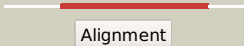

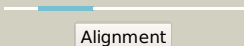
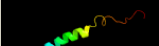
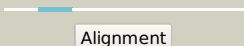

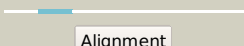

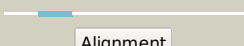

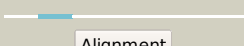

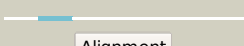











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0431 (-)_519076_519570
Date	Tue Jul 23 14:50:50 BST 2019
Unique Job ID	46b98d032c40efd5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2m5yA_	 Alignment		100.0	100	PDB header: unknown function Chain: A: PDB Molecule: putative tuberculin related peptide; PDBTitle: solution structure of the c-terminal domain of rv0431
2	c6f0kA_	 Alignment		31.3	7	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
3	c3j1rO_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: O: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
4	c3j1rP_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: P: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
5	c3j1rQ_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: Q: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
6	c3j1rR_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: R: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
7	c3j1rT_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: T: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
8	c3j1rN_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: N: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
9	c3j1rE_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: E: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
10	c3j1rG_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: G: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
11	c3j1rH_	 Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: H: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices

12	c3j1rF_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: F: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
13	c3j1rI_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: I: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
14	c3j1rM_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: M: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
15	c3j1rC_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: C: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
16	c3j1rA_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: A: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
17	c3j1rB_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: B: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
18	c3j1rS_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: S: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
19	c3j1rL_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: L: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
20	c3j1rD_	Alignment		31.0	17	PDB header: cell adhesion, structural protein Chain: D: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
21	c3j1rK_	Alignment	not modelled	31.0	17	PDB header: cell adhesion, structural protein Chain: K: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
22	c3j1rU_	Alignment	not modelled	31.0	17	PDB header: cell adhesion, structural protein Chain: U: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
23	c3j1rJ_	Alignment	not modelled	31.0	17	PDB header: cell adhesion, structural protein Chain: J: PDB Molecule: archaeal adhesion filament core; PDBTitle: filaments from ignicoccus hospitalis show diversity of packing in2 proteins containing n-terminal type iv pilin helices
24	c2mniA_	Alignment	not modelled	29.9	47	PDB header: unknown function Chain: A: PDB Molecule: hp_q4d059; PDBTitle: chemical shift assignments and structure of q4d059, a hypothetical2 protein from trypanosoma cruzi
25	d2axth1	Alignment	not modelled	25.9	25	Fold: Single transmembrane helix Superfamily: Photosystem II 10 kDa phosphoprotein PsbH Family: PsbH-like
26	c2axth_	Alignment	not modelled	25.9	25	PDB header: electron transport Chain: H: PDB Molecule: photosystem ii reaction center h protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
27	d1xjca_	Alignment	not modelled	22.4	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
28	c4lfmA_	Alignment	not modelled	20.8	17	PDB header: isomerase Chain: A: PDB Molecule: galactose-6-phosphate isomerase subunit a; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with2 d-psicose

