







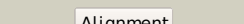

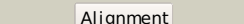
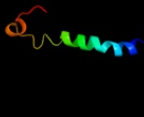
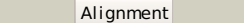
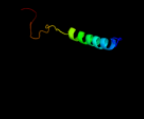
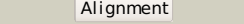

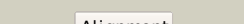

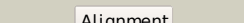
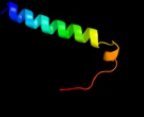
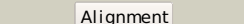
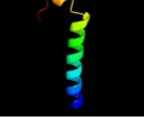
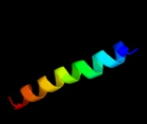

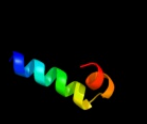
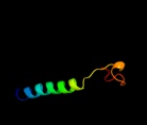
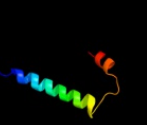


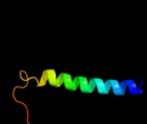
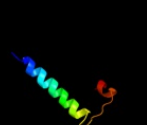


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P45562
Date	Thu Jan 5 12:03:15 GMT 2012
Unique Job ID	aac1e034efbd585c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pv7a_	 Alignment		100.0	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
2	d1pw4a_	 Alignment		100.0	12	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
3	c2xutC_	 Alignment		100.0	17	PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
4	c3o7pA_	 Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
5	c2gfpA_	 Alignment		100.0	11	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
6	d1fftb2	 Alignment		56.6	15	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
7	c2kncA_	 Alignment		51.6	18	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
8	c3qngD_	 Alignment		38.0	15	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
9	c2w8aC_	 Alignment		25.4	7	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
10	d3dtub2	 Alignment		15.9	14	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
11	d3ehbb2	 Alignment		12.4	11	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region

12	c2rddB_	Alignment		9.2	12	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
13	c2g9pA_	Alignment		8.7	21	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide latarcin 2a; PDBTitle: nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
14	d2fnoa1	Alignment		8.1	17	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
15	c2jo1A_	Alignment		7.7	18	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
16	d1j4na_	Alignment		7.5	15	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
17	c3b9yA_	Alignment		7.1	8	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
18	c1qleB_	Alignment		6.1	8	PDB header: oxidoreductase/immune system Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
19	c1ar1B_	Alignment		6.1	8	PDB header: complex (oxidoreductase/antibody) Chain: B: PDB Molecule: cytochrome c oxidase; PDBTitle: structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
20	c1ymgA_	Alignment		5.3	5	PDB header: membrane protein Chain: A: PDB Molecule: lens fiber major intrinsic protein; PDBTitle: the channel architecture of aquaporin o at 2.2 angstrom resolution
21	d1ymga1	Alignment	not modelled	5.3	5	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like