







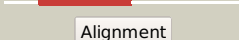

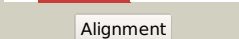

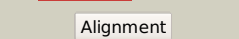










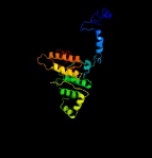
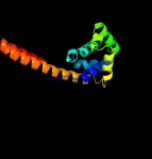


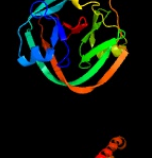

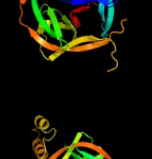
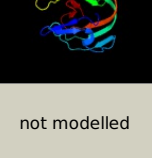


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0058_(dnaB)_60393_63017
Date	Tue Jul 23 14:50:09 BST 2019
Unique Job ID	1228c615ee4e645e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nmnA_	 Alignment		100.0	36	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
2	c6qeIB_	 Alignment		100.0	37	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
3	c4zc0A_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
4	c2vyeA_	 Alignment		100.0	46	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
5	c2q6tB_	 Alignment		100.0	44	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
6	c3bgwD_	 Alignment		100.0	33	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
7	c6bbmA_	 Alignment		100.0	39	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
8	c1dq3A_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease; PDBTitle: crystal structure of an archaeal intein-encoded homing2 endonuclease pi-pfui
9	c4a1fB_	 Alignment		100.0	37	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
10	c2cw8A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease pi-pk0ii; PDBTitle: crystal structure of intein homing endonuclease ii
11	c1vdeA_	 Alignment		100.0	17	PDB header: endonuclease Chain: A: PDB Molecule: pi-scei; PDBTitle: pi-scei, a homing endonuclease with protein splicing2 activity

12	c3bh0A_	Alignment		100.0	38	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
13	c1q57G_	Alignment		100.0	19	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
14	c2r5uD_	Alignment		100.0	99	PDB header: hydrolase Chain: D: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the n-terminal domain of dnab helicase from2 mycobacterium tuberculosis
15	d1mi8a_	Alignment		100.0	48	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
16	c4o1rA_	Alignment		99.9	49	PDB header: splicing Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of npudnab intein
17	c1zd7B_	Alignment		99.9	37	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: 1.7 angstrom crystal structure of post-splicing form of a dnae intein2 from synechocystis sp. pcc 6803
18	c4zc0D_	Alignment		99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
19	c2imzA_	Alignment		99.9	50	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease pi-mtui; PDBTitle: crystal structure of mtu reca intein splicing domain
20	d1am2a_	Alignment		99.9	36	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
21	c5o9jB_	Alignment	not modelled	99.9	30	PDB header: hydrolase Chain: B: PDB Molecule: transcription initiation factor iib,transcription PDBTitle: crystal structure of transcription factor iib mja mini-intein
22	d1jwea_	Alignment	not modelled	99.9	40	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
23	c2keqA_	Alignment	not modelled	99.9	38	PDB header: splicing Chain: A: PDB Molecule: dna polymerase iii alpha subunit, nucleic acid PDBTitle: solution structure of dnae intein from nostoc punctiforme
24	d1mo6a1	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
25	c3ldaA_	Alignment	not modelled	99.9	18	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
26	d1cr2a_	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
27	c1szpC_	Alignment	not modelled	99.9	21	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
28	c3io5B_	Alignment	not modelled	99.9	18	PDB header: dna binding protein Chain: B: PDB Molecule: recombination and repair protein; PDBTitle: crystal structure of a dimeric form of the uvx recombinase core2 domain from enterobacteria phage t4
29	c2imzA_	Alignment	not modelled	99.9	22	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein mj0781;

