










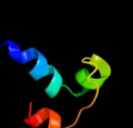

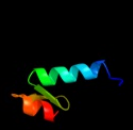





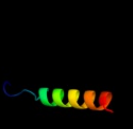




Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ADK0
Date	Thu Jan 5 11:21:12 GMT 2012
Unique Job ID	3a110f580723d51b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2c8sa1	 Alignment		60.6	18	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
2	d1fc2c_	 Alignment		59.7	36	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
3	d1lp1b_	 Alignment		59.3	38	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
4	c2d0wA_	 Alignment		49.7	25	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c1; PDBTitle: crystal structure of cytochrome c1 from hyphomicrobium2 denitrificans
5	d1deeg_	 Alignment		47.0	43	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
6	c1zdbA_	 Alignment		47.0	25	PDB header: igg binding domain Chain: A: PDB Molecule: mini protein a domain, z38; PDBTitle: phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
7	d2jwda1	 Alignment		46.5	32	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
8	d2gc4d1	 Alignment		42.3	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
9	d1lp1a_	 Alignment		42.3	33	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
10	c2g38A_	 Alignment		38.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
11	d2g38a1	 Alignment		38.3	16	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE

12	c3fggA_	Alignment		36.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bce2196; PDBTitle: crystal structure of putative ecf-type sigma factor negative effector2 from bacillus cereus
13	c3lueP_	Alignment		31.9	24	PDB header: structural protein Chain: P: PDB Molecule: alpha-actinin-3; PDBTitle: model of alpha-actinin ch1 bound to f-actin
14	d1edla_	Alignment		24.8	44	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
15	d2iy5a1	Alignment		20.3	13	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Phenylalanyl-tRNA synthetase (PheRS)
16	d1ojqa_	Alignment		18.0	4	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins
17	c3uc2A_	Alignment		15.8	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein with immunoglobulin-like fold; PDBTitle: crystal structure of a hypothetical protein with immunoglobulin-like2 fold (pa0388) from pseudomonas aeruginosa pao1 at 2.09 a resolution
18	c2xglB_	Alignment		14.2	33	PDB header: antibiotic Chain: B: PDB Molecule: colicin-m immunity protein; PDBTitle: the x-ray structure of the escherichia coli colicin m immunity2 protein demonstrates the presence of a disulphide bridge, which is3 functionally essential
19	c1hynQ_	Alignment		13.9	27	PDB header: membrane protein Chain: Q: PDB Molecule: band 3 anion transport protein; PDBTitle: crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein
20	c1g5gA_	Alignment		13.8	24	PDB header: viral protein Chain: A: PDB Molecule: fusion protein; PDBTitle: fragment of fusion protein from newcastle disease virus
21	d1r45a_	Alignment	not modelled	12.1	13	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins
22	d1fqva1	Alignment	not modelled	11.8	38	Fold: F-box domain Superfamily: F-box domain Family: F-box domain
23	c2kv5A_	Alignment	not modelled	11.7	36	PDB header: toxin Chain: A: PDB Molecule: putative uncharacterized protein rnai; PDBTitle: solution structure of the par toxin fst in dpc micelles
24	c2yskA_	Alignment	not modelled	10.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein tha1432; PDBTitle: crystal structure of a hypothetical protein tha1432 from thermus2 thermophilus
25	d1qn2a_	Alignment	not modelled	10.6	13	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
26	d1qhma_	Alignment	not modelled	10.4	14	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: PFL-like
27	c2dbhA_	Alignment	not modelled	10.3	22	PDB header: signaling protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily PDBTitle: solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
28	d1eiya1	Alignment	not modelled	10.3	12	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Phenylalanyl-tRNA synthetase (PheRS)
						Fold: Periplasmic binding protein-like II

29	d1y9ua_	Alignment	not modelled	10.1	15	Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
30	c3ermD_	Alignment	not modelled	10.0	16	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved protein with unknown function2 from pseudomonas syringae pv. tomato str. dc3000
31	d4icba_	Alignment	not modelled	9.7	31	Fold: EF Hand-like Superfamily: EF-hand Family: Calbindin D9K
32	c3swyB_	Alignment	not modelled	8.8	18	PDB header: transport protein Chain: B: PDB Molecule: cyclic nucleotide-gated cation channel alpha-3; PDBTitle: cnga3 626-672 containing clz domain
33	d1j3sa_	Alignment	not modelled	8.3	21	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
34	c2x7aB_	Alignment	not modelled	8.0	22	PDB header: immune system Chain: B: PDB Molecule: bone marrow stromal antigen 2; PDBTitle: structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
35	c2kwhA_	Alignment	not modelled	7.6	27	PDB header: transport protein Chain: A: PDB Molecule: rala-binding protein 1; PDBTitle: ral binding domain of rliip76 (ralbp1)
36	d1sh5a1	Alignment	not modelled	7.6	10	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
37	d1hynp_	Alignment	not modelled	7.2	24	Fold: Phosphotransferase/anion transport protein Superfamily: Phosphotransferase/anion transport protein Family: Anion transport protein, cytoplasmic domain
38	d1y4ta_	Alignment	not modelled	7.1	26	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
39	c2zykA_	Alignment	not modelled	7.0	14	PDB header: sugar binding protein Chain: A: PDB Molecule: solute-binding protein; PDBTitle: crystal structure of cyclo/maltodextrin-binding protein2 complexed with gamma-cyclodextrin
40	c3bw8B_	Alignment	not modelled	7.0	17	PDB header: transferase Chain: B: PDB Molecule: mono-adp-ribosyltransferase c3; PDBTitle: crystal structure of the clostridium limosum c3 exoenzyme
41	c3d0wD_	Alignment	not modelled	6.9	36	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: yflh protein; PDBTitle: crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326
42	d1lmsa_	Alignment	not modelled	6.8	21	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
43	d1ccra_	Alignment	not modelled	6.8	23	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
44	d1l8ya_	Alignment	not modelled	6.7	42	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
45	d1nmla2	Alignment	not modelled	6.4	28	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
46	c3gdzA_	Alignment	not modelled	6.3	18	PDB header: ligase Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae
47	d3ctda1	Alignment	not modelled	6.2	0	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
48	c2pt1A_	Alignment	not modelled	6.0	24	PDB header: metal transport Chain: A: PDB Molecule: iron transport protein; PDBTitle: futa1 synechocystis pcc 6803
49	c3oeoD_	Alignment	not modelled	6.0	78	PDB header: signaling protein Chain: D: PDB Molecule: spheroplast protein y; PDBTitle: the crystal structure e. coli spy
50	c1sj8A_	Alignment	not modelled	5.9	12	PDB header: structural protein Chain: A: PDB Molecule: talín 1; PDBTitle: crystal structure of talin residues 482-789
51	c1sszA_	Alignment	not modelled	5.8	33	PDB header: surface active protein Chain: A: PDB Molecule: pulmonary surfactant-associated protein b; PDBTitle: conformational mapping of mini-b: an n-terminal/c-terminal2 construct of surfactant protein b using 13c-enhanced3 fourier transform infrared (ftir) spectroscopy
52	d1aoaa1	Alignment	not modelled	5.7	8	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
53	c3m97X_	Alignment	not modelled	5.7	21	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c-552; PDBTitle: structure of the soluble domain of cytochrome c552 with its flexible2 linker segment from paracoccus denitrificans
54	d1ycca_	Alignment	not modelled	5.6	21	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
55	c2z6vA_	Alignment	not modelled	5.6	14	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of sulfotransferase stf9 from2

					mycobacterium avium
56	d1hywa_	Alignment	not modelled	5.3	36 Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
57	d1cl1a_	Alignment	not modelled	5.2	35 Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
58	d1hroa_	Alignment	not modelled	5.2	23 Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
59	c2qk1A_	Alignment	not modelled	5.2	13 PDB header: protein binding Chain: A: PDB Molecule: protein stu2; PDBTitle: structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1