







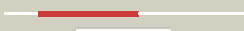



















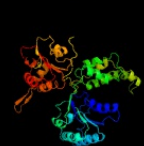
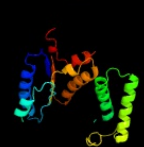


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3871 (-) _4349005_4350780
Date	Sat Aug 10 22:05:05 BST 2019
Unique Job ID	446253eee2f72959

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4n1aE_</a>	 Alignment		100.0	41	<b>PDB header:</b> protein binding/protein binding <b>Chain:</b> E; <b>PDB Molecule:</b> cell divisionftsk/spoiii; <b>PDBTitle:</b> thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
2	<a href="#">c4nh0A_</a>	 Alignment		100.0	40	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> cell divisionftsk/spoiii; <b>PDBTitle:</b> cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
3	<a href="#">c4lyaA_</a>	 Alignment		100.0	21	<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)
4	<a href="#">c2iuuE_</a>	 Alignment		100.0	16	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> dna translocase ftsk; <b>PDBTitle:</b> p. aeruginosa ftsk motor domain, hexamer
5	<a href="#">c2iutA_</a>	 Alignment		100.0	16	<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
6	<a href="#">c2iusB_</a>	 Alignment		100.0	18	<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
7	<a href="#">c4kfuC_</a>	 Alignment		99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> genome packaging ntpase b204; <b>PDBTitle:</b> structure of the genome packaging ntpase b204 from sulfolobus turreted2 icosahedral virus 2 in complex with amppcp
8	<a href="#">c4d2iB_</a>	 Alignment		99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> hera; <b>PDBTitle:</b> crystal structure of the hera hexameric dna translocase2 from sulfolobus solfataricus bound to amp-pnp
9	<a href="#">c4ag5A_</a>	 Alignment		99.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> type iv secretory pathway virb4 components-like protein; <b>PDBTitle:</b> structure of virb4 of thermoanaerobacter pseudethanolicus
10	<a href="#">c5g4gF_</a>	 Alignment		99.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> structure of the atpgs-bound vat complex
11	<a href="#">c6matE_</a>	 Alignment		99.3	17	<b>PDB header:</b> ribosomal protein <b>Chain:</b> E; <b>PDB Molecule:</b> rix7 mutant; <b>PDBTitle:</b> cryo-em structure of the essential ribosome assembly aaa-atpase rix7

12	<a href="#">c1u9iA_</a>	Alignment		99.3	17	<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
13	<a href="#">c5ifwB_</a>	Alignment		99.2	15	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
14	<a href="#">d1e9ra_</a>	Alignment		99.2	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)
15	<a href="#">c5e7pA_</a>	Alignment		99.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein cdc48; <b>PDBTitle:</b> crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
16	<a href="#">c5jwqA_</a>	Alignment		99.2	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
17	<a href="#">c3cf2B_</a>	Alignment		99.2	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/amp-pnp
18	<a href="#">c3cf1C_</a>	Alignment		99.1	16	<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
19	<a href="#">c4ag5D_</a>	Alignment		98.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> type iv secretory pathway virb4 components-like protein; <b>PDBTitle:</b> structure of virb4 of thermoanaerobacter pseudethanolicus
20	<a href="#">c3j96F_</a>	Alignment		98.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vesicle-fusing atpase; <b>PDBTitle:</b> structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
21	<a href="#">c1yqtA_</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> rnase-I inhibitor
22	<a href="#">c3cmvG_</a>	Alignment	not modelled	98.5	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-ssdna/dsdna2 structures
23	<a href="#">c5vq9D_</a>	Alignment	not modelled	98.4	14	<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
24	<a href="#">c4finA_</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> etta (yjjk) abcf family protein; <b>PDBTitle:</b> crystal structure of etta (formerly yjjk) - an e. coli abc-type atpase
25	<a href="#">c2zamA_</a>	Alignment	not modelled	98.3	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4b; <b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form
26	<a href="#">c5udbD_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
27	<a href="#">c3bk7A_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abce1/rnaase-I inhibitor protein from2 pyrococcus abyssi
28	<a href="#">c1xwiA_</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
						<b>PDB header:</b> hydrolase

29	<a href="#">c3d8bB_</a>	Alignment	not modelled	98.2	18	<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
30	<a href="#">c4xguB_</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative pachytene checkpoint protein 2; <b>PDBTitle:</b> structure of c. elegans pch-2
31	<a href="#">c6b5cA_</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> katanin p60 atpase-containing subunit a-like 1; <b>PDBTitle:</b> structural basis for katanin self-assembly
32	<a href="#">c3hu2C_</a>	Alignment	not modelled	98.1	20	<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
33	<a href="#">c3l0aA_</a>	Alignment	not modelled	98.1	25	<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 from <i>thermotoga maritima</i>
34	<a href="#">c3j16B_</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> rli1p; <b>PDBTitle:</b> models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
35	<a href="#">c4b4tj_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s protease regulatory subunit 8 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
36	<a href="#">c5kzfj_</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
37	<a href="#">c3b9pA_</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
38	<a href="#">c5w0tA_</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein msp1; <b>PDBTitle:</b> crystal structure of monomeric msp1 from <i>s. cerevisiae</i>
39	<a href="#">c3l0oB_</a>	Alignment	not modelled	98.0	25	<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 from <i>thermotoga maritima</i>
40	<a href="#">c6opcf_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> motor protein <b>Chain:</b> F: <b>PDB Molecule:</b> cell division control protein 48; <b>PDBTitle:</b> cdc48 hexamer in a complex with substrate and shp1(ubx domain)
41	<a href="#">c5wc0D_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> motor protein <b>Chain:</b> D: <b>PDB Molecule:</b> meiotic spindle formation protein mei-1; <b>PDBTitle:</b> katanin hexamer in spiral conformation
42	<a href="#">c6epcj_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 8; <b>PDBTitle:</b> ground state 26s proteasome (gs2)
43	<a href="#">c6nyyC_</a>	Alignment	not modelled	98.0	23	<b>PDB header:</b> translocase <b>Chain:</b> C: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
44	<a href="#">c3vfdA_</a>	Alignment	not modelled	98.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain
45	<a href="#">c1s3sA_</a>	Alignment	not modelled	98.0	17	<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
46	<a href="#">c4b4tH_</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> 26s protease regulatory subunit 7 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
47	<a href="#">c2q6tB_</a>	Alignment	not modelled	97.9	20	<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
48	<a href="#">c5mpaL_</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> 26s proteasome in presence of atp (s2)
49	<a href="#">c4b4tK_</a>	Alignment	not modelled	97.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> K: <b>PDB Molecule:</b> 26s protease regulatory subunit 6b homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
50	<a href="#">c4xgcD_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
51	<a href="#">c4z8xC_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> truncated ftsh from <i>a. aeolicus</i>
52	<a href="#">c1xpuB_</a>	Alignment	not modelled	97.9	22	<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)
53	<a href="#">c4lcbA_</a>	Alignment	not modelled	97.9	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein cdvc, vps4; <b>PDBTitle:</b> structure of vps4 homolog from <i>acidianus hospitalis</i>
54	<a href="#">d1xpuA3</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> RecA protein-like (ATPase-domain)
55	<a href="#">c2ja1A</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
56	<a href="#">c6hecH</a>	Alignment	not modelled	97.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
57	<a href="#">d1tf7a2</a>	Alignment	not modelled	97.8	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)
58	<a href="#">c4nmmA</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
59	<a href="#">c3bh0A</a>	Alignment	not modelled	97.8	17	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p
60	<a href="#">c2r2aB</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
61	<a href="#">c4l16A</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of figl-1 aaa domain in complex with adp
62	<a href="#">c3ldaA</a>	Alignment	not modelled	97.8	20	<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
63	<a href="#">c2dhrC</a>	Alignment	not modelled	97.8	25	<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)
64	<a href="#">c3eihB</a>	Alignment	not modelled	97.8	24	<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
65	<a href="#">c5gjql</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease regulatory subunit 10b; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
66	<a href="#">c4xgcE</a>	Alignment	not modelled	97.7	10	<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
67	<a href="#">c4b4tM</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s protease regulatory subunit 6a; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
68	<a href="#">c4kxfF</a>	Alignment	not modelled	97.7	22	<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 nlrc4 reveals its autoinhibition mechanism
69	<a href="#">c4b4tL</a>	Alignment	not modelled	97.7	16	<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
70	<a href="#">c2vyeA</a>	Alignment	not modelled	97.7	18	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnac-ssdna complex
71	<a href="#">c5vy9C</a>	Alignment	not modelled	97.7	24	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> s. cerevisiae hsp104:casein complex, middle domain conformation
72	<a href="#">c6epdM</a>	Alignment	not modelled	97.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 6a; <b>PDBTitle:</b> substrate processing state 26s proteasome (sps1)
73	<a href="#">c2ce7B</a>	Alignment	not modelled	97.7	26	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
74	<a href="#">c2v1uA</a>	Alignment	not modelled	97.6	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
75	<a href="#">c2ztsB</a>	Alignment	not modelled	97.6	12	<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
76	<a href="#">d2did3</a>	Alignment	not modelled	97.6	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)
77	<a href="#">c4b4tI</a>	Alignment	not modelled	97.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> 26s protease regulatory subunit 4 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
78	<a href="#">c5l3rC</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
79	<a href="#">d1w5sa2</a>	Alignment	not modelled	97.6	12	<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
						<b>PDB header:</b> hydrolase

80	<a href="#">c5t0gA_</a>	Alignment	not modelled	97.6	23	<b>Chain:</b> A: <b>PDB Molecule:</b> 26s protease regulatory subunit 7; <b>PDBTitle:</b> structural basis for dynamic regulation of the human 26s proteasome
81	<a href="#">d2ce7a2</a>	Alignment	not modelled	97.6	25	<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
82	<a href="#">c3te6A_</a>	Alignment	not modelled	97.6	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
83	<a href="#">c4wiaA_</a>	Alignment	not modelled	97.6	13	<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
84	<a href="#">c4kxfP_</a>	Alignment	not modelled	97.6	22	<b>PDB header:</b> immune system <b>Chain:</b> P: <b>PDB Molecule:</b> nlr family card domain-containing protein 4; <b>PDBTitle:</b> crystal structure of nlrc4 reveals its autoinhibition mechanism
85	<a href="#">c3pvsA_</a>	Alignment	not modelled	97.5	22	<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
86	<a href="#">d1fnna2</a>	Alignment	not modelled	97.5	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
87	<a href="#">c4ydsA_</a>	Alignment	not modelled	97.5	11	<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
88	<a href="#">c5uj7B_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
89	<a href="#">c3bgwD_</a>	Alignment	not modelled	97.5	16	<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
90	<a href="#">c6qeIB_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> e. coli dnabc apo complex
91	<a href="#">c2x8aA_</a>	Alignment	not modelled	97.5	13	<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
92	<a href="#">d1skyb3</a>	Alignment	not modelled	97.5	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)
93	<a href="#">d1n0wa_</a>	Alignment	not modelled	97.5	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)
94	<a href="#">d1tf7a1</a>	Alignment	not modelled	97.5	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="#">c4ypnA_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lon protease; <b>PDBTitle:</b> crystal structure of a lon fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
96	<a href="#">c1iy2A_</a>	Alignment	not modelled	97.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent metalloprotease ftsh; <b>PDBTitle:</b> crystal structure of the ftsh atpase domain from thermus2 thermophilus
97	<a href="#">d1nlfa_</a>	Alignment	not modelled	97.5	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)
98	<a href="#">d1fx0b3</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)
99	<a href="#">d1skye3</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)
100	<a href="#">c2qz4A_</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> paraplegin; <b>PDBTitle:</b> human paraplegin, aaa domain in complex with adp
101	<a href="#">c5x06G_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein
102	<a href="#">c2j7pA_</a>	Alignment	not modelled	97.4	17	<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
103	<a href="#">c1iqpF_</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> rfcs; <b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
104	<a href="#">c6bbmA_</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
105	<a href="#">d1u94a1</a>	Alignment	not modelled	97.4	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)
						<b>PDB header:</b> hydrolase

106	<a href="#">c4a1fB_</a>	Alignment	not modelled	97.4	17	<b>Chain:</b> B; <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
107	<a href="#">c2hcbC_</a>	Alignment	not modelled	97.4	21	<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
108	<a href="#">d2qy9a2</a>	Alignment	not modelled	97.4	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
109	<a href="#">d2jdia3</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)
110	<a href="#">c4ciua_</a>	Alignment	not modelled	97.4	28	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> crystal structure of e. coli clpb
111	<a href="#">c6gefB_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> type iv secretion system protein dotb; <b>PDBTitle:</b> x-ray structure of the yersinia pseudotuberculosis atpase dotb
112	<a href="#">c1szpC_</a>	Alignment	not modelled	97.4	21	<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
113	<a href="#">d1qvra2</a>	Alignment	not modelled	97.4	20	<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
114	<a href="#">c6focD_</a>	Alignment	not modelled	97.3	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
115	<a href="#">c1fnnB_</a>	Alignment	not modelled	97.3	16	<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
116	<a href="#">c1q57G_</a>	Alignment	not modelled	97.3	15	<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
117	<a href="#">c5l3sF_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> protein transport <b>Chain:</b> F; <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
118	<a href="#">c5ujmE_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> replication <b>Chain:</b> E; <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> structure of the active form of human origin recognition complex and2 its atpase motor module
119	<a href="#">c5l3qB_</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> protein transport <b>Chain:</b> B; <b>PDB Molecule:</b> signal recognition particle receptor subunit alpha; <b>PDBTitle:</b> structure of the gtpase heterodimer of human srp54 and sralpha
120	<a href="#">c3pfiB_</a>	Alignment	not modelled	97.3	21	<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