
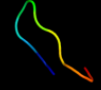
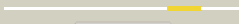




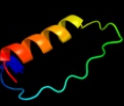









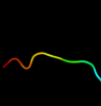










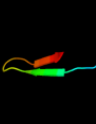




Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q5F267
Date	Wed Jul 10 14:18:19 BST 2013
Unique Job ID	c7eba2d3692eca70

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ok5a4	 Alignment		77.9	46	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
2	d1k3ra2	 Alignment		74.8	42	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
3	c1k3rA_	 Alignment		58.6	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
4	d1b93a_	 Alignment		56.5	18	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
5	d1vmda_	 Alignment		26.6	13	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
6	c2fwtA_	 Alignment		23.9	21	PDB header: electron transport Chain: A: PDB Molecule: dhc, diheme cytochrome c; PDBTitle: crystal structure of dhc purified from rhodobacter2 sphaeroides
7	c4a8xB_	 Alignment		23.2	30	PDB header: transcription Chain: B: PDB Molecule: hook-like, isoform a; PDBTitle: structure of the core asap complex
8	c3eopB_	 Alignment		22.4	50	PDB header: unknown function Chain: B: PDB Molecule: thymocyte nuclear protein 1; PDBTitle: crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
9	d2gbsa1	 Alignment		20.4	40	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
10	d1zcea1	 Alignment		19.0	40	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
11	d2g2xa1	 Alignment		18.8	40	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like

12	d2ar1a1	Alignment		18.2	30	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
13	d2evea1	Alignment		17.4	40	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
14	d2dkya1	Alignment		16.6	33	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
15	c3u99A_	Alignment		15.9	18	PDB header: electron transport Chain: A: PDB Molecule: diheme cytochrome c; PDBTitle: the experimental x-ray structure of the new diheme cytochrome type c2 from shewanella baltica os155 sb-dhc
16	d1y5ia1	Alignment		14.4	40	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
17	c2k8qA_	Alignment		12.4	29	PDB header: structural protein Chain: A: PDB Molecule: protein shq1; PDBTitle: nmr structure of shq1p n-terminal domain
18	c3eudE_	Alignment		12.2	28	PDB header: nuclear protein Chain: E: PDB Molecule: protein shq1; PDBTitle: structure of the cs domain of the essential h/aca rnp2 assembly protein shq1p
19	d1w4ma_	Alignment		11.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
20	c2jy0A_	Alignment		11.0	55	PDB header: membrane protein, viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution nmr structure of hcv ns2 protein, membrane segment2 (1-27)
21	c1qcrD_	Alignment	not modelled	10.9	19	PDB header: oxidoreductase Chain: D: PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
22	d2h80a1	Alignment	not modelled	10.8	32	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
23	d2r5fa1	Alignment	not modelled	9.8	16	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
24	c2i6sA_	Alignment	not modelled	9.5	21	PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
25	c3h5jA_	Alignment	not modelled	9.3	50	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
26	c3q3wB_	Alignment	not modelled	8.8	33	PDB header: transferase Chain: B: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from campylobacter jejuni.
27	c2hcuA_	Alignment	not modelled	8.8	50	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus2 mutans
28	d1uhwa_	Alignment	not modelled	8.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain

						Family: DEP domain
29	c2ct6A_	Alignment	not modelled	8.8	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sh3 domain-binding glutamic acid-rich-like PDBTitle: solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
30	c3a0bL_	Alignment	not modelled	8.4	50	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
31	d1v3fa_	Alignment	not modelled	8.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
32	d1t0ia_	Alignment	not modelled	8.2	26	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
33	d1sxra_	Alignment	not modelled	8.0	15	Fold: N-acetylmuramoyl-L-alanine amidase-like Superfamily: N-acetylmuramoyl-L-alanine amidase-like Family: N-acetylmuramoyl-L-alanine amidase-like
34	c3a0hL_	Alignment	not modelled	7.8	50	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
35	c3a0hL_	Alignment	not modelled	7.8	50	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of i-substituted photosystem ii complex
36	c3a0bL_	Alignment	not modelled	7.8	50	PDB header: electron transport Chain: L: PDB Molecule: photosystem ii reaction center protein I; PDBTitle: crystal structure of br-substituted photosystem ii complex
37	d2cu8a2	Alignment	not modelled	7.7	27	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
38	c3t7hB_	Alignment	not modelled	7.6	13	PDB header: ligase Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: atg8 transfer from atg7 to atg3: a distinctive e1-e2 architecture and2 mechanism in the autophagy pathway
39	d1wo8a1	Alignment	not modelled	7.3	14	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
40	c3ju3A_	Alignment	not modelled	7.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; PDBTitle: crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
41	c3mbfA_	Alignment	not modelled	7.1	16	PDB header: lyase Chain: A: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose bisphosphate aldolase from2 encephalitozoon cuniculi, bound to fructose 1,6-bisphosphate
42	d1gl0i_	Alignment	not modelled	6.4	60	Fold: PMP inhibitors Superfamily: PMP inhibitors Family: PMP inhibitors
43	d1xmeb2	Alignment	not modelled	6.4	33	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
44	d1ixsa_	Alignment	not modelled	6.2	58	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
45	d2iv2x1	Alignment	not modelled	6.1	20	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
46	d1vfsa1	Alignment	not modelled	5.9	21	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Alanine racemase
47	c1rpqW_	Alignment	not modelled	5.9	43	PDB header: membrane protein Chain: W: PDB Molecule: peptide e131; PDBTitle: high affinity ige receptor (alpha chain) complexed with tight-binding2 e131 'zeta' peptide from phage display
48	c1kcoA_	Alignment	not modelled	5.9	43	PDB header: protein binding Chain: A: PDB Molecule: e131 zeta peptide; PDBTitle: structure of e131 zeta peptide, a potent antagonist of the2 high-affinity ige receptor
49	c1rpqZ_	Alignment	not modelled	5.9	43	PDB header: membrane protein Chain: Z: PDB Molecule: peptide e131; PDBTitle: high affinity ige receptor (alpha chain) complexed with tight-binding2 e131 'zeta' peptide from phage display
50	c1rpqX_	Alignment	not modelled	5.9	43	PDB header: membrane protein Chain: X: PDB Molecule: peptide e131; PDBTitle: high affinity ige receptor (alpha chain) complexed with tight-binding2 e131 'zeta' peptide from phage display
51	d1g1xc_	Alignment	not modelled	5.6	50	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Ribosomal protein S18 Family: Ribosomal protein S18
52	c3kl4B_	Alignment	not modelled	5.6	60	PDB header: hydrolase Chain: B: PDB Molecule: signal peptide of yeast dipeptidyl aminopeptidase b; PDBTitle: recognition of a signal peptide by the signal recognition particle
53	d1ea0a1	Alignment	not modelled	5.5	27	Fold: Single-stranded right-handed beta-helix Superfamily: Alpha subunit of glutamate synthase, C-terminal domain Family: Alpha subunit of glutamate synthase, C-terminal domain
54	c1rpqY_	Alignment	not modelled	5.2	43	PDB header: membrane protein Chain: Y: PDB Molecule: peptide e131; PDBTitle: high affinity ige receptor (alpha chain) complexed with

