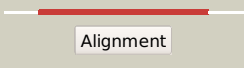

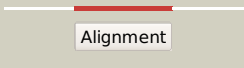

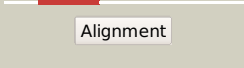

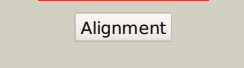

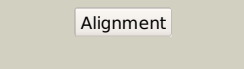

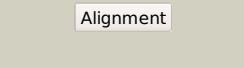

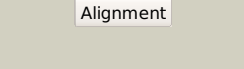

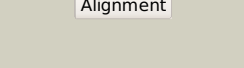

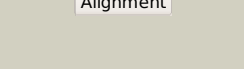

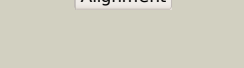

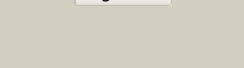
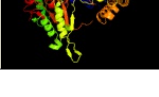

















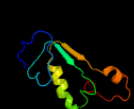






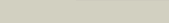
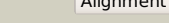



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0631c_(recC)_725016_728309
 Date Fri Jul 26 01:50:19 BST 2019
 Unique Job ID 04b0d1383d4de2f1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w36F_	 Alignment		100.0	29	PDB header: recombination Chain: F: PDB Molecule: exodeoxyribonuclease v gamma chain; PDBTitle: recbcd:dna complex
2	d1w36c2	 Alignment		100.0	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
3	d1w36c1	 Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
4	c3u44B_	 Alignment		100.0	12	PDB header: hydrolase/dna Chain: B: PDB Molecule: atp-dependent helicase/deoxyribonuclease subunit b; PDBTitle: crystal structure of addab-dna complex
5	d1w36c3	 Alignment		100.0	22	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Exodeoxyribonuclease V beta chain (RecC), C-terminal domain
6	c3u4qA_	 Alignment		100.0	12	PDB header: hydrolase/dna Chain: A: PDB Molecule: atp-dependent helicase/nuclease subunit a; PDBTitle: structure of addab-dna complex at 2.8 angstroms
7	c1w36E_	 Alignment		100.0	16	PDB header: recombination Chain: E: PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
8	c2is6B_	 Alignment		100.0	12	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of uvrd-dna-adpmgf3 ternary complex
9	c1uuaB_	 Alignment		100.0	13	PDB header: hydrolase/dna Chain: B: PDB Molecule: protein (atp-dependent dna helicase rep.); PDBTitle: e. coli rep helicase/dna complex
10	d1uuaa2	 Alignment		100.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
11	c4c30I_	 Alignment		100.0	15	PDB header: hydrolase/dna Chain: I: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of deinococcus radiodurans uvrd in2 complex with dna, form 2

12	c3lfuA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of e. coli uvrd
13	d1pjra2	 Alignment		100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
14	c1pjrA_	 Alignment		100.0	15	PDB header: helicase Chain: A: PDB Molecule: pcra; PDBTitle: structure of dna helicase
15	d1w36b2	 Alignment		100.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
16	c2pjrF_	 Alignment		100.0	13	PDB header: hydrolase/dna Chain: F: PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
17	c1qhhB_	 Alignment		99.9	11	PDB header: hydrolase Chain: B: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
18	c2pjrB_	 Alignment		99.6	27	PDB header: hydrolase/dna Chain: B: PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
19	c1qhhD_	 Alignment		99.5	27	PDB header: hydrolase Chain: D: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
20	c3dmnA_	 Alignment		99.2	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dna helicase; PDBTitle: the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcf51
21	d1w36d2	 Alignment	not modelled	98.8	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
22	d1uaaa1	 Alignment	not modelled	98.5	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
23	d1w36b1	 Alignment	not modelled	98.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
24	d1pjra1	 Alignment	not modelled	98.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
25	c3upuC_	 Alignment	not modelled	97.8	16	PDB header: hydrolase/dna Chain: C: PDB Molecule: atp-dependent dna helicase dda; PDBTitle: crystal structure of the t4 phage sf1b helicase dda
26	c3e1sA_	 Alignment	not modelled	97.3	15	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
27	c5ld2D_	 Alignment	not modelled	97.1	18	PDB header: hydrolase Chain: D: PDB Molecule: recbcd enzyme subunit recd; PDBTitle: cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain
28	c1w36G_	 Alignment	not modelled	97.1	16	PDB header: recombination Chain: G: PDB Molecule: exodeoxyribonuclease v alpha chain; PDBTitle: recbcd:dna complex
29	c1qhhA_	 Alignment	not modelled	97.1	22	PDB header: hydrolase Chain: A: PDB Molecule: protein (pcra (subunit));

