
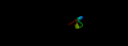

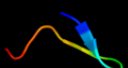

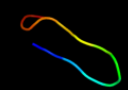





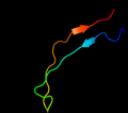

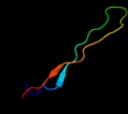

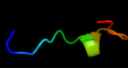



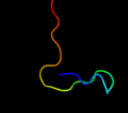

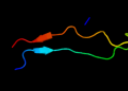
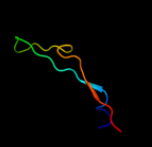
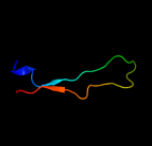
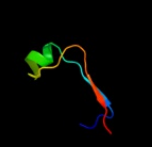

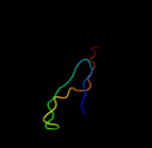


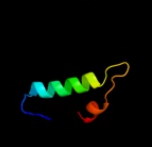
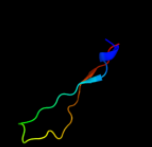


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P28915
Date	Thu Jan 5 11:45:25 GMT 2012
Unique Job ID	9be07ed3549734fc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlgzs_b	 Alignment		50.3	77	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
2	d2joka1	 Alignment		48.8	62	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
3	dlr6ea_	 Alignment		46.9	62	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
4	cljqsB_	 Alignment		33.4	50	PDB header: ribosome Chain: B: PDB Molecule: elongation factor g; PDBTitle: fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmpcp, a nonhydrolysable gtp analog
5	d1beca1	 Alignment		27.9	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
6	d2ntsp1	 Alignment		25.2	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
7	d2cdeb1	 Alignment		24.2	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
8	d2oeza1	 Alignment		18.4	35	Fold: YacF-like Superfamily: YacF-like Family: YacF-like
9	c3i5dC_	 Alignment		17.7	24	PDB header: transport protein Chain: C: PDB Molecule: p2x purinoceptor; PDBTitle: crystal structure of the atp-gated p2x4 ion channel in the closed, apo2 state at 3.5 angstroms (r3)
10	dlgsoa1	 Alignment		15.8	32	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
11	d2rhea_	 Alignment		15.1	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)

12	dlj8hd1	Alignment		14.9	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
13	d2nxyz1	Alignment		13.9	35	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
14	d2axha1	Alignment		13.1	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
15	d2rcja1	Alignment		12.7	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
16	d1nl0l1	Alignment		12.4	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
17	c2rf4A_	Alignment		11.2	16	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase i subunit rpa4; PDBTitle: crystal structure of the rna polymerase i subcomplex a14/43
18	d1hnga1	Alignment		11.1	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
19	c2rnnA_	Alignment		10.2	26	PDB header: ligase Chain: A: PDB Molecule: e3 sumo-protein ligase siz1; PDBTitle: solution structure of the n-terminal sap domain of sumo e3 ligases2 from saccharomyces cerevisiae
20	d1kgce1	Alignment		9.4	35	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
21	d1aql1	Alignment	not modelled	8.8	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
22	d1nfdb1	Alignment	not modelled	8.6	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
23	d1u3hb1	Alignment	not modelled	8.5	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
24	c2ckzB_	Alignment	not modelled	8.2	15	PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase iii 25 kd PDBTitle: x-ray structure of rna polymerase iii subcomplex c17-c25.
25	c3l15A_	Alignment	not modelled	7.6	30	PDB header: transcription Chain: A: PDB Molecule: transcriptional enhancer factor tef-4; PDBTitle: human tead2 transcriptional factor
26	c2kuyA_	Alignment	not modelled	7.5	43	PDB header: antimicrobial protein Chain: A: PDB Molecule: prebacteriocin glycosin f; PDBTitle: structure of glycosin f
27	d1ktke1	Alignment	not modelled	7.2	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
28	d1q1jl1	Alignment	not modelled	7.2	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
29	d2aw2a1	Alignment	not modelled	6.9	52	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin

						Family: V set domains (antibody variable domain-like)
30	c3fd9C_	Alignment	not modelled	6.9	25	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the transcriptional anti-activator exsd2 from pseudomonas aeruginosa
31	d1lc0a2	Alignment	not modelled	6.9	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Biliverdin reductase
32	d1nfda1	Alignment	not modelled	6.8	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
33	c1ye9E_	Alignment	not modelled	6.7	35	PDB header: oxidoreductase Chain: E: PDB Molecule: catalase hp11; PDBTitle: crystal structure of proteolytically truncated catalase2 hp11 from e. coli
34	d1xaau_	Alignment	not modelled	6.6	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
35	d1nzpa_	Alignment	not modelled	6.5	29	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
36	c2hpaA_	Alignment	not modelled	6.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
37	d1vmaa1	Alignment	not modelled	6.2	17	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
38	c3ayhB_	Alignment	not modelled	6.2	8	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase iii subunit rpc8; PDBTitle: crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
39	d2pxyd2	Alignment	not modelled	6.1	57	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
40	d2bnub1	Alignment	not modelled	5.9	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
41	c3fe7A_	Alignment	not modelled	5.8	15	PDB header: cell cycle Chain: A: PDB Molecule: mdm4 protein; PDBTitle: crystal structure of hdmx bound to the p53-peptidomimetic2 ac-phe-met-aib-pmp-trp-glu-ac3c-leu-nh2 at 1.35a
42	d2ak4d1	Alignment	not modelled	5.6	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
43	d2ho2a1	Alignment	not modelled	5.5	55	Fold: WW domain-like Superfamily: WW domain Family: WW domain
44	d2j6el1	Alignment	not modelled	5.4	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
45	d1w72l1	Alignment	not modelled	5.2	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
46	c2l0eA_	Alignment	not modelled	5.2	67	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: structural and functional analysis of tm vi of the nhe1 isoform of the2 na+/h+ exchanger
47	d2axia1	Alignment	not modelled	5.1	15	Fold: SWIB/MDM2 domain Superfamily: SWIB/MDM2 domain Family: SWIB/MDM2 domain