
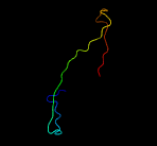
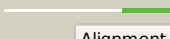
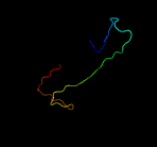


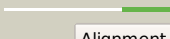
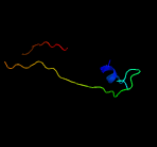


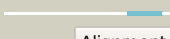
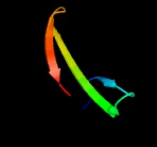







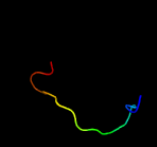







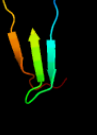

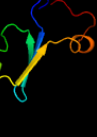



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0556 (-)_647962_648477
Date	Fri Jul 26 01:50:11 BST 2019
Unique Job ID	1f263d6a0c6db37f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qqpG_	 Alignment		66.5	10	PDB header: virus Chain: G; PDB Molecule: large capsid protein; PDBTitle: crystal structure of authentic providence virus
2	d1ohfa_	 Alignment		57.0	18	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tetraviridae-like VP
3	c3k6oA_	 Alignment		55.1	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein duf1344; PDBTitle: crystal structure of protein of unknown function duf13442 (yp_001299214.1) from bacteroides vulgatus atcc 8482 at 2.00 a3 resolution
4	d1ohfc_	 Alignment		53.7	24	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Tetraviridae-like VP
5	c4pqxC_	 Alignment		40.8	13	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a nigd-like protein (baccac_02139) from2 bacteroides caccae atcc 43185 at 2.39 a resolution
6	c3wknG_	 Alignment		39.8	29	PDB header: immune system Chain: G; PDB Molecule: affinger p17; PDBTitle: crystal structure of the artificial protein affinger p17 (af.p17)2 complexed with fc fragment of human igg
7	c1jy2O_	 Alignment		39.3	39	PDB header: blood clotting Chain: O; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of the central region of bovine fibrinogen (e52 fragment) at 1.4 angstroms resolution
8	c3db3A_	 Alignment		36.2	26	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase uhrf1; PDBTitle: crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide
9	c3askC_	 Alignment		34.8	26	PDB header: ligase/dna binding protein Chain: C; PDB Molecule: e3 ubiquitin-protein ligase uhrf1; PDBTitle: structure of uhrf1 in complex with histone tail
10	c6b9mC_	 Alignment		34.5	42	PDB header: transferase Chain: C; PDB Molecule: e3 ubiquitin-protein ligase uhrf1; PDBTitle: crystal structure of uhrf1 ttd domain in complex with the polybasic2 region
11	c4tvrA_	 Alignment		34.2	37	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase uhrf2; PDBTitle: tandem tudor and phd domains of uhrf2

12	c3s6pC_	Alignment		31.6	17	PDB header: virus Chain: C: PDB Molecule: capsid protein; PDBTitle: crystal structure of helicoverpa armigera stunt virus
13	c1ohfB_	Alignment		30.4	15	PDB header: virus Chain: B: PDB Molecule: nudaurelia capensis omega virus capsid protein; PDBTitle: the refined structure of nudaurelia capensis omega virus
14	c2q6oB_	Alignment		29.1	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: hypothetical protein; PDBTitle: sall-y70t with sam and cl
15	c3k0yA_	Alignment		24.7	16	PDB header: toxin Chain: A: PDB Molecule: putative toxin related protein; PDBTitle: crystal structure of putative toxin related protein (yp_001303978.1)2 from parabacteroides distasonis atcc 8503 at 2.16 a resolution
16	c2jx2A_	Alignment		24.5	14	PDB header: transcription Chain: A: PDB Molecule: negative elongation factor e; PDBTitle: solution conformation of rna-bound nelf-e rrm
17	c3f6zB_	Alignment		23.1	29	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pseudomonas aeruginosa mlic in complex2 with hen egg white lysozyme
18	c4j8qA_	Alignment		21.4	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a nigd-like protein (bf0700) from bacteroides2 fragilis nctc 9343 at 2.50 a resolution
19	c2zbcC_	Alignment		20.8	20	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from thermotoga2 maritima
20	c2kpiA_	Alignment		20.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sco3027; PDBTitle: solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
21	c2e26A_	Alignment	not modelled	19.8	11	PDB header: signaling protein Chain: A: PDB Molecule: reelin; PDBTitle: crystal structure of two repeat fragment of reelin
22	c2a45H_	Alignment	not modelled	19.4	60	PDB header: hydrolase/hydrolase inhibitor Chain: H: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin
23	c2js4A_	Alignment	not modelled	18.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0434 protein bb2007; PDBTitle: solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
24	c4gy5A_	Alignment	not modelled	18.3	26	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase uhrf1; PDBTitle: crystal structure of the tandem tudor domain and plant homeodomain of2 uhrf1 with histone h3k9me3
25	c2ka3C_	Alignment	not modelled	18.2	30	PDB header: structural protein Chain: C: PDB Molecule: emilin-1; PDBTitle: structure of emilin-1 c1q-like domain
26	c3d0fA_	Alignment	not modelled	17.2	23	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718
27	c1rqra_	Alignment	not modelled	17.0	20	PDB header: transferase Chain: A: PDB Molecule: 5'-fluoro-5'-deoxyadenosine synthase; PDBTitle: crystal structure and mechanism of a bacterial fluorinating enzyme,2 product complex
28	d1x4fa1	Alignment	not modelled	16.4	24	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD

29	c4oumA	Alignment	not modelled	15.9	30	PDB header: signaling protein Chain: A: PDB Molecule: caprin-2; PDBTitle: crystal structure of human caprin-2 c1q domain
30	d1gr3a	Alignment	not modelled	15.8	10	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
31	c1gr3A	Alignment	not modelled	15.8	10	PDB header: collagen Chain: A: PDB Molecule: collagen x; PDBTitle: structure of the human collagen x nc1 trimer
32	c5hbaA	Alignment	not modelled	15.5	30	PDB header: immune system Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: globular domain of zebrafish complement 1qa protein
33	c4obyA	Alignment	not modelled	15.4	14	PDB header: ligase Chain: A: PDB Molecule: arginine--trna ligase; PDBTitle: crystal structure of e.coli arginyl-trna synthetase and ligand binding2 studies revealed key residues in arginine recognition
34	c4r3zB	Alignment	not modelled	15.2	22	PDB header: protein binding/ligase Chain: B: PDB Molecule: arginine--trna ligase, cytoplasmic; PDBTitle: crystal structure of human argrs-glnrs-aimp1 complex
35	d1kl9a2	Alignment	not modelled	15.1	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
36	c4b03D	Alignment	not modelled	14.9	14	PDB header: virus Chain: D: PDB Molecule: dengue virus 1 prm protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
37	c1o91B	Alignment	not modelled	14.8	13	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha 1(viii) chain; PDBTitle: crystal structure of a collagen viii nc1 domain trimer
38	d1o91a	Alignment	not modelled	14.8	13	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
39	d1pk6a	Alignment	not modelled	14.7	40	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
40	c3c6rE	Alignment	not modelled	14.1	20	PDB header: virus Chain: E: PDB Molecule: peptide pr; PDBTitle: low ph immature dengue virus
41	c3ixxE	Alignment	not modelled	13.9	30	PDB header: virus Chain: E: PDB Molecule: peptide pr; PDBTitle: the pseudo-atomic structure of west nile immature virus in complex2 with fab fragments of the anti-fusion loop antibody e53
42	d1c3ha	Alignment	not modelled	13.8	20	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
43	d1pk6c	Alignment	not modelled	13.4	20	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
44	d1m5ha1	Alignment	not modelled	13.4	50	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
45	c2jr6A	Alignment	not modelled	13.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0434 protein nma0874; PDBTitle: solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
46	c2zufA	Alignment	not modelled	13.2	30	PDB header: ligase/rna Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
47	c4bg0A	Alignment	not modelled	12.9	26	PDB header: cell adhesion Chain: A: PDB Molecule: complement regulator-acquiring surface protein 2 (crasp-2) PDBTitle: crystal structure of complement factors h and fh-1 binding protein2 bbh06 or crasp-2 from borrelia burgdorferi
48	d1rqpa2	Alignment	not modelled	12.9	24	Fold: Bacterial fluorinating enzyme, N-terminal domain Superfamily: Bacterial fluorinating enzyme, N-terminal domain Family: Bacterial fluorinating enzyme, N-terminal domain
49	c4f3jA	Alignment	not modelled	12.9	20	PDB header: signaling protein Chain: A: PDB Molecule: complement c1q tumor necrosis factor-related protein 5; PDBTitle: crystal structure of trimeric gc1q domain of human c1qtnf5 associated2 with late-onset retinal macular degeneration
50	d2jnya1	Alignment	not modelled	12.9	9	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
51	d1bcoa1	Alignment	not modelled	12.8	11	Fold: mu transposase, C-terminal domain Superfamily: mu transposase, C-terminal domain Family: mu transposase, C-terminal domain
52	c3c6eC	Alignment	not modelled	12.8	20	PDB header: viral protein Chain: C: PDB Molecule: prm; PDBTitle: crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the dengue 2 virus at neutral ph
53	d2bz2a1	Alignment	not modelled	12.3	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
54	c2wh7A	Alignment	not modelled	12.2	31	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-phage associated; PDBTitle: the partial structure of a group a streptococcal phage-2

						encoded tail fibre hyaluronate lyase hylp2 PDB header: hormone Chain: A: PDB Molecule: adiponectin; PDBTitle: crystal structure of a single-chain trimer of human adiponectin2 globular domain
55	c4douA_	Alignment	not modelled	12.1	20	
56	d1khba2	Alignment	not modelled	12.0	16	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
57	c6bj5F_	Alignment	not modelled	11.6	24	PDB header: immunosuppressant Chain: F: PDB Molecule: serine proteinase inhibitor 1; PDBTitle: structure of the clinically used myxomaviral serine protease inhibitor2 1 (serp-1)
58	c6bl5A_	Alignment	not modelled	10.9	40	PDB header: viral protein Chain: A: PDB Molecule: head decoration protein; PDBTitle: head decoration protein from the hyperthermophilic phage p74-26
59	d2pk7a1	Alignment	not modelled	10.8	13	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
60	d1x4da1	Alignment	not modelled	10.8	13	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
61	c6epkB_	Alignment	not modelled	10.7	30	PDB header: viral protein Chain: B: PDB Molecule: precursor membrane protein; PDBTitle: crystal structure of the precursor membrane protein-envelope protein2 heterodimer from the yellow fever virus
62	c4d7yA_	Alignment	not modelled	10.6	14	PDB header: signaling protein Chain: A: PDB Molecule: c1q-related factor; PDBTitle: crystal structure of mouse c1q1 globular domain
63	c3g4hB_	Alignment	not modelled	10.6	6	PDB header: hydrolase Chain: B: PDB Molecule: regucalcin; PDBTitle: crystal structure of human senescence marker protein-30 (zinc bound)
64	d2hf1a1	Alignment	not modelled	10.3	9	Fold: Trm112p-like Superfamily: Trm112p-like Family: Trm112p-like
65	d1ftra1	Alignment	not modelled	9.9	40	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
66	c1m5hF_	Alignment	not modelled	9.9	50	PDB header: transferase Chain: F: PDB Molecule: formylmethanofuran--tetrahydromethanopterin PDBTitle: formylmethanofuran:tetrahydromethanopterin2 formyltransferase from archaeoglobus fulgidus
67	d2gcxa1	Alignment	not modelled	9.7	17	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
68	c2bvba_	Alignment	not modelled	9.7	11	PDB header: adhesion Chain: A: PDB Molecule: micronemal protein 1; PDBTitle: the c-terminal domain from micronemal protein 1 (mic1) from2 toxoplasma gondii
69	c5xxul_	Alignment	not modelled	9.7	38	PDB header: ribosome Chain: I: PDB Molecule: ribosomal protein es8; PDBTitle: small subunit of toxoplasma gondii ribosome
70	c2vovA_	Alignment	not modelled	9.4	27	PDB header: metal-binding protein Chain: A: PDB Molecule: surface-associated protein; PDBTitle: an oxidized tryptophan facilitates copper-binding in2 methylococcus capsulatus secreted protein mope. the3 structure of wild-type mope to 1.35aa
71	c5hkiA_	Alignment	not modelled	9.4	40	PDB header: signaling protein Chain: A: PDB Molecule: complement c1q subcomponent subunit a,complement c1q PDBTitle: single chain recombinant globular head of the complement system2 protein c1q
72	c3zey5_	Alignment	not modelled	9.1	38	PDB header: ribosome Chain: 5: PDB Molecule: 40s ribosomal protein s8; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
73	c5lj3Y_	Alignment	not modelled	8.8	29	PDB header: splicing Chain: Y: PDB Molecule: u2 small nuclear ribonucleoprotein b"; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
74	d1nyra3	Alignment	not modelled	8.8	15	Fold: RRF/tRNA synthetase additional domain-like Superfamily: ThrRS/AlaRS common domain Family: Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
75	d1pk6b_	Alignment	not modelled	8.6	20	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
76	d3brda1	Alignment	not modelled	8.5	45	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
77	c2xzn2_	Alignment	not modelled	8.4	38	PDB header: ribosome Chain: 2: PDB Molecule: 40s ribosomal protein s8; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
78	c4rt5A_	Alignment	not modelled	8.4	9	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase protein from planctomyces limnophilus dsm 3776
						PDB header: ligase/rna