29	c4jw2A	Alignment	not modelled	99.9	32	PDBTitle: solution structure of a klba intein precursor from2 methanococcus jannaschii
30	d1b79a	Alignment	not modelled	99.9	42	Fold: N-terminal domain of DnaB helicase Superfamily: N-terminal domain of DnaB helicase Family: N-terminal domain of DnaB helicase
31	d1ubea1	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
32	c5jzcG	Alignment	not modelled	99.9	18	PDB header: dna binding protein Chain: G; PDB Molecule: dna repair protein rad51 homolog 1; PDBTitle: helical filament
33	c4e2uA	Alignment	not modelled	99.9	31	PDB header: unknown function Chain: A; PDB Molecule: pho rada intein; PDBTitle: crystal structures of radamin intein from pyrococcus horikoshii
34	c2in0A	Alignment	not modelled	99.9	42	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease pi-mtui; PDBTitle: crystal structure of mtu reca intein splicing domain
35	c2lcjA	Alignment	not modelled	99.9	31	PDB header: hydrolase Chain: A; PDB Molecule: pab polc intein; PDBTitle: solution nmr structure of pab polii intein
36	c2df1A	Alignment	not modelled	99.9	13	PDB header: recombination Chain: A; PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
37	c1t4gA	Alignment	not modelled	99.9	15	PDB header: recombination Chain: A; PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
38	c4o1sB	Alignment	not modelled	99.9	39	PDB header: splicing Chain: B; PDB Molecule: v-type atp synthase alpha chain; PDBTitle: crystal structure of tvovma intein
39	c3gxvA	Alignment	not modelled	99.9	21	PDB header: hydrolase/replication Chain: A; PDB Molecule: replicative dna helicase; PDBTitle: three-dimensional structure of n-terminal domain of dnab2 helicase from helicobacter pylori and its interactions with3 primase
40	d1u94a1	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
41	c1pznA	Alignment	not modelled	99.9	16	PDB header: recombination Chain: A; PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
42	d1xp8a1	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
43	c2zroA	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A; PDB Molecule: protein reca; PDBTitle: msreca adp form iv
44	d1dq3a1	Alignment	not modelled	99.8	38	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
45	c5z51A	Alignment	not modelled	99.8	11	PDB header: transferase Chain: A; PDB Molecule: dna primase; PDBTitle: helicase binding domain of primase from mycobacterium tuberculosis
46	d1szpa2	Alignment	not modelled	99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
47	c1xp8A	Alignment	not modelled	99.8	18	PDB header: dna binding protein Chain: A; PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
48	c2recB	Alignment	not modelled	99.8	21	PDB header: helicase PDB COMPND:
49	c2ztsB	Alignment	not modelled	99.8	17	PDB header: atp-binding protein Chain: B; PDB Molecule: putative uncharacterized protein ph0186; PDBTitle: crystal structure of kaic-like protein ph0186 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
50	d1n0wa	Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
51	c1b24A	Alignment	not modelled	99.8	17	PDB header: intron-encoded Chain: A; PDB Molecule: protein (i-dmoi); PDBTitle: i-dmoi, intron-encoded endonuclease
52	d1tf7a1	Alignment	not modelled	99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
53	d2i1qa2	Alignment	not modelled	99.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
54	d1tf7a2	Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
55	c2cvhB	Alignment	not modelled	99.8	20	PDB header: dna binding protein Chain: B; PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase PDB header: dna binding protein

56	c5lkmB_	Alignment	not modelled	99.8	33	Chain: B: PDB Molecule: dna repair protein rada; PDBTitle: rada bound to dtdp
57	c3hr8A_	Alignment	not modelled	99.8	18	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
58	d1v5wa_	Alignment	not modelled	99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
59	c4ydsA_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfolobus acidocaldarius with atp and mg-ion
60	c2zjbB_	Alignment	not modelled	99.8	15	PDB header: recombination Chain: B: PDB Molecule: meiotic recombination protein dmc1/lim15 homolog; PDBTitle: crystal structure of the human dmc1-m200v polymorphic2 variant
61	c1u9iA_	Alignment	not modelled	99.7	14	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
62	c2w0mA_	Alignment	not modelled	99.7	21	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus p2
63	d1dq3a4	Alignment	not modelled	99.7	22	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
64	c1pznG_	Alignment	not modelled	99.7	15	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
65	c2lwyA_	Alignment	not modelled	99.7	37	PDB header: unknown function Chain: A: PDB Molecule: bacterial intein-like domain; PDBTitle: solution structure of bacterial intein-like domain from clostridium2 thermocellum
66	d1nlfa_	Alignment	not modelled	99.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
67	c5o15B_	Alignment	not modelled	99.7	20	PDB header: splicing Chain: B: PDB Molecule: dna polymerase iii subunit alpha,dna polymerase iii subunit PDBTitle: crystal structure of an inactivated ssp siclopps intein with cfahpq2 extein
68	d1pzna2	Alignment	not modelled	99.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
69	c5jwqA_	Alignment	not modelled	99.7	15	PDB header: transcription regulator Chain: A: PDB Molecule: circadian clock protein kinase kaic; PDBTitle: crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
70	c4wiaA_	Alignment	not modelled	99.7	16	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
71	d1jvaa3	Alignment	not modelled	99.6	15	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
72	c2r6cG_	Alignment	not modelled	99.6	19	PDB header: replication Chain: G: PDB Molecule: dnag primase, helicase binding domain; PDBTitle: crystal form bh2
73	c3cmuA_	Alignment	not modelled	99.6	17	PDB header: recombination/dna Chain: A: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
74	d1at0a_	Alignment	not modelled	99.6	16	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Hedgehog C-terminal (Hog) autoprocessing domain
75	c5o17A_	Alignment	not modelled	99.5	24	PDB header: splicing Chain: A: PDB Molecule: dna-directed dna polymerase,dna-directed dna polymerase; PDBTitle: crystal structure of an inactivated npu siclopps intein with cfahpq2 extein
76	c2dr3A_	Alignment	not modelled	99.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0273 protein ph0284; PDBTitle: crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
77	c2lznA_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: solution structure of s. aureus primase c-terminal domain
78	c3cmvG_	Alignment	not modelled	99.4	22	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
79	c3bs4A_	Alignment	not modelled	99.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ph0321; PDBTitle: crystal structure of uncharacterized protein ph0321 from pyrococcus2 horikoshii in complex with an unknown peptide
80	c6bs8C_	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: C: PDB Molecule: replicative dna helicase; PDBTitle: the class 3 dnab intein from mycobacterium smegmatis
81	c3cmwA_	Alignment	not modelled	99.1	18	PDB header: recombination/dna Chain: A: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
						Fold: AXH domain

