





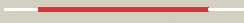
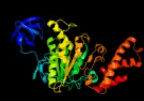




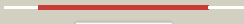



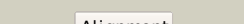







#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dpyA_	 Alignment		100.0	95	PDB header: hydrolase Chain: A: PDB Molecule: flagellum-specific atp synthase; PDBTitle: crystal structure of the flagellar type iii atpase flII
2	c2r9vA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of atp synthase subunit alpha (tm1612) from <i>Thermotoga maritima</i> at 2.10 Å resolution
3	c1fx0B_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase beta chain; PDBTitle: crystal structure of the chloroplast f1-atpase from spinach
4	c3a5dM_	 Alignment		100.0	28	PDB header: hydrolase Chain: M: PDB Molecule: v-type atp synthase beta chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
5	c2qe7C_	 Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium <i>Bacillus sp. ta2.a1</i>
6	c2w6jD_	 Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: atp synthase subunit beta, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
7	c2w6fA_	 Alignment		100.0	23	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.
8	c2jizD_	 Alignment		100.0	25	PDB header: hydrolase Chain: D: PDB Molecule: atp synthase subunit beta; PDBTitle: the structure of f1-atpase inhibited by resveratrol.
9	c1skyE_	 Alignment		100.0	26	PDB header: atp synthase Chain: E: PDB Molecule: f1-atpase; PDBTitle: crystal structure of the nucleotide free alpha3beta3 sub-complex of f1-atpase from the thermophilic <i>Bacillus ps3</i>
10	c3oaaC_	 Alignment		100.0	22	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
11	c1w0jB_	 Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase alpha chain heart isoform, PDBTitle: beryllium fluoride inhibited bovine f1-atpase

12	c1kmhA_	Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: atpase alpha subunit; PDBTitle: crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
13	c3a5dB_	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: v-type atp synthase alpha chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
14	c2c61A_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: a-type atp synthase non-catalytic subunit b; PDBTitle: crystal structure of the non-catalytic b subunit of a-type2 atpase from m. maei go1
15	c2ob1A_	Alignment		100.0	45	PDB header: hydrolase Chain: A: PDB Molecule: escn; PDBTitle: structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria
16	c1vdzA_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: a-type atpase subunit a; PDBTitle: crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
17	d2jdia3	Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
18	d1skyb3	Alignment		100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
19	d1fx0a3	Alignment		100.0	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
20	d2jdid3	Alignment		100.0	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
21	d1skye3	Alignment	not modelled	100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
22	d1fx0b3	Alignment	not modelled	100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
23	c3l0oB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
24	c1xpuB_	Alignment	not modelled	100.0	20	PDB header: transcription/rna Chain: B: PDB Molecule: rho transcription termination factor; PDBTitle: structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
25	d1xpua3	Alignment	not modelled	100.0	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
26	d2jdid1	Alignment	not modelled	99.0	13	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
27	d1skye1	Alignment	not modelled	99.0	17	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
						Fold: Left-handed superhelix

28	d1fx0b1	Alignment	not modelled	98.9	17	Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
29	c1u9iA_	Alignment	not modelled	98.6	14	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
30	d1tf7a2	Alignment	not modelled	98.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
31	d1tf7a1	Alignment	not modelled	98.3	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
32	d1fx0a1	Alignment	not modelled	98.3	13	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
33	d1skyb2	Alignment	not modelled	98.3	16	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
34	d2jdia2	Alignment	not modelled	98.3	10	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
35	d2jdia1	Alignment	not modelled	98.2	14	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
36	d1fx0a2	Alignment	not modelled	98.2	15	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
37	d1skyb1	Alignment	not modelled	98.1	10	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
38	d2i1qa2	Alignment	not modelled	98.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
39	d1mo6a1	Alignment	not modelled	97.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
40	d1xp8a1	Alignment	not modelled	97.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
41	c2recB_	Alignment	not modelled	97.9	18	PDB header: helicase PDB COMPND:
42	c2dr3A_	Alignment	not modelled	97.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0273 protein ph0284; PDBTitle: crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
43	d2f43a1	Alignment	not modelled	97.9	14	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
44	d1n0wa_	Alignment	not modelled	97.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
45	d1maba2	Alignment	not modelled	97.8	11	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
46	c3ldaA_	Alignment	not modelled	97.8	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
47	c3hr8A_	Alignment	not modelled	97.8	17	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
48	d1v5wa_	Alignment	not modelled	97.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
49	c2w0mA_	Alignment	not modelled	97.8	16	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus2 p2
50	c2zroA_	Alignment	not modelled	97.8	22	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
51	d1ubea1	Alignment	not modelled	97.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)

