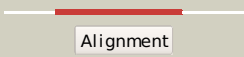

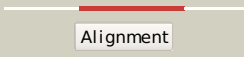

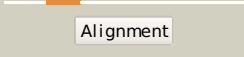



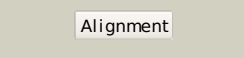

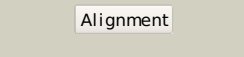

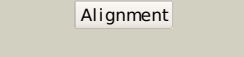

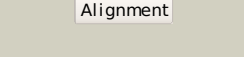
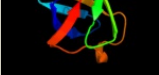
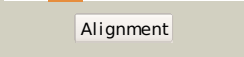

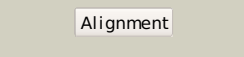
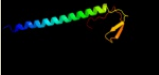
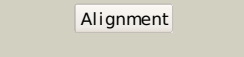

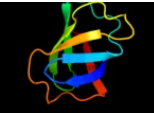
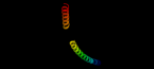





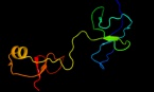



Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P16926
Date	Thu Jan 5 11:35:56 GMT 2012
Unique Job ID	d33cdbbe8354893e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j5uB_	 Alignment		100.0	28	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
2	c2qf4A_	 Alignment		100.0	23	PDB header: structural protein Chain: A: PDB Molecule: cell shape determining protein mrec; PDBTitle: high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
3	c2wvrB_	 Alignment		89.5	26	PDB header: replication Chain: B: PDB Molecule: geminin; PDBTitle: human cdt1:geminin complex
4	c2zxxA_	 Alignment		89.0	28	PDB header: cell cycle/replication Chain: A: PDB Molecule: geminin; PDBTitle: crystal structure of cdt1/geminin complex
5	c1t6fA_	 Alignment		86.3	31	PDB header: cell cycle Chain: A: PDB Molecule: geminin; PDBTitle: crystal structure of the coiled-coil dimerization motif of2 geminin
6	c3m9bK_	 Alignment		85.9	18	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
7	c1ci6B_	 Alignment		81.3	25	PDB header: transcription Chain: B: PDB Molecule: transcription factor c/ebp beta; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
8	d2jdia2	 Alignment		81.0	14	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
9	c1dipA_	 Alignment		80.7	24	PDB header: acetylation Chain: A: PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
10	d1fxkc_	 Alignment		80.6	11	Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
11	d1fx0a2	 Alignment		80.4	14	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase

12	d1skyb2	Alignment		77.3	20	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
13	c2xzaA_	Alignment		76.4	16	PDB header: cell adhesion Chain: A: PDB Molecule: immunoglobulin-binding protein eibd; PDBTitle: escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
14	c2jeeA_	Alignment		74.6	22	PDB header: cell cycle Chain: A: PDB Molecule: yiii; PDBTitle: xray structure of e. coli yiii
15	c2yy0D_	Alignment		71.1	32	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
16	d1maba2	Alignment		70.6	14	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
17	c2oqqB_	Alignment		70.1	28	PDB header: transcription Chain: B: PDB Molecule: transcription factor hy5; PDBTitle: crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
18	c1debA_	Alignment		69.8	33	PDB header: structural protein Chain: A: PDB Molecule: adenomatous polyposis coli protein; PDBTitle: crystal structure of the n-terminal coiled coil domain from2 apc
19	c3pv4A_	Alignment		67.0	15	PDB header: hydrolase Chain: A: PDB Molecule: degq; PDBTitle: structure of legionella fallonii degq (delta-pdz2 variant)
20	c3mudA_	Alignment		66.1	19	PDB header: contractile protein Chain: A: PDB Molecule: dna repair protein xrcc4, tropomyosin alpha-1 chain; PDBTitle: structure of the tropomyosin overlap complex from chicken smooth2 muscle
21	c1ce0B_	Alignment	not modelled	60.5	25	PDB header: hiv-1 envelope protein Chain: B: PDB Molecule: protein (leucine zipper model h38-p1); PDBTitle: trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
22	c1t2kD_	Alignment	not modelled	59.3	24	PDB header: transcription/dna Chain: D: PDB Molecule: cyclic-amp-dependent transcription factor atf-2; PDBTitle: structure of the dna binding domains of irf3, atf-2 and jun2 bound to dna
23	c2e43A_	Alignment	not modelled	58.4	19	PDB header: transcription/dna Chain: A: PDB Molecule: ccaat/enhancer-binding protein beta; PDBTitle: crystal structure of c/ebpbeta bzip homodimer k269a mutant2 bound to a high affinity dna fragment
24	c2wukD_	Alignment	not modelled	58.2	3	PDB header: cell cycle Chain: D: PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant
25	c3qh9A_	Alignment	not modelled	58.2	21	PDB header: structural protein Chain: A: PDB Molecule: liprin-beta-2; PDBTitle: human liprin-beta2 coiled-coil
26	c1fosE_	Alignment	not modelled	57.7	24	PDB header: transcription/dna Chain: E: PDB Molecule: p55-c-fos proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
27	c2w6aB_	Alignment	not modelled	57.3	30	PDB header: signaling protein Chain: B: PDB Molecule: arf gtpase-activating protein git1; PDBTitle: x-ray structure of the dimeric git1 coiled-coil domain
28	c2r9vA_	Alignment	not modelled	57.0	15	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
29	c3c2aA_	Alignment	not modelled	53.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein;

29	c2c2yA	Alignment	not modelled	55.8	14	PDBTitle: crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2 PDB header: protein transport Chain: A: PDB Molecule: trafficking protein particle complex subunit 4; PDBTitle: solution structure of the atypical pdz-like domain of2 synbindin
30	c2jsnA	Alignment	not modelled	53.6	25	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: RimM C-terminal domain-like
31	d2f1la1	Alignment	not modelled	52.5	22	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.
32	c1go4F	Alignment	not modelled	50.3	44	PDB header: cell cycle Chain: A: PDB Molecule: kinetochore protein hec1, kinetochore protein spc25; PDBTitle: crystal structure of a bonsai version of the human ndc802 complex
33	c2ve7A	Alignment	not modelled	50.2	21	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
34	d1f6ga	Alignment	not modelled	47.6	9	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
35	c1rb1B	Alignment	not modelled	45.6	26	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
36	c3k7zA	Alignment	not modelled	45.6	26	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
37	c3k7zB	Alignment	not modelled	45.6	26	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
38	c1rb1A	Alignment	not modelled	45.6	26	PDB header: dna binding protein Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
39	c1swiA	Alignment	not modelled	45.6	26	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
40	c1rb6C	Alignment	not modelled	45.6	26	Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
41	d1nppa2	Alignment	not modelled	45.6	21	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvt coiled-coil trimer with threonine at the a(16)2 position
42	d1uklc	Alignment	not modelled	44.5	21	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
43	c1ij2C	Alignment	not modelled	44.4	26	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvs1 coiled-coil trimer with serine at the a(16)2 position
44	d1nz9a	Alignment	not modelled	43.3	23	PDB header: transcription Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
45	c1ij3C	Alignment	not modelled	43.3	26	PDB header: dna-binding motif Chain: A: PDB Molecule: leucine zipper monomer; PDBTitle: the solution structure of a leucine-zipper motif peptide
46	c1ij3B	Alignment	not modelled	43.3	26	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvt coiled-coil trimer with threonine at the a(16)2 position
47	c2ywxA	Alignment	not modelled	42.8	13	PDB header: transcription regulator/dna Chain: B: PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
48	c1ztaA	Alignment	not modelled	42.2	26	PDB header: chaperone Chain: C: PDB Molecule: prefoldin subunit alpha; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
49	c1ij2B	Alignment	not modelled	42.2	26	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
50	c3a5tB	Alignment	not modelled	41.5	26	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
51	c2zdiC	Alignment	not modelled	41.3	18	PDB header: vimentin Chain: A: PDB Molecule: vimentin;
52	c2kvqG	Alignment	not modelled	40.9	23	
53	c2jvvA	Alignment	not modelled	40.9	23	
54	c1gk7A	Alignment	not modelled	40.6	17	

					PDBTitle: human vimentin coil 1a fragment (1a)
55	c2qe7C_	Alignment	not modelled	40.0	23 PDB header: hydrolase Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
56	c3q4fG_	Alignment	not modelled	39.5	17 PDB header: dna binding protein/protein binding Chain: G: PDB Molecule: dna repair protein xrcc4; PDBTitle: crystal structure of xrcc4/xf-cernunnos complex
57	c1ik9B_	Alignment	not modelled	39.5	16 PDB header: gene regulation/ligase Chain: B: PDB Molecule: dna repair protein xrcc4; PDBTitle: crystal structure of a xrcc4-dna ligase iv complex
58	c2o7hF_	Alignment	not modelled	38.1	23 PDB header: transcription Chain: F: PDB Molecule: general control protein gcn4; PDBTitle: crystal structure of trimeric coiled coil gcn4 leucine zipper
59	c1ci6A_	Alignment	not modelled	37.0	20 PDB header: transcription Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
60	d1am9a_	Alignment	not modelled	36.6	21 Fold: HLH-like Superfamily: HLH, helix-loop-helix DNA-binding domain Family: HLH, helix-loop-helix DNA-binding domain
61	c2nn6l_	Alignment	not modelled	35.5	16 PDB header: hydrolase/transferase Chain: I: PDB Molecule: 3'-5' exoribonuclease csl4 homolog; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
62	d1xi8a3	Alignment	not modelled	35.3	17 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
63	c1fosF_	Alignment	not modelled	35.1	14 PDB header: transcription/dna Chain: F: PDB Molecule: c-jun proto-oncogene protein; PDBTitle: two human c-fos:c-jun:dna complexes
64	c2gd7B_	Alignment	not modelled	34.6	29 PDB header: transcription Chain: B: PDB Molecule: hexim1 protein; PDBTitle: the structure of the cyclin t-binding domain of hexim12 reveals the molecular basis for regulation of3 transcription elongation
65	d2z1ca1	Alignment	not modelled	33.1	25 Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
66	c1w5kB_	Alignment	not modelled	32.0	35 PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle
67	c1w5kC_	Alignment	not modelled	32.0	35 PDB header: four helix bundle Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle
68	c1w5kD_	Alignment	not modelled	32.0	35 PDB header: four helix bundle Chain: D: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle
69	c1w5kA_	Alignment	not modelled	32.0	35 PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle
70	c1unxA_	Alignment	not modelled	31.0	29 PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
71	c2j66A_	Alignment	not modelled	31.0	20 PDB header: lyase Chain: A: PDB Molecule: btrk; PDBTitle: structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
72	c2w5eB_	Alignment	not modelled	30.6	19 PDB header: hydrolase Chain: B: PDB Molecule: putative serine protease; PDBTitle: structural and biochemical analysis of human pathogenic2 astrovirus serine protease at 2.0 angstrom resolution
73	c1p9iA_	Alignment	not modelled	30.4	23 PDB header: unknown function Chain: A: PDB Molecule: cortexillin i/gcn4 hybrid peptide; PDBTitle: coiled-coil x-ray structure at 1.17 a resolution
74	c3ipkA_	Alignment	not modelled	30.0	18 PDB header: cell adhesion Chain: A: PDB Molecule: agi/ii; PDBTitle: crystal structure of a3vp1 of agi/ii of streptococcus mutans
75	d2nn6i1	Alignment	not modelled	29.9	16 Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
76	c2je6l_	Alignment	not modelled	29.9	18 PDB header: hydrolase Chain: I: PDB Molecule: exosome complex rna-binding protein 1; PDBTitle: structure of a 9-subunit archaean exosome
77	c1gc1C_	Alignment	not modelled	29.6	29 PDB header: leucine zipper Chain: C: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
78	c1gc1B_	Alignment	not modelled	29.6	29 PDB header: leucine zipper Chain: B: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
79	c1gc1A_	Alignment	not modelled	29.6	29 PDB header: leucine zipper Chain: A: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
80	c3bboW_	Alignment	not modelled	29.5	25 PDB header: ribosome Chain: W: PDB Molecule: ribosomal protein l24; PDBTitle: homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
					PDB header: four helix bundle

