




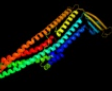




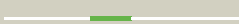




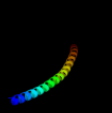





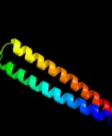
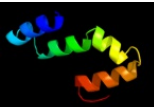
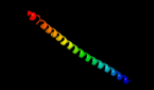
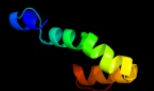




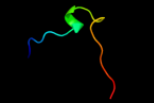


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77211
Date	Thu Jan 5 12:26:21 GMT 2012
Unique Job ID	20b15102de8ff044

Detailed template information

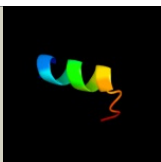
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pikA_	 Alignment		100.0	100	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusc; PDBTitle: outer membrane protein cusc
2	dlwplA_	 Alignment		100.0	44	Fold: Outer membrane efflux proteins (OEP) Superfamily: Outer membrane efflux proteins (OEP) Family: Outer membrane efflux proteins (OEP)
3	c1yc9A_	 Alignment		100.0	27	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein; PDBTitle: the crystal structure of the outer membrane protein vcec from the 2 bacterial pathogen vibrio cholerae at 1.8 resolution
4	c1tqgC_	 Alignment		100.0	17	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	17	Fold: Outer membrane efflux proteins (OEP) Superfamily: Outer membrane efflux proteins (OEP) Family: Outer membrane efflux proteins (OEP)
6	c3fppB_	 Alignment		51.6	15	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
7	c1lurqC_	 Alignment		20.8	17	PDB header: transport protein Chain: C: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: crystal structure of neuronal q-snares in complex with 2 r-snares motif of tomosyn
8	c3b5nC_	 Alignment		15.4	7	PDB header: membrane protein Chain: C: PDB Molecule: protein transport protein sec9; PDBTitle: structure of the yeast plasma membrane snare complex
9	c3sogA_	 Alignment		10.0	7	PDB header: structural protein Chain: A: PDB Molecule: amphiphysin; PDBTitle: crystal structure of the bar domain of human amphiphysin, isoform 1
10	c1nhlA_	 Alignment		9.8	8	PDB header: protein transport Chain: A: PDB Molecule: synaptosomal-associated protein 23; PDBTitle: snap-23n structure
11	c2f1mA_	 Alignment		8.7	18	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
						PDB header: protein binding

12	c2l06A_	Alignment		8.2	16	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
13	c1l4aC_	Alignment		7.4	11	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
14	c2l3wA_	Alignment		6.6	20	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
15	c3ohwB_	Alignment		6.6	14	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
16	c2v7sA_	Alignment		6.6	8	PDB header: unknown function Chain: A: PDB Molecule: probable conserved lipoprotein lppa; PDBTitle: crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
17	c3pruD_	Alignment		6.4	18	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
18	c2ky4A_	Alignment		6.2	14	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
19	d1yuda1	Alignment		5.9	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: YML079-like

20

[c2d7cD_](#)

Alignment



5.2

13

PDB header:protein transport
Chain: D: **PDB Molecule:**rab11 family-interacting protein 3;
PDBTitle: crystal structure of human rab11 in complex with fip3
rab-2 binding domain