52	c2ztsB	Alignment	not modelled	97.7	17	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
53	c2dflA	Alignment	not modelled	97.7	17	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
54	c1t4gA	Alignment	not modelled	97.7	19	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
55	d1pzna2	Alignment	not modelled	97.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
56	d1szpa2	Alignment	not modelled	97.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
57	c1pznG	Alignment	not modelled	97.6	19	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
58	c1xp8A	Alignment	not modelled	97.5	16	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: "deinococcus radiodurans reca in complex with atp-gamma-s"
59	c2cvhB	Alignment	not modelled	97.5	16	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase
60	c2zjbB	Alignment	not modelled	97.5	13	PDB header: recombination Chain: B: PDB Molecule: meiotic recombination protein dmc1/lim15 homolog; PDBTitle: crystal structure of the human dmc1-m200v polymorphic2 variant
61	c1szpC	Alignment	not modelled	97.5	21	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
62	d1skye2	Alignment	not modelled	97.5	15	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
63	d1fx0b2	Alignment	not modelled	97.4	17	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
64	d2jdid2	Alignment	not modelled	97.3	18	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
65	d1u94a1	Alignment	not modelled	97.3	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
66	d1mabb2	Alignment	not modelled	97.2	16	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
67	c3io5B	Alignment	not modelled	97.2	21	PDB header: dna binding protein Chain: B: PDB Molecule: recombination and repair protein; PDBTitle: crystal structure of a dimeric form of the uvx recombinase core2 domain from enterobacteria phage t4
68	c3bh0A	Alignment	not modelled	97.1	13	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
69	d1cr2a	Alignment	not modelled	96.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
70	c2vyeA	Alignment	not modelled	96.9	13	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
71	c3pvsA	Alignment	not modelled	96.7	27	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
72	c2q6tB	Alignment	not modelled	96.6	20	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
73	c3bs4A	Alignment	not modelled	96.6	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ph0321; PDBTitle: crystal structure of uncharacterized protein ph0321 from pyrococcus2 horikoshii in complex with an unknown peptide
74	c2a5yB	Alignment	not modelled	96.0	17	PDB header: apoptosis Chain: B: PDB Molecule: ced-4; PDBTitle: structure of a ced-4/ced-9 complex
75	c2zamA	Alignment	not modelled	96.0	19	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
76	c2w0cB	Alignment	not modelled	95.9	15	PDB header: transferase Chain: B: PDB Molecule: thymidylate kinase;

76	c2wv5B	Alignment	not modelled	95.9	19	PDBTitle: crystal structure of vaccinia virus thymidylate kinase2 bound to brivudin-5'-monophosphate
77	c1yqtA	Alignment	not modelled	95.9	30	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: rnase-l inhibitor
78	c1zu4A	Alignment	not modelled	95.9	15	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
79	c2og2A	Alignment	not modelled	95.8	17	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
80	c3bgwD	Alignment	not modelled	95.7	15	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
81	c3p1jC	Alignment	not modelled	95.7	16	PDB header: hydrolase Chain: C: PDB Molecule: gtpase imap family member 2; PDBTitle: crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
82	c2j7pA	Alignment	not modelled	95.7	13	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
83	c3pfiB	Alignment	not modelled	95.7	19	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
84	d2awna2	Alignment	not modelled	95.7	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
85	c3geiB	Alignment	not modelled	95.6	26	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
86	d2qy9a2	Alignment	not modelled	95.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c3cmvG	Alignment	not modelled	95.5	15	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
88	c3b9qA	Alignment	not modelled	95.5	17	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
89	c3iytG	Alignment	not modelled	95.5	18	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
90	c3d8bB	Alignment	not modelled	95.4	15	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
91	c2x8aA	Alignment	not modelled	95.4	20	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
92	c3dmdA	Alignment	not modelled	95.4	18	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
93	c2vb6A	Alignment	not modelled	95.4	19	PDB header: motor protein Chain: A: PDB Molecule: myosin vi; PDBTitle: myosin vi (md-insert2-cam, delta insert1) post-rigor state (2 crystal form 2)
94	d1l7vc	Alignment	not modelled	95.3	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
95	c2yyzA	Alignment	not modelled	95.3	24	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
96	c3u5zM	Alignment	not modelled	95.3	15	PDB header: dna binding protein/dna Chain: M: PDB Molecule: dna polymerase accessory protein 44; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
97	d1qvra2	Alignment	not modelled	95.3	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
98	c3p1jB	Alignment	not modelled	95.3	14	PDB header: hydrolase Chain: B: PDB Molecule: gtpase imap family member 2; PDBTitle: crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
99	c1xwiA	Alignment	not modelled	95.3	21	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
100	c1z6tC	Alignment	not modelled	95.3	16	PDB header: apoptosis Chain: C: PDB Molecule: apoptotic protease activating factor 1; PDBTitle: structure of the apoptotic protease-activating factor 12 bound to adp

101	d1ye8a1	Alignment	not modelled	95.3	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
102	c1z47B_	Alignment	not modelled	95.2	30	PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
103	c2pjzA_	Alignment	not modelled	95.2	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st1066; PDBTitle: the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066
104	c3bosA_	Alignment	not modelled	95.2	8	PDB header: hydrolase regulator,dna binding protein Chain: A: PDB Molecule: putative dna replication factor; PDBTitle: crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
105	c2d62A_	Alignment	not modelled	95.2	21	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
106	c1oxtB_	Alignment	not modelled	95.2	24	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
107	d1okkd2	Alignment	not modelled	95.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
108	d1tmka_	Alignment	not modelled	95.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
109	d1vmaa2	Alignment	not modelled	95.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
110	c2ce7B_	Alignment	not modelled	95.1	14	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
111	d1zpa1	Alignment	not modelled	95.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like
112	d2ak3a1	Alignment	not modelled	95.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
113	c2v1uA_	Alignment	not modelled	95.1	17	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
114	c2ihyB_	Alignment	not modelled	95.1	29	PDB header: hydrolase Chain: B: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter
115	d1jj7a_	Alignment	not modelled	95.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
116	c2iw3B_	Alignment	not modelled	95.0	30	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
117	c3b9pA_	Alignment	not modelled	95.0	19	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
118	d2pmka1	Alignment	not modelled	95.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
119	d1nlfa_	Alignment	not modelled	95.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
120	c2j41A_	Alignment	not modelled	95.0	21	PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase