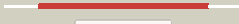



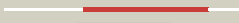




























# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1297\_(rho)\_1453210\_1455018  
 Date Wed Jul 31 22:05:39 BST 2019  
 Unique Job ID 6b701a6ca143baf0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3l0oA_</a>	 Alignment		100.0	52	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> transcription termination factor rho; <b>PDBTitle:</b> structure of rna-free rho transcription termination factor from2 thermotoga maritima
2	<a href="#">c1xpuB_</a>	 Alignment		100.0	56	<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)
3	<a href="#">c3l0oB_</a>	 Alignment		100.0	52	<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
4	<a href="#">d1xpuA3</a>	 Alignment		100.0	61	<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)
5	<a href="#">c2dpyA_</a>	 Alignment		100.0	23	<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="#">c1skyE_</a>	 Alignment		100.0	21	<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
7	<a href="#">c5b0oB_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase/motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellum-specific atp synthase; <b>PDBTitle:</b> structure of the flih-flii complex
8	<a href="#">c2w6jD_</a>	 Alignment		100.0	20	<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-atpase during2 controlled dehydration: hydration state 5.
9	<a href="#">c2jizD_</a>	 Alignment		100.0	20	<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.
10	<a href="#">c6focD_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit beta; <b>PDBTitle:</b> f1-atpase from mycobacterium smegmatis
11	<a href="#">c6npjC_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> translocator escn; <b>PDBTitle:</b> structure of the assembled atpase escn in complex with its central2 stalk esco from the enteropathogenic e. coli (epec) type iii3 secretion system

12	<a href="#">c1fx0B_</a>	Alignment		100.0	19	<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
13	<a href="#">c6f5dE_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> atp synthase subunit beta, mitochondrial; <b>PDBTitle:</b> trypanosoma brucei f1-atpase
14	<a href="#">c2ob1A_</a>	Alignment		100.0	23	<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 the 2 type III secretion system of pathogenic bacteria
15	<a href="#">c5bn4A_</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> v-type atp synthase alpha chain; <b>PDBTitle:</b> structure of a unique atp synthase neqa-neqb in complex with anp from Nanoarchaeum equitans
16	<a href="#">c6rdtY_</a>	Alignment		100.0	20	<b>PDB header:</b> proton transport <b>Chain:</b> Y: <b>PDB Molecule:</b> atp synthase subunit beta; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 composite map
17	<a href="#">c5bo5B_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> neq263; <b>PDBTitle:</b> structure of a unique atp synthase subunit neqb from nanoarchaeum2 equitans
18	<a href="#">c6fkhA_</a>	Alignment		100.0	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 2
19	<a href="#">c2r9vA_</a>	Alignment		100.0	17	<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) from Thermotoga maritima at 2.10 Å resolution
20	<a href="#">c3a5dB_</a>	Alignment		100.0	20	<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 rearrangement 2 defined by the central stalk of prokaryotic v1-atpase
21	<a href="#">c2w6fA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha heart isoform, mitochondrial; <b>PDBTitle:</b> low resolution structures of bovine mitochondrial f1-atpase during controlled dehydration: hydration state 2.
22	<a href="#">c3vr5C_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> v-type sodium atpase catalytic subunit a; <b>PDBTitle:</b> crystal structure of nucleotide-free enterococcus hirae v1-atpase2 [ev1(l)]
23	<a href="#">c3vr5D_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> v-type sodium atpase subunit b; <b>PDBTitle:</b> crystal structure of nucleotide-free enterococcus hirae v1-atpase2 [ev1(l)]
24	<a href="#">c5syrA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp synthase spa/mxib; <b>PDBTitle:</b> crystal structure of atpase delta1-79 spa47 r350a
25	<a href="#">c2qe7C_</a>	Alignment	not modelled	100.0	21	<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 thermoalkaliphilic bacterium bacillus sp. ta2.a1
26	<a href="#">c1w0jB_</a>	Alignment	not modelled	100.0	17	<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
27	<a href="#">c6f5dB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit alpha, mitochondrial; <b>PDBTitle:</b> trypanosoma brucei f1-atpase
28	<a href="#">c3j9uD_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> v-type proton atpase subunit b; <b>PDBTitle:</b> yeast v-atpase state 2

29	<a href="#">c6re7U</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> proton transport <b>Chain:</b> U: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 2c,2 focussed refinement of f1 head and rotor
30	<a href="#">c6q45C</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> f1-atpase from fusobacterium nucleatum
31	<a href="#">c3a5dM</a>	Alignment	not modelled	100.0	17	<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
32	<a href="#">c2c61A</a>	Alignment	not modelled	100.0	18	<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. mazei go1
33	<a href="#">c5dn6A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> atp synthase from paracoccus denitrificans
34	<a href="#">c4b2qA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha, mitochondrial; <b>PDBTitle:</b> model of the yeast f1fo-atp synthase dimer based on subtomogram2 average
35	<a href="#">d2jdia3</a>	Alignment	not modelled	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)
36	<a href="#">c3j9vC</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> v-type proton atpase catalytic subunit a; <b>PDBTitle:</b> yeast v-atpase state 3
37	<a href="#">c6focB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit alpha,atp synthase subunit alpha,atp <b>PDBTitle:</b> f1-atpase from mycobacterium smegmatis
38	<a href="#">c30aaC</a>	Alignment	not modelled	100.0	16	<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
39	<a href="#">c4xd7B</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> structure of thermophilic f1-atpase inhibited by epsilon subunit
40	<a href="#">c1kmhA</a>	Alignment	not modelled	100.0	17	<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-atpase complexed with2 tentoxin
41	<a href="#">d1skyb3</a>	Alignment	not modelled	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)
42	<a href="#">d2jdid3</a>	Alignment	not modelled	100.0	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)
43	<a href="#">d1fx0a3</a>	Alignment	not modelled	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)
44	<a href="#">c5t4oA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> autoinhibited e. coli atp synthase state 1
45	<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)
46	<a href="#">d1skye3</a>	Alignment	not modelled	100.0	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)
47	<a href="#">c4nphA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> probable secretion system apparatus atp synthase ssan; <b>PDBTitle:</b> crystal structure of ssan from salmonella enterica
48	<a href="#">c1vdzA</a>	Alignment	not modelled	100.0	21	<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
49	<a href="#">c3sdzA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> v-type atp synthase alpha chain; <b>PDBTitle:</b> structural characterization of the subunit a mutant f427w of the a-atp2 synthase from pyrococcus horikoshii
50	<a href="#">c2a8vA</a>	Alignment	not modelled	99.9	51	<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
51	<a href="#">d1a62a2</a>	Alignment	not modelled	99.9	39	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
52	<a href="#">c4ydsA</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagella-related protein h; <b>PDBTitle:</b> flah from sulfobolus acidocaldarius with atp and mg-ion
53	<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)
54	<a href="#">c1u9iA</a>	Alignment	not modelled	98.7	19	<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
55	<a href="#">d1xp8a1</a>	Alignment	not modelled	98.4	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)
56	<a href="#">c2recB_</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
57	<a href="#">d1tf7a1</a>	Alignment	not modelled	98.3	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)
58	<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)
59	<a href="#">c3hr8A_</a>	Alignment	not modelled	98.2	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
60	<a href="#">c2ztsB_</a>	Alignment	not modelled	98.1	15	<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 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
61	<a href="#">c2zroA_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
62	<a href="#">c4wiaA_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flagella-related protein h; <b>PDBTitle:</b> crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
63	<a href="#">d2i1qa2</a>	Alignment	not modelled	98.0	12	<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)
64	<a href="#">d1ubea1</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)
65	<a href="#">c2w0mA_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfobolus solfataricus p2
66	<a href="#">c1xp8A_</a>	Alignment	not modelled	97.9	23	<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
67	<a href="#">c2z4rB_</a>	Alignment	not modelled	97.9	21	<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
68	<a href="#">d1n0wa_</a>	Alignment	not modelled	97.9	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)
69	<a href="#">c1pznA_</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
70	<a href="#">c3io5B_</a>	Alignment	not modelled	97.9	23	<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
71	<a href="#">c2dr3A_</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cupf0273 protein ph0284; <b>PDBTitle:</b> crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
72	<a href="#">c2df1A_</a>	Alignment	not modelled	97.8	11	<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
73	<a href="#">c1pznG_</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
74	<a href="#">c3ldaA_</a>	Alignment	not modelled	97.8	13	<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
75	<a href="#">d1u94a1</a>	Alignment	not modelled	97.8	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)
76	<a href="#">c5x06G_</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein
77	<a href="#">c4lyaA_</a>	Alignment	not modelled	97.7	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
78	<a href="#">c1szpC_</a>	Alignment	not modelled	97.7	13	<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
79	<a href="#">d1pzna2</a>	Alignment	not modelled	97.7	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)
80	<a href="#">d1v5wa_</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> RecA protein-like (ATPase-domain)
81	<a href="#">c1t4gA_</a>	Alignment	not modelled	97.6	16	<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 <b>PDB header:</b> cell cycle

82	<a href="#">c4nh0A_</a>	Alignment	not modelled	97.6	18	<b>Chain:</b> A: <b>PDB Molecule:</b> cell divisionftsks/spoiii; <b>PDBTitle:</b> cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
83	<a href="#">c3dmdA_</a>	Alignment	not modelled	97.6	21	<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
84	<a href="#">d1qvrA2</a>	Alignment	not modelled	97.6	26	<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
85	<a href="#">c4xgcE_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
86	<a href="#">c6cy1B_</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
87	<a href="#">c2qbyA_</a>	Alignment	not modelled	97.5	16	<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)
88	<a href="#">c2zjbB_</a>	Alignment	not modelled	97.5	18	<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
89	<a href="#">c2cvhB_</a>	Alignment	not modelled	97.5	20	<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
90	<a href="#">c3pvsA_</a>	Alignment	not modelled	97.5	24	<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
91	<a href="#">c2vyeA_</a>	Alignment	not modelled	97.5	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnc-ssdna complex
92	<a href="#">c2q6tB_</a>	Alignment	not modelled	97.5	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
93	<a href="#">c5jzcG_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair protein rad51 homolog 1; <b>PDBTitle:</b> helical filament
94	<a href="#">d1szpa2</a>	Alignment	not modelled	97.4	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)
95	<a href="#">c3cmvG_</a>	Alignment	not modelled	97.4	22	<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-ssdna/dsdna2 structures
96	<a href="#">d1cr2a_</a>	Alignment	not modelled	97.4	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)
97	<a href="#">c4kxfF_</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> immune system <b>Chain:</b> F: <b>PDB Molecule:</b> nlr family card domain-containing protein 4; <b>PDBTitle:</b> crystal structure of nlr4 reveals its autoinhibition mechanism
98	<a href="#">c5jwqA_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> circadian clock protein kinase kaic; <b>PDBTitle:</b> crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
99	<a href="#">c5uj7C_</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
100	<a href="#">c1vt4J_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> J: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
101	<a href="#">c1vt4P_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> P: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
102	<a href="#">c1vt4L_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> L: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
103	<a href="#">c1vt4O_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> O: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
104	<a href="#">c3iz8D_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
105	<a href="#">c3iz8G_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> G: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
106	<a href="#">c1vt4K_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> K: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
107	<a href="#">c3iz8H_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> H: <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome

108	<a href="#">c3iz8E_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> E; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
109	<a href="#">c1vt4N_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> N; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
110	<a href="#">c3iz8F_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> F; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
111	<a href="#">c1vt4I_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> I; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
112	<a href="#">c3iz8B_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
113	<a href="#">c1vt4M_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> M; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
114	<a href="#">c3iz8A_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
115	<a href="#">c3iz8C_</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> apoptosis <b>Chain:</b> C; <b>PDB Molecule:</b> apaf-1 related killer dark; <b>PDBTitle:</b> structure of the drosophila apoptosome
116	<a href="#">d1w5sa2</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> Extended AAA-ATPase domain
117	<a href="#">c6hecH_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
118	<a href="#">c4b4tL_</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> L; <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
119	<a href="#">c3uk6L_</a>	Alignment	not modelled	97.3	32	<b>PDB header:</b> hydrolase <b>Chain:</b> L; <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> crystal structure of the tip48 (tip49b) hexamer
120	<a href="#">c5vq9D_</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> pachytene checkpoint protein 2 homolog; <b>PDBTitle:</b> structure of human trip13, apo form