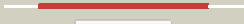



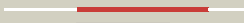





















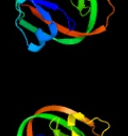



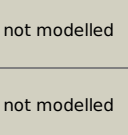


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2737c_(recA)_3049062_3051434
Date	Wed Aug 7 12:50:39 BST 2019
Unique Job ID	8b114dc393d4da33

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cmwA_</a>	 Alignment		100.0	39	<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-ssdna/dsdna2 structures
2	<a href="#">c3cmuA_</a>	 Alignment		100.0	37	<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-ssdna/dsdna2 structures
3	<a href="#">c1dq3A_</a>	 Alignment		100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease; <b>PDBTitle:</b> crystal structure of an archaeal intein-encoded homing2 endonuclease pi-pfui
4	<a href="#">c3hr8A_</a>	 Alignment		100.0	65	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
5	<a href="#">c2zroA_</a>	 Alignment		100.0	91	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
6	<a href="#">c3cmvG_</a>	 Alignment		100.0	66	<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
7	<a href="#">c2cw8A_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease pi-pkoi; <b>PDBTitle:</b> crystal structure of intein homing endonuclease ii
8	<a href="#">c2recB_</a>	 Alignment		100.0	63	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
9	<a href="#">c1xp8A_</a>	 Alignment		100.0	66	<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
10	<a href="#">d1mo6a1</a>	 Alignment		100.0	99	<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="#">c1vdeA_</a>	 Alignment		100.0	23	<b>PDB header:</b> endonuclease <b>Chain:</b> A: <b>PDB Molecule:</b> pi-scei; <b>PDBTitle:</b> pi-scei, a homing endonuclease with protein splicing2 activity

12	<a href="#">d1u94a1</a>	Alignment		100.0	64	<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)
13	<a href="#">d1ubea1</a>	Alignment		100.0	90	<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="#">d1xp8a1</a>	Alignment		100.0	65	<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="#">c3io5B_</a>	Alignment		100.0	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 uvx3 recombinase core2 domain from enterobacteria phage t4
16	<a href="#">c2imzA_</a>	Alignment		100.0	100	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease pi-mtui; <b>PDBTitle:</b> crystal structure of mtu reca intein splicing domain
17	<a href="#">d1mi8a_</a>	Alignment		100.0	42	<b>Fold:</b> Hedgehog/intein (Hint) domain <b>Superfamily:</b> Hedgehog/intein (Hint) domain <b>Family:</b> Intein (protein splicing domain)
18	<a href="#">d1am2a_</a>	Alignment		99.9	38	<b>Fold:</b> Hedgehog/intein (Hint) domain <b>Superfamily:</b> Hedgehog/intein (Hint) domain <b>Family:</b> Intein (protein splicing domain)
19	<a href="#">c1zd7B_</a>	Alignment		99.9	39	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii alpha subunit; <b>PDBTitle:</b> 1.7 angstrom crystal structure of post-splicing form of a dnae intein2 from synechocystis sp. pcc 6803
20	<a href="#">c4o1rA_</a>	Alignment		99.9	43	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of npudnab intein
21	<a href="#">c3ldaA_</a>	Alignment	not modelled	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
22	<a href="#">c5jzcG_</a>	Alignment	not modelled	99.9	23	<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
23	<a href="#">c2keqA_</a>	Alignment	not modelled	99.9	36	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii alpha subunit, nucleic acid <b>PDBTitle:</b> solution structure of dnae intein from nostoc punctiforme
24	<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
25	<a href="#">c2in0A_</a>	Alignment	not modelled	99.9	100	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease pi-mtui; <b>PDBTitle:</b> crystal structure of mtu reca intein splicing domain
26	<a href="#">c2df1A_</a>	Alignment	not modelled	99.9	27	<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
27	<a href="#">c1pznA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
28	<a href="#">c5o9jB_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> transcription initiation factor iib,transcription <b>PDBTitle:</b> crystal structure of transcription factor iib mja mini-intein
						<b>PDB header:</b> dna binding protein