82	d1oa8a_	Alignment	not modelled	98.9	25	Superfamily: AXH domain Family: AXH domain
83	c3hyiA_	Alignment	not modelled	98.8	19	PDB header: transcription regulator Chain: A: PDB Molecule: protein duf199/whia; PDBTitle: crystal structure of full-length duf199/whia from thermatoga maritima
84	c3hyjD_	Alignment	not modelled	98.2	14	PDB header: transcription regulator Chain: D: PDB Molecule: protein duf199/whia; PDBTitle: crystal structure of the n-terminal laglidadg domain of duf199/whia
85	c2og2A_	Alignment	not modelled	98.2	9	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
86	c2cnwF_	Alignment	not modelled	98.1	16	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
87	c3b9qA_	Alignment	not modelled	98.1	10	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
88	c5gafi_	Alignment	not modelled	98.0	15	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
89	c2q9cA_	Alignment	not modelled	98.0	15	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmppnp with mgcl complex
90	c1vmaA_	Alignment	not modelled	97.9	15	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
91	c6cy1B_	Alignment	not modelled	97.9	12	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
92	c4ak9A_	Alignment	not modelled	97.9	13	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
93	c2yhsA_	Alignment	not modelled	97.9	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
94	c5l3qB_	Alignment	not modelled	97.8	10	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
95	c2qy9A_	Alignment	not modelled	97.8	15	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
96	c2j7pA_	Alignment	not modelled	97.8	17	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
97	c5l3sF_	Alignment	not modelled	97.8	14	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
98	c2qmoA_	Alignment	not modelled	97.7	15	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
99	c5l3rC_	Alignment	not modelled	97.7	12	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
100	d1gppa_	Alignment	not modelled	97.7	23	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
101	c3dmdA_	Alignment	not modelled	97.7	12	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
102	d1jvaa1	Alignment	not modelled	97.6	23	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
103	d1skye3	Alignment	not modelled	97.5	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
104	c2j37W_	Alignment	not modelled	97.5	17	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
105	c1zu4A_	Alignment	not modelled	97.5	12	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
106	c3fkqA_	Alignment	not modelled	97.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
107	c2j289_	Alignment	not modelled	97.4	14	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs

108	c1v06A_	 Alignment	not modelled	97.4	20	PDB header: dna-binding protein Chain: A: PDB Molecule: hmg box-containing protein 1; PDBTitle: axh domain of the transcription factor hbp1 from m.musculus
109	c2v3cC_	 Alignment	not modelled	97.4	16	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
110	c1r7mA_	 Alignment	not modelled	97.3	8	PDB header: hydrolase/dna Chain: A: PDB Molecule: intron-encoded endonuclease i-scei; PDBTitle: the homing endonuclease i-scei bound to its dna recognition2 region
111	c6ah0D_	 Alignment	not modelled	97.3	22	PDB header: splicing Chain: D: PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: the cryo-em structure of the precursor of human pre-catalytic2 spliceosome (pre-b complex)
112	d1x6va3	 Alignment	not modelled	97.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'phosphosulfate kinase (APS kinase)
113	c3fmfA_	 Alignment	not modelled	97.3	10	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
114	c1qzWC_	 Alignment	not modelled	97.3	16	PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
115	c3jcrC_	 Alignment	not modelled	97.2	23	PDB header: splicing Chain: C: PDB Molecule: hbr2; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrrp complex
116	c2dchX_	 Alignment	not modelled	97.2	21	PDB header: hydrolase Chain: X: PDB Molecule: putative homing endonuclease; PDBTitle: crystal structure of archaeal intron-encoded homing endonuclease i-2 tsp061i
117	c4f92B_	 Alignment	not modelled	97.2	16	PDB header: hydrolase Chain: B: PDB Molecule: u5 small nuclear ribonucleoprotein 200 kda helicase; PDBTitle: brr2 helicase region s1087I
118	c2i1vB_	 Alignment	not modelled	97.2	11	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6- PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
119	c5dcaA_	 Alignment	not modelled	97.2	17	PDB header: hydrolase Chain: A: PDB Molecule: pre-mrna-splicing helicase brr2; PDBTitle: crystal structure of yeast full length brr2 in complex with prp8 jab12 domain
120	c5do7B_	 Alignment	not modelled	97.2	17	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8