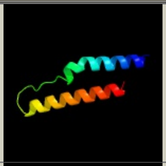
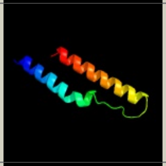
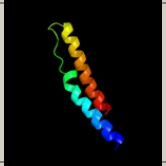
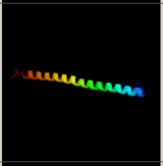
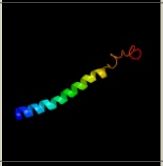
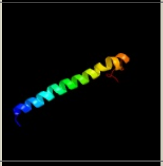
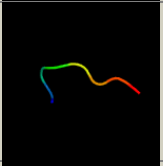
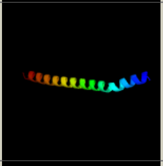
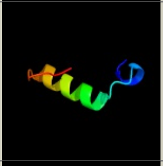
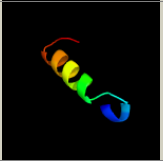
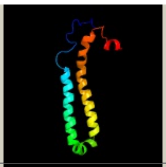
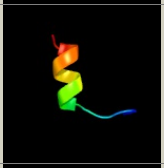
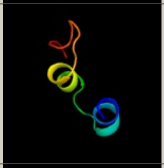
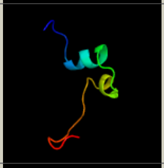
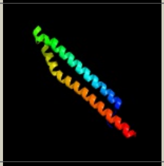
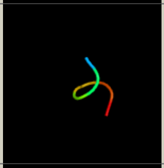
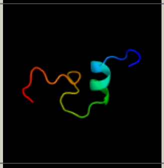
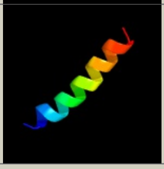
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD3746c_(PE34)_4196349_4196684
Date	Fri Aug 9 18:20:44 BST 2019
Unique Job ID	a69803421ccbf387

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g38A_	Alignment		94.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
2	d2g38a1	Alignment		94.9	22	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PE
3	c5xfsA_	Alignment		94.6	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**pe family protein pe8; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
4	c4wj2A_	Alignment		90.3	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**antigen mtb48; **PDBTitle:** mycobacterial protein
5	c2r18A_	Alignment		29.9	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid assembly protein vp3; **PDBTitle:** structural insights into the multifunctional protein vp3 of2 birnaviruses
6	d1wa8a1	Alignment		28.8	23	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
7	d1wa8b1	Alignment		25.8	6	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
8	c5ujhA_	Alignment		19.3	88	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**granulin; **PDBTitle:** ov-grn12-34
9	c3zbhC_	Alignment		18.1	18	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**esxa; **PDBTitle:** geobacillus thermodenitrificans esxa crystal form i
10	c3hgkE_	Alignment		16.8	19	**PDB header:**transferase **Chain:** E: **PDB Molecule:**effector protein hopab2; **PDBTitle:** crystal structure of effect protein avrptob complexed with2 kinase pto
11	c3sviA_	Alignment		16.7	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**type iii effector hopab2; **PDBTitle:** structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion

12	c2kg7B_	Alignment		14.2	10	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**esat-6-like protein esxh; **PDBTitle:** structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
13	d1jnsa_	Alignment		12.0	33	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
14	d2pv2a1	Alignment		11.4	18	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
15	c1zk6A_	Alignment		10.4	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** nmr solution structure of b. subtilis prsa ppiase
16	c3gvmA_	Alignment		9.4	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
17	c2l53B_	Alignment		9.2	86	**PDB header:**ca-binding protein/proton transport **Chain:** B: **PDB Molecule:**voltage-gated sodium channel type v alpha isoform b **PDBTitle:** solution nmr structure of apo-calmodulin in complex with the iq motif2 of human cardiac sodium channel nav1.5
18	c3gpkA_	Alignment		8.8	40	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
19	d1m5ya3	Alignment		8.0	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
20	c1wrgA_	Alignment		7.5	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
21	c2jzvA_	Alignment	not modelled	7.4	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** solution structure of s. aureus prsa-ppiase
22	d1ecfa1	Alignment	not modelled	7.2	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
23	c4e40A_	Alignment	not modelled	7.1	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the haptoglobin-hemoglobin receptor of trypanosoma congolense
24	d1gph11	Alignment	not modelled	7.0	32	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
25	c5ujgA_	Alignment	not modelled	7.0	75	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**granulin; **PDBTitle:** ovgrn12-35_3s
26	d1eq3a_	Alignment	not modelled	6.6	40	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
27	d1wd5a_	Alignment	not modelled	6.5	30	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
28	c6et5u_	Alignment	not modelled	6.5	32	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
29	d1nera_	Alignment	not modelled	6.2	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains

						Family: Phage repressors
30	d1lghb_	Alignment	not modelled	6.2	36	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
31	c2rqsA_	Alignment	not modelled	6.1	47	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase; **PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin)
32	c1y66D_	Alignment	not modelled	5.4	33	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**engrailed homeodomain; **PDBTitle:** dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
33	c2vs0B_	Alignment	not modelled	5.3	15	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
34	d1dc1a_	Alignment	not modelled	5.3	47	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BsobI
35	d1jo5a_	Alignment	not modelled	5.2	14	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits