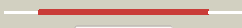


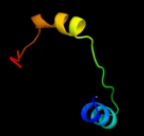



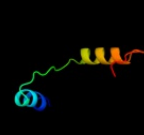

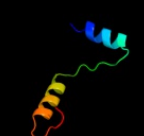



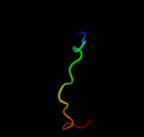

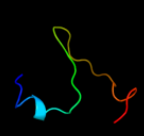





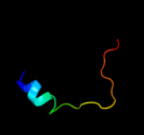


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A0Q4
Date	Tue Jul 17 17:05:08 BST 2012
Unique Job ID	110c69bdc90a068

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kbyB_	 Alignment		100.0	95	PDB header: unknown function Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hypothetical protein from staphylococcus aureus
2	d2w6ka1	 Alignment		31.4	27	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
3	c2l9sa_	 Alignment		25.1	33	PDB header: transcription Chain: A; PDB Molecule: phd finger protein 12; PDBTitle: solution structure of pf1 sid1-msin3a pah2 complex
4	c3by5A_	 Alignment		22.5	28	PDB header: biosynthetic protein Chain: A; PDB Molecule: cobalamin biosynthesis protein; PDBTitle: crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
5	d3by5a1	 Alignment		22.5	28	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
6	c3bpcC_	 Alignment		18.1	67	PDB header: toxin Chain: C; PDB Molecule: antitoxin relb3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
7	d1eu3a1	 Alignment		14.8	47	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Superantigen toxins, N-terminal domain
8	d1uf0a_	 Alignment		14.5	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
9	c1jrxA_	 Alignment		13.9	30	PDB header: oxidoreductase Chain: A; PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
10	d1r17a2	 Alignment		12.2	19	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Fibrinogen-binding domain
11	c2qneA_	 Alignment		12.1	17	PDB header: transferase Chain: A; PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution

12	c3o0lB_	Alignment		11.1	70	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf1425 family member (shew_1734) from <i>Shewanella</i> sp. pv-4 at 1.81 Å resolution
13	c2bpsA_	Alignment		9.2	18	PDB header: ubiquitin Chain: A: PDB Molecule: yukd protein; PDBTitle: ubiquitin-like protein yukd of <i>Bacillus subtilis</i>
14	c3l9kZ_	Alignment		8.8	38	PDB header: motor protein Chain: Z: PDB Molecule: dynein intermediate chain, cytosolic; PDBTitle: insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
15	c2ysfA_	Alignment		8.7	33	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: solution structure of the fourth ww domain from the human e3 ubiquitin-protein ligase itchy homolog, itch
16	d1xg0c_	Alignment		8.2	40	Fold: Globin-like Superfamily: Globin-like Family: Phycocyanin-like phycobilisome proteins
17	d1eyxb_	Alignment		8.2	40	Fold: Globin-like Superfamily: Globin-like Family: Phycocyanin-like phycobilisome proteins
18	d1j3ka_	Alignment		7.1	44	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
19	c2ysgA_	Alignment		7.1	17	PDB header: protein binding Chain: A: PDB Molecule: syntaxin-binding protein 4; PDBTitle: solution structure of the ww domain from the human syntaxin-2 binding protein 4
20	c2y9xG_	Alignment		6.9	75	PDB header: oxidoreductase Chain: G: PDB Molecule: lectin-like fold protein; PDBTitle: crystal structure of ppo3, a tyrosinase from <i>Agaricus bisporus</i> , in 2 deoxy-form that contains additional unknown lectin-like subunit, 3 with inhibitor tropolone
21	c3ctrA_	Alignment	not modelled	6.9	12	PDB header: hydrolase Chain: A: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of the rrm-domain of the poly(a)-specific 2 ribonuclease parn bound to m7gtp
22	c2dmvA_	Alignment	not modelled	6.9	33	PDB header: ligase Chain: A: PDB Molecule: itchy homolog e3 ubiquitin protein ligase; PDBTitle: solution structure of the second ww domain of itchy homolog 2 e3 ubiquitin protein ligase (itch)
23	d1a21a2	Alignment	not modelled	6.7	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
24	c2dnfA_	Alignment	not modelled	6.6	16	PDB header: protein binding Chain: A: PDB Molecule: doublecortin domain-containing protein 2; PDBTitle: solution structure of rsgi ruh-062, a dcx domain from human
25	d1df7a_	Alignment	not modelled	6.6	33	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
26	d1mjda_	Alignment	not modelled	6.5	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Doublecortin (DC) Family: Doublecortin (DC)
27	d1ha7b_	Alignment	not modelled	6.3	30	Fold: Globin-like Superfamily: Globin-like Family: Phycocyanin-like phycobilisome proteins
28	d2fzia1	Alignment	not modelled	6.3	67	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases

29	d1kmva_	Alignment	not modelled	6.2	44	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
30	c1ymzA_	Alignment	not modelled	6.2	18	PDB header: unknown function Chain: A: PDB Molecule: cc45; PDBTitle: cc45, an artificial ww domain designed using statistical2 coupling analysis
31	c2zajA_	Alignment	not modelled	6.2	44	PDB header: protein binding Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz PDBTitle: solution structure of the short-isoform of the second ww2 domain from the human membrane-associated guanylate kinase,3 ww and pdz domain-containing protein 1 (magi-1)
32	c2blcA_	Alignment	not modelled	6.2	44	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase-thymidylate synthase; PDBTitle: sp21 double mutant p. vivax dihydrofolate reductase in2 complex with des-chloropyrimethamine
33	c3cseA_	Alignment	not modelled	6.1	67	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
34	c1wr4A_	Alignment	not modelled	6.1	56	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-protein ligase nedd4-2; PDBTitle: solution structure of the second ww domain of nedd4-2
35	d1aoea_	Alignment	not modelled	6.0	67	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
36	c1zdrB_	Alignment	not modelled	5.9	67	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: dhfr from bacillus stearothermophilus
37	c4ehpB_	Alignment	not modelled	5.9	22	PDB header: cell adhesion Chain: B: PDB Molecule: catenin alpha-1; PDBTitle: crystal structure of human vinculin head domain (residues 1-252) in2 complex with alpha-catenin (residues 277-382)
38	d2f21a1	Alignment	not modelled	5.9	33	Fold: WW domain-like Superfamily: WW domain Family: WW domain
39	c3opwA_	Alignment	not modelled	5.7	38	PDB header: oxidoreductase Chain: A: PDB Molecule: dna damage-responsive transcriptional repressor rph1; PDBTitle: crystal structure of the rph1 catalytic core
40	c3dgsB_	Alignment	not modelled	5.7	44	PDB header: oxidoreductase, transferase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump PDBTitle: quadruple mutant (n51i+c59r+s108n+i164l) plasmodium2 falciparum dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump
41	c2ysdA_	Alignment	not modelled	5.7	18	PDB header: protein binding Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz PDBTitle: solution structure of the first ww domain from the human2 membrane-associated guanylate kinase, ww and pdz domain-3 containing protein 1. magi-1
42	d1phnb_	Alignment	not modelled	5.7	30	Fold: Globin-like Superfamily: Globin-like Family: Phycocyanin-like phycobilisome proteins
43	d2jmf1	Alignment	not modelled	5.6	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
44	c3tq8A_	Alignment	not modelled	5.5	44	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of the dihydrofolate reductase (fo1a) from coxiella burnetii2 in complex with trimethoprim
45	d1js8a2	Alignment	not modelled	5.5	15	Fold: C-terminal domain of mollusc hemocyanin Superfamily: C-terminal domain of mollusc hemocyanin Family: C-terminal domain of mollusc hemocyanin
46	c3f0uX_	Alignment	not modelled	5.5	67	PDB header: oxidoreductase Chain: X: PDB Molecule: trimethoprim-sensitive dihydrofolate reductase; PDBTitle: staphylococcus aureus f98y mutant dihydrofolate reductase2 complexed with nadph and 2,4-diamino-5-[3-(3-methoxy-5-3 phenylphenyl)but-1-ynyl]-6-methyl pyrimidine
47	c2j96B_	Alignment	not modelled	5.5	25	PDB header: photosynthesis Chain: B: PDB Molecule: phycoerythrocyanin alpha chain; PDBTitle: the e-configuration of alfa-phycoerythrocyanin
48	c2lawA_	Alignment	not modelled	5.4	33	PDB header: signaling protein/transcription Chain: A: PDB Molecule: yorkie homolog; PDBTitle: structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
49	c4ei0B_	Alignment	not modelled	5.4	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized hypothetical protein; PDBTitle: crystal structure of a hypothetical protein (parmer_03218) from2 parabacteroides merdae atcc 43184 at 2.00 a resolution
50	d8dfra_	Alignment	not modelled	5.4	44	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
51	c2yadA_	Alignment	not modelled	5.4	53	PDB header: surfactant protein Chain: A: PDB Molecule: surfactant protein c brichos domain; PDBTitle: brichos domain of surfactant protein c precursor protein
52	d1tk7a2	Alianment	not modelled	5.3	44	Fold: WW domain-like Superfamily: WW domain

						Family: WW domain
53	d1ra9a_	Alignment	not modelled	5.3	56	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
54	c1jmuE_	Alignment	not modelled	5.2	64	PDB header: viral protein Chain: E: PDB Molecule: protein mu-1; PDBTitle: crystal structure of the reovirus mu1/sigma3 complex
55	d1lnla2	Alignment	not modelled	5.2	20	Fold: C-terminal domain of mollusc hemocyanin Superfamily: C-terminal domain of mollusc hemocyanin Family: C-terminal domain of mollusc hemocyanin
56	c2lazA_	Alignment	not modelled	5.1	0	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
57	c2lb0A_	Alignment	not modelled	5.1	0	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
58	c1mhmA_	Alignment	not modelled	5.0	23	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: crystal structure of s-adenosylmethionine decarboxylase2 from potato