29	c2hkoA	Alignment	not modelled	19.9	33	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1
30	d2dw4a2	Alignment	not modelled	18.9	31	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
31	d2e74f1	Alignment	not modelled	18.5	29	Fold: Single transmembrane helix Superfamily: PetM subunit of the cytochrome b6f complex Family: PetM subunit of the cytochrome b6f complex
32	c2x2oA	Alignment	not modelled	18.2	15	PDB header: flavoprotein Chain: A: PDB Molecule: nrdi protein; PDBTitle: the flavoprotein nrdi from bacillus cereus with the initially oxidized2 fmn cofactor in an intermediate radiation reduced state
33	d2fzva1	Alignment	not modelled	17.9	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
34	c4gutA	Alignment	not modelled	16.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1b; PDBTitle: crystal structure of lsd2-npac
35	c3d11B	Alignment	not modelled	15.1	24	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
36	d1t70a	Alignment	not modelled	14.7	29	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
37	c4nkrB	Alignment	not modelled	13.6	16	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
38	c2xagA	Alignment	not modelled	12.4	33	PDB header: transcription Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
39	c2v1dA	Alignment	not modelled	12.4	33	PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
40	c6navl	Alignment	not modelled	12.0	18	PDB header: structural protein Chain: I: PDB Molecule: m9ud72; PDBTitle: cryo-em reconstruction of sulfolobus islandicus lal14/1 pilus
41	c3a91B	Alignment	not modelled	11.4	7	PDB header: hydrolase Chain: B: PDB Molecule: poly-gamma-glutamate hydrolase; PDBTitle: structure of bacteriophage poly-gamma-glutamate hydrolase
42	c6gcsW	Alignment	not modelled	10.9	18	PDB header: oxidoreductase Chain: W: PDB Molecule: nb6m subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
43	d2z06a1	Alignment	not modelled	10.6	29	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
44	d1yt8a4	Alignment	not modelled	10.1	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
45	d1nyra1	Alignment	not modelled	10.1	22	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
46	d1rlja	Alignment	not modelled	9.8	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavoprotein NrdI
47	d2fgca2	Alignment	not modelled	9.6	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
48	c5lnkq	Alignment	not modelled	9.2	21	PDB header: oxidoreductase Chain: Q: PDB Molecule: PDBTitle: entire ovine respiratory complex i
49	c4b2oB	Alignment	not modelled	9.2	21	PDB header: hydrolase Chain: B: PDB Molecule: yymb phosphodiesterase; PDBTitle: crystal structure of bacillus subtilis yymb, a global2 regulator of late adaptive responses.
50	c6et5b	Alignment	not modelled	9.1	25	PDB header: photosynthesis Chain: B: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
51	d1t71a	Alignment	not modelled	8.6	29	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
52	c5mjiA	Alignment	not modelled	8.6	13	PDB header: flavoprotein Chain: A: PDB Molecule: bramp domain protein; PDBTitle: crystal structure of rosb with bound intermediate ohc-rp (8-demethyl-2 8-formylriboflavin-5'-phosphate)
53	d2pc6a2	Alignment	not modelled	8.6	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
54	c4v0pA	Alignment	not modelled	8.2	12	PDB header: immune system Chain: A: PDB Molecule: melanoma-associated antigen 3; PDBTitle: crystal structure of the mage homology domain of human mage-a3
55	c4onyB	Alignment	not modelled	8.1	30	PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein family 5; PDBTitle: crystal structure of a abc transporter, periplasmic

						substrate-binding2 protein from brucella melitensis PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus influenzae
56	c1gqqA_	Alignment	not modelled	8.1	19	
57	c1wv9B_	Alignment	not modelled	7.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: rhodanese homolog tt1651; PDBTitle: crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
58	c4alnE_	Alignment	not modelled	7.7	16	PDB header: oxidoreductase Chain: E: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadph]; PDBTitle: crystal structure of s. aureus fabi (p32)
59	c2vvID_	Alignment	not modelled	7.5	15	PDB header: oxidoreductase Chain: D: PDB Molecule: monoamine oxidase n; PDBTitle: the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
60	d2f1fa1	Alignment	not modelled	7.5	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: llvH-like
61	c6fxsA_	Alignment	not modelled	7.4	18	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase, putative; PDBTitle: structure of trypanosoma brucei type b ribose 5-phosphate isomerase
62	d1m0da_	Alignment	not modelled	7.0	15	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
63	c4em8A_	Alignment	not modelled	6.9	26	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
64	c1ps9A_	Alignment	not modelled	6.5	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
65	d1xrdA1	Alignment	not modelled	6.4	33	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
66	c1xrdA_	Alignment	not modelled	6.4	33	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, alpha chain; PDBTitle: light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum
67	d1qf6a1	Alignment	not modelled	6.3	21	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
68	c2f1rA_	Alignment	not modelled	6.2	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
69	c3wmmY_	Alignment	not modelled	6.0	30	PDB header: photosynthesis Chain: Y: PDB Molecule: lh1 alpha polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
70	d1dwka1	Alignment	not modelled	5.9	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
71	c5onkA_	Alignment	not modelled	5.9	23	PDB header: hydrolase Chain: A: PDB Molecule: yndl; PDBTitle: native yndl
72	c3k7pA_	Alignment	not modelled	5.8	23	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from2 trypanosoma cruzi.
73	c6hwhB_	Alignment	not modelled	5.8	13	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
74	c3m1pA_	Alignment	not modelled	5.7	23	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
75	d1szpa1	Alignment	not modelled	5.5	14	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: DNA repair protein Rad51, N-terminal domain
76	c2kvcA_	Alignment	not modelled	5.3	41	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c.2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a