29	<a href="#">c1szpC_</a>	Alignment	not modelled	99.9	24	<b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> a crystal structure of the rad51 filament
30	<a href="#">d1szpa2</a>	Alignment	not modelled	99.9	27	<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="#">d1v5wa_</a>	Alignment	not modelled	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)
32	<a href="#">c2jmzA_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein mj0781; <b>PDBTitle:</b> solution structure of a kba intein precursor from2 methanococcus jannaschii
33	<a href="#">d1n0wa_</a>	Alignment	not modelled	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)
34	<a href="#">c4e2uA_</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pho rada intein; <b>PDBTitle:</b> crystal structures of radamin intein from pyrococcus horikoshii
35	<a href="#">d1pzna2</a>	Alignment	not modelled	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)
36	<a href="#">c2lcjA_</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pab polc intein; <b>PDBTitle:</b> solution nmr structure of pab polii intein
37	<a href="#">c2zjbB_</a>	Alignment	not modelled	99.9	28	<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
38	<a href="#">d2i1qa2</a>	Alignment	not modelled	99.9	27	<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="#">c4o1sB_</a>	Alignment	not modelled	99.8	35	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> v-type atp synthase alpha chain; <b>PDBTitle:</b> crystal structure of tvovma intein
40	<a href="#">c1b24A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> intron-encoded <b>Chain:</b> A: <b>PDB Molecule:</b> protein (i-dmoi); <b>PDBTitle:</b> i-dmoi, intron-encoded endonuclease
41	<a href="#">d1tf7a2</a>	Alignment	not modelled	99.8	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)
42	<a href="#">d1tf7a1</a>	Alignment	not modelled	99.8	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)
43	<a href="#">c2cvhB_</a>	Alignment	not modelled	99.8	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
44	<a href="#">c3bh0A_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p
45	<a href="#">c2ztsB_</a>	Alignment	not modelled	99.8	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 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
46	<a href="#">d1dq3a4</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Intein endonuclease
47	<a href="#">c2q6tB_</a>	Alignment	not modelled	99.8	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="#">c1pznG_</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
49	<a href="#">c4nmnA_</a>	Alignment	not modelled	99.8	16	<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
50	<a href="#">c2vyeA_</a>	Alignment	not modelled	99.7	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
51	<a href="#">c3bgwD_</a>	Alignment	not modelled	99.7	18	<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
52	<a href="#">c6qeIB_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> e. coli dnabc apo complex
53	<a href="#">c1u9iA_</a>	Alignment	not modelled	99.7	24	<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
54	<a href="#">d1dq3a1</a>	Alignment	not modelled	99.7	47	<b>Fold:</b> Hedgehog/intein (Hint) domain <b>Superfamily:</b> Hedgehog/intein (Hint) domain <b>Family:</b> Intein (protein splicing domain)
55	<a href="#">c6bbmA_</a>	Alignment	not modelled	99.7	21	<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 <b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from <i>sulfolobus solfataricus</i> p2
56	<a href="#">c2w0mA</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagella-related protein h; <b>PDBTitle:</b> flah from <i>sulfolobus acidocaldarius</i> with atp and mg-ion
57	<a href="#">c4ydsA</a>	Alignment	not modelled	99.7	24	<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 from <i>Methanocaldococcus jannaschii</i>
58	<a href="#">c4wiaA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> structure of a dodecameric bacterial helicase
59	<a href="#">c4zc0A</a>	Alignment	not modelled	99.7	19	<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 of <i>T. bacteriophage t7</i>
60	<a href="#">c1q57G</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of c-terminal domain of <i>Helicobacter pylori</i> dnab helicase
61	<a href="#">c4a1fB</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Homing endonucleases <b>Family:</b> Intein endonuclease
62	<a href="#">d1jvaa3</a>	Alignment	not modelled	99.7	21	<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 <i>Pyrococcus2 horikoshii</i> ot3
63	<a href="#">c2dr3A</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii subunit alpha,dna polymerase iii subunit <b>PDBTitle:</b> crystal structure of an inactivated ssp siclopps intein with cfahpq2 extein
64	<a href="#">c5ol5B</a>	Alignment	not modelled	99.6	24	<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 <i>Thermosynechococcus elongatus</i>
65	<a href="#">c5jwqA</a>	Alignment	not modelled	99.6	28	<b>PDB header:</b> splicing <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed dna polymerase,dna-directed dna polymerase; <b>PDBTitle:</b> crystal structure of an inactivated npu siclopps intein with cfahpq2 extein
66	<a href="#">c5ol7A</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rada; <b>PDBTitle:</b> rada bound to dtdp
67	<a href="#">c5lkmB</a>	Alignment	not modelled	99.5	19	<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 <i>Pyrococcus2 horikoshii</i> in complex with an unknown peptide
68	<a href="#">c3bs4A</a>	Alignment	not modelled	99.5	11	<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="#">d1nlfa</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> Hedgehog/intein (Hint) domain <b>Superfamily:</b> Hedgehog/intein (Hint) domain <b>Family:</b> Hedgehog C-terminal (Hog) autoprocessing domain
70	<a href="#">d1at0a</a>	Alignment	not modelled	99.5	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)
71	<a href="#">d1cr2a</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial intein-like domain; <b>PDBTitle:</b> solution structure of bacterial intein-like domain from <i>Clostridium2 thermocellum</i>
72	<a href="#">c2lwyA</a>	Alignment	not modelled	99.3	29	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> the class 3 dnab intein from <i>Mycobacterium smegmatis</i>
73	<a href="#">c6bs8C</a>	Alignment	not modelled	99.2	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein duf199/whia; <b>PDBTitle:</b> crystal structure of full-length duf199/whia from <i>Thermatoga maritima</i>
74	<a href="#">c3hyiA</a>	Alignment	not modelled	99.0	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> protein duf199/whia; <b>PDBTitle:</b> crystal structure of the n-terminal laglidagd domain of duf199/whia
75	<a href="#">c3hyjD</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> AXH domain <b>Superfamily:</b> AXH domain <b>Family:</b> AXH domain
76	<a href="#">d1oa8a</a>	Alignment	not modelled	98.6	21	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
77	<a href="#">d1mo6a2</a>	Alignment	not modelled	98.3	100	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> intron-encoded endonuclease i-scei; <b>PDBTitle:</b> the homing endonuclease i-scei bound to its dna recognition2 region
78	<a href="#">c1r7mA</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
79	<a href="#">d1ubea2</a>	Alignment	not modelled	98.2	87	<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
80	<a href="#">c2cnwF</a>	Alignment	not modelled	98.2	16	<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 <i>Arabidopsis2</i>
81	<a href="#">c2og2A</a>	Alignment	not modelled	98.1	16	

