
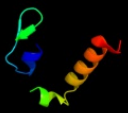



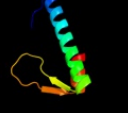
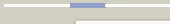

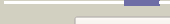



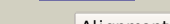

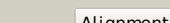
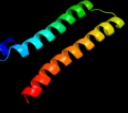








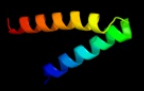


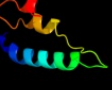


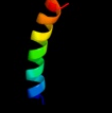


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P75968
Date	Thu Jan 5 12:16:35 GMT 2012
Unique Job ID	5e0b4ddb0e88b484

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qgia_	 Alignment		47.0	14	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Chitosanase
2	d1eysh2	 Alignment		38.3	38	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
3	d3ckca1	 Alignment		31.3	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: SusD-like
4	c3pr3B_	 Alignment		26.7	33	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
5	c1sqwA_	 Alignment		16.4	21	PDB header: unknown function Chain: A: PDB Molecule: saccharomyces cerevisiae nip7p homolog; PDBTitle: crystal structure of kd93, a novel protein expressed in the2 human pro
6	d2ajta1	 Alignment		16.0	67	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Fucl/AraA C-terminal domain-like Family: AraA C-terminal domain-like
7	c1w8jD_	 Alignment		15.8	18	PDB header: motor protein Chain: D: PDB Molecule: myosin va; PDBTitle: crystal structure of myosin v motor domain -2 nucleotide-free
8	d1oeda_	 Alignment		15.4	14	Fold: Neurotransmitter-gated ion-channel transmembrane pore Superfamily: Neurotransmitter-gated ion-channel transmembrane pore Family: Neurotransmitter-gated ion-channel transmembrane pore
9	d1lkxa_	 Alignment		13.2	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Motor proteins
10	d2h8pc1	 Alignment		12.8	15	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
11	d1mnda2	 Alignment		12.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Motor proteins

12	c1eysH_	Alignment		12.0	38	PDB header: electron transport Chain: H: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
13	c1br2C_	Alignment		10.8	13	PDB header: muscle protein Chain: C: PDB Molecule: myosin; PDBTitle: smooth muscle myosin motor domain complexed with mgadp.alf4
14	d2b0ja1	Alignment		10.5	15	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HMD dimerization domain-like
15	d1kx5b_	Alignment		9.8	36	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
16	d1nh1a_	Alignment		9.3	29	Fold: Antivirulence factor Superfamily: Antivirulence factor Family: Antivirulence factor
17	c1nh1A_	Alignment		9.3	29	PDB header: avirulence protein Chain: A: PDB Molecule: avirulence b protein; PDBTitle: crystal structure of the type iii effector avrb from2 pseudomonas syringae.
18	c3ujhB_	Alignment		8.7	31	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
19	c2zw3B_	Alignment		8.4	20	PDB header: cell adhesion Chain: B: PDB Molecule: gap junction beta-2 protein; PDBTitle: structure of the connexin-26 gap junction channel at 3.52 angstrom resolution
20	c2rndA_	Alignment		7.8	22	PDB header: endocytosis Chain: A: PDB Molecule: myc box-dependent-interacting protein 1; PDBTitle: structure of the n-terminal barpeptide in dpc micelles
21	c2erpA_	Alignment	not modelled	7.7	22	PDB header: toxin Chain: A: PDB Molecule: vascular apoptosis-inducing protein 1; PDBTitle: crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
22	c3lhnB_	Alignment	not modelled	7.4	83	PDB header: lipid binding protein Chain: B: PDB Molecule: lipoprotein; PDBTitle: crystal structure of putative lipoprotein (np_718719.1) from2 shewanella oneidensis at 1.42 a resolution
23	d2foka1	Alignment	not modelled	7.4	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Restriction endonuclease FokI, N-terminal (recognition) domain
24	d1ul1a2	Alignment	not modelled	7.2	25	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydropyridine reductase-like
25	c2kjaA_	Alignment	not modelled	7.1	45	PDB header: signaling protein Chain: A: PDB Molecule: protein phosphatase 1 regulatory subunit 12a; PDBTitle: mypt1(658-714)
26	c2fcgF_	Alignment	not modelled	6.9	50	PDB header: antimicrobial protein Chain: F: PDB Molecule: antibacterial protein fall-39, core peptide; PDBTitle: solution structure of the c-terminal fragment of human II-37
27	d1kha1	Alignment	not modelled	6.3	12	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
28	c1w9iA_	Alignment	not modelled	6.2	21	PDB header: myosin Chain: A: PDB Molecule: myosin ii heavy chain;

28	c1w91A	Alignment	not modelled	6.2	41	PDBTitle: myosin ii dictyostelium discoideum motor domain s456y bound2 with mgadp-befx PDB header: photosynthesis
29	c1k6nH	Alignment	not modelled	6.2	47	Chain: H: PDB Molecule: photosynthetic reaction center h subunit; PDBTitle: e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
30	c1g8xB	Alignment	not modelled	6.0	18	PDB header: structural protein Chain: B: PDB Molecule: myosin ii heavy chain fused to alpha-actinin 3; PDBTitle: structure of a genetically engineered molecular motor
31	d1cfea	Alignment	not modelled	5.9	38	Fold: PR-1-like Superfamily: PR-1-like Family: PR-1-like
32	d1d0xa2	Alignment	not modelled	5.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Motor proteins
33	d1vjpa2	Alignment	not modelled	5.7	40	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydropyridine reductase-like
34	d1rzh2	Alignment	not modelled	5.7	41	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
35	c2vb6A	Alignment	not modelled	5.3	24	PDB header: motor protein Chain: A: PDB Molecule: myosin vi; PDBTitle: myosin vi (md-insert2-cam, delta insert1) post-rigor state (2 crystal form 2)