79	c1f7uA_	Alignment	not modelled	8.3	11	Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of the arginyl-trna synthetase complexed with the 2 trna(arg) and l-arg
80	c3mhxB_	Alignment	not modelled	8.2	25	PDB header: metal transport Chain: B: PDB Molecule: putative ferrous iron transport protein a; PDBTitle: crystal structure of stentrophomonas maltophilia feoa complexed with 2 zinc: a unique prokaryotic sh3 domain protein possibly acting as a 3 bacterial ferrous iron transport activating factor
81	c3fo8D_	Alignment	not modelled	8.2	25	PDB header: viral protein Chain: D: PDB Molecule: tail sheath protein gp18; PDBTitle: crystal structure of the bacteriophage t4 tail sheath protein, 2 protease resistant fragment gp18pr
82	d1x4ga1	Alignment	not modelled	8.1	20	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
83	d2f09a1	Alignment	not modelled	8.1	15	Fold: Streptavidin-like Superfamily: YdhA-like Family: YdhA-like
84	c5xyil_	Alignment	not modelled	7.8	43	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8; PDBTitle: small subunit of trichomonas vaginalis ribosome
85	c2fhjD_	Alignment	not modelled	7.8	40	PDB header: transferase Chain: D: PDB Molecule: formylmethanofuran--tetrahydromethanopterin PDBTitle: crystal structure of formylmethanofuran:2 tetrahydromethanopterin formyltransferase in complex with 3 its coenzymes
86	c3dlmA_	Alignment	not modelled	7.7	15	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setdb1; PDBTitle: crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
87	d2cpja1	Alignment	not modelled	7.7	20	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
88	c5kc5A_	Alignment	not modelled	7.7	20	PDB header: signaling protein Chain: A: PDB Molecule: cerebellin-1; PDBTitle: crystal structure of the cbln1 c1q domain trimer
89	d1m5sa1	Alignment	not modelled	7.6	40	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
90	c4wiuA_	Alignment	not modelled	7.6	26	PDB header: lyase, transferase Chain: A: PDB Molecule: phosphoenolpyruvate carboxykinase [gtp]; PDBTitle: crystal structure of pepck (rv0211) from mycobacterium tuberculosis in 2 complex with oxalate and mn2+
91	c5gslB_	Alignment	not modelled	7.6	12	PDB header: hydrolase Chain: B: PDB Molecule: 778aa long hypothetical beta-galactosidase; PDBTitle: glycoside hydrolase a
92	c1m5sC_	Alignment	not modelled	7.5	40	PDB header: transferase Chain: C: PDB Molecule: formylmethanofuran--tetrahydromethanopterin PDBTitle: formylmethanofuran:tetrahydromethanopterin2 fromyltransferase from methanosarcina barkeri
93	c3j3a1_	Alignment	not modelled	7.4	50	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8; PDBTitle: structure of the human 40s ribosomal proteins
94	c2ks1B_	Alignment	not modelled	7.4	29	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
95	d1f7ua2	Alignment	not modelled	7.4	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
96	c3u5cl_	Alignment	not modelled	7.2	36	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this 2 entry contains proteins of the 40s subunit, ribosome a
97	d2awna1	Alignment	not modelled	7.1	15	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
98	c4q2tB_	Alignment	not modelled	7.0	10	PDB header: ligase Chain: B: PDB Molecule: arginine--trna ligase, cytoplasmic; PDBTitle: crystal structure of arginyl-trna synthetase complexed with l-arginine
99	d1aуда_	Alignment	not modelled	6.9	14	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD