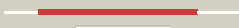



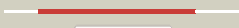






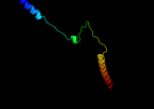







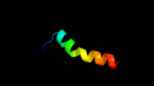


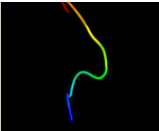


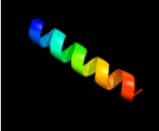



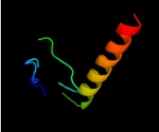
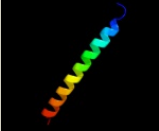


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P59048
Date	Wed Jul 10 14:04:54 BST 2013
Unique Job ID	eba552cc3c21b6c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zdiC_	 Alignment		96.6	15	PDB header: chaperone Chain: C; PDB Molecule: prefoldin subunit alpha; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
2	d1fxkc_	 Alignment		96.3	15	Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
3	c2zdiA_	 Alignment		96.0	14	PDB header: chaperone Chain: A; PDB Molecule: prefoldin subunit beta; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
4	d1fxka_	 Alignment		85.3	19	Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
5	c3aeiA_	 Alignment		69.8	18	PDB header: chaperone Chain: A; PDB Molecule: prefoldin beta subunit 2; PDBTitle: crystal structure of the prefoldin beta2 subunit from thermococcus2 strain ks-1
6	c1go4F_	 Alignment		51.8	26	PDB header: cell cycle Chain: F; PDB Molecule: mad1 (mitotic arrest deficient)-like 1; PDBTitle: crystal structure of mad1-mad2 reveals a conserved mad22 binding motif in mad1 and cdc20.
7	c2ke4A_	 Alignment		41.5	22	PDB header: membrane protein Chain: A; PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
8	c2gboB_	 Alignment		27.5	14	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: upf0358 protein ef2458; PDBTitle: protein of unknown function ef2458 from enterococcus faecalis
9	d2gboa1	 Alignment		27.5	14	Fold: Open three-helical up-and-down bundle Superfamily: EF2458-like Family: EF2458-like
10	c4dncD_	 Alignment		20.0	33	PDB header: transcription Chain: D; PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of human mof in complex with msl1
11	c3lyvF_	 Alignment		18.6	27	PDB header: chaperone Chain: F; PDB Molecule: ribosome-associated factor y; PDBTitle: crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a

12	c3ka5A	Alignment		16.4	38	PDB header: chaperone Chain: A: PDB Molecule: ribosome-associated protein y (psrp-1); PDBTitle: crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
13	d1wpga2	Alignment		16.3	18	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
14	c3hdeA	Alignment		15.5	22	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of full-length endolysin r21 from phage 21
15	c3he4A	Alignment		14.5	32	PDB header: de novo protein Chain: A: PDB Molecule: synzip6; PDBTitle: heterospecific coiled-coil pair synzip5:synzip6
16	d1lpya	Alignment		13.9	14	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
17	c2kz6A	Alignment		13.8	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2
18	c3kyzA	Alignment		13.1	27	PDB header: transferase Chain: A: PDB Molecule: sensor protein pfes; PDBTitle: the crystal structure of the sensor domain of two-component2 sensor pfes from pseudomonas aeruginosa pa01
19	d176la	Alignment		12.5	19	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
20	c1t3jA	Alignment		12.2	20	PDB header: membrane protein Chain: A: PDB Molecule: mitofusin 1; PDBTitle: mitofusin domain hr2 v686m/i708m mutant
21	d1p37a	Alignment	not modelled	12.2	21	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
22	c3b8cB	Alignment	not modelled	11.6	26	PDB header: hydrolase Chain: B: PDB Molecule: atpase 2, plasma membrane-type; PDBTitle: crystal structure of a plasma membrane proton pump
23	c1mhsA	Alignment	not modelled	11.5	15	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
24	c2y0mB	Alignment	not modelled	11.0	35	PDB header: transcription Chain: B: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and mof
25	c3rkgA	Alignment	not modelled	10.8	11	PDB header: metal transport Chain: A: PDB Molecule: magnesium transporter mrs2, mitochondrial; PDBTitle: structural and functional characterization of the yeast mg2+ channel2 mrs2
26	c2ka6B	Alignment	not modelled	10.4	41	PDB header: transcription regulator Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: nmr structure of the cbp-taz2/stat1-tad complex
27	d1hqz1	Alignment	not modelled	9.8	10	Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Cofilin-like
28	d1hh8a	Alignment	not modelled	9.7	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
29	d1oqya1	Alignment	not modelled	9.7	26	Fold: RuvA C-terminal domain-like Superfamily: UBA-like

