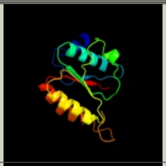
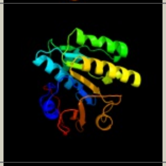
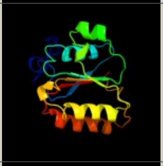
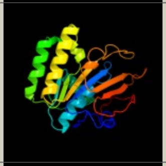
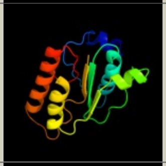
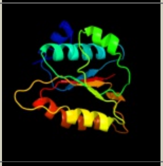
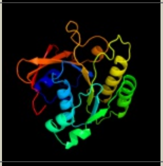
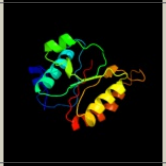
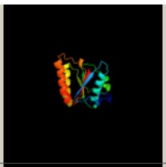
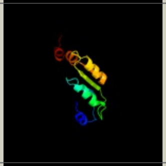
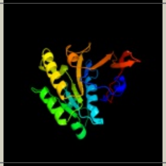
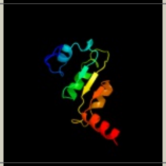
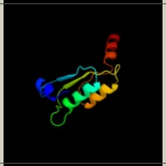
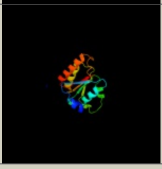
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P37657
Date	Thu Jan 5 11:56:30 GMT 2012
Unique Job ID	51df013406728e6c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ubea1	Alignment		95.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
2	d1mo6a1	Alignment		94.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
3	c1u9iA_	Alignment		94.0	7	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
4	d1xp8a1	Alignment		92.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
5	d1u94a1	Alignment		91.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
6	d1tf7a2	Alignment		88.7	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
7	d1n0wa_	Alignment		85.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
8	c2zroA_	Alignment		85.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
9	c2cvhB_	Alignment		84.3	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair and recombination protein radb; **PDBTitle:** crystal structure of the radb recombinase
10	c2recB_	Alignment		83.9	15	**PDB header:**helicase **PDB COMPND:**
11	c1xp8A_	Alignment		79.3	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"

12	c3hr8A_	Alignment		79.0	12	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
13	c3c85A_	Alignment		70.5	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative glutathione-regulated potassium-efflux system **PDBTitle:** crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
14	d1szpa2	Alignment		69.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
15	d7reqa2	Alignment		59.2	12	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
16	c2ztsB_	Alignment		57.4	11	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186; **PDBTitle:** crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
17	c2g1uA_	Alignment		53.3	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
18	d1tf7a1	Alignment		52.0	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
19	c3fwzA_	Alignment		45.9	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
20	c2q6tB_	Alignment		42.8	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
21	d1id1a_	Alignment	not modelled	40.8	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
22	d2i1qa2	Alignment	not modelled	35.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
23	d1fmfa_	Alignment	not modelled	34.1	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
24	c1szpC_	Alignment	not modelled	33.0	13	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** a crystal structure of the rad51 filament
25	d1b74a1	Alignment	not modelled	33.0	7	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
26	d3bula2	Alignment	not modelled	29.9	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
27	c3eywA_	Alignment	not modelled	28.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
28	c1y80A_	Alignment	not modelled	27.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein from2 moorella thermoacetica
						PDB header:unknown function

29	c2w0mA_	Alignment	not modelled	23.7	8	**Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
30	d1lssa_	Alignment	not modelled	22.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
31	c3mjsA_	Alignment	not modelled	22.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amphb; **PDBTitle:** structure of a-type ketoreductases from modular polyketide synthase
32	c3cq0B_	Alignment	not modelled	20.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative transaldolase ygr043c; **PDBTitle:** crystal structure of tal2_yeast
33	c2dflA_	Alignment	not modelled	19.1	15	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** crystal structure of left-handed rada filament
34	c3qatB_	Alignment	not modelled	19.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
35	c2zjbB_	Alignment	not modelled	18.3	13	**PDB header:**recombination **Chain:** B: **PDB Molecule:**meiotic recombination protein dmc1/lim15 homolog; **PDBTitle:** crystal structure of the human dmc1-m200v polymorphic2 variant
36	c2xoaA_	Alignment	not modelled	16.7	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of the n-terminal three domains of the2 skeletal muscle ryanodine receptor (ryr1)
37	d1skyb3	Alignment	not modelled	15.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
38	c3s93B_	Alignment	not modelled	15.4	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**tudor domain-containing protein 5; **PDBTitle:** crystal structure of conserved motif in tdrd5
39	d1oaia_	Alignment	not modelled	15.3	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
40	c3bh0A_	Alignment	not modelled	15.2	9	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
41	d1go5a_	Alignment	not modelled	15.1	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
42	c1yqtA_	Alignment	not modelled	14.8	10	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
43	d1ccwa_	Alignment	not modelled	14.3	12	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
44	c2vyeA_	Alignment	not modelled	13.5	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
45	c1yodB_	Alignment	not modelled	13.0	30	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**water-solublized phospholamban; **PDBTitle:** crystal structure of a water soluble analog of phospholamban
46	c2iy3A_	Alignment	not modelled	12.8	16	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
47	d3dhwc1	Alignment	not modelled	12.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
48	c3io5B_	Alignment	not modelled	12.4	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination and repair protein; **PDBTitle:** crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
49	c1yodA_	Alignment	not modelled	12.1	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**water-solublized phospholamban; **PDBTitle:** crystal structure of a water soluble analog of phospholamban
50	d3e9la1	Alignment	not modelled	12.0	50	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Prp8 beta-finger domain-like
51	d3e9oa1	Alignment	not modelled	11.9	31	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Prp8 beta-finger domain-like
52	c2yhsA_	Alignment	not modelled	11.5	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
53	d1t6sa1	Alignment	not modelled	11.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ScpB/YpuH-like
54	d2g1la1	Alignment	not modelled	10.7	25	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
55	c3e66B_	Alignment	not modelled	10.6	31	**PDB header:**splicing **Chain:** B: **PDB Molecule:**prp8;

						PDBTitle: crystal structure of the beta-finger domain of yeast prp8
56	c3f6cB_	Alignment	not modelled	10.4	9	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
57	c1vciA_	Alignment	not modelled	10.4	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar-binding transport atp-binding protein; **PDBTitle:** crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
58	c2j37W_	Alignment	not modelled	10.4	7	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
59	d1nlfa_	Alignment	not modelled	10.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
60	d2b4aa1	Alignment	not modelled	10.2	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c3dm5A_	Alignment	not modelled	10.2	14	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
62	d1oi7a1	Alignment	not modelled	10.1	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
63	c2it1B_	Alignment	not modelled	9.9	6	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin **PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii
64	c1oxtB_	Alignment	not modelled	9.8	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, atp binding protein; **PDBTitle:** crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
65	d2fy8a1	Alignment	not modelled	9.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
66	c3r1fO_	Alignment	not modelled	9.7	17	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
67	c2qy9A_	Alignment	not modelled	9.7	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
68	c1wr4A_	Alignment	not modelled	9.7	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-protein ligase nedd4-2; **PDBTitle:** solution structure of the second ww domain of nedd4-2
69	d1vpra1	Alignment	not modelled	9.7	38	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Dinoflagellate luciferase repeat
70	d1np7a2	Alignment	not modelled	9.7	13	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
71	c2d62A_	Alignment	not modelled	9.5	10	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**multiple sugar-binding transport atp-binding **PDBTitle:** crystal structure of multiple sugar binding transport atp-2 binding protein
72	c3pfmA_	Alignment	not modelled	9.4	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ggdef domain protein; **PDBTitle:** crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
73	d1v5wa_	Alignment	not modelled	9.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
74	c1xnlA_	Alignment	not modelled	9.2	42	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**membrane protein gp37; **PDBTitle:** aslv fusion peptide
75	c3t8yA_	Alignment	not modelled	9.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
76	c3eulB_	Alignment	not modelled	9.1	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**possible nitrate/nitrite response transcriptional **PDBTitle:** structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
77	d1jbea_	Alignment	not modelled	9.0	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
78	c3ldaA_	Alignment	not modelled	9.0	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
79	c2jp7A_	Alignment	not modelled	8.9	10	**PDB header:**translation **Chain:** A: **PDB Molecule:**mrna export factor mex67; **PDBTitle:** nmr structure of the mex67 uba domain
						PDB header:hydrolase **Chain:** D: **PDB Molecule:**exodeoxyribonuclease vii small subunit;

80	c1vp7D_	Alignment	not modelled	8.8	21	**PDBTitle:** crystal structure of exodeoxyribonuclease vii small subunit2 (np_881400.1) from bordetella pertussis at 2.40 a resolution
81	d1owla2	Alignment	not modelled	8.5	20	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
82	c1m7lA_	Alignment	not modelled	8.4	27	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d
83	c2r8rB_	Alignment	not modelled	8.2	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
84	c1t4gA_	Alignment	not modelled	8.2	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** atpase in complex with amp-pnp
85	d1fx0a3	Alignment	not modelled	8.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
86	c3hv9A_	Alignment	not modelled	8.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx eal domain from pseudomonas aeruginosa
87	c3pihA_	Alignment	not modelled	8.0	20	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
88	c2knjA_	Alignment	not modelled	7.9	33	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**microplusin preprotein; **PDBTitle:** nmr structure of microplusin a antimicrobial peptide from2 rhipicephalus (boophilus) microplus
89	c1y7pB_	Alignment	not modelled	7.8	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
90	c2lf3A_	Alignment	not modelled	7.8	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**effector protein hopab3; **PDBTitle:** solution nmr structure of hoppmal_281_385 from pseudomonas syringae2 pv. maculicola str. es4326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
91	c1skyE_	Alignment	not modelled	7.7	17	**PDB header:**atp synthase **Chain:** E: **PDB Molecule:**f1-atpase; **PDBTitle:** crystal structure of the nucleotide free alpha3beta3 sub-complex of2 f1-atpase from the thermophilic bacillus ps3
92	c1qzwC_	Alignment	not modelled	7.7	13	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
93	d1a8oa_	Alignment	not modelled	7.6	18	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
94	c2nq2C_	Alignment	not modelled	7.5	10	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**hypothetical abc transporter atp-binding protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
95	d1p6qa_	Alignment	not modelled	7.5	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	d1qrjb1	Alignment	not modelled	7.3	22	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**Retrovirus capsid protein C-terminal domain
97	d1tu1a_	Alignment	not modelled	7.2	18	**Fold:**Mog1p/PsbP-like **Superfamily:**Mog1p/PsbP-like **Family:**PA0094-like
98	d2veaa2	Alignment	not modelled	7.2	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**Phytochrome-specific domain
99	c3d31B_	Alignment	not modelled	7.2	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sulfate/molybdate abc transporter, atp-binding **PDBTitle:** modbc from methanosarcina acetivorans