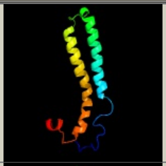
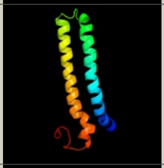
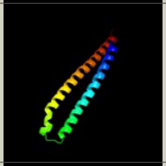
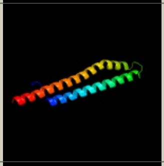
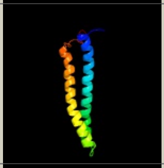
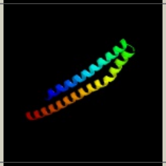
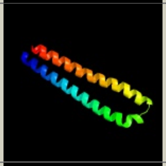
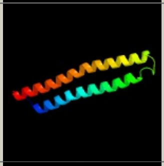
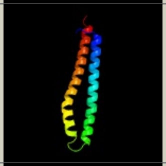
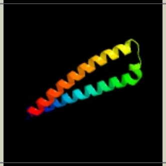
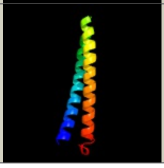
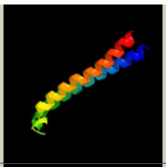
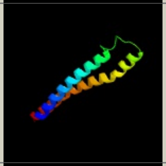
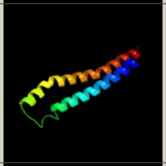
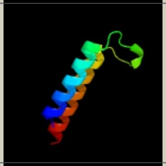
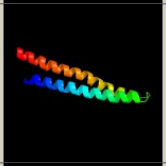
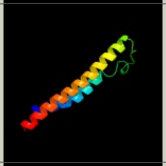
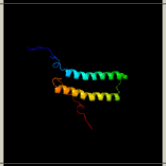
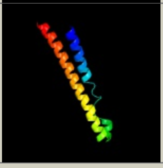
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3019c_(esxR)_3378721_3379011
Date	Thu Aug 8 16:20:19 BST 2019
Unique Job ID	b0f3caa0b624be2b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kg7B_	Alignment		99.9	84	**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
2	d1wa8b1	Alignment		99.9	23	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
3	c4lwsA_	Alignment		99.8	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
4	c3gvmA_	Alignment		99.8	15	**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	d1wa8a1	Alignment		99.8	14	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
6	c3zbhC_	Alignment		99.8	11	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**esxa; **PDBTitle:** geobacillus thermodenitrificans esxa crystal form i
7	c4lwsB_	Alignment		99.8	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
8	c4iogD_	Alignment		99.8	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
9	c2vs0B_	Alignment		99.7	13	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
10	c4i0xJ_	Alignment		99.0	15	**PDB header:**structural genomics, unknown function **Chain:** J: **PDB Molecule:**esat-6-like protein mab_3113; **PDBTitle:** crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
11	c4i0xA_	Alignment		98.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**esat-6-like protein mab_3112; **PDBTitle:** crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex

12	c3q4hB_	Alignment		98.6	62	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**low molecular weight protein antigen 7; **PDBTitle:** crystal structure of the mycobacterium smegmatis esxgh complex2 (msmeg_0620-msmeg_0621)
13	d2g38b1	Alignment		97.7	14	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PPE
14	c2g38B_	Alignment		97.7	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ppe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
15	d2gtsa1	Alignment		97.4	8	**Fold:**Ferritin-like **Superfamily:**HP0062-like **Family:**HP0062-like
16	c3h6pD_	Alignment		97.2	100	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**esat-6-like protein esxr; **PDBTitle:** crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
17	c5xfsB_	Alignment		97.1	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**ppe family protein ppe15; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
18	c4wj2A_	Alignment		94.8	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**antigen mtb48; **PDBTitle:** mycobacterial protein
19	c2kg7A_	Alignment		94.1	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein esxg (pe family protein); **PDBTitle:** structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
20	c4xy3A_	Alignment		87.1	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**esx-1 secretion-associated protein espb; **PDBTitle:** structure of esx-1 secreted protein espb
21	c3h6pB_	Alignment	not modelled	71.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**esat-6 like protein esxs; **PDBTitle:** crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
22	c5wlqA_	Alignment	not modelled	66.9	17	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**capsid assembly scaffolding protein,myosin-7,microtubule- **PDBTitle:** crystal structure of amino acids 1677-1755 of human beta cardiac2 myosin fused to gp7 and eb1
23	d1aepa_	Alignment	not modelled	53.1	16	**Fold:**Apolipophorin-III **Superfamily:**Apolipophorin-III **Family:**Apolipophorin-III
24	c1ls4A_	Alignment	not modelled	52.8	16	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipophorin-iii; **PDBTitle:** nmr structure of apolipophorin-iii from locusta migratoria
25	c4gzrA_	Alignment	not modelled	51.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**esat-6-like protein 6; **PDBTitle:** crystal structure of the mycobacterium tuberculosis h37rv esxop2 (rv2346c-rv2347c) complex in space group c2221
26	c3ogiC_	Alignment	not modelled	50.7	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative esat-6-like protein 6; **PDBTitle:** crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
27	c4njlA_	Alignment	not modelled	48.3	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**s protein; **PDBTitle:** crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
28	c3n8uB_	Alignment	not modelled	42.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**imelysin peptidase; **PDBTitle:** crystal structure of an imelysin peptidase (bacova_03801) from2 bacteroides ovatus at 1.44 a resolution

29	c1wdfA_	Alignment	not modelled	38.7	8	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** crystal structure of mhv spike protein fusion core
30	c1p68A_	Alignment	not modelled	34.6	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed protein s-824; **PDBTitle:** solution structure of s-824, a de novo designed four helix2 bundle
31	c6b3oB_	Alignment	not modelled	30.4	8	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**spike glycoprotein; **PDBTitle:** tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
32	c1qu7A_	Alignment	not modelled	29.0	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein i; **PDBTitle:** four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
33	c4ug1A_	Alignment	not modelled	23.1	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell cycle protein gpsb; **PDBTitle:** gpsb n-terminal domain
34	c2bezC_	Alignment	not modelled	20.9	13	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** structure of a proteolitically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein
35	c5x5fC_	Alignment	not modelled	20.5	10	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**s protein; **PDBTitle:** prefusion structure of mers-cov spike glycoprotein, conformation 2
36	c6nb3B_	Alignment	not modelled	19.1	10	**PDB header:**virus **Chain:** B: **PDB Molecule:**spike glycoprotein; **PDBTitle:** mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
37	c6nzkB_	Alignment	not modelled	19.0	8	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**spike surface glycoprotein; **PDBTitle:** structural basis for human coronavirus attachment to sialic acid2 receptors
38	d2j0na1	Alignment	not modelled	19.0	11	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
39	c6gqaD_	Alignment	not modelled	19.0	22	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cell cycle protein gpsb; **PDBTitle:** cell division regulator s. pneumoniae gpsb
40	c5i08A_	Alignment	not modelled	17.0	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**spike glycoprotein, envelope glycoprotein chimera; **PDBTitle:** prefusion structure of a human coronavirus spike protein
41	c2wukD_	Alignment	not modelled	16.3	6	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
42	c3iv1F_	Alignment	not modelled	15.6	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**tumor susceptibility gene 101 protein; **PDBTitle:** coiled-coil domain of tumor susceptibility gene 101
43	c4y66D_	Alignment	not modelled	15.6	6	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**putative tbpip family protein; **PDBTitle:** crystal structure of giardia lamblia hop2-mnd1 complex
44	c3vp8B_	Alignment	not modelled	15.4	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general transcriptional corepressor tup1; **PDBTitle:** crystal structure of the n-terminal domain of the yeast general2 corepressor tup1p
45	c3jclC_	Alignment	not modelled	14.3	8	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
46	d1st6a6	Alignment	not modelled	14.1	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
47	c2l10A_	Alignment	not modelled	13.9	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** structure of the talin rod residues, domain c
48	c3ok8A_	Alignment	not modelled	13.1	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein **PDBTitle:** i-bar of pinkbar
49	c3g67A_	Alignment	not modelled	12.8	7	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of a soluble chemoreceptor from thermotoga2 maritima
50	c5xlrC_	Alignment	not modelled	12.8	13	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** structure of sars-cov spike glycoprotein
51	c1nohB_	Alignment	not modelled	12.8	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**head morphogenesis protein; **PDBTitle:** the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
52	c1wyyB_	Alignment	not modelled	11.9	13	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
53	c2d5kC_	Alignment	not modelled	11.8	8	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**dps family protein; **PDBTitle:** crystal structure of dps from staphylococcus aureus
54	d1h6ga1	Alignment	not modelled	11.5	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
55	c2pybC_	Alignment	not modelled	10.8	13	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**neutrophil activating protein;

						PDBTitle: napa protein from borrelia burgdorferi
56	c5wrgB_	Alignment	not modelled	10.6	13	**PDB header:**virus like particle **Chain:** B: **PDB Molecule:**spike glycoprotein; **PDBTitle:** sars-cov spike glycoprotein
57	c6cs2A_	Alignment	not modelled	10.2	13	**PDB header:**viral protein/hydrolase **Chain:** A: **PDB Molecule:**spike glycoprotein,fibritin; **PDBTitle:** sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
