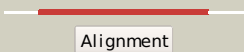

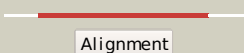

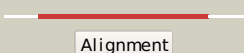

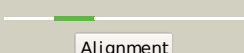

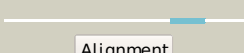

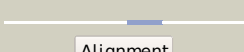
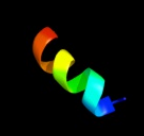


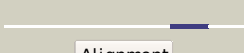
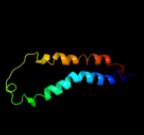










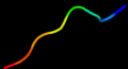






Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AFF0
Date	Thu Jan 5 11:26:04 GMT 2012
Unique Job ID	9176c9f773beec16

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rkoN_	 Alignment		100.0	99	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-quinone oxidoreductase subunit n; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
2	c3rkoL_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-quinone oxidoreductase subunit l; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	c3rkoM_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit m; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
4	c3rkoK_	 Alignment		54.7	21	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
5	d1a6qa1	 Alignment		39.8	11	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain
6	c2l3iA_	 Alignment		21.6	46	PDB header: antimicrobial protein Chain: A: PDB Molecule: aoxki4a, antimicrobial peptide in spider venom; PDBTitle: oxki4a, spider derived antimicrobial peptide
7	c3mesB_	 Alignment		8.8	15	PDB header: transferase Chain: B: PDB Molecule: choline kinase; PDBTitle: crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
8	d1fftb2	 Alignment		8.0	10	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
9	c2kncA_	 Alignment		7.2	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIiB-beta3 transmembrane-cytoplasmic2 heterocomplex
10	c1r6rA_	 Alignment		6.8	26	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of dengue virus capsid protein reveals a2 new fold
11	d1r6ra_	 Alignment		6.8	26	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C

12	c1ceuA	Alignment		6.6	25	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 regulatory protein n-terminal) PDBTitle: nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
13	d1n9wa2	Alignment		6.5	50	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
14	c3r24A	Alignment		6.5	44	PDB header: transferase, viral protein Chain: A: PDB Molecule: 2'-o-methyl transferase; PDBTitle: crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible
15	c3c25A	Alignment		6.3	67	PDB header: hydrolase/dna Chain: A: PDB Molecule: noti restriction endonuclease; PDBTitle: crystal structure of noti restriction endonuclease bound to cognate2 dna
16	c1n9wA	Alignment		6.2	50	PDB header: biosynthetic protein Chain: A: PDB Molecule: aspartyl-trna synthetase 2; PDBTitle: crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
17	d3dtub2	Alignment		6.1	9	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
18	c3bjub	Alignment		5.8	50	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna2 synthetase
19	c1b8aB	Alignment		5.4	50	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
20	c2xteH	Alignment		5.3	40	PDB header: transcription Chain: H: PDB Molecule: f-box-like/wd repeat-containing protein tbl1x; PDBTitle: structure of the tbl1 tetramerisation domain
21	c1wydB	Alignment	not modelled	5.2	50	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
22	c2jwaA	Alignment	not modelled	5.1	21	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure