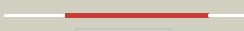
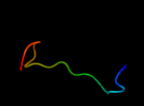
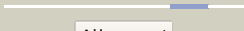
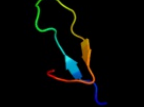
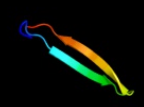
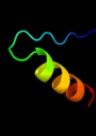
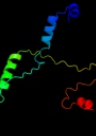
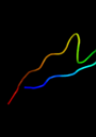
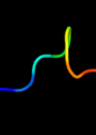


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8U0
Date	Thu Jan 5 11:08:44 GMT 2012
Unique Job ID	34463450d2d53420

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ffvA_	 Alignment		100.0	100	PDB header: protein binding Chain: A: PDB Molecule: protein syd; PDBTitle: crystal structure analysis of syd
2	c3d5pB_	 Alignment		97.7	13	PDB header: gene regulation Chain: B: PDB Molecule: putative glucan synthesis regulator of smi1/knr4 family; PDBTitle: crystal structure of a putative glucan synthesis regulator of2 smi1/knr4 family (bf1740) from bacteroides fragilis nctc 9343 at 1.453 a resolution
3	d2prva1	 Alignment		97.1	10	Fold: SMI1/KNR4-like Superfamily: SMI1/KNR4-like Family: SMI1/KNR4-like
4	d2icga1	 Alignment		96.2	11	Fold: SMI1/KNR4-like Superfamily: SMI1/KNR4-like Family: SMI1/KNR4-like
5	d2paga1	 Alignment		83.0	15	Fold: SMI1/KNR4-like Superfamily: SMI1/KNR4-like Family: SMI1/KNR4-like
6	c1hf9B_	 Alignment		32.2	26	PDB header: atpase inhibitor Chain: B: PDB Molecule: atpase inhibitor (mitochondrial); PDBTitle: c-terminal coiled-coil domain from bovine if1
7	c1z5sD_	 Alignment		30.0	53	PDB header: ligase Chain: D: PDB Molecule: ran-binding protein 2; PDBTitle: crystal structure of a complex between ubc9, sumo-1,2 rangap1 and nup358/ranbp2
8	c3o27B_	 Alignment		28.5	5	PDB header: dna binding protein Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of c68 from the hybrid virus-plasmid pssvx
9	d2bv3a4	 Alignment		23.6	17	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
10	c2wryA_	 Alignment		20.1	22	PDB header: immune system Chain: A: PDB Molecule: interleukin-1beta; PDBTitle: crystal structure of chicken cytokine interleukin 1 beta
11	d1e2wa2	 Alignment		19.3	15	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain

12	d1ci3m2	Alignment		17.2	10	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
13	c3kepA_	Alignment		16.4	17	PDB header: protein transport, rna binding protein Chain: A: PDB Molecule: nucleoporin nup145; PDBTitle: crystal structure of the autoproteolytic domain from the2 nuclear pore complex component nup145 from saccharomyces3 cerevisiae
14	c1q2lA_	Alignment		14.3	13	PDB header: hydrolase Chain: A: PDB Molecule: protease iii; PDBTitle: crystal structure of pitrilysin
15	c2jbuB_	Alignment		13.9	12	PDB header: hydrolase Chain: B: PDB Molecule: insulin-degrading enzyme; PDBTitle: crystal structure of human insulin degrading enzyme2 complexed with co-purified peptides.
16	c3dx5A_	Alignment		12.2	16	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
17	c2wk3A_	Alignment		11.7	12	PDB header: hydrolase Chain: A: PDB Molecule: insulin degrading enzyme; PDBTitle: crystal structure of human insulin-degrading enzyme in2 complex with amyloid-beta (1-42)
18	d1j83a_	Alignment		11.5	31	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 17 carbohydrate binding module, CBM17
19	c3lgeF_	Alignment		11.4	11	PDB header: lyase/protein binding Chain: F: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
20	c3lgeG_	Alignment		11.4	11	PDB header: lyase/protein binding Chain: G: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
21	c3d22A_	Alignment	not modelled	11.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h-type; PDBTitle: crystal structure of a poplar thioredoxin h mutant,2 ptxrh4c61s
22	d1ilr1_	Alignment	not modelled	10.9	30	Fold: beta-Trefoil Superfamily: Cytokine Family: Interleukin-1 (IL-1)
23	c1m45B_	Alignment	not modelled	10.6	25	PDB header: cell cycle protein Chain: B: PDB Molecule: iq2 motif from myo2p, a class v myosin; PDBTitle: crystal structure of mlc1p bound to iq2 of myo2p, a class v2 myosin
24	c2j57J_	Alignment	not modelled	10.5	18	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: x-ray reduced paraccocus denitrificans methylamine2 dehydrogenase n-quinol in complex with amicyanin.
25	d2a6qb1	Alignment	not modelled	10.5	14	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
26	d1st9a_	Alignment	not modelled	10.4	34	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
27	d8ilba_	Alignment	not modelled	10.1	30	Fold: beta-Trefoil Superfamily: Cytokine Family: Interleukin-1 (IL-1)
28	d2bg1a1	Alignment	not modelled	10.1	17	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
						PDB header: cytokine

29	c2klIA_	Alignment	not modelled	10.0	33	Chain: A: PDB Molecule: interleukin-33; PDBTitle: solution structure of human interleukin-33
30	c2hlwA_	Alignment	not modelled	9.2	15	PDB header: ligase, signaling protein Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 variant 1; PDBTitle: solution structure of the human ubiquitin-conjugating2 enzyme variant uev1a
31	c2a7oA_	Alignment	not modelled	8.9	16	PDB header: transcription Chain: A: PDB Molecule: huntingtin interacting protein b; PDBTitle: solution structure of the hset2/hypb sri domain
32	dlsmya1	Alignment	not modelled	8.8	24	Fold: DCoH-like Superfamily: RBP11-like subunits of RNA polymerase Family: RNA polymerase alpha subunit dimerisation domain
33	dlmd6a_	Alignment	not modelled	8.0	17	Fold: beta-Trefoil Superfamily: Cytokine Family: Interleukin-1 (IL-1)
34	d2v0ea1	Alignment	not modelled	7.8	16	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
35	c3psiA_	Alignment	not modelled	7.6	11	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
36	dltu2b2	Alignment	not modelled	7.6	26	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
37	c2nogA_	Alignment	not modelled	7.1	6	PDB header: dna binding protein Chain: A: PDB Molecule: iswi protein; PDBTitle: sant domain structure of xenopus remodeling factor iswi
38	c3kh7A_	Alignment	not modelled	7.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbe; PDBTitle: crystal structure of the periplasmic soluble domain of reduced ccmg2 from pseudomonas aeruginosa
39	c3iu6A_	Alignment	not modelled	6.8	9	PDB header: transcription Chain: A: PDB Molecule: protein polybromo-1; PDBTitle: crystal structure of the sixth bromodomain of human poly-bromodomain2 containing protein 1 (pb1)
40	c2jciA_	Alignment	not modelled	6.8	17	PDB header: drug-binding protein Chain: A: PDB Molecule: penicillin-binding protein 1b; PDBTitle: structural insights into the catalytic mechanism and the2 role of streptococcus pneumoniae pbp1b
41	c2j04C_	Alignment	not modelled	6.6	13	PDB header: transcription Chain: C: PDB Molecule: hypothetical protein ypl007c; PDBTitle: the tau60-tau91 subcomplex of yeast transcription factor2 iiic
42	dlqy9a1	Alignment	not modelled	6.1	20	Fold: Diaminopimelate epimerase-like Superfamily: Diaminopimelate epimerase-like Family: PhzC/PhzF-like
43	dlil2a2	Alignment	not modelled	6.0	32	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
44	c3uinD_	Alignment	not modelled	5.9	70	PDB header: ligase/isomerase/protein binding Chain: D: PDB Molecule: e3 sumo-protein ligase ranbp2; PDBTitle: complex between human rangap1-sumo2, ubc9 and the ir1 domain from2 ranbp2
45	dlwb9a3	Alignment	not modelled	5.6	20	Fold: Ribonuclease H-like motif Superfamily: DNA repair protein MutS, domain II Family: DNA repair protein MutS, domain II
46	dlzma2	Alignment	not modelled	5.6	14	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
47	dlrvra1	Alignment	not modelled	5.5	21	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
48	c3b79A_	Alignment	not modelled	5.5	20	PDB header: nucleotide binding protein Chain: A: PDB Molecule: toxin secretion atp-binding protein; PDBTitle: crystal structure of the n-terminal peptidase c39 like2 domain of the toxin secretion atp-binding protein from3 vibrio parahaemolyticus
49	c1n2dC_	Alignment	not modelled	5.5	25	PDB header: cell cycle Chain: C: PDB Molecule: iq2 and iq3 motifs from myo2p, a class v myosin; PDBTitle: ternary complex of mlc1p bound to iq2 and iq3 of myo2p, a2 class v myosin
50	c2o3oD_	Alignment	not modelled	5.5	23	PDB header: signaling protein Chain: D: PDB Molecule: yyci protein; PDBTitle: crystal structure of the sensor histidine kinase regulator yyci from2 bacillus subtilis
51	dltf5a1	Alignment	not modelled	5.4	22	Fold: Pre-protein crosslinking domain of SecA Superfamily: Pre-protein crosslinking domain of SecA Family: Pre-protein crosslinking domain of SecA
52	c1mzwB_	Alignment	not modelled	5.4	38	PDB header: isomerase Chain: B: PDB Molecule: u4/u6 snrnp 60kda protein; PDBTitle: crystal structure of a u4/u6 snrnp complex between human2 spliceosomal cyclophilin h and a u4/u6-60k peptide
53	c2wadB_	Alignment	not modelled	5.3	17	PDB header: peptide binding protein Chain: B: PDB Molecule: penicillin-binding protein 2b; PDBTitle: penicillin-binding protein 2b (pbp-2b) from streptococcus2 pneumoniae (strain 5204)
54	d2olua2	Alignment	not modelled	5.2	8	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
						PDB header: phosphotransferase

55	c1ezaA_	Alignment	not modelled	5.2	14	Chain: A: PDB Molecule: enzyme i; PDBTitle: amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
56	c1qy9B_	Alignment	not modelled	5.1	19	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ydde; PDBTitle: crystal structure of e. coli se-met protein ydde
57	d2gw6a1	Alignment	not modelled	5.1	22	Fold: Restriction endonuclease-like Superfamily: tRNA-intron endonuclease catalytic domain-like Family: tRNA-intron endonuclease catalytic domain-like
58	dls1qa_	Alignment	not modelled	5.1	19	Fold: UBC-like Superfamily: UBC-like Family: UEV domain
59	c3udiA_	Alignment	not modelled	5.1	17	PDB header: penicillin-binding protein/antibiotic Chain: A: PDB Molecule: penicillin-binding protein 1a; PDBTitle: crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g