81	c1w5jD_	Alignment	not modelled	29.3	35	Chain: D: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle
82	c1w5jA_	Alignment	not modelled	29.3	35	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle
83	c1w5jB_	Alignment	not modelled	29.3	35	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle
84	c1w5jC_	Alignment	not modelled	29.3	35	PDB header: four helix bundle Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: an anti-parallel four helix bundle
85	c2xv5A_	Alignment	not modelled	29.1	24	PDB header: structural protein Chain: A: PDB Molecule: lamin-a/c; PDBTitle: human lamin a coil 2b fragment
86	c2rjzA_	Alignment	not modelled	29.1	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pilo protein; PDBTitle: crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
87	c3e98B_	Alignment	not modelled	28.1	28	PDB header: unknown function Chain: B: PDB Molecule: gaf domain of unknown function; PDBTitle: crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
88	d1fx0b2	Alignment	not modelled	28.1	19	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
89	c1kmhA_	Alignment	not modelled	28.0	14	PDB header: hydrolase Chain: A: PDB Molecule: atpase alpha subunit; PDBTitle: crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
90	c3e0eA_	Alignment	not modelled	27.9	14	PDB header: replication Chain: A: PDB Molecule: replication protein a; PDBTitle: crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
91	c2dyiA_	Alignment	not modelled	27.7	32	PDB header: ribosome Chain: A: PDB Molecule: probable 16s rrna-processing protein rimm; PDBTitle: crystal structure of 16s ribosomal rna processing protein rimm from2 thermus thermophilus hb8
92	c1w5iA_	Alignment	not modelled	27.7	29	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: aba does not affect topology of pli.
93	c1uo2A_	Alignment	not modelled	27.7	29	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
94	c1uo1B_	Alignment	not modelled	27.7	29	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
95	c1unwB_	Alignment	not modelled	27.6	29	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
96	c2ccfA_	Alignment	not modelled	27.6	29	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel configuration of pli e20s
97	c1uo0A_	Alignment	not modelled	27.6	29	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
98	c1uo0B_	Alignment	not modelled	27.6	29	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
99	d1x87a_	Alignment	not modelled	27.5	50	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
100	c1unxB_	Alignment	not modelled	27.5	29	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
101	d1skye2	Alignment	not modelled	27.4	29	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
102	d1mabb2	Alignment	not modelled	27.3	24	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
103	c2w6fA_	Alignment	not modelled	27.2	15	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha heart isoform, PDBTitle: low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 2.
104	d2oa5a1	Alignment	not modelled	27.0	17	Fold: BLRF2-like Superfamily: BLRF2-like Family: BLRF2-like
105	d2jdjd2	Alignment	not modelled	26.9	24	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase

106	c1w5iB_	Alignment	not modelled	26.2	29	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: aba does not affect topology of pli.
107	c1uo2B_	Alignment	not modelled	26.2	29	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
108	d1uwka_	Alignment	not modelled	25.5	46	Fold: Urocanase Superfamily: Urocanase Family: Urocanase
109	c3trhl_	Alignment	not modelled	25.1	12	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
110	c3h9nA_	Alignment	not modelled	24.5	25	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome maturation factor rimm; PDBTitle: crystal structure of the ribosome maturation factor rimm2 (hi0203) from h.influenzae. northeast structural genomics3 consortium target ir66.
111	d1j2za_	Alignment	not modelled	24.5	9	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
112	c2f1lA_	Alignment	not modelled	23.6	18	PDB header: unknown function Chain: A: PDB Molecule: 16s rna processing protein; PDBTitle: crystal structure of a putative 16s ribosomal rna processing protein2 rimm (pa3744) from pseudomonas aeruginosa at 2.46 a resolution
113	c1gd2G_	Alignment	not modelled	23.4	23	PDB header: transcription/dna Chain: G: PDB Molecule: transcription factor pap1; PDBTitle: crystal structure of bzip transcription factor pap1 bound2 to dna
114	d2otma1	Alignment	not modelled	23.3	26	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
115	c3l31B_	Alignment	not modelled	23.3	38	PDB header: hydrolase Chain: B: PDB Molecule: probable manganese-dependent inorganic PDBTitle: crystal structure of the cbs and drtg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
116	c2vpmB_	Alignment	not modelled	23.2	25	PDB header: ligase Chain: B: PDB Molecule: trypanothione synthetase; PDBTitle: trypanothione synthetase
117	d1wzua1	Alignment	not modelled	22.9	19	Fold: NadA-like Superfamily: NadA-like Family: NadA-like
118	d1jjcb3	Alignment	not modelled	22.9	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Myf domain
119	c2p3eA_	Alignment	not modelled	22.9	25	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of aq1208 from aquifex aeolicus
120	d2jf2a1	Alignment	not modelled	22.8	0	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase