



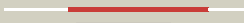


















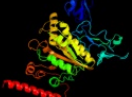









#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1xpuB_</a>	 Alignment		100.0	100	<b>PDB header:</b> transcription/rna <b>Chain:</b> B: <b>PDB Molecule:</b> rho transcription termination factor; <b>PDBTitle:</b> structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
2	<a href="#">c3l0oB_</a>	 Alignment		100.0	58	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transcription termination factor rho; <b>PDBTitle:</b> structure of rna-free rho transcription termination factor from2 thermotoga maritima
3	<a href="#">d1xpua3</a>	 Alignment		100.0	100	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
4	<a href="#">c1skyE_</a>	 Alignment		100.0	18	<b>PDB header:</b> atp synthase <b>Chain:</b> E: <b>PDB Molecule:</b> f1-atpase; <b>PDBTitle:</b> crystal structure of the nucleotide free alpha3beta3 sub-complex of f1-atpase from the thermophilic bacillus ps3
5	<a href="#">c2dpyA_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagellum-specific atp synthase; <b>PDBTitle:</b> crystal structure of the flagellar type iii atpase flII
6	<a href="#">c2jizD_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit beta; <b>PDBTitle:</b> the structure of f1-atpase inhibited by resveratrol.
7	<a href="#">c2w6jD_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit beta, mitochondrial; <b>PDBTitle:</b> low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
8	<a href="#">c1fx0B_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase beta chain; <b>PDBTitle:</b> crystal structure of the chloroplast f1-atpase from spinach
9	<a href="#">c2r9vA_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
10	<a href="#">c2w6fA_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha heart isoform, <b>PDBTitle:</b> low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 2.
11	<a href="#">c2qe7C_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1

12	<a href="#">c2oblA_</a>	Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> escn; <b>PDBTitle:</b> structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria
13	<a href="#">c3a5dB_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> v-type atp synthase alpha chain; <b>PDBTitle:</b> inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
14	<a href="#">c1w0jB_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase alpha chain heart isoform, <b>PDBTitle:</b> beryllium fluoride inhibited bovine f1-atpase
15	<a href="#">c1kmhA_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atpase alpha subunit; <b>PDBTitle:</b> crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
16	<a href="#">c3oaaC_</a>	Alignment		100.0	17	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> structure of the e.coli f1-atp synthase inhibited by subunit epsilon
17	<a href="#">c3a5dM_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> v-type atp synthase beta chain; <b>PDBTitle:</b> inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
18	<a href="#">c2c61A_</a>	Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> a-type atp synthase non-catalytic subunit b; <b>PDBTitle:</b> crystal structure of the non-catalytic b subunit of a-type2 atpase from m. maezi go1
19	<a href="#">d2jdia3</a>	Alignment		100.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
20	<a href="#">d1skyb3</a>	Alignment		100.0	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
21	<a href="#">d2jdid3</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
22	<a href="#">d1fx0a3</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
23	<a href="#">d1fx0b3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
24	<a href="#">c1vdzA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> a-type atpase subunit a; <b>PDBTitle:</b> crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
25	<a href="#">d1skye3</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
26	<a href="#">c2a8vA_</a>	Alignment	not modelled	100.0	100	<b>PDB header:</b> protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> rna binding domain of rho transcription <b>PDBTitle:</b> rho transcription termination factor/rna complex
27	<a href="#">d1a62a2</a>	Alignment	not modelled	99.9	100	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
28	<a href="#">d1tf7a2</a>	Alignment	not modelled	98.8	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain) <b>PDB header:</b> circadian clock protein

