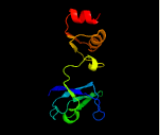

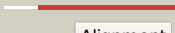
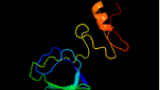









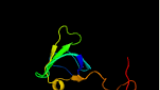

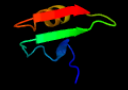

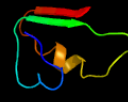

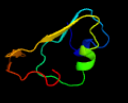

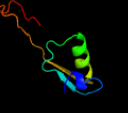




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2311 (-) _2583894_2584418
Date	Mon Aug 5 13:25:46 BST 2019
Unique Job ID	eca80f05d794dc42

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ld2D_	 Alignment		99.9	24	PDB header: hydrolase Chain: D; PDB Molecule: recbcd enzyme subunit recd; PDBTitle: cryo-em structure of recbcd+dna complex revealing activated nuclease2 domain
2	c3e1sA_	 Alignment		99.8	25	PDB header: hydrolase Chain: A; PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
3	c5n8oA_	 Alignment		99.8	21	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
4	c3gp8A_	 Alignment		99.8	26	PDB header: hydrolase/dna Chain: A; PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
5	c5ftbA_	 Alignment		99.7	23	PDB header: hydrolase Chain: A; PDB Molecule: tpr domain protein; PDBTitle: crystal structure of pif1 helicase from bacteroides in2 complex with ampnp
6	c5fhhA_	 Alignment		99.6	22	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of human pif1 helicase domain residues 200-641
7	c1w36G_	 Alignment		99.6	29	PDB header: recombination Chain: G; PDB Molecule: exodeoxyribonuclease v alpha chain; PDBTitle: recbcd:dna complex
8	d1w36d2	 Alignment		99.5	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
9	c4l0jA_	 Alignment		99.5	16	PDB header: hydrolase Chain: A; PDB Molecule: dna helicase i; PDBTitle: structure of a translocation signal domain mediating conjugative2 transfer by type iv secretion systems
10	c5o6dB_	 Alignment		99.4	20	PDB header: hydrolase Chain: B; PDB Molecule: atp-dependent dna helicase pif1; PDBTitle: structure of scpif1 in complex with polydt and atpgs
11	c3upuC_	 Alignment		99.1	21	PDB header: hydrolase/dna Chain: C; PDB Molecule: atp-dependent dna helicase dda; PDBTitle: crystal structure of the t4 phage sf1b helicase dda

12	c4n0oC_	Alignment		98.9	26	PDB header: hydrolase/dna Chain: C; PDB Molecule: replicase polyprotein 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
13	c5wwpA_	Alignment		98.7	19	PDB header: hydrolase Chain: A; PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
14	c5wwpB_	Alignment		98.7	21	PDB header: hydrolase Chain: B; PDB Molecule: orf1ab; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus2 helicase (mers-cov nsp13)
15	c3dmnA_	Alignment		98.6	13	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 wcfs1
16	c1pjrA_	Alignment		98.4	19	PDB header: helicase Chain: A; PDB Molecule: pcra; PDBTitle: structure of dna helicase
17	c4c30I_	Alignment		98.3	21	PDB header: hydrolase/dna Chain: I; PDB Molecule: dna helicase ii; PDBTitle: crystal structure of deinococcus radiodurans uvrd in2 complex with dna, form 2
18	d1w36b2	Alignment		98.3	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
19	c1uaaB_	Alignment		98.3	34	PDB header: hydrolase/dna Chain: B; PDB Molecule: protein (atp-dependent dna helicase rep.); PDBTitle: e. coli rep helicase/dna complex
20	c1qhhD_	Alignment		98.3	18	PDB header: hydrolase Chain: D; PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
21	c4b3gA_	Alignment	not modelled	98.3	21	PDB header: hydrolase/rna Chain: A; PDB Molecule: dna-binding protein smubp-2; PDBTitle: crystal structure of ighmbp2 helicase in complex with rna
22	c3lfuA_	Alignment	not modelled	98.3	24	PDB header: hydrolase Chain: A; PDB Molecule: dna helicase ii; PDBTitle: crystal structure of e. coli uvrd
23	c2is6B_	Alignment	not modelled	98.3	28	PDB header: hydrolase/dna Chain: B; PDB Molecule: dna helicase ii; PDBTitle: crystal structure of uvrd-dna-adpmgf3 ternary complex
24	c2pjrB_	Alignment	not modelled	98.2	18	PDB header: hydrolase/dna Chain: B; PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
25	d1pjra2	Alignment	not modelled	98.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
26	c2gk7A_	Alignment	not modelled	98.0	26	PDB header: hydrolase Chain: A; PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: structural and functional insights into the human upf1 helicase core
27	c3vkwA_	Alignment	not modelled	98.0	26	PDB header: transferase Chain: A; PDB Molecule: replicase large subunit; PDBTitle: crystal structure of the superfamily 1 helicase from tomato mosaic2 virus
28	d1uaaa2	Alignment	not modelled	97.9	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
29	c5eayB_	Alignment	not modelled	97.6	24	PDB header: hydrolase/dna Chain: B; PDB Molecule: dna replication atp-dependent