					Family:UBA domain
30	c2ykqC_	Alignment	not modelled	9.5	13 PDB header: rna-binding protein Chain: C: PDB Molecule: line-1 orf1p; PDBTitle: structure of the human line-1 orf1p trimer
31	c3hdfA_	Alignment	not modelled	9.1	22 PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of truncated endolysin r21 from phage 21
32	c2anxB_	Alignment	not modelled	8.7	19 PDB header: hydrolase Chain: B: PDB Molecule: lysozyme; PDBTitle: crystal structure of bacteriophage p22 lysozyme mutant l87m
33	c1y4mC_	Alignment	not modelled	8.7	33 PDB header: membrane protein Chain: C: PDB Molecule: herv-frd_6p24.1 provirus ancestral env polyprotein; PDBTitle: crystal structure of human endogenous retrovirus herv-frd envelope2 protein (syncitin-2)
34	c2ko2A_	Alignment	not modelled	8.4	15 PDB header: membrane protein Chain: A: PDB Molecule: reticulon-4; PDBTitle: nogo66
35	d1xjta_	Alignment	not modelled	8.3	12 Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
36	c1mofA_	Alignment	not modelled	8.3	24 PDB header: viral protein Chain: A: PDB Molecule: moloney murine leukemia virus p15; PDBTitle: coat protein
37	c2l5gB_	Alignment	not modelled	8.0	18 PDB header: transcription regulator Chain: B: PDB Molecule: putative uncharacterized protein ncor2; PDBTitle: co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
38	c1lb1C_	Alignment	not modelled	7.9	13 PDB header: signaling protein Chain: C: PDB Molecule: guanine nucleotide exchange factor dbs; PDBTitle: crystal structure of the dbl and pleckstrin homology2 domains of dbs in complex with rhoa
39	d2a8ea1	Alignment	not modelled	7.4	20 Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: YktB-like
40	c2odmA_	Alignment	not modelled	7.4	15 PDB header: unknown function Chain: A: PDB Molecule: upf0358 protein mw0995; PDBTitle: crystal structure of s. aureus ylan, an essential leucine rich protein2 involved in the control of cell shape
41	d1zl8a1	Alignment	not modelled	7.3	16 Fold: L27 domain Superfamily: L27 domain Family: L27 domain
42	d2b8ea1	Alignment	not modelled	7.3	22 Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
43	d1ubea2	Alignment	not modelled	7.2	3 Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
44	c2l3aA_	Alignment	not modelled	7.2	33 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
45	d1mo6a2	Alignment	not modelled	7.2	5 Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
46	c1a3wB_	Alignment	not modelled	7.1	24 PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
47	d1xp8a2	Alignment	not modelled	6.9	18 Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
48	d189la_	Alignment	not modelled	6.8	21 Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
49	c3virA_	Alignment	not modelled	6.8	14 PDB header: recombination activator Chain: A: PDB Molecule: mating-type switching protein swi5; PDBTitle: crystal strcture of swi5 from fission yeast
50	c2q7cC_	Alignment	not modelled	6.8	25 PDB header: viral protein Chain: C: PDB Molecule: fusion protein between yeast variant gcn4 and PDBTitle: crystal structure of iqn17
51	c3t07D_	Alignment	not modelled	6.8	26 PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
52	c4exmB_	Alignment	not modelled	6.8	17 PDB header: toxin, hydrolase Chain: B: PDB Molecule: pesticin, lysozyme chimera; PDBTitle: the crystal structure of an engineered phage lysin containing the2 binding domain of pesticin and the killing domain of t4-lysozyme
53	c1d6uB_	Alignment	not modelled	6.6	47 PDB header: oxidoreductase Chain: B: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
54	d1y74a1	Alignment	not modelled	6.6	13 Fold: L27 domain Superfamily: L27 domain Family: L27 domain
55	c3uuxD_	Alignment	not modelled	6.4	15 PDB header: apoptosis Chain: D: PDB Molecule: mitochondrial division protein 1; PDBTitle: crystal structure of yeast fis1 in complex with mdv1

						fragment2 containing n-terminal extension and coiled coil domains
56	d1u94a2	Alignment	not modelled	6.3	10	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
57	d1udma_	Alignment	not modelled	6.3	21	Fold: Gelsolin-like Superfamily: Actin depolymerizing proteins Family: Cofilin-like
58	d1is1a_	Alignment	not modelled	6.2	13	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
59	d2j0111	Alignment	not modelled	6.1	44	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
60	d1vdra_	Alignment	not modelled	6.0	16	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: Dihydrofolate reductases
61	d191la_	Alignment	not modelled	5.9	21	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: Phage lysozyme
62	c2w9yA_	Alignment	not modelled	5.8	18	PDB header: lipid transport Chain: A: PDB Molecule: fatty acid/retinol binding protein protein 7, PDBTitle: the structure of the lipid binding protein ce-far-7 from2 caenorhabditis elegans
63	c3tnuB_	Alignment	not modelled	5.7	12	PDB header: cytosolic protein Chain: B: PDB Molecule: keratin, type ii cytoskeletal 5; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
64	c3b9bA_	Alignment	not modelled	5.6	15	PDB header: hydrolase Chain: A: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
65	c2la3A_	Alignment	not modelled	5.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
66	d1vega_	Alignment	not modelled	5.5	17	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
67	c1b89A_	Alignment	not modelled	5.5	20	PDB header: clathrin Chain: A: PDB Molecule: protein (clathrin heavy chain); PDBTitle: clathrin heavy chain proximal leg segment (bovine)
68	d1b89a_	Alignment	not modelled	5.5	20	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: Clathrin heavy chain proximal leg segment
69	c3mqzA_	Alignment	not modelled	5.5	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein duf1054; PDBTitle: crystal structure of conserved protein duf1054 from pink subaerial2 biofilm microbial leptospirillum sp. group ii uba.
70	c3ma8A_	Alignment	not modelled	5.3	24	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
71	d1ifya_	Alignment	not modelled	5.3	26	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
72	c4aj5M_	Alignment	not modelled	5.3	9	PDB header: cell cycle Chain: M: PDB Molecule: spindle and kinetochore-associated protein 2; PDBTitle: crystal structure of the ska core complex
73	c2ivfB_	Alignment	not modelled	5.2	20	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum