



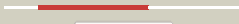


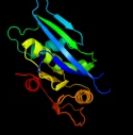


























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3m6aC_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent protease la 1; <b>PDBTitle:</b> crystal structure of bacillus subtilis lon c-terminal domain
2	<a href="#">c3k1jA_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent protease lon; <b>PDBTitle:</b> crystal structure of lon protease from thermococcus onnurineus na1
3	<a href="#">c2zroA_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
4	<a href="#">d1xhka_</a>	 Alignment		100.0	24	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> ATP-dependent protease Lon (La), catalytic domain
5	<a href="#">c1z0eF_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> putative protease la homolog type; <b>PDBTitle:</b> crystal structure of a. fulgidus lon proteolytic domain
6	<a href="#">c2x36F_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> lon protease homolog, mitochondrial; <b>PDBTitle:</b> structure of the proteolytic domain of the human2 mitochondrial lon protease
7	<a href="#">c2recB_</a>	 Alignment		100.0	20	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
8	<a href="#">d1rrea_</a>	 Alignment		99.9	23	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> ATP-dependent protease Lon (La), catalytic domain
9	<a href="#">d1mo6a1</a>	 Alignment		99.9	23	<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)
10	<a href="#">d1xp8a1</a>	 Alignment		99.9	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)
11	<a href="#">c2cvhB_</a>	 Alignment		99.9	23	<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

12	<a href="#">c3ldaA_</a>	Alignment		99.9	25	<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
13	<a href="#">dlu94a1</a>	Alignment		99.9	23	<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)
14	<a href="#">d1tf7a1</a>	Alignment		99.9	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)
15	<a href="#">c1xp8A_</a>	Alignment		99.9	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"
16	<a href="#">d1tf7a2</a>	Alignment		99.9	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)
17	<a href="#">c2q6tB_</a>	Alignment		99.9	22	<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
18	<a href="#">d1n0wa_</a>	Alignment		99.9	24	<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)
19	<a href="#">d2ilqa2</a>	Alignment		99.9	23	<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="#">d1szpa2</a>	Alignment		99.9	25	<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="#">d1ubea1</a>	Alignment	not modelled	99.9	24	<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="#">d1v5wa_</a>	Alignment	not modelled	99.9	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)
23	<a href="#">c3bgwD_</a>	Alignment	not modelled	99.9	19	<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
24	<a href="#">c1szpC_</a>	Alignment	not modelled	99.9	26	<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
25	<a href="#">c2zjbB_</a>	Alignment	not modelled	99.9	21	<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
26	<a href="#">c2ztsB_</a>	Alignment	not modelled	99.9	21	<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
27	<a href="#">c2dflA_</a>	Alignment	not modelled	99.9	26	<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
28	<a href="#">c3bh0A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p

29	<a href="#">c1t4gA_</a>	Alignment	not modelled	99.9	25	<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
30	<a href="#">d1nlfa_</a>	Alignment	not modelled	99.9	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)
31	<a href="#">c3hr8A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
32	<a href="#">c1u9iA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> circadian clock protein <b>Chain:</b> A: <b>PDB Molecule:</b> kaic; <b>PDBTitle:</b> crystal structure of circadian clock protein kaic with phosphorylation2 sites
33	<a href="#">d1pzna2</a>	Alignment	not modelled	99.9	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)
34	<a href="#">c2w0mA_</a>	Alignment	not modelled	99.9	24	<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
35	<a href="#">c2vyeA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dna-ssdna complex
36	<a href="#">c1pznG_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
37	<a href="#">c1q57G_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> dna primase/helicase; <b>PDBTitle:</b> the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
38	<a href="#">c2dr3A_</a>	Alignment	not modelled	99.8	26	<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
39	<a href="#">c3io5B_</a>	Alignment	not modelled	99.8	13	<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
40	<a href="#">c3cmvG_</a>	Alignment	not modelled	99.8	23	<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
41	<a href="#">d1cr2a_</a>	Alignment	not modelled	99.8	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)
42	<a href="#">c3bs4A_</a>	Alignment	not modelled	99.8	15	<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
43	<a href="#">c3cmwA_</a>	Alignment		99.6	22	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
44	<a href="#">c3cmuA_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> recombination/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
45	<a href="#">c1xwiA_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
46	<a href="#">c2cnwF_</a>	Alignment	not modelled	98.3	16	<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
47	<a href="#">c2j7pA_</a>	Alignment	not modelled	98.3	20	<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
48	<a href="#">c3dhwC_</a>	Alignment	not modelled	98.2	26	<b>PDB header:</b> membrane protein/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> methionine import atp-binding protein metn; <b>PDBTitle:</b> crystal structure of methionine importer metni
49	<a href="#">c3cf1C_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx
50	<a href="#">c2qy9A_</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
51	<a href="#">c1s3sA_</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase (ter <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
52	<a href="#">c3b9qA_</a>	Alignment	not modelled	98.2	22	<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 cpfts from arabidopsis thaliana
53	<a href="#">c1nsfA_</a>	Alignment	not modelled	98.2	16	<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)
54	<a href="#">c2og2A</a>	Alignment	not modelled	98.2	18	<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
55	<a href="#">c2j37W</a>	Alignment	not modelled	98.1	18	<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
56	<a href="#">c1vmaA</a>	Alignment	not modelled	98.1	18	<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
57	<a href="#">c2yhsA</a>	Alignment	not modelled	98.1	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
58	<a href="#">c1zu4A</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsy; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
59	<a href="#">d1d2na</a>	Alignment	not modelled	98.1	16	<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
60	<a href="#">c3eihB</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4; <b>PDBTitle:</b> crystal structure of s.cerevisiae vps4 in the presence of atpgammas
61	<a href="#">d2jdid3</a>	Alignment	not modelled	98.1	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)
62	<a href="#">d3dhwc1</a>	Alignment	not modelled	98.1	27	<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
63	<a href="#">c3hu2C</a>	Alignment	not modelled	98.1	23	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
64	<a href="#">d1skyb3</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)
65	<a href="#">d2jdia3</a>	Alignment	not modelled	98.0	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)
66	<a href="#">d1skye3</a>	Alignment	not modelled	98.0	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)
67	<a href="#">c2hbcC</a>	Alignment	not modelled	98.0	15	<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
68	<a href="#">c2zamA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associating protein 4b; <b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form
69	<a href="#">c3pvsA</a>	Alignment	not modelled	98.0	14	<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
70	<a href="#">c2dhrC</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ftsh; <b>PDBTitle:</b> whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
71	<a href="#">c3b9pA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
72	<a href="#">c3dmdA</a>	Alignment	not modelled	98.0	16	<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
73	<a href="#">c3ec2A</a>	Alignment	not modelled	98.0	15	<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
74	<a href="#">c2r65A</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protease ftsh homolog; <b>PDBTitle:</b> crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
75	<a href="#">c3d8bB</a>	Alignment	not modelled	98.0	24	<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
76	<a href="#">c2iy3A</a>	Alignment	not modelled	98.0	22	<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
77	<a href="#">d1fx0a3</a>	Alignment	not modelled	98.0	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)
78	<a href="#">d1fx0b3</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) <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="#">d2ce7a2</a>	Alignment	not modelled	97.9	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
80	<a href="#">d1vmaa2</a>	Alignment	not modelled	97.9	11	<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
81	<a href="#">c1skyE_</a>	Alignment	not modelled	97.9	19	<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
82	<a href="#">c30aaC_</a>	Alignment	not modelled	97.9	19	<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
83	<a href="#">d1l8qa2</a>	Alignment	not modelled	97.9	16	<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
84	<a href="#">c2ce7B_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsH; <b>PDBTitle:</b> edta treated
85	<a href="#">c3dm5A_</a>	Alignment	not modelled	97.9	14	<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 assembling the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
86	<a href="#">d2awna2</a>	Alignment	not modelled	97.9	22	<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
87	<a href="#">d1ls1a2</a>	Alignment	not modelled	97.9	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
88	<a href="#">c1w0jB_</a>	Alignment	not modelled	97.8	20	<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
89	<a href="#">d1l2ta_</a>	Alignment	not modelled	97.8	23	<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
90	<a href="#">c3d31B_</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, atp-binding <b>PDBTitle:</b> modbc from methanosarcina acetivorans
91	<a href="#">c3pfiB_</a>	Alignment	not modelled	97.8	17	<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
92	<a href="#">c2qe7C_</a>	Alignment	not modelled	97.8	20	<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
93	<a href="#">c2w6jD_</a>	Alignment	not modelled	97.8	19	<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.
94	<a href="#">c2jizD_</a>	Alignment	not modelled	97.8	19	<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.
95	<a href="#">c3gfoA_</a>	Alignment	not modelled	97.8	25	<b>PDB header:</b> atp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cobalt import atp-binding protein cbio 1; <b>PDBTitle:</b> structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.
96	<a href="#">d1qzxa3</a>	Alignment	not modelled	97.8	14	<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
97	<a href="#">d1vpla_</a>	Alignment	not modelled	97.8	23	<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
98	<a href="#">c3h4mC_</a>	Alignment	not modelled	97.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> aaa atpase domain of the proteasome- activating nucleotidase
99	<a href="#">c2oblA_</a>	Alignment	not modelled	97.8	19	<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
100	<a href="#">d1e32a2</a>	Alignment	not modelled	97.8	23	<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
101	<a href="#">c1z47B_</a>	Alignment	not modelled	97.8	23	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc-transporter atp-binding protein; <b>PDBTitle:</b> structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
102	<a href="#">c2dpyA_</a>	Alignment	not modelled	97.8	18	<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
						<b>PDB header:</b> hydrolase



103	<a href="#">c2c61A_</a>	Alignment	not modelled	97.8	13	<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. maei go1
104	<a href="#">c2w58B_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> primosome component (helicase loader); <b>PDBTitle:</b> crystal structure of the dna1
105	<a href="#">c2x8aA_</a>	Alignment	not modelled	97.8	23	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear valosin-containing protein-like; <b>PDBTitle:</b> human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
106	<a href="#">clsxjA_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> activator 1 95 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
107	<a href="#">c2z4rB_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> dna binding protein <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
108	<a href="#">dlg2912</a>	Alignment	not modelled	97.8	22	<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
109	<a href="#">c2r9vA_</a>	Alignment	not modelled	97.8	21	<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
110	<a href="#">c2w6fA_</a>	Alignment	not modelled	97.8	20	<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.
111	<a href="#">c3fvqB_</a>	Alignment	not modelled	97.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fe(3+) ions import atp-binding protein fbpc; <b>PDBTitle:</b> crystal structure of the nucleotide binding domain fbpc2 complexed with atp
112	<a href="#">clvciaA_</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transport atp-binding protein; <b>PDBTitle:</b> crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
113	<a href="#">c2it1B_</a>	Alignment	not modelled	97.7	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> 362aa long hypothetical maltose/maltodextrin <b>PDBTitle:</b> structure of ph0203 protein from pyrococcus horikoshii
114	<a href="#">c2olkD_</a>	Alignment	not modelled	97.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> amino acid abc transporter; <b>PDBTitle:</b> abc protein artp in complex with adp-beta-s
115	<a href="#">dlr7ra3</a>	Alignment	not modelled	97.7	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
116	<a href="#">dlfnna2</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> Extended AAA-ATPase domain
117	<a href="#">dlbifa1</a>	Alignment	not modelled	97.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
118	<a href="#">dlxpua3</a>	Alignment	not modelled	97.7	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)
119	<a href="#">c2d62A_</a>	Alignment	not modelled	97.7	24	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multiple sugar-binding transport atp-binding <b>PDBTitle:</b> crystal structure of multiple sugar binding transport atp-2 binding protein
120	<a href="#">dlb0ua_</a>	Alignment	not modelled	97.7	25	<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