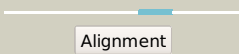

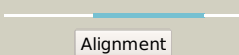
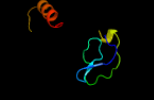
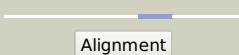

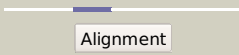
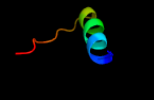


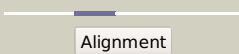
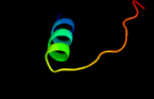
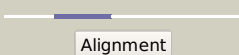

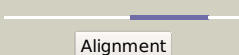



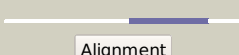

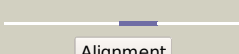
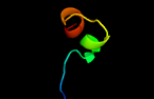


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1974 (-) _2217667_2218044
Date	Mon Aug 5 13:25:07 BST 2019
Unique Job ID	ba1fa0226f2c260e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xglB_	 Alignment		33.0	25	PDB header: antibiotic Chain: B; PDB Molecule: colicin-m immunity protein; PDBTitle: the x-ray structure of the escherichia coli colicin m immunity protein2 demonstrates the presence of a disulphide bridge, which is3 functionally essential
2	c4evxA_	 Alignment		31.2	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative phage endolysin; PDBTitle: crystal structure of putative phage endolysin from s. enterica
3	c2lqvA_	 Alignment		28.9	38	PDB header: protein transport Chain: A; PDB Molecule: protein yebf; PDBTitle: yebf
4	c1x5bA_	 Alignment		17.0	14	PDB header: protein binding Chain: A; PDB Molecule: signal transducing adaptor molecule 2; PDBTitle: the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
5	d2pmra1	 Alignment		16.8	27	Fold: immunoglobulin/albumin-binding domain-like Superfamily: AF1782-like Family: AF1782-like
6	c3zyqA_	 Alignment		16.4	17	PDB header: signaling Chain: A; PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.48 a3 resolution
7	d1dvpa1	 Alignment		15.3	10	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
8	d1nh2b_	 Alignment		14.5	24	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
9	d1nvpb_	 Alignment		13.0	27	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
10	c1nvpB_	 Alignment		13.0	27	PDB header: transcription/dna Chain: B; PDB Molecule: transcription initiation factor iia alpha chain; PDBTitle: human tfiia/tbp/dna complex
11	c4rwrB_	 Alignment		12.2	33	PDB header: viral protein Chain: B; PDB Molecule: stage ii sporulation protein d; PDBTitle: 2.1 angstrom crystal structure of stage ii sporulation protein d from2 bacillus anthracis

12	c1spfA_	Alignment		11.7	78	PDB header: lipoprotein(surface film) Chain: A: PDB Molecule: pulmonary surfactant-associated polypeptide c; PDBTitle: the nmr structure of the pulmonary surfactant-associated2 polypeptide sp-c in an apolar solvent contains a valyl-3 rich alpha-helix
13	d2oo2a1	Alignment		10.4	7	Fold: immunoglobulin/albumin-binding domain-like Superfamily: AF1782-like Family: AF1782-like
14	c2la3A_	Alignment		10.3	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
15	c4k90A_	Alignment		9.5	23	PDB header: hydrolase Chain: A: PDB Molecule: extracellular metalloproteinase mep; PDBTitle: extracellular metalloproteinase from aspergillus
16	d1oqya2	Alignment		9.4	36	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
17	c5i1tA_	Alignment		9.3	33	PDB header: hydrolase Chain: A: PDB Molecule: stage ii sporulation protein d; PDBTitle: 2.6 angstrom resolution crystal structure of stage ii sporulation2 protein d (spoiiid) from clostridium difficile in complex with3 triacetylchitotriose
18	c1qoyA_	Alignment		9.2	17	PDB header: toxin Chain: A: PDB Molecule: hemolysin e; PDBTitle: e.coli hemolysin e (hlye, clya, shea)
19	c3hdeA_	Alignment		8.8	18	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of full-length endolysin r21 from phage 21
20	c3j9oJ_	Alignment		7.7	24	PDB header: structural protein Chain: J: PDB Molecule: intracellular growth locus protein b; PDBTitle: cryoem structure of a type vi secretion system
21	c2d56A_	Alignment	not modelled	7.5	50	PDB header: antibiotic Chain: A: PDB Molecule: asabf; PDBTitle: solution structure of asabf, antibacterial peptide isolated2 from a nematode, ascaris suum
22	d1m0wa1	Alignment	not modelled	7.4	24	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Eukaryotic glutathione synthetase, substrate-binding domain
23	c2f95B_	Alignment	not modelled	7.3	53	PDB header: membrane protein Chain: B: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: m intermediate structure of sensory rhodopsin ii/transducer complex in2 combination with the ground state structure
24	c2uuvC_	Alignment	not modelled	7.0	25	PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1
25	c2f93B_	Alignment	not modelled	6.9	39	PDB header: membrane protein Chain: B: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: k intermediate structure of sensory rhodopsin ii/transducer complex in2 combination with the ground state structure
26	d2f93b1	Alignment	not modelled	6.9	39	Fold: Transmembrane helix hairpin Superfamily: Htr2 transmembrane domain-like Family: Htr2 transmembrane domain-like
27	d1dv0a_	Alignment	not modelled	6.6	31	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
28	c3vocA_	Alignment	not modelled	6.2	21	PDB header: hydrolase Chain: A: PDB Molecule: beta/alpha-amylase; PDBTitle: crystal structure of the catalytic domain of beta-amylase

						from2 paenibacillus polymyxa
29	c5nfvA_	Alignment	not modelled	6.0	35	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated endonuclease cpf1; PDBTitle: crystal structure of catalytically inactive fncas12 mutant bound to an2 r-loop structure containing a pre-crrna mimic and full-length dna3 target
30	c5ix5A_	Alignment	not modelled	6.0	50	PDB header: antibiotic Chain: A: PDB Molecule: antibacterial factor-related peptide 2; PDBTitle: nmr structure of antibacterial factor-2
31	c5b2oA_	Alignment	not modelled	5.6	22	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of francisella novicida cas9 in complex with sgrna2 and target dna (tgg pam)
32	c5n8nR_	Alignment	not modelled	5.6	18	PDB header: structural protein Chain: R: PDB Molecule: evpb family type vi secretion protein; PDBTitle: contracted sheath of a pseudomonas aeruginosa type six secretion2 system consisting of tssb1 and tssc1
33	c6ijfA_	Alignment	not modelled	5.5	19	PDB header: antitoxin Chain: A: PDB Molecule: tai4; PDBTitle: crystal structure of the type vi effector-immunity complex (tae4-tai4)2 from agrobacterium tumefaciens
34	c3rafA_	Alignment	not modelled	5.4	26	PDB header: isomerase/dna/antibiotic Chain: A: PDB Molecule: dna topoisomerase 4 subunit a; PDBTitle: quinazolinone-dna cleavage complex of type iv topoisomerase from s.2 pneumoniae
35	c4w8yA_	Alignment	not modelled	5.4	15	PDB header: rna binding protein Chain: A: PDB Molecule: crispr system cmr subunit cmr2; PDBTitle: structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
36	c1hgzA_	Alignment	not modelled	5.4	50	PDB header: virus Chain: A: PDB Molecule: ph75 inovirus major coat protein; PDBTitle: filamentous bacteriophage ph75
37	c1hgvA_	Alignment	not modelled	5.4	50	PDB header: virus Chain: A: PDB Molecule: ph75 inovirus major coat protein; PDBTitle: filamentous bacteriophage ph75
38	c5mxnA_	Alignment	not modelled	5.2	22	PDB header: transport protein Chain: A: PDB Molecule: type vi secretion protein; PDBTitle: atomic model of the vipa/vipb/hcp, the type six secretion system non-2 contractile sheath-tube of vibrio cholerae from cryo-em