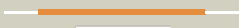
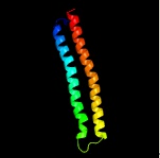



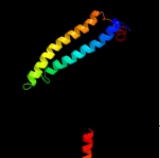
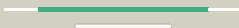
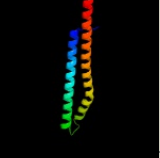

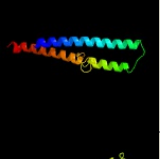
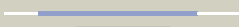
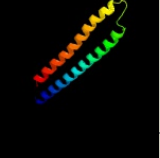

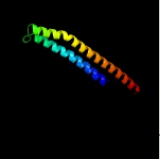

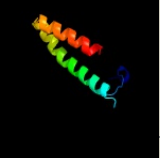



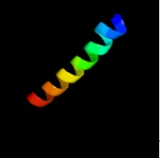




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0027 (-)_31189_31506
Date	Tue Jul 23 14:50:05 BST 2019
Unique Job ID	758d4c8861938612

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4iogD_	 Alignment		89.4	20	PDB header: unknown function Chain: D; PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
2	c2vs0B_	 Alignment		87.3	16	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
3	d1wa8a1	 Alignment		82.0	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
4	c3gvmA_	 Alignment		49.4	17	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
5	c4lwsA_	 Alignment		31.7	21	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
6	c4lwsB_	 Alignment		24.1	10	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
7	c3zbhC_	 Alignment		18.6	14	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
8	c3a98A_	 Alignment		16.9	22	PDB header: signaling protein Chain: A; PDB Molecule: dedicator of cytokinesis protein 2; PDBTitle: crystal structure of the complex of the interacting regions of dock22 and elmo1
9	c6fueC_	 Alignment		15.6	50	PDB header: protein transport Chain: C; PDB Molecule: fapf; PDBTitle: periplasmic coiled coil domain of the fapf amyloid transporter
10	c6fueA_	 Alignment		15.6	50	PDB header: protein transport Chain: A; PDB Molecule: fapf; PDBTitle: periplasmic coiled coil domain of the fapf amyloid transporter
11	c3bboZ_	 Alignment		13.3	23	PDB header: ribosome Chain: Z; PDB Molecule: ribosomal protein l29; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome

12	c5jzrA_	Alignment		13.1	56	PDB header: viral protein Chain: A: PDB Molecule: coat protein; PDBTitle: solid-state mas nmr structure of acinetobacter phage 205 (ap205) coat2 protein in assembled capsid particles
13	c3l8jA_	Alignment		12.9	29	PDB header: protein binding Chain: A: PDB Molecule: programmed cell death protein 10; PDBTitle: crystal structure of ccm3, a cerebral cavernous malformation protein2 critical for vascular integrity
14	c1pyvA_	Alignment		11.4	73	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase beta chain, mitochondrial precursor; PDBTitle: nmr solution structure of the mitochondrial f1b presequence2 peptide from nicotiana plumbaginifolia
15	c2pl9D_	Alignment		11.0	50	PDB header: signaling protien Chain: D: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
16	c2e8pA_	Alignment		10.9	16	PDB header: signaling protein Chain: A: PDB Molecule: elf3 protein; PDBTitle: solution structure of the n-terminal sam-domain of e74-like2 factor 3
17	c5mlcZ_	Alignment		10.5	20	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l29, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
18	c4m70A_	Alignment		8.7	69	PDB header: plant protein Chain: A: PDB Molecule: rx protein; PDBTitle: crystal structure of potato rx-cc domain in complex with rangap2-wpp2 domain
19	c2odmA_	Alignment		8.6	44	PDB header: unknown function Chain: A: PDB Molecule: upf0358 protein mw0995; PDBTitle: crystal structure of s. aureus ylan, an essential leucine rich protein2 involved in the control of cell shape
20	c2lndA_	Alignment		7.9	41	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein, pfk fold; PDBTitle: solution nmr structure of de novo designed protein, pfk fold,2 northeast structural genomics consortium target or134
21	c2lpeA_	Alignment	not modelled	7.7	23	PDB header: signaling protein Chain: A: PDB Molecule: kinase suppressor of ras 1; PDBTitle: solution nmr structure of the ksr1 ca1-ca1a domain
22	c3j3wX_	Alignment	not modelled	7.6	27	PDB header: ribosome Chain: X: PDB Molecule: 50s ribosomal protein l29; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
23	c2pl9F_	Alignment	not modelled	6.9	54	PDB header: signaling protien Chain: F: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
24	c2pl9E_	Alignment	not modelled	6.9	54	PDB header: signaling protien Chain: E: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of chey-mg(2+)-bef(3)(-) in complex with chez(c19)2 peptide solved from a p2(1)2(1)2 crystal
25	c1i7wB_	Alignment	not modelled	6.8	38	PDB header: cell adhesion Chain: B: PDB Molecule: epithelial-cadherin; PDBTitle: beta-catenin/phosphorylated e-cadherin complex
26	c6dlmB_	Alignment	not modelled	6.4	41	PDB header: de novo protein Chain: B: PDB Molecule: dhd127_b; PDBTitle: dhd127
27	d1vqov1	Alignment	not modelled	6.4	25	Fold: Long alpha-hairpin Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
28	c2w0cT_	Alignment	not modelled	6.1	75	PDB header: virus Chain: T: PDB Molecule: protein p6; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
						Fold: Long alpha-hairpin

29	d1r73a_	Alignment	not modelled	6.1	27	Superfamily: Ribosomal protein L29 (L29p) Family: Ribosomal protein L29 (L29p)
30	c5o60Z_	Alignment	not modelled	5.9	23	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l29; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
31	c6fikC_	Alignment	not modelled	5.6	50	PDB header: biosynthetic protein Chain: C: PDB Molecule: polyketide synthase; PDBTitle: acp2 crosslinked to the ks of the loading/condensing region of the2 ctb1 pks
32	d1fnoa3	Alignment	not modelled	5.5	33	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain