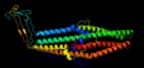
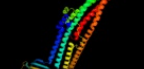
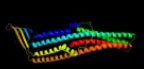
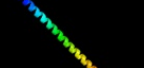
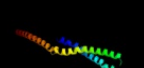
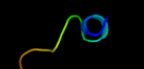
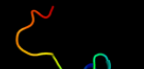
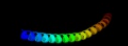
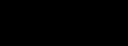
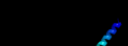


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P32714
Date	Thu Jan 5 11:50:35 GMT 2012
Unique Job ID	7311320105746526

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlwpla_	 Alignment		100.0	22	Fold: Outer membrane efflux proteins (OEP) Superfamily: Outer membrane efflux proteins (OEP) Family: Outer membrane efflux proteins (OEP)
2	c3pikA_	 Alignment		100.0	27	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusc; PDBTitle: outer membrane protein cusc
3	c1yc9A_	 Alignment		100.0	28	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein; PDBTitle: the crystal structure of the outer membrane protein vcec from the2 bacterial pathogen vibrio cholerae at 1.8 resolution
4	c1tqgC_	 Alignment		100.0	14	PDB header: transport protein Chain: C: PDB Molecule: outer membrane protein tolC; PDBTitle: structure of tolC in complex with hexammincobalt
5	d1ek9a_	 Alignment		100.0	14	Fold: Outer membrane efflux proteins (OEP) Superfamily: Outer membrane efflux proteins (OEP) Family: Outer membrane efflux proteins (OEP)
6	c3fppB_	 Alignment		47.9	12	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
7	c1urqC_	 Alignment		28.1	12	PDB header: transport protein Chain: C: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: crystal structure of neuronal q-snares in complex with2 r-snares motif of tomosyn
8	d2ijra1	 Alignment		27.7	14	Fold: Api92-like Superfamily: Api92-like Family: Api92-like
9	c3sogA_	 Alignment		22.3	10	PDB header: structural protein Chain: A: PDB Molecule: amphiphysin; PDBTitle: crystal structure of the bar domain of human amphiphysin, isoform 1
10	c2zroA_	 Alignment		19.0	47	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
11	d1mo6a1	 Alignment		14.9	47	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)

12	c3b5nC_	Alignment		14.7	15	PDB header: membrane protein Chain: C: PDB Molecule: protein transport protein sec9; PDBTitle: structure of the yeast plasma membrane snare complex
13	d1v5ra1	Alignment		14.7	50	Fold: N domain of copper amine oxidase-like Superfamily: GAS2 domain-like Family: GAS2 domain
14	d1xp8a1	Alignment		14.4	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
15	c1xp8A_	Alignment		13.8	41	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: "deinococcus radiodurans reca in complex with atp-gamma-s"
16	d1ubea1	Alignment		13.3	47	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
17	c2recB_	Alignment		12.0	47	PDB header: helicase PDB COMPND:
18	d2vdfa1	Alignment		9.8	38	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane adhesin/invasin OpcA
19	c1l4aC_	Alignment		8.1	8	PDB header: endocytosis/exocytosis Chain: C: PDB Molecule: s-snap25 fusion protein; PDBTitle: x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
20	c2l06A_	Alignment		8.0	18	PDB header: protein binding Chain: A: PDB Molecule: phycobilisome lcm core-membrane linker polypeptide; PDBTitle: solution nmr structure of the pbs linker polypeptide domain (fragment2 254-400) of phycobilisome linker protein apce from synechocystis sp.3 pcc 6803. northeast structural genomics consortium target sgr209c
21	c3ohwB_	Alignment	not modelled	7.3	12	PDB header: protein binding Chain: B: PDB Molecule: phycobilisome lcm core-membrane linker polypeptide; PDBTitle: x-ray structure of phycobilisome lcm core-membrane linker polypeptide2 (fragment 721-860) from synechocystis sp. pcc 6803, northeast3 structural genomics consortium target sgr209e
22	c3hr8A_	Alignment	not modelled	7.2	41	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
23	c2f1mA_	Alignment	not modelled	6.8	8	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
24	c2ky4A_	Alignment	not modelled	6.7	11	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
25	c2l3wA_	Alignment	not modelled	6.6	14	PDB header: photosynthesis Chain: A: PDB Molecule: phycobilisome rod linker polypeptide; PDBTitle: solution nmr structure of the pbs linker domain of phycobilisome rod2 linker polypeptide from synechococcus elongatus, northeast structural3 genomics consortium target snr168a
26	c3pruD_	Alignment	not modelled	6.5	16	PDB header: photosynthesis Chain: D: PDB Molecule: phycobilisome 32.1 kda linker polypeptide, phycocyanin- PDBTitle: crystal structure of phycobilisome 32.1 kda linker polypeptide,2 phycocyanin-associated, rod 1 (fragment 14-158) from synechocystis3 sp. pcc 6803, northeast structural genomics consortium target sgr182a
						PDB header: transport protein

27	c3brzA_	Alignment	not modelled	6.5	11	Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
28	c1nhlA_	Alignment	not modelled	6.3	12	PDB header: protein transport Chain: A: PDB Molecule: synaptosomal-associated protein 23; PDBTitle: snap-23n structure
29	c3zqbB_	Alignment	not modelled	5.9	11	PDB header: cell invasion Chain: B: PDB Molecule: protein prgi, cell invasion protein sipd; PDBTitle: prgi-sipd from salmonella typhimurium