29	<a href="#">c1u9iA_</a>	Alignment	not modelled	98.8	12	<b>Chain:</b> A: <b>PDB Molecule:</b> kaic; <b>PDBTitle:</b> crystal structure of circadian clock protein kaic with phosphorylation2 sites
30	<a href="#">d1tf7a1</a>	Alignment	not modelled	98.3	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
31	<a href="#">c2recB_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
32	<a href="#">d1mo6a1</a>	Alignment	not modelled	98.2	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
33	<a href="#">c2ztsB_</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ph0186; <b>PDBTitle:</b> crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
34	<a href="#">c2zroA_</a>	Alignment	not modelled	98.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
35	<a href="#">c3hr8A_</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
36	<a href="#">d1xp8a1</a>	Alignment	not modelled	98.1	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
37	<a href="#">c2w0mA_</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfolobus solfataricus2 p2
38	<a href="#">d1ubea1</a>	Alignment	not modelled	98.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
39	<a href="#">d1n0wa_</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
40	<a href="#">d2i1qa2</a>	Alignment	not modelled	97.9	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
41	<a href="#">c1xp8A_</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> reca protein; <b>PDBTitle:</b> "deinococcus radiodurans reca in complex with atp-gamma-s"
42	<a href="#">d1u94a1</a>	Alignment	not modelled	97.8	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
43	<a href="#">c2df1A_</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rada; <b>PDBTitle:</b> crystal structure of left-handed rada filament
44	<a href="#">d1v5wa_</a>	Alignment	not modelled	97.8	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
45	<a href="#">c3ldaA_</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> yeast rad51 h352y filament interface mutant
46	<a href="#">d1pzna2</a>	Alignment	not modelled	97.7	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
47	<a href="#">c3io5B_</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination and repair protein; <b>PDBTitle:</b> crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
48	<a href="#">c1t4ga_</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rada; <b>PDBTitle:</b> atpase in complex with amp-pnp
49	<a href="#">c1szpC_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> a crystal structure of the rad51 filament
50	<a href="#">c2zjbB_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> meiotic recombination protein dmc1/lim15 homolog; <b>PDBTitle:</b> crystal structure of the human dmc1-m200v polymorphic2 variant
51	<a href="#">d1szpa2</a>	Alignment	not modelled	97.5	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
52	<a href="#">c1pznG_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
53	<a href="#">c2cvhB_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair and recombination protein radb; <b>PDBTitle:</b> crystal structure of the radb recombinase
54	<a href="#">c2vyeA_</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnac-ssdna complex
						<b>PDB header:</b> dna binding protein

55	<a href="#">c2z4rB_</a>	Alignment	not modelled	97.5	25	<b>Chain:</b> B: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
56	<a href="#">c3bh0A_</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p
57	<a href="#">d1cr2a_</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
58	<a href="#">c2q6tB_</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dnab replication fork helicase; <b>PDBTitle:</b> crystal structure of the thermus aquaticus dnab monomer
59	<a href="#">c3dmdA_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle receptor; <b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
60	<a href="#">c2dr3A_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0273 protein ph0284; <b>PDBTitle:</b> crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
61	<a href="#">c3pvsA_</a>	Alignment	not modelled	97.3	27	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> replication-associated recombination protein a; <b>PDBTitle:</b> structure and biochemical activities of escherichia coli mgsa
62	<a href="#">c3bs4A_</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ph0321; <b>PDBTitle:</b> crystal structure of uncharacterized protein ph0321 from pyrococcus2 horikoshii in complex with an unknown peptide
63	<a href="#">d1a62a1</a>	Alignment	not modelled	97.2	94	<b>Fold:</b> LEM/SAP HeH motif <b>Superfamily:</b> Rho N-terminal domain-like <b>Family:</b> Rho termination factor, N-terminal domain
64	<a href="#">c2qbyA_</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> replication/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog 1; <b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
65	<a href="#">c3b9qA_</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpftsy from arabidopsis thaliana
66	<a href="#">c2og2A_</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
67	<a href="#">c3cmvG_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
68	<a href="#">c2j7pA_</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
69	<a href="#">c2cnwF_</a>	Alignment	not modelled	97.1	11	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsy
70	<a href="#">d1vmaa2</a>	Alignment	not modelled	97.1	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
71	<a href="#">d1nlfa_</a>	Alignment	not modelled	97.1	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
72	<a href="#">c1fnnb_</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6; <b>PDBTitle:</b> crystal structure of cdc6p from pyrobaculum aerophilum
73	<a href="#">d1ye8a1</a>	Alignment	not modelled	97.0	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
74	<a href="#">d1w5sa2</a>	Alignment	not modelled	97.0	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
75	<a href="#">c1vmaA_</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
76	<a href="#">d1okkd2</a>	Alignment	not modelled	96.9	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
77	<a href="#">d1fnaa2</a>	Alignment	not modelled	96.9	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
78	<a href="#">d1qvra2</a>	Alignment	not modelled	96.8	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
79	<a href="#">c2gksB_</a>	Alignment	not modelled	96.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional sat/aps kinase; <b>PDBTitle:</b> crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

80	<a href="#">d1lw7a2</a>	Alignment	not modelled	96.8	14	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
81	<a href="#">d1qzxa3</a>	Alignment	not modelled	96.8	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
82	<a href="#">d2i3ba1</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
83	<a href="#">c1zu4A</a>	Alignment	not modelled	96.8	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsyt; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
84	<a href="#">c2v1uA</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog; <b>PDBTitle:</b> structure of the aeropyrum pernix orc1 protein in complex2 with dna
85	<a href="#">c3bosA</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> hydrolase regulator,dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna replication factor; <b>PDBTitle:</b> crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
86	<a href="#">c2w58B</a>	Alignment	not modelled	96.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> primosome component (helicase loader); <b>PDBTitle:</b> crystal structure of the dnaI
87	<a href="#">d1x6va3</a>	Alignment	not modelled	96.7	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Adenosine-5'phosphosulfate kinase (APS kinase)
88	<a href="#">d1ls1a2</a>	Alignment	not modelled	96.7	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
89	<a href="#">d2qy9a2</a>	Alignment	not modelled	96.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
90	<a href="#">c2j37W</a>	Alignment	not modelled	96.7	13	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
91	<a href="#">d1d2na</a>	Alignment	not modelled	96.6	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
92	<a href="#">c2hcbC</a>	Alignment	not modelled	96.6	22	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of amppcp-bound dnaa from aquifex aeolicus
93	<a href="#">d1np6a</a>	Alignment	not modelled	96.6	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
94	<a href="#">c3b85A</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate starvation-inducible protein; <b>PDBTitle:</b> crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
95	<a href="#">c1nsfA</a>	Alignment	not modelled	96.6	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide sensitive factor; <b>PDBTitle:</b> d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
96	<a href="#">c1yqtA</a>	Alignment	not modelled	96.6	23	<b>PDB header:</b> hydrolase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase l inhibitor; <b>PDBTitle:</b> rnase-l inhibitor
97	<a href="#">c3d8bB</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of human fidgetin-like protein 1 in complex with adp
98	<a href="#">c3bgwD</a>	Alignment	not modelled	96.5	25	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> the structure of a dnab-like replicative helicase and its interactions2 with primase
99	<a href="#">c3ec2A</a>	Alignment	not modelled	96.5	21	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna replication protein dnac; <b>PDBTitle:</b> crystal structure of the dnac helicase loader
100	<a href="#">d2ak3a1</a>	Alignment	not modelled	96.5	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
101	<a href="#">c3pfiB</a>	Alignment	not modelled	96.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 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
102	<a href="#">c2iy3A</a>	Alignment	not modelled	96.5	17	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein ffh; <b>PDBTitle:</b> structure of the e. coli signal recognition particle2 bound to a translating ribosome
103	<a href="#">c2a5yB</a>	Alignment	not modelled	96.5	8	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> ced-4; <b>PDBTitle:</b> structure of a ced-4/ced-9 complex
104	<a href="#">c2chvE</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> dna-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c adpnp complex
						<b>PDB header:</b> hydrolase



105	<a href="#">c2qz4A_</a>	Alignment	not modelled	96.4	19	<b>Chain:</b> A: <b>PDB Molecule:</b> paraplegin; <b>PDBTitle:</b> human paraplegin, aaa domain in complex with adp
106	<a href="#">c3iytG_</a>	Alignment	not modelled	96.4	10	<b>PDB header:</b> apoptosis <b>Chain:</b> G: <b>PDB Molecule:</b> apoptotic protease-activating factor 1; <b>PDBTitle:</b> structure of an apoptosome-procaspase-9 card complex
107	<a href="#">c3te6A_</a>	Alignment	not modelled	96.4	11	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sir3; <b>PDBTitle:</b> crystal structure of the s. cerevisiae sir3 aaa+ domain
108	<a href="#">d1l8qa2</a>	Alignment	not modelled	96.4	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
109	<a href="#">d1ki9a_</a>	Alignment	not modelled	96.4	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
110	<a href="#">c2iutA_</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> p. aeruginosa ftsk motor domain, dimeric
111	<a href="#">c2wjyA_</a>	Alignment	not modelled	96.4	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of nonsense transcripts 1; <b>PDBTitle:</b> crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
112	<a href="#">c1lw7A_</a>	Alignment	not modelled	96.3	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator nadr; <b>PDBTitle:</b> nadr protein from haemophilus influenzae
113	<a href="#">d2qm8a1</a>	Alignment	not modelled	96.3	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
114	<a href="#">d2awna2</a>	Alignment	not modelled	96.3	37	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
115	<a href="#">c1z6tC_</a>	Alignment	not modelled	96.3	9	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> apoptotic protease activating factor 1; <b>PDBTitle:</b> structure of the apoptotic protease-activating factor 12 bound to adp
116	<a href="#">c2yhsA_</a>	Alignment	not modelled	96.3	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy
117	<a href="#">d1tmka_</a>	Alignment	not modelled	96.3	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
118	<a href="#">c2iusB_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> e. coli ftsk motor domain
119	<a href="#">c2c9oC_</a>	Alignment	not modelled	96.2	38	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1
120	<a href="#">c3dm5A_</a>	Alignment	not modelled	96.2	18	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaean pyrococcus furiosus.