						thaliana
82	<a href="#">c4ak9A_</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cpftsy; <b>PDBTitle:</b> structure of chloroplast ftsy from physcomitrella patens
83	<a href="#">d1skyb3</a>	Alignment	not modelled	98.1	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)
84	<a href="#">c2q9cA_</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of ftsy:gmpnp with mgcl complex
85	<a href="#">c3b9qA_</a>	Alignment	not modelled	98.0	18	<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
86	<a href="#">c6epdM_</a>	Alignment	not modelled	97.9	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)
87	<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
88	<a href="#">c2yhsA_</a>	Alignment	not modelled	97.9	16	<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
89	<a href="#">c30aaC_</a>	Alignment	not modelled	97.9	21	<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
90	<a href="#">c2qe7C_</a>	Alignment	not modelled	97.9	19	<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
91	<a href="#">c6focD_</a>	Alignment	not modelled	97.9	23	<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
92	<a href="#">c4xd7B_</a>	Alignment	not modelled	97.9	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
93	<a href="#">d1u94a2</a>	Alignment	not modelled	97.9	53	<b>Fold:</b> Anti-LPS factor/recA domain <b>Superfamily:</b> RecA protein, C-terminal domain <b>Family:</b> RecA protein, C-terminal domain
94	<a href="#">c3fkqA_</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc-like two-domain protein; <b>PDBTitle:</b> crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
95	<a href="#">d2did3</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)
96	<a href="#">c4b4tH_</a>	Alignment	not modelled	97.9	17	<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
97	<a href="#">c6f5dE_</a>	Alignment	not modelled	97.9	24	<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
98	<a href="#">c6cy1B_</a>	Alignment	not modelled	97.9	15	<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
99	<a href="#">c2iy3A_</a>	Alignment	not modelled	97.9	23	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein,signal recognition <b>PDBTitle:</b> structure of the e. coli signal recognition particle
100	<a href="#">d1skye3</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> RecA protein-like (ATPase-domain)
101	<a href="#">c4b4tI_</a>	Alignment	not modelled	97.9	18	<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
102	<a href="#">c5mpaL_</a>	Alignment	not modelled	97.8	25	<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)
103	<a href="#">c4b4tJ_</a>	Alignment	not modelled	97.8	17	<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
104	<a href="#">c1vmaA_</a>	Alignment	not modelled	97.8	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
105	<a href="#">c2r9vA_</a>	Alignment	not modelled	97.8	22	<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
106	<a href="#">c1zu4A_</a>	Alignment	not modelled	97.8	15	<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
107	<a href="#">c6rdtY_</a>	Alignment	not modelled	97.8	22	<b>PDB header:</b> proton transport <b>Chain:</b> Y: <b>PDB Molecule:</b> atp synthase subunit beta;

107	<a href="#">c0ruct_</a>	Alignment	not modelled	97.8	22	<b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 composite map
108	<a href="#">c5dn6A_</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> atp synthase from paracoccus denitrificans
109	<a href="#">c6q45C_</a>	Alignment	not modelled	97.8	21	<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
110	<a href="#">c2j7pA_</a>	Alignment	not modelled	97.8	23	<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
111	<a href="#">d1fx0a3</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)
112	<a href="#">c5l3rC_</a>	Alignment	not modelled	97.8	20	<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
113	<a href="#">c4b4tK_</a>	Alignment	not modelled	97.8	24	<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
114	<a href="#">c4b4tL_</a>	Alignment	not modelled	97.8	24	<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
115	<a href="#">d1xpua3</a>	Alignment	not modelled	97.8	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)
116	<a href="#">c4b4tM_</a>	Alignment	not modelled	97.8	20	<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
117	<a href="#">c6hecH_</a>	Alignment	not modelled	97.7	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
118	<a href="#">d2jdia3</a>	Alignment	not modelled	97.7	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)
119	<a href="#">c1s3sA_</a>	Alignment	not modelled	97.7	24	<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
120	<a href="#">c5syrA_</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp synthase spa1/mxib; <b>PDBTitle:</b> crystal structure of atpase delta1-79 spa47 r350a