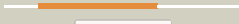
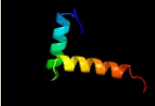
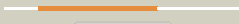
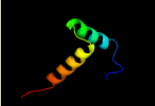
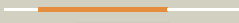
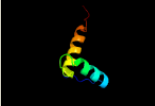



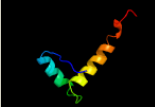

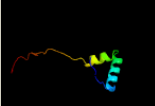


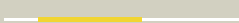


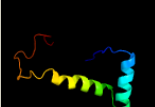





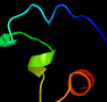
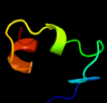
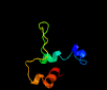



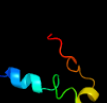



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2530A (-)_2854693_2854917
Date	Wed Aug 7 12:50:16 BST 2019
Unique Job ID	898af746a6114af0

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2bsqe1	 Alignment		89.9	16	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Trafficking protein A-like
2	c2h1oH	 Alignment		89.3	16	PDB header: gene regulation/dna complex Chain: H: PDB Molecule: trafficking protein a; PDBTitle: structure of fitab bound to ir36 dna fragment
3	c1q5vB	 Alignment		87.2	25	PDB header: transcription Chain: B: PDB Molecule: nickel responsive regulator; PDBTitle: apo-nikr
4	c3kk4B	 Alignment		87.1	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
5	c2bj3D	 Alignment		86.5	19	PDB header: transcription Chain: D: PDB Molecule: nickel responsive regulator; PDBTitle: nikr-apo
6	c5x3tA	 Alignment		85.0	25	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapp26; PDBTitle: vapbc from mycobacterium tuberculosis
7	d2bj7a1	 Alignment		81.1	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
8	c2ca9B	 Alignment		77.1	16	PDB header: transcription Chain: B: PDB Molecule: putative nickel-responsive regulator; PDBTitle: apo-nikr from helicobacter pylori in closed trans-2 conformation
9	c2k5jB	 Alignment		75.9	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
10	c6a7vU	 Alignment		69.3	24	PDB header: toxin/antitoxin Chain: U: PDB Molecule: antitoxin vapp11; PDBTitle: crystal structure of mycobacterium tuberculosis vappc11 toxin-2 antitoxin complex
11	d2hzaa1	 Alignment		68.5	32	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like

12	d2hzab1	Alignment		62.5	32	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
13	d1rxal	Alignment		54.9	35	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
14	c1rxrD	Alignment		54.9	35	PDB header: replication inhibitor Chain: D: PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
15	d1xd7a	Alignment		47.5	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Transcriptional regulator Rrf2
16	c4a1qB	Alignment		42.7	26	PDB header: viral protein Chain: B: PDB Molecule: orf e73; PDBTitle: solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
17	c4aaiB	Alignment		42.7	26	PDB header: viral protein Chain: B: PDB Molecule: orf e73; PDBTitle: thermostable protein from hyperthermophilic virus ssv-rh
18	c2k29A	Alignment		38.5	13	PDB header: transcription Chain: A: PDB Molecule: antitoxin relb; PDBTitle: structure of the dbd domain of e. coli antitoxin relb
19	c2d86A	Alignment		37.1	25	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: vav-3 protein; PDBTitle: solution structure of the ch domain from human vav-3 protein
20	c1t01B	Alignment		32.2	42	PDB header: cell adhesion, structural protein Chain: B: PDB Molecule: talin 1; PDBTitle: vinculin complexed with the vbs1 helix from talin
21	d1xrsa	Alignment	not modelled	29.0	20	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: D-lysine 5,6-aminomutase alpha subunit, KamD
22	c3h87D	Alignment	not modelled	28.5	32	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
23	c1syqB	Alignment	not modelled	28.4	42	PDB header: cell adhesion Chain: B: PDB Molecule: talin 1; PDBTitle: human vinculin head domain vh1, residues 1-258, in complex with human2 talin's vinculin binding site 1, residues 607-636
24	c3lwfD	Alignment	not modelled	22.5	25	PDB header: transcription regulator Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
25	d1ro0a	Alignment	not modelled	18.3	17	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: Bifunctional DNA primase/polymerase N-terminal domain
26	c5htIA	Alignment	not modelled	17.9	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: msha biogenesis protein mshe; PDBTitle: structure of mshe with cdg
27	c3t8tA	Alignment	not modelled	17.2	23	PDB header: unknown function Chain: A: PDB Molecule: staphylococcus aureus cymr (oxidized form); PDBTitle: crystal structure of staphylococcus aureus cymr oxidized form
28	c3fmtF	Alignment	not modelled	16.2	19	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna

29	c6hsdB	Alignment	not modelled	15.2	25	PDB header: transcription Chain: B: PDB Molecule: rrf2 family transcriptional regulator; PDBTitle: crystal structure of the oxidized form of the transcription regulator2 rsrr
30	c3m8jA	Alignment	not modelled	15.1	22	PDB header: transcription Chain: A: PDB Molecule: focb protein; PDBTitle: crystal structure of e.coli focb at 1.4 a resolution
31	c4hv0B	Alignment	not modelled	14.8	36	PDB header: transcription, viral protein Chain: B: PDB Molecule: avtr; PDBTitle: structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrivirus
32	c4cicB	Alignment	not modelled	14.7	25	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator, badm/rrf2 family; PDBTitle: t. potens iscr
33	c2gpyB	Alignment	not modelled	14.5	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of putative o-methyltransferase from bacillus2 halodurans
34	c2mdvB	Alignment	not modelled	12.7	36	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
35	c3gzaB	Alignment	not modelled	11.6	10	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-l-fucosidase; PDBTitle: crystal structure of putative alpha-l-fucosidase (np_812709.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.60 a resolution
36	c3k69A	Alignment	not modelled	11.5	14	PDB header: transcription Chain: A: PDB Molecule: putative transcription regulator; PDBTitle: crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
37	d1wuda1	Alignment	not modelled	10.7	16	Fold: SAM domain-like Superfamily: HRDC-like Family: HRDC domain from helicases
38	c6ejfQ	Alignment	not modelled	10.6	15	PDB header: motor protein Chain: Q: PDB Molecule: type iv pilus assembly protein pilf; PDBTitle: thermus thermophilus pilf atpase (apoprotein form)
39	c5n07A	Alignment	not modelled	10.5	25	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor nsrr; PDBTitle: structure of the [4fe-4s] form of the no response regulator nsrr
40	c3t98C	Alignment	not modelled	10.3	24	PDB header: protein transport Chain: C: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
41	c1ea4K	Alignment	not modelled	9.8	40	PDB header: gene regulation/dna Chain: K: PDB Molecule: transcriptional repressor copg; PDBTitle: transcriptional repressor copg/22bp dsdna complex
42	d2cpga	Alignment	not modelled	9.8	40	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
43	c6f36N	Alignment	not modelled	9.8	26	PDB header: proton transport Chain: N: PDB Molecule: mitochondrial atp synthase subunit asa6; PDBTitle: polytomella fo model
44	c2c4rL	Alignment	not modelled	8.8	60	PDB header: hydrolase Chain: L: PDB Molecule: ribonuclease e; PDBTitle: catalytic domain of e. coli rnase e
45	c3m1mA	Alignment	not modelled	8.7	20	PDB header: replication Chain: A: PDB Molecule: orf904; PDBTitle: crystal structure of the primase-polymerase from sulfolobus islandicus
46	c5h2sA	Alignment	not modelled	8.6	50	PDB header: antimicrobial protein Chain: A: PDB Molecule: piscidin-4; PDBTitle: solution structure of tilapia piscidin 4 (tp4) from oreochromis2 niloticus
47	c2qezC	Alignment	not modelled	8.4	32	PDB header: lyase Chain: C: PDB Molecule: ethanolamine ammonia-lyase heavy chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase heavy chain2 (yp_013784.1) from listeria monocytogenes 4b f2365 at 2.15 a3 resolution
48	c3t98A	Alignment	not modelled	8.2	24	PDB header: protein transport Chain: A: PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
49	c4dmzB	Alignment	not modelled	8.2	13	PDB header: nucleotide-binding protein Chain: B: PDB Molecule: putative uncharacterized protein peld; PDBTitle: peld 156-455 from pseudomonas aeruginosa pa14, apo form
50	c2y75F	Alignment	not modelled	8.1	28	PDB header: transcription Chain: F: PDB Molecule: hth-type transcriptional regulator cymr; PDBTitle: the structure of cymr (yrzc) the global cysteine regulator of b.2 subtilis
51	c4wv4A	Alignment	not modelled	7.9	31	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 10; PDBTitle: heterodimer of taf8/taf10
52	c5x7fA	Alignment	not modelled	7.6	36	PDB header: transferase Chain: A: PDB Molecule: putative o-methyltransferase rv1220c; PDBTitle: structure of a o-methyltransferase from mycobacterium tuberculosis at2 2.0 resolution
53	c4dbgB	Alignment	not modelled	7.4	31	PDB header: ligase Chain: B: PDB Molecule: ring finger protein 31; PDBTitle: crystal structure of hoil-1l-ubl complexed with a hoip-uba derivative
54	c1dl5A	Alignment	not modelled	7.0	13	PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-

54	c10f2A_	Alignment	not modelled	7.0	13	PDB header: methyltransferase; PDBTitle: protein-l-isoaspartate o-methyltransferase
55	c2wvsD_	Alignment	not modelled	7.0	19	PDB header: hydrolase Chain: D; PDB Molecule: alpha-l-fucosidase; PDBTitle: crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant
56	c6orfA_	Alignment	not modelled	6.9	14	PDB header: hydrolase Chain: A; PDB Molecule: spgh29; PDBTitle: crystal structure of spgh29
57	c5lvtC_	Alignment	not modelled	6.7	21	PDB header: dna binding protein Chain: C; PDB Molecule: dna-binding protein hu; PDBTitle: structure of hu protein from lactococcus lactis
58	c1zw2B_	Alignment	not modelled	6.6	55	PDB header: protein binding Chain: B; PDB Molecule: talain; PDBTitle: vinculin head (0-258) in complex with the talin rod2 residues 2345-2369
59	c3ntvB_	Alignment	not modelled	6.5	20	PDB header: transferase Chain: B; PDB Molecule: mw1564 protein; PDBTitle: crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus
60	c6a6xC_	Alignment	not modelled	6.5	28	PDB header: toxin Chain: C; PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex
61	c5k9hA_	Alignment	not modelled	6.4	10	PDB header: hydrolase Chain: A; PDB Molecule: 0940_gh29; PDBTitle: crystal structure of a glycoside hydrolase 29 family member from an2 unknown rumen bacterium
62	c2an7A_	Alignment	not modelled	6.4	21	PDB header: dna binding protein Chain: A; PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
63	c6dy3G_	Alignment	not modelled	6.4	26	PDB header: hydrolase Chain: G; PDB Molecule: n-acylethanolamine-hydrolyzing acid amidase alpha-subunit; PDBTitle: caenorhabditis elegans n-acylethanolamine-hydrolyzing acid amidase2 (naaa) ortholog
64	c4hf1B_	Alignment	not modelled	6.3	18	PDB header: transcription/dna Chain: B; PDB Molecule: hth-type transcriptional regulator iscr; PDBTitle: crystal structure of iscr bound to its promoter
65	c3pc3A_	Alignment	not modelled	6.2	22	PDB header: lyase Chain: A; PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
66	c2o8xA_	Alignment	not modelled	6.0	33	PDB header: transcription Chain: A; PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
67	c3abqA_	Alignment	not modelled	5.6	15	PDB header: lyase Chain: A; PDB Molecule: ethanolamine ammonia-lyase heavy chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and 2-amino-1-propanol
68	c2owvB_	Alignment	not modelled	5.6	20	PDB header: dna binding protein Chain: B; PDB Molecule: recombination-associated protein rdgc; PDBTitle: the recombination-associated protein rdgc adopts a novel toroidal2 architecture for dna binding
69	c4fxeB_	Alignment	not modelled	5.5	13	PDB header: toxin/toxin inhibitor Chain: B; PDB Molecule: antitoxin relb; PDBTitle: crystal structure of the intact e. coli relbe toxin-antitoxin complex
70	c6re86_	Alignment	not modelled	5.4	26	PDB header: proton transport Chain: 6; PDB Molecule: mitochondrial atp synthase subunit asa6; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 2d,2 composite map
71	c4ni3B_	Alignment	not modelled	5.3	26	PDB header: hydrolase Chain: B; PDB Molecule: alpha-fucosidase gh29; PDBTitle: crystal structure of gh29 family alpha-l-fucosidase from fusarium2 graminearum in the closed form
72	c6gn6A_	Alignment	not modelled	5.3	24	PDB header: hydrolase Chain: A; PDB Molecule: alpha-l-fucosidase; PDBTitle: alpha-l-fucosidase isoenzyme 1 from paenibacillus thiaminolyticus
73	d1s4ka_	Alignment	not modelled	5.2	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like