29	c2gaaB	Alignment	not modelled	97.8	24	helicase/nuclease dna2; PDBTitle: crystal structure of dna2 in complex with an ssdna
30	c2wjyA	Alignment	not modelled	97.4	26	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
31	c1w36E	Alignment	not modelled	97.4	27	PDB header: recombination Chain: E; PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
32	c2xzaA	Alignment	not modelled	97.3	21	PDB header: hydrolase/rna Chain: A; PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
33	c5mznA	Alignment	not modelled	97.1	19	PDB header: hydrolase Chain: A; PDB Molecule: helicase sen1,helicase sen1; PDBTitle: helicase sen1
34	c4pj3A	Alignment	not modelled	96.9	24	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
35	c6jimA	Alignment	not modelled	96.3	23	PDB header: viral protein/rna Chain: A; PDB Molecule: helicase; PDBTitle: viral helicase protein
36	c3u4qA	Alignment	not modelled	96.3	32	PDB header: hydrolase/dna Chain: A; PDB Molecule: atp-dependent helicase/nuclease subunit a; PDBTitle: structure of addab-dna complex at 2.8 angstroms
37	c3jb9X	Alignment	not modelled	96.1	19	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
38	c3u44B	Alignment	not modelled	95.0	18	PDB header: hydrolase/dna Chain: B; PDB Molecule: atp-dependent helicase/deoxyribonuclease subunit b; PDBTitle: crystal structure of addab-dna complex
39	d1w36c2	Alignment	not modelled	80.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
40	c1w36F	Alignment	not modelled	52.4	16	PDB header: recombination Chain: F; PDB Molecule: exodeoxyribonuclease v gamma chain; PDBTitle: recbcd:dna complex
41	c2e6zA	Alignment	not modelled	34.0	13	PDB header: transcription Chain: A; PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5
42	c4ytiB	Alignment	not modelled	31.7	15	PDB header: transcription Chain: B; PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
43	d1nz9a	Alignment	not modelled	26.1	13	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
44	c2mi6A	Alignment	not modelled	24.6	19	PDB header: transcription Chain: A; PDB Molecule: transcription termination/antitermination protein nusg; PDBTitle: solution structure of the carboxy terminal domain of nusg from2 mycobacterium tuberculosis
45	c3p8bB	Alignment	not modelled	21.6	15	PDB header: transferase/transcription Chain: B; PDB Molecule: transcription antitermination protein nusg; PDBTitle: x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
46	c2kvqG	Alignment	not modelled	20.8	24	PDB header: transcription Chain: G; PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
47	c2jvvA	Alignment	not modelled	20.8	24	PDB header: transcription Chain: A; PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
48	d1mhna	Alignment	not modelled	19.1	16	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
49	d1nppa2	Alignment	not modelled	18.1	15	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
50	c3b79A	Alignment	not modelled	16.3	18	PDB header: nucleotide binding protein Chain: A; PDB Molecule: toxin secretion atp-binding protein; PDBTitle: crystal structure of the n-terminal peptidase c39 like2 domain of the toxin secretion atp-binding protein from3 vibrio parahaemolyticus
51	d2d9ta1	Alignment	not modelled	16.1	13	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
52	c1g5vA	Alignment	not modelled	15.4	17	PDB header: translation Chain: A; PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein
53	c4a4fA	Alignment	not modelled	15.2	19	PDB header: rna binding protein Chain: A; PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with symmetrically2 dimethylated arginine
54	c3pnwX	Alignment	not modelled	14.7	13	PDB header: protein binding/immune system Chain: X; PDB Molecule: tudor domain-containing protein 3; PDBTitle: crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab

55	c2d9tA_	Alignment	not modelled	10.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tudor domain-containing protein 3; PDBTitle: solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse
56	c2lo9A_	Alignment	not modelled	8.5	62	PDB header: toxin Chain: A: PDB Molecule: mu-conotoxin buiiiib; PDBTitle: nmr solution structure of mu-conotoxin buiiiib
57	c1m1gB_	Alignment	not modelled	8.4	15	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
58	c2n5uA_	Alignment	not modelled	7.4	14	PDB header: photosynthesis Chain: A: PDB Molecule: tsr0524 protein; PDBTitle: solution structure of the cyanobacterial cytochrome b6f complex2 subunit petp
59	c3cgnA_	Alignment	not modelled	7.2	25	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of thermophilic slyd
60	c5y4oA_	Alignment	not modelled	7.1	15	PDB header: membrane protein Chain: A: PDB Molecule: low conductance mechanosensitive channel ynai; PDBTitle: cryo-em structure of mscs channel, ynai
61	d1lb8a1	Alignment	not modelled	7.1	3	Fold: Sm-like fold Superfamily: YhbC-like, C-terminal domain Family: YhbC-like, C-terminal domain
62	c4ui9D_	Alignment	not modelled	7.1	13	PDB header: cell cycle Chain: D: PDB Molecule: anaphase-promoting complex subunit 15; PDBTitle: atomic structure of the human anaphase-promoting complex
63	c4ytkA_	Alignment	not modelled	7.0	8	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow1-linker1 domain of transcription elongation2 factor spt5
64	c2axcA_	Alignment	not modelled	6.7	16	PDB header: hydrolase Chain: A: PDB Molecule: colicin e7; PDBTitle: crystal structure of cole7 translocation domain
65	c3t9nG_	Alignment	not modelled	5.7	20	PDB header: membrane protein Chain: G: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: crystal structure of a membrane protein
66	c3zuaA_	Alignment	not modelled	5.7	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-hemolysin translocation atp-binding protein hlyb; PDBTitle: a c39-like domain
67	c3d3rA_	Alignment	not modelled	5.6	29	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hycp/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hycp/hupf2 family protein from shewanella oneidensis mr-1
68	c4tseA_	Alignment	not modelled	5.6	13	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mib repeat domain of mind bomb 1
69	c3prdA_	Alignment	not modelled	5.3	6	PDB header: chaperone, isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase; PDBTitle: structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
70	d1pn0a3	Alignment	not modelled	5.3	10	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: PHBH-like