58	c5ijnS_	Alignment	not modelled	10.1	8	**PDB header:**transport protein **Chain:** S: **PDB Molecule:**nuclear pore complex protein nup58; **PDBTitle:** composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
59	c2oszA_	Alignment	not modelled	9.8	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**nucleoporin p58/p45; **PDBTitle:** structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
60	c2pnvA_	Alignment	not modelled	8.9	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
61	c2ym0B_	Alignment	not modelled	8.7	12	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**cell invasion protein sipd; **PDBTitle:** truncated sipd from salmonella typhimurium
62	c3swyB_	Alignment	not modelled	8.5	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cyclic nucleotide-gated cation channel alpha-3; **PDBTitle:** cnga3 626-672 containing clz domain
63	d2fjca1	Alignment	not modelled	7.8	11	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
64	c5x5bB_	Alignment	not modelled	7.6	13	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**spike glycoprotein; **PDBTitle:** prefusion structure of sars-cov spike glycoprotein, conformation 2
65	c1nfoA_	Alignment	not modelled	7.6	9	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**apolipoprotein e2; **PDBTitle:** apolipoprotein e2 (apoe2, d154a mutation)
66	d1icha_	Alignment	not modelled	7.1	6	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
67	c1ichA_	Alignment	not modelled	7.1	6	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor-1; **PDBTitle:** solution structure of the tumor necrosis factor receptor-12 death domain
68	c3swfA_	Alignment	not modelled	6.8	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
69	c3cazA_	Alignment	not modelled	6.6	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**bar protein; **PDBTitle:** crystal structure of a bar protein from galdieria sulphuraria
70	c1kmiZ_	Alignment	not modelled	6.6	14	**PDB header:**signaling protein **Chain:** Z: **PDB Molecule:**chemotaxis protein chez; **PDBTitle:** crystal structure of an e.coli chemotaxis protein, chez
71	c5t58N_	Alignment	not modelled	6.5	11	**PDB header:**cell cycle **Chain:** N: **PDB Molecule:**klla0c15939p; **PDBTitle:** structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
72	c6h9mA_	Alignment	not modelled	6.4	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**coiled-coil domain-containing protein 90b, mitochondrial, **PDBTitle:** coiled-coil domain-containing protein 90b residues 43-125 from homo2 sapiens fused to a gcn4 adaptor
73	c5lkdB_	Alignment	not modelled	6.3	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase omega-like 2; **PDBTitle:** crystal structure of the xi glutathione transferase ecm4 from2 saccharomyces cerevisiae in complex with glutathione
74	c3tnuA_	Alignment	not modelled	6.2	12	**PDB header:**cytosolic protein **Chain:** A: **PDB Molecule:**keratin, type i cytoskeletal 14; **PDBTitle:** heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
75	c5uxtA_	Alignment	not modelled	6.1	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coiled-coil trimer with glu:trp:lys triad; **PDBTitle:** coiled-coil trimer with glu:trp:lys triad
76	d1h6gb1	Alignment	not modelled	6.0	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
77	c2of5K_	Alignment	not modelled	6.0	9	**PDB header:**apoptosis **Chain:** K: **PDB Molecule:**leucine-rich repeat and death domain-containing protein; **PDBTitle:** oligomeric death domain complex
78	c1zv8I_	Alignment	not modelled	6.0	13	**PDB header:**viral protein **Chain:** I: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
79	c2c6rA_	Alignment	not modelled	5.9	13	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**dna-binding stress response protein, dps family; **PDBTitle:** fe-soaked crystal structure of the dps92 from deinococcus2 radiodurans
80	c6cv0C_	Alignment	not modelled	5.8	6	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein

81	d1hy5a_	Alignment	not modelled	5.8	20	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain
82	c4o6xA_	Alignment	not modelled	5.6	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-3; **PDBTitle:** crystal structure of human ankyrin g death domain
83	c4zrjB_	Alignment	not modelled	5.6	13	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**merlin; **PDBTitle:** structure of merlin-ferm and ctd
84	c2ieqC_	Alignment	not modelled	5.5	11	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
85	c2kbbA_	Alignment	not modelled	5.4	14	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin-1; **PDBTitle:** nmr structure of the talin rod domain, 1655-1822
86	c4modB_	Alignment	not modelled	5.4	11	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hr1 of s protein, linker, hr2 of s protein; **PDBTitle:** structure of the mers-cov fusion core
87	c2p90B_	Alignment	not modelled	5.1	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032