						PDBTitle: structure of dna helicase with adpnp
30	c5o6dB_	Alignment	not modelled	97.0	12	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of scpif1 in complex with polydt and atpgs
31	c5n8oA_	Alignment	not modelled	96.8	14	PDB header: transferase Chain: A: PDB Molecule: dna helicase i; PDBTitle: cryo em structure of the conjugative relaxase trai of the f/r1 plasmid2 system
32	c3gp8A_	Alignment	not modelled	96.5	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
33	c4b3gA_	Alignment	not modelled	96.3	19	PDB header: hydrolase/rna Chain: A: PDB Molecule: dna-binding protein smubp-2; PDBTitle: crystal structure of ighmbp2 helicase in complex with rna
34	c4onbA_	Alignment	not modelled	96.3	17	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated exonuclease, cas4 family; PDBTitle: crystal structure of crispr-associated exonuclease (cas4 family) from2 pyrobaculum calidifontis jcm 11548
35	c5fhhA_	Alignment	not modelled	95.9	11	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of human pif1 helicase domain residues 200-641
36	c5eaxB_	Alignment	not modelled	95.3	18	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna replication atp-dependent helicase/nuclease dna2; PDBTitle: crystal structure of dna2 in complex with an ssdna
37	c5wwpA_	Alignment	not modelled	95.1	19	PDB header: hydrolase Chain: A: PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
38	c5wwpB_	Alignment	not modelled	94.4	15	PDB header: hydrolase Chain: B: PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
39	c2gk7A_	Alignment	not modelled	94.1	14	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: structural and functional insights into the human upf1 helicase core
40	c5ftbA_	Alignment	not modelled	93.9	10	PDB header: hydrolase Chain: A: PDB Molecule: tpr domain protein; PDBTitle: crystal structure of pif1 helicase from bacteroides in2 complex with amppnp
41	c4n0oC_	Alignment	not modelled	91.6	27	PDB header: hydrolase/dna Chain: C: PDB Molecule: replicase polyprotein 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
42	c2wjyA_	Alignment	not modelled	91.1	12	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
43	c5mznA_	Alignment	not modelled	90.0	14	PDB header: hydrolase Chain: A: PDB Molecule: helicase sen1,helicase sen1; PDBTitle: helicase sen1
44	c2xzlA_	Alignment	not modelled	89.1	16	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
45	c3h4rA_	Alignment	not modelled	87.1	9	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease 8; PDBTitle: crystal structure of e. coli rece exonuclease
46	c4pj3A_	Alignment	not modelled	86.9	20	PDB header: rna binding protein Chain: A: PDB Molecule: intron-binding protein aquarius; PDBTitle: structural insight into the function and evolution of the spliceosomal2 helicase aquarius, structure of aquarius in complex with amppnp
47	c4ic1D_	Alignment	not modelled	84.2	9	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of sso0001
48	c3vkwA_	Alignment	not modelled	71.0	22	PDB header: transferase Chain: A: PDB Molecule: replicase large subunit; PDBTitle: crystal structure of the superfamily 1 helicase from tomato mosaic2 virus
49	c4nl8E_	Alignment	not modelled	37.0	20	PDB header: dna binding protein Chain: E: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to ssb c-terminal tail peptide
50	c4nl4H_	Alignment	not modelled	25.7	20	PDB header: dna binding protein Chain: H: PDB Molecule: primosome assembly protein pria; PDBTitle: pria helicase bound to adp
51	c6hegA_	Alignment	not modelled	22.3	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent rna helicase hrpb; PDBTitle: crystal structure of escherichia coli deah/rha helicase hrpb
52	d1w36d1	Alignment	not modelled	20.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
53	c5lopC_	Alignment	not modelled	15.4	28	PDB header: rna binding protein Chain: C: PDB Molecule: klla0a11308p; PDBTitle: structure of the active form of /k. lactis/ dcp1-dcp2-edc3 decapping2 complex bound to m7gdp
54	c2vbcA_	Alignment	not modelled	12.4	12	PDB header: hydrolase Chain: A: PDB Molecule: dengue 4 ns3 full-length protein; PDBTitle: crystal structure of the ns3 protease-helicase from dengue2 virus
						PDB header: dna binding protein/dna

55	c5zyuA_	Alignment	not modelled	12.3	8	Chain: A: PDB Molecule: mitochondrial genome maintenance exonuclease 1; PDBTitle: the crystal structure of humanmgme1 with single strand dna2
56	c5exvD_	Alignment	not modelled	12.1	35	PDB header: heme-binding protein Chain: D: PDB Molecule: hemin-degrading hems.chux domain protein; PDBTitle: crystal structure of heme binding protein hutx from vibrio cholerae
57	c5lqwO_	Alignment	not modelled	11.5	15	PDB header: splicing Chain: O: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase-like PDBTitle: yeast activated spliceosome
58	d2h5na1	Alignment	not modelled	11.5	14	Fold: TerB-like Superfamily: TerB-like Family: PG1108-like
59	c4tpsD_	Alignment	not modelled	11.3	16	PDB header: replication Chain: D: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: sporulation inhibitor of dna replication, sira, in complex with domain2 i of dnaa
60	c2l2qA_	Alignment	not modelled	11.3	11	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
61	c2v1xB_	Alignment	not modelled	11.0	9	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase q1; PDBTitle: crystal structure of human recq-like dna helicase
62	c4q47A_	Alignment	not modelled	10.9	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna helicase recq; PDBTitle: structure of the drrecq catalytic core in complex with adp
63	c4cdgA_	Alignment	not modelled	10.6	16	PDB header: hydrolase Chain: A: PDB Molecule: bloom syndrome protein; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
64	d1zrra1	Alignment	not modelled	10.6	14	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Acireductone dioxygenase
65	d1gm5a4	Alignment	not modelled	10.4	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
66	c5lj5Q_	Alignment	not modelled	10.0	15	PDB header: splicing Chain: Q: PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp16; PDBTitle: overall structure of the yeast spliceosome immediately after2 branching.
67	d1oywa2	Alignment	not modelled	9.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
68	d1wnaa1	Alignment	not modelled	9.1	13	Fold: TTHA1528-like Superfamily: TTHA1528-like Family: TTHA1528-like
69	c5z58x_	Alignment	not modelled	9.0	15	PDB header: splicing Chain: X: PDB Molecule: smad nuclear-interacting protein 1; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
70	c1oywA_	Alignment	not modelled	8.9	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of the recq catalytic core
71	c4on9B_	Alignment	not modelled	8.9	11	PDB header: hydrolase Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: dech box helicase domain
72	c3e2iA_	Alignment	not modelled	8.7	9	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from s. aureus
73	c4mgeB_	Alignment	not modelled	8.6	9	PDB header: transferase Chain: B: PDB Molecule: pts system, cellobiose-specific iib component; PDBTitle: 1.85 angstrom resolution crystal structure of pts system cellobiose-2 specific transporter subunit iib from bacillus anthracis.
74	d1vr3a1	Alignment	not modelled	8.6	20	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Acireductone dioxygenase
75	c4cbmA_	Alignment	not modelled	8.4	16	PDB header: hydrolase Chain: A: PDB Molecule: serine protease ns3; PDBTitle: pestivirus ns3 helicase
76	c4qglA_	Alignment	not modelled	8.1	7	PDB header: oxidoreductase Chain: A: PDB Molecule: acireductone dioxygenase; PDBTitle: acireductone dioxygenase from bacillus anthracis with three cadmium2 ions
77	c1z63A_	Alignment	not modelled	8.1	13	PDB header: hydrolase/dna complex Chain: A: PDB Molecule: helicase of the snf2/rad54 family; PDBTitle: sulfolobus solfataricus swi2/snf2 atpase core in complex with dsdna
78	d1tlea2	Alignment	not modelled	8.0	21	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Subtilase propeptides/inhibitors
79	c5gn1D_	Alignment	not modelled	8.0	23	PDB header: hydrolase Chain: D: PDB Molecule: atp-dependent helicase fun30; PDBTitle: crystal structure of the c-terminal part of fun30 atpase domain PDB header: hydrolase

80	c3kx2A_	Alignment	not modelled	7.9	13	Chain: A; PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase prp43; PDBTitle: crystal structure of prp43p in complex with adp
81	c5eomF_	Alignment	not modelled	7.8	11	PDB header: transferase Chain: F; PDB Molecule: protein mab-21-like 1; PDBTitle: structure of full-length human mab2111 with bound ctp
82	c6hwyB_	Alignment	not modelled	7.8	21	PDB header: viral protein Chain: B; PDB Molecule: putative gag polyprotein; PDBTitle: mature mlv capsid pentamer structure in intact virus particles
83	c4km5A_	Alignment	not modelled	7.8	9	PDB header: transferase Chain: A; PDB Molecule: cyclic gmp-amp synthase; PDBTitle: x-ray crystal structure of human cyclic gmp-amp synthase (cgas)
84	c3nctC_	Alignment	not modelled	7.5	9	PDB header: dna binding protein, chaperone Chain: C; PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
85	c2x7mA_	Alignment	not modelled	7.4	28	PDB header: hydrolase Chain: A; PDB Molecule: archaemetzincin; PDBTitle: crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
86	c5n8zA_	Alignment	not modelled	7.4	12	PDB header: hydrolase Chain: A; PDB Molecule: cg9323, isoform a; PDBTitle: crystal structure of drosophila dhx36 helicase in complex with2 ctctccctt
87	c2l25A_	Alignment	not modelled	7.3	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: np_888769.1
88	c2ja1A_	Alignment	not modelled	7.2	8	PDB header: transferase Chain: A; PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
89	c4k8vA_	Alignment	not modelled	7.2	12	PDB header: transferase Chain: A; PDB Molecule: cyclic gmp-amp synthase; PDBTitle: structure of cyclic gmp-amp synthase (cgas)
90	d1xx6a1	Alignment	not modelled	7.0	5	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
91	c5xdrA_	Alignment	not modelled	6.9	10	PDB header: hydrolase Chain: A; PDB Molecule: pre-mrna-splicing factor atp-dependent rna helicase dhx15; PDBTitle: crystal structure of human deah-box rna helicase dhx15 in complex with2 adp
92	d1tdja3	Alignment	not modelled	6.8	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Allosteric threonine deaminase C-terminal domain
93	c2z83A_	Alignment	not modelled	6.4	16	PDB header: viral protein Chain: A; PDB Molecule: helicase/nucleoside triphosphatase; PDBTitle: crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
94	c3jb9X_	Alignment	not modelled	6.4	17	PDB header: rna binding protein/rna Chain: X; PDB Molecule: pre-mrna-splicing factor cwf11; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
95	d1nkt4	Alignment	not modelled	6.4	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
96	c3b85A_	Alignment	not modelled	6.3	3	PDB header: hydrolase Chain: A; PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 pho2 from corynebacterium glutamicum
97	c3tbkA_	Alignment	not modelled	6.2	7	PDB header: hydrolase Chain: A; PDB Molecule: rig-i helicase domain; PDBTitle: mouse rig-i atpase domain
98	c1xx6B_	Alignment	not modelled	6.1	6	PDB header: transferase Chain: B; PDB Molecule: thymidine kinase; PDBTitle: x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
99	c2zxxA_	Alignment	not modelled	6.0	24	PDB header: cell cycle/replication Chain: A; PDB Molecule: geminin; PDBTitle: crystal structure of cdt1/geminin complex