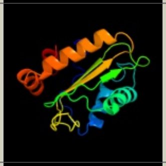
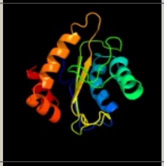
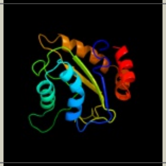
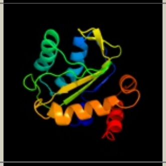
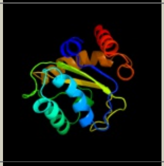
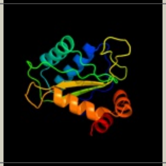
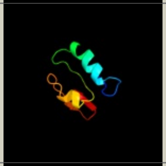
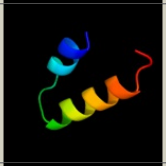
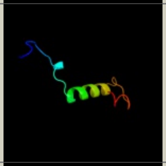
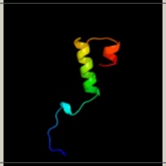
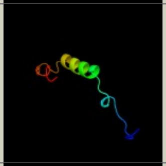
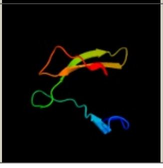
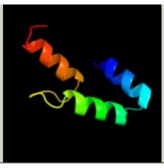
Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
Description	P69829
Date	Thu Jan 5 12:12:11 GMT 2012
Unique Job ID	3d506d72a0e4cf8a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a6ja_	Alignment		100.0	100	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
2	c2a0jA_	Alignment		100.0	39	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, nitrogen regulatory iia protein; **PDBTitle:** crystal structure of nitrogen regulatory protein iia-ntr from2 neisseria meningitidis
3	c3urrB_	Alignment		100.0	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts iia-like nitrogen-regulatory protein ptsn; **PDBTitle:** structure of pts iia-like nitrogen-regulatory protein ptsn (bth_i0484)2 (ptsn)
4	c3oxpB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
5	c3oxpA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
6	c2oq3A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific cryptic phosphotransferase **PDBTitle:** solution structure of the mannitol- specific cryptic2 phosphotransferase enzyme iia cmtb from escherichia coli
7	c3bjvA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpa; **PDBTitle:** the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans
8	c2oqtD_	Alignment		100.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein spy0176; **PDBTitle:** structural genomics, the crystal structure of a putative2 pts iia domain from streptococcus pyogenes m1 gas
9	d1a3aa_	Alignment		100.0	25	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
10	d1xiza_	Alignment		100.0	18	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
11	c1hynQ_	Alignment		98.2	19	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein

12	d1hynp_	Alignment		98.2	20	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
13	c3ntvB_	Alignment		8.9	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mw1564 protein; **PDBTitle:** crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus
14	c3n6oB_	Alignment		7.9	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide exchange factor; **PDBTitle:** crystal structure of the gef and p4m domain of drra/sidm from2 legionella pneumophila
15	d1vcoa2	Alignment		6.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
16	c3nvaB_	Alignment		6.1	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
17	c1vcnA_	Alignment		5.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
18	d1nyca_	Alignment		5.5	16	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Staphostatin

19	c2p9xB_	Alignment		5.2	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph0832; **PDBTitle:** crystal structure of ph0832 from pyrococcus horikoshii ot3