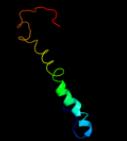
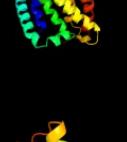
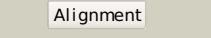
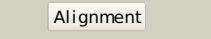
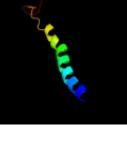


Phyre²

Email	I.a.kelley@imperial.ac.uk
Description	P0ABK2
Date	Thu Jan 5 11:15:40 GMT 2012
Unique Job ID	ace989a84af3a6b7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fftb2	 Alignment		20.9	14	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
2	clar1B_	 Alignment		16.5	10	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
3	c1gleB_	 Alignment		15.8	10	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
4	d1ejxc2	 Alignment		11.7	25	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
5	d1e9yb2	 Alignment		11.0	22	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: alpha-subunit of urease, catalytic domain
6	c3m7bA_	 Alignment		10.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tellurite resistance protein teha homolog; PDBTitle: crystal structure of plant slac1 homolog teha
7	c2ktaA_	 Alignment		6.8	26	PDB header: hydrolase Chain: A: PDB Molecule: putative helicase; PDBTitle: solution nmr structure of a domain of protein a6ky75 from bacteroides2 vulgaris, northeast structural genomics target bvr106a
8	c2knca_	 Alignment		6.2	16	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfa1b-beta3 transmembrane-cytoplasmic2 heterocomplex

9 c2f3oB_

Alignment



5.6

19

PDB header:unknown function
Chain: B; **PDB Molecule:**pyruvate formate-lyase 2;
PDBTitle: crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus