonuclease-like **Superfamily:**tRNA-intron endonuclease catalytic domain-like **Family:**tRNA-intron endonuclease catalytic domain-like
24	d1tuwa_	Alignment	not modelled	5.5	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Polyketide synthesis cyclase
25	c2vofA_	Alignment	not modelled	5.4	4	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**bcl-2-related protein a1; **PDBTitle:** structure of mouse a1 bound to the puma bh3-domain
26	c1ei0A_	Alignment	not modelled	5.3	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**p8mtcp1; **PDBTitle:** nmr structure of the alpha-helical hairpin of p8mtcp1
27	c3a0hX_	Alignment	not modelled	5.3	23	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
28	c3a0hx_	Alignment	not modelled	5.3	23	**PDB header:**electron transport **Chain:** X: **PDB Molecule:**photosystem ii reaction center protein x; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
29	c1s5lx_	Alignment	not modelled	5.1	25	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**photosystem ii psbx protein;

PDBTitle: architecture of the photosynthetic oxygen evolving center