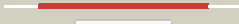



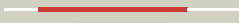


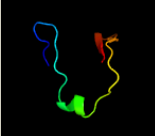

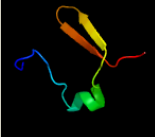

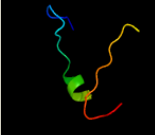

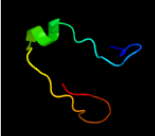



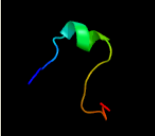






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2166c (-) _2429435_2429866
Date	Mon Aug 5 13:25:29 BST 2019
Unique Job ID	16611007f5e005d7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1n0fF_	 Alignment		100.0	28	PDB header: biosynthetic protein Chain: F: PDB Molecule: protein mrz; PDBTitle: crystal structure of a cell division and cell wall2 biosynthesis protein upf0040 from mycoplasma pneumoniae:3 indication of a novel fold with a possible new conserved4 sequence motif
2	d1n0ea_	 Alignment		100.0	28	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: Hypothetical protein MraZ
3	c2glwA_	 Alignment		95.7	17	PDB header: transcription Chain: A: PDB Molecule: 92aa long hypothetical protein; PDBTitle: the solution structure of phs018 from pyrococcus horikoshii
4	c2w1tB_	 Alignment		94.5	26	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: crystal structure of b. subtilis spovt
5	d1yfa1	 Alignment		90.5	22	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
6	d2fy9a1	 Alignment		90.4	31	Fold: Double-split beta-barrel Superfamily: AbrB/MazE/MraZ-like Family: AbrB N-terminal domain-like
7	c2ro5B_	 Alignment		88.2	26	PDB header: transcription Chain: B: PDB Molecule: stage v sporulation protein t; PDBTitle: rdc-refined solution structure of the n-terminal dna recognition2 domain of the bacillus subtilis transition-state regulator spovt
8	c3oeiB_	 Alignment		58.7	14	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
9	c2l66B_	 Alignment		54.5	24	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, abrb family; PDBTitle: the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea.
10	c2dgyA_	 Alignment		31.6	18	PDB header: translation Chain: A: PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
11	d2a6qb1	 Alignment		31.5	14	Fold: YefM-like Superfamily: YefM-like Family: YefM-like

12	c3hs2H_	Alignment		25.3	20	PDB header: antitoxin Chain: H: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
13	d2a6qa1	Alignment		23.6	14	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
14	c4mnoA_	Alignment		23.0	18	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssi
15	c2k2eA_	Alignment		22.8	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bp2786; PDBTitle: solution nmr structure of bordetella pertussis protein2 bp2786, a mth938-like domain. northeast structural3 genomics consortium target ber31
16	c3nngA_	Alignment		22.6	29	PDB header: viral protein Chain: A: PDB Molecule: n-terminal domain of moloney murine leukemia virus PDBTitle: crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
17	c3hryA_	Alignment		22.3	21	PDB header: antitoxin Chain: A: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd in a trigonal space group and partially2 disordered
18	c3qq5A_	Alignment		17.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydF
19	c2c45F_	Alignment		15.3	25	PDB header: lyase Chain: F: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: native precursor of pyruvoyl dependent aspartate decarboxylase
20	c1pt1B_	Alignment		14.4	10	PDB header: lyase Chain: B: PDB Molecule: aspartate 1-decarboxylase; PDBTitle: unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
21	d2odka1	Alignment	not modelled	14.1	21	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
22	c5os9A_	Alignment	not modelled	14.1	23	PDB header: dna binding protein Chain: A: PDB Molecule: b3 domain-containing transcription factor nga1; PDBTitle: structure of the b3 dna-binding domain of nga1
23	d1wida_	Alignment	not modelled	14.0	23	Fold: DNA-binding pseudobarrel domain Superfamily: DNA-binding pseudobarrel domain Family: B3 DNA binding domain
24	c5l2dA_	Alignment	not modelled	14.0	28	PDB header: cell adhesion Chain: A: PDB Molecule: surface-associated protein csha; PDBTitle: streptococcal surface adhesin - csha nr2
25	c3g5oA_	Alignment	not modelled	13.8	10	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
26	d1s6la1	Alignment	not modelled	13.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MerB N-terminal domain-like
27	d2q4qa1	Alignment	not modelled	13.8	14	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
28	d1ppya_	Alignment	not modelled	13.2	10	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Pyruvoyl dependent aspartate decarboxylase, ADC
29	d2fi9a1	Alignment	not modelled	13.2	15	Fold: MTH938-like Superfamily: MTH938-like

						Family: MTH938-like
30	c2zcpA_	Alignment	not modelled	13.2	16	PDB header: transferase Chain: A: PDB Molecule: dehydro-squalene synthase; PDBTitle: crystal structure of the c(30) carotenoid dehydro-squalene synthase2 from staphylococcus aureus complexed with farnesyl thiopyrophosphate
31	c2gm2A_	Alignment	not modelled	12.9	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: nmr structure of xanthomonas campestris xcc1710: northeast2 structural genomics consortium target xcr35
32	d2zgwa1	Alignment	not modelled	12.9	56	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: Biotin repressor (BirA)
33	c3d55A_	Alignment	not modelled	12.7	18	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
34	c4hd1A_	Alignment	not modelled	12.6	21	PDB header: transferase Chain: A: PDB Molecule: squalene synthase hpnc; PDBTitle: crystal structure of squalene synthase hpnc from alicyclobacillus2 acidocaldarius
35	c2odkD_	Alignment	not modelled	12.4	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
36	c2kdnA_	Alignment	not modelled	12.2	7	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein pfe0790c; PDBTitle: solution structure of pfe0790c, a putative bola-like protein from the2 protozoan parasite plasmodium falciparum.
37	c5iysA_	Alignment	not modelled	11.7	21	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: phytoene synthase; PDBTitle: crystal structure of a dehydro-squalene synthase in complex with ligand
38	c3dwmA_	Alignment	not modelled	10.6	13	PDB header: transferase Chain: A: PDB Molecule: 9.5 kda culture filtrate antigen cfp10a; PDBTitle: crystal structure of mycobacterium tuberculosis cyso, an antigen
39	c5l6mA_	Alignment	not modelled	10.6	17	PDB header: hydrolase Chain: A: PDB Molecule: vapb family protein; PDBTitle: structure of caulobacter crescentus vapbc1 (vapb1deltac:vapc1 form)
40	d1d7qa_	Alignment	not modelled	10.0	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
41	d1lpfa2	Alignment	not modelled	10.0	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
42	c3df0C_	Alignment	not modelled	10.0	27	PDB header: hydrolase Chain: C: PDB Molecule: calpastatin; PDBTitle: calcium-dependent complex between m-calpain and calpastatin
43	d2fvta1	Alignment	not modelled	9.4	14	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
44	c4n6eB_	Alignment	not modelled	9.1	14	PDB header: lyase/biosynthetic protein Chain: B: PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
45	c6h3cC_	Alignment	not modelled	8.9	17	PDB header: signaling protein Chain: C: PDB Molecule: brisc and brca1-a complex member 2; PDBTitle: cryo-em structure of the brisc complex bound to shmt2
46	c6h9xA_	Alignment	not modelled	8.9	32	PDB header: ligase Chain: A: PDB Molecule: serine--trna ligase; PDBTitle: klebsiella pneumoniae seryl-trna synthetase in complex with the2 intermediate analog 5'-o-(n-(l-seryl)-sulfamoyl)adenosine
47	c3j81i_	Alignment	not modelled	8.2	13	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
48	c3errB_	Alignment	not modelled	7.9	18	PDB header: ligase Chain: B: PDB Molecule: fusion protein of microtubule binding domain from mouse PDBTitle: microtubule binding domain from mouse cytoplasmic dynein as a fusion2 with seryl-trna synthetase
49	c2oqkA_	Alignment	not modelled	7.9	13	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
50	c3r5tA_	Alignment	not modelled	7.8	17	PDB header: metal transport Chain: A: PDB Molecule: ferric vibriobactin abc transporter, periplasmic ferric PDBTitle: crystal structure of holo-viup
51	c2dq3A_	Alignment	not modelled	7.4	15	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
52	d2gv8a2	Alignment	not modelled	7.3	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
53	d1m7ja1	Alignment	not modelled	7.0	23	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: D-aminoacylase
54	c3j39O_	Alignment	not modelled	6.6	15	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
						Fold: SH3-like barrel

55	d1xova1	Alignment	not modelled	6.5	50	Superfamily: Prokaryotic SH3-related domain Family: Ply C-terminal domain-like
56	d1v59a2	Alignment	not modelled	6.5	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
57	c3if4C	Alignment	not modelled	6.5	31	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: integron cassette protein hfx_cass5; PDBTitle: structure from the mobile metagenome of north west arm sewage outfall:2 integron cassette protein hfx_cass5
58	c2ubpC	Alignment	not modelled	6.5	26	PDB header: hydrolase Chain: C: PDB Molecule: protein (urease alpha subunit); PDBTitle: structure of native urease from bacillus pasteurii
59	c2dq0A	Alignment	not modelled	6.3	12	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
60	c3qoqC	Alignment	not modelled	6.3	32	PDB header: transcription/dna Chain: C: PDB Molecule: alginate and motility regulator z; PDBTitle: crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
61	d1d6za4	Alignment	not modelled	6.2	10	Fold: N domain of copper amine oxidase-like Superfamily: Copper amine oxidase, domain N Family: Copper amine oxidase, domain N
62	d1jt8a	Alignment	not modelled	6.2	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
63	c4e54B	Alignment	not modelled	6.1	21	PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna damage-binding protein 2; PDBTitle: damaged dna induced uv-damaged dna-binding protein (uv-ddb)2 dimerization and its roles in chromatinized dna repair
64	c2mhdA	Alignment	not modelled	6.0	58	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein bacuni_03114 from bacteroides uniformis2 atcc 8492
65	d1seta2	Alignment	not modelled	5.8	15	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
66	c6bdcA	Alignment	not modelled	5.7	23	PDB header: protein transport Chain: A: PDB Molecule: hcp1; PDBTitle: structure of hcp1 from flavobacterium johnsoniae
67	c3crcB	Alignment	not modelled	5.7	28	PDB header: hydrolase Chain: B: PDB Molecule: protein mazg; PDBTitle: crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
68	d1lva2	Alignment	not modelled	5.7	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
69	c1sryB	Alignment	not modelled	5.6	16	PDB header: ligase(synthetase) Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
70	d2j7ja2	Alignment	not modelled	5.6	30	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
71	c3zvkg	Alignment	not modelled	5.5	11	PDB header: antitoxin/toxin/dna Chain: G: PDB Molecule: antitoxin of toxin-antitoxin system vapb; PDBTitle: crystal structure of vapbc2 from rickettsia felis bound to2 a dna fragment from their promoter
72	d1ihna	Alignment	not modelled	5.5	9	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
73	c3vqzA	Alignment	not modelled	5.4	15	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase, smb-1, in a complex with2 mercaptoacetic acid
74	c3jywM	Alignment	not modelled	5.4	14	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l16(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
75	d1k1da1	Alignment	not modelled	5.2	29	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
76	c5k92C	Alignment	not modelled	5.1	22	PDB header: de novo protein Chain: C: PDB Molecule: apo-(csl16c)3; PDBTitle: crystal structure of an apo tris-thiolate binding site in a de novo2 three stranded coiled coil peptide
77	c5k92B	Alignment	not modelled	5.1	22	PDB header: de novo protein Chain: B: PDB Molecule: apo-(csl16c)3; PDBTitle: crystal structure of an apo tris-thiolate binding site in a de novo2 three stranded coiled coil peptide
78	c5k92A	Alignment	not modelled	5.1	22	PDB header: de novo protein Chain: A: PDB Molecule: apo-(csl16c)3; PDBTitle: crystal structure of an apo tris-thiolate binding site in a de novo2 three stranded coiled coil peptide