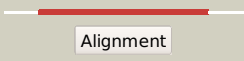

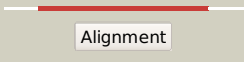

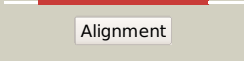

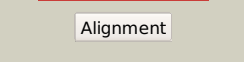

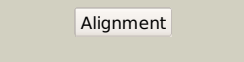

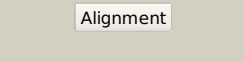

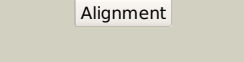

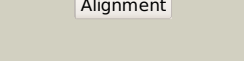

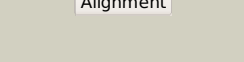

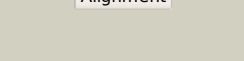

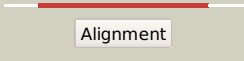









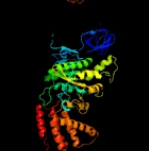


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1308_(atpA)_1463234_1464883
Date	Wed Jul 31 22:05:40 BST 2019
Unique Job ID	162732d6afee7d01

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6re7U_</a>	 Alignment		100.0	52	<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
2	<a href="#">c5dn6A_</a>	 Alignment		100.0	55	<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
3	<a href="#">c6fkhA_</a>	 Alignment		100.0	58	<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
4	<a href="#">c4b2qA_</a>	 Alignment		100.0	56	<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
5	<a href="#">c2w6fA_</a>	 Alignment		100.0	56	<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 during2 controlled dehydration: hydration state 2.
6	<a href="#">c2r9vA_</a>	 Alignment		100.0	58	<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
7	<a href="#">c1w0jB_</a>	 Alignment		100.0	56	<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
8	<a href="#">c5t4oA_</a>	 Alignment		100.0	52	<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
9	<a href="#">c1kmhA_</a>	 Alignment		100.0	59	<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
10	<a href="#">c2qe7C_</a>	 Alignment		100.0	65	<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
11	<a href="#">c6q45C_</a>	 Alignment		100.0	62	<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

12	<a href="#">c6focB_</a>	Alignment		100.0	88	<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
13	<a href="#">c30aaC_</a>	Alignment		100.0	54	<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
14	<a href="#">c6f5dB_</a>	Alignment		100.0	47	<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
15	<a href="#">c6rdtY_</a>	Alignment		100.0	23	<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
16	<a href="#">c3j9vC_</a>	Alignment		100.0	23	<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
17	<a href="#">c3a5dB_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> v-type atp synthase alpha chain; <b>PDBTitle:</b> inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
18	<a href="#">c6f5dE_</a>	Alignment		100.0	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
19	<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
20	<a href="#">c5bn4A_</a>	Alignment		100.0	21	<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 from2 nanoarchaeum equitans
21	<a href="#">c3a5dM_</a>	Alignment	not modelled	100.0	22	<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
22	<a href="#">c3vr5C_</a>	Alignment	not modelled	100.0	23	<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="#">c2w6jD_</a>	Alignment	not modelled	100.0	24	<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.
24	<a href="#">c1skyE_</a>	Alignment	not modelled	100.0	27	<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 of2 f1-atpase from the thermophilic bacillus ps3
25	<a href="#">c2jizD_</a>	Alignment	not modelled	100.0	24	<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.
26	<a href="#">c3vr5D_</a>	Alignment	not modelled	100.0	25	<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)]
27	<a href="#">c6focD_</a>	Alignment	not modelled	100.0	25	<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
28	<a href="#">c1fx0B_</a>	Alignment	not modelled	100.0	24	<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
						<b>PDB header:</b> hydrolase

29	<a href="#">c2dpyA_</a>	Alignment	not modelled	100.0	24	<b>Chain:</b> A: <b>PDB Molecule:</b> flagellum-specific atp synthase; <b>PDBTitle:</b> crystal structure of the flagellar type iii atpase fliii
30	<a href="#">c6npjC_</a>	Alignment	not modelled	100.0	23	<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 central stalk esco from the enteropathogenic e. coli (epec) type iii3 secretion system
31	<a href="#">c3j9uD_</a>	Alignment	not modelled	100.0	24	<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
32	<a href="#">c4xd7B_</a>	Alignment	not modelled	100.0	54	<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
33	<a href="#">c2c61A_</a>	Alignment	not modelled	100.0	25	<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
34	<a href="#">c5bo5B_</a>	Alignment	not modelled	100.0	25	<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
35	<a href="#">c3sdzA_</a>	Alignment	not modelled	100.0	25	<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
36	<a href="#">c2oblA_</a>	Alignment	not modelled	100.0	24	<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
37	<a href="#">c5syrA_</a>	Alignment	not modelled	100.0	30	<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
38	<a href="#">c1vdzA_</a>	Alignment	not modelled	100.0	23	<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
39	<a href="#">d2jdia3</a>	Alignment	not modelled	100.0	62	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
40	<a href="#">c4nphA_</a>	Alignment	not modelled	100.0	29	<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
41	<a href="#">d1skyb3</a>	Alignment	not modelled	100.0	67	<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="#">d1fx0a3</a>	Alignment	not modelled	100.0	66	<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="#">d2jdid3</a>	Alignment	not modelled	100.0	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)
44	<a href="#">d1skye3</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
45	<a href="#">d1fx0b3</a>	Alignment	not modelled	100.0	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)
46	<a href="#">c3l0oB_</a>	Alignment	not modelled	100.0	19	<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
47	<a href="#">c3l0oA_</a>	Alignment	not modelled	100.0	17	<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
48	<a href="#">c1xpuB_</a>	Alignment	not modelled	100.0	17	<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 dihydrocyclomycin (fpdb)
49	<a href="#">d1xpuA3</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
50	<a href="#">d1fx0a1</a>	Alignment	not modelled	100.0	51	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
51	<a href="#">d2jdia1</a>	Alignment	not modelled	100.0	47	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
52	<a href="#">d1skyb1</a>	Alignment	not modelled	100.0	53	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
53	<a href="#">d2f43a1</a>	Alignment	not modelled	100.0	46	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase

54	<a href="#">d1skyb2</a>	Alignment	not modelled	99.6	47	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
55	<a href="#">d1maba2</a>	Alignment	not modelled	99.6	42	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
56	<a href="#">d2dia2</a>	Alignment	not modelled	99.5	46	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
57	<a href="#">d1fx0a2</a>	Alignment	not modelled	99.5	48	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
58	<a href="#">d2did1</a>	Alignment	not modelled	99.0	29	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
59	<a href="#">d1skye1</a>	Alignment	not modelled	98.9	32	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
60	<a href="#">c1u9iA_</a>	Alignment	not modelled	98.8	14	<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
61	<a href="#">c4ydsA_</a>	Alignment	not modelled	98.8	14	<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
62	<a href="#">d1fx0b1</a>	Alignment	not modelled	98.7	29	<b>Fold:</b> Left-handed superhelix <b>Superfamily:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> C-terminal domain of alpha and beta subunits of F1 ATP synthase
63	<a href="#">d1tf7a1</a>	Alignment	not modelled	98.4	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
64	<a href="#">d1tf7a2</a>	Alignment	not modelled	98.4	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)
65	<a href="#">c2recB_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
66	<a href="#">c1pznA_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
67	<a href="#">c2zroA_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
68	<a href="#">d2i1qa2</a>	Alignment	not modelled	98.2	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)
69	<a href="#">d1xp8a1</a>	Alignment	not modelled	98.1	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)
70	<a href="#">c3ldaA_</a>	Alignment	not modelled	98.1	15	<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
71	<a href="#">c3hr8A_</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
72	<a href="#">c2dr3A_</a>	Alignment	not modelled	98.1	19	<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
73	<a href="#">d1mo6a1</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)
74	<a href="#">d1n0wa_</a>	Alignment	not modelled	98.1	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)
75	<a href="#">d1ubea1</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)
76	<a href="#">c2dfiA_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rada; <b>PDBTitle:</b> crystal structure of left-handed rada filament
77	<a href="#">c1xp8A_</a>	Alignment	not modelled	98.0	18	<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
78	<a href="#">c1pznG_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)

79	<a href="#">c5lkmB</a>	Alignment	not modelled	98.0	19	<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
80	<a href="#">d1pzna2</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)
81	<a href="#">c1szpC</a>	Alignment	not modelled	97.9	17	<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
82	<a href="#">c2ztsB</a>	Alignment	not modelled	97.9	14	<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
83	<a href="#">c1t4gA</a>	Alignment	not modelled	97.9	19	<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
84	<a href="#">c2w0mA</a>	Alignment	not modelled	97.8	20	<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
85	<a href="#">d1u94a1</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)
86	<a href="#">c2zjbB</a>	Alignment	not modelled	97.8	15	<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
87	<a href="#">d1szpa2</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)
88	<a href="#">d1v5wa</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> RecA protein-like (ATPase-domain)
89	<a href="#">c2cvhB</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> dna repair and recombination protein radb; <b>PDBTitle:</b> crystal structure of the radb recombinase
90	<a href="#">c5jzcG</a>	Alignment	not modelled	97.7	17	<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
91	<a href="#">c3io5B</a>	Alignment	not modelled	97.7	15	<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 uvx recombinase core2 domain from enterobacteria phage t4
92	<a href="#">c5jwqA</a>	Alignment	not modelled	97.7	20	<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
93	<a href="#">c4wiaA</a>	Alignment	not modelled	97.5	15	<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
94	<a href="#">c3bs4A</a>	Alignment	not modelled	97.4	11	<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
95	<a href="#">c3bh0A</a>	Alignment	not modelled	97.4	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
96	<a href="#">c2vyeA</a>	Alignment	not modelled	97.3	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
97	<a href="#">c2q6tB</a>	Alignment	not modelled	97.2	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
98	<a href="#">c4nmnA</a>	Alignment	not modelled	97.2	21	<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
99	<a href="#">d2did2</a>	Alignment	not modelled	97.2	21	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
100	<a href="#">d1fx0b2</a>	Alignment	not modelled	97.2	21	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
101	<a href="#">d1skye2</a>	Alignment	not modelled	97.2	16	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase
102	<a href="#">c3cmvG</a>	Alignment	not modelled	97.1	19	<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
103	<a href="#">d1mabb2</a>	Alignment	not modelled	97.1	20	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>Family:</b> N-terminal domain of alpha and beta subunits of F1 ATP synthase <b>PDB header:</b> hydrolase



104	<a href="#">c4a1fB_</a>	Alignment	not modelled	97.1	12	<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
105	<a href="#">d1cr2a_</a>	Alignment	not modelled	96.8	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)
106	<a href="#">c4lyaA_</a>	Alignment	not modelled	96.6	13	<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)
107	<a href="#">c3bgwD_</a>	Alignment	not modelled	96.3	21	<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
108	<a href="#">c4zc0A_</a>	Alignment	not modelled	96.3	18	<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
109	<a href="#">c5x06G_</a>	Alignment	not modelled	96.3	13	<b>PDB header:</b> replication <b>Chain:</b> G; <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein
110	<a href="#">c4kxfF_</a>	Alignment	not modelled	96.2	17	<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
111	<a href="#">c6bbmA_</a>	Alignment	not modelled	96.2	14	<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
112	<a href="#">c2a5yB_</a>	Alignment	not modelled	96.1	10	<b>PDB header:</b> apoptosis <b>Chain:</b> B; <b>PDB Molecule:</b> ced-4; <b>PDBTitle:</b> structure of a ced-4/ced-9 complex
113	<a href="#">c5eaxB_</a>	Alignment	not modelled	96.1	11	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B; <b>PDB Molecule:</b> dna replication atp-dependent helicase/nuclease dna2; <b>PDBTitle:</b> crystal structure of dna2 in complex with an ssdna
114	<a href="#">c5zr1A_</a>	Alignment	not modelled	96.1	12	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A; <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
115	<a href="#">c5bq5A_</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> insertion sequence is5376 putative atp-binding protein; <b>PDBTitle:</b> crystal structure of the istb aaa+ domain bound to adp-bef3
116	<a href="#">c6qe1B_</a>	Alignment	not modelled	96.1	13	<b>PDB header:</b> replication <b>Chain:</b> B; <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> e. coli dnabc apo complex
117	<a href="#">c6cy1B_</a>	Alignment	not modelled	96.0	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
118	<a href="#">c2og2A_</a>	Alignment	not modelled	96.0	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 arabidopsis2 thaliana
119	<a href="#">c3dmdA_</a>	Alignment	not modelled	96.0	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
120	<a href="#">c5udbD_</a>	Alignment	not modelled	96.0	19	<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