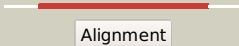



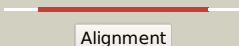

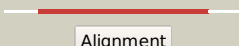
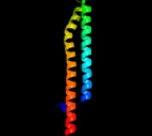
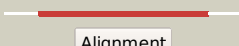

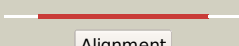
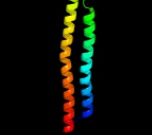
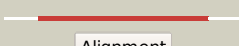
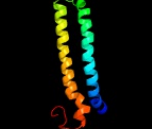







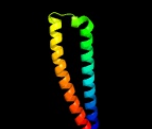
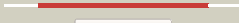
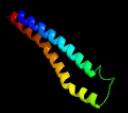
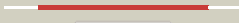
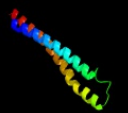











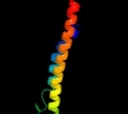


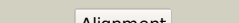

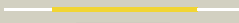

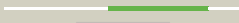
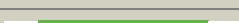
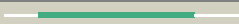



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3905c_(esxF)_4390898_4391209
 Date Sat Aug 10 22:05:09 BST 2019
 Unique Job ID b208cbe76d87c655

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4lwsA_	 Alignment		99.8	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
2	d1wa8a1	 Alignment		99.8	23	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
3	c3zbcC_	 Alignment		99.8	17	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
4	c3gvmA_	 Alignment		99.8	11	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	c2vs0B_	 Alignment		99.7	12	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
6	c4iogD_	 Alignment		99.7	13	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
7	d1wa8b1	 Alignment		99.7	21	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
8	c4lwsB_	 Alignment		99.7	25	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
9	c2kg7B_	 Alignment		99.6	17	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
10	c4i0xA_	 Alignment		99.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex
11	c4i0xJ_	 Alignment		98.8	25	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex

12	d2g38b1	 Alignment		97.6	14	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
13	c2g38B_	 Alignment		97.6	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
14	d2gtsa1	 Alignment		97.5	15	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
15	c5xfsB_	 Alignment		97.0	15	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
16	c3q4hB_	 Alignment		96.3	15	PDB header: metal transport Chain: B: PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esx9 complex2 (msmeg_0620-msmeg_0621)
17	c3h6pD_	 Alignment		91.3	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
18	c3ogiD_	 Alignment		87.6	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative esat-6-like protein 7; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
19	c4wj2A_	 Alignment		87.5	14	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
20	c4xy3A_	 Alignment		85.1	10	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
21	c2kg7A_	 Alignment	not modelled	84.3	16	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
22	c4nj1A_	 Alignment	not modelled	74.1	6	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
23	c3h6pB_	 Alignment	not modelled	73.6	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
24	c1wdfA_	 Alignment	not modelled	60.3	10	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of mhv spike protein fusion core
25	c6b3oB_	 Alignment	not modelled	57.3	10	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
26	c1qu7A_	 Alignment	not modelled	56.1	15	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
27	c3n8uB_	 Alignment	not modelled	46.8	15	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
28	c5j0hA_	 Alignment	not modelled	45.0	16	PDB header: de novo protein Chain: A: PDB Molecule: design construct 2l6hc3_13; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity

29	c2bezC	Alignment	not modelled	43.4	6	PDB header: viral protein Chain: C: PDB Molecule: e2 glycoprotein; PDBTitle: structure of a proteolytically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein
30	c5zhyA	Alignment	not modelled	43.1	8	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
31	c3ogiC	Alignment	not modelled	41.8	16	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxp2 complex (rv2346c-rv2347c)
32	c4gzaA	Alignment	not modelled	40.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxp2 (rv2346c-rv2347c) complex in space group c2221
33	c3g67A	Alignment	not modelled	38.3	6	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
34	c5ijnS	Alignment	not modelled	32.0	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)
35	c2of5K	Alignment	not modelled	31.1	14	PDB header: apoptosis Chain: K: PDB Molecule: leucine-rich repeat and death domain-containing protein; PDBTitle: oligomeric death domain complex
36	c3ci9B	Alignment	not modelled	30.4	3	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
37	c3jclC	Alignment	not modelled	30.0	10	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
38	c4modB	Alignment	not modelled	29.8	8	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
39	c1zv8L	Alignment	not modelled	28.3	8	PDB header: viral protein Chain: I: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
40	c2oszA	Alignment	not modelled	27.6	8	PDB header: structural protein Chain: A: PDB Molecule: nucleoporin p58/p45; PDBTitle: structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
41	d1st6a6	Alignment	not modelled	27.1	5	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
42	c6nzkB	Alignment	not modelled	25.3	10	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
43	c1wyyB	Alignment	not modelled	24.2	6	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
44	c5x5fC	Alignment	not modelled	23.7	6	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
45	c6nb3B	Alignment	not modelled	22.4	6	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
46	c1wncE	Alignment	not modelled	22.3	8	PDB header: viral protein Chain: E: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of the sars-cov spike protein fusion core
47	c3ur1C	Alignment	not modelled	21.0	6	PDB header: immune system Chain: C: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: the structure of a ternary complex between chea domains p4 and p5 with2 chew and with a truncated fragment of tm14, a chemoreceptor analog3 from thermotoga maritima.
48	c5zuvB	Alignment	not modelled	20.4	7	PDB header: viral protein, inhibitor Chain: B: PDB Molecule: spike glycoprotein,spike glycoprotein,inhibitor ek1; PDBTitle: crystal structure of the human coronavirus 229e hr1 motif in complex2 with pan-covs inhibitor ek1
49	c5i08A	Alignment	not modelled	20.3	8	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
50	d1h6ga1	Alignment	not modelled	20.2	7	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
51	c6cs2A	Alignment	not modelled	17.7	6	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrinin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
52	c3sjbC	Alignment	not modelled	17.6	11	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: golgi to er traffic protein 1; PDBTitle: crystal structure of s. cerevisiae get3 in the open state in complex2 with get1 cytosolic domain
53	d2j0na1	Alignment	not modelled	16.5	8	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
54	c5xlrC	Alignment	not modelled	16.3	6	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein

55	c1ichA_	Alignment	not modelled	16.0	14	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor-1; PDBTitle: solution structure of the tumor necrosis factor receptor-12 death domain
56	d1icha_	Alignment	not modelled	16.0	14	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
57	c4kp4B_	Alignment	not modelled	15.9	11	PDB header: transferase/signaling protein Chain: B: PDB Molecule: osmolarity sensor protein envz, histidine kinase; PDBTitle: deciphering cis-trans directionality and visualizing2 autophosphorylation in histidine kinases.
58	c6ckoC_	Alignment	not modelled	15.9	8	PDB header: dna binding protein/transferase Chain: C: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-79 specific; PDBTitle: crystal structure of an af10 fragment
59	c6ckoD_	Alignment	not modelled	15.9	8	PDB header: dna binding protein/transferase Chain: D: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-79 specific; PDBTitle: crystal structure of an af10 fragment
60	d1h6gb1	Alignment	not modelled	15.5	7	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
61	c3viqC_	Alignment	not modelled	15.2	13	PDB header: recombination activator Chain: C: PDB Molecule: swi5-dependent recombination dna repair protein 1; PDBTitle: crystal structure of swi5-sfr1 complex from fission yeast
62	c5wrgB_	Alignment	not modelled	15.0	6	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
63	c2ym0B_	Alignment	not modelled	14.5	10	PDB header: cell invasion Chain: B: PDB Molecule: cell invasion protein sipd; PDBTitle: truncated sipd from salmonella typhimurium
64	c2yy0D_	Alignment	not modelled	13.9	20	PDB header: transcription Chain: D: PDB Molecule: c-myc-binding protein; PDBTitle: crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
65	c3vp8B_	Alignment	not modelled	13.5	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
66	c6b7nC_	Alignment	not modelled	12.6	12	PDB header: viral protein Chain: C: PDB Molecule: spike protein; PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
67	c5xuaB_	Alignment	not modelled	12.2	13	PDB header: signaling protein Chain: B: PDB Molecule: methyl-accepting chemotaxis sensory transducer; PDBTitle: the ligand-free dimer of chemoreceptor mcp2201 ligand binding domain
68	c3iv1F_	Alignment	not modelled	11.9	17	PDB header: hydrolase Chain: F: PDB Molecule: tumor susceptibility gene 101 protein; PDBTitle: coiled-coil domain of tumor susceptibility gene 101
69	d1aepa_	Alignment	not modelled	11.7	21	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
70	c1p68A_	Alignment	not modelled	11.3	19	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
71	c2ym9C_	Alignment	not modelled	11.2	12	PDB header: cell invasion Chain: C: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium
72	c2ym9D_	Alignment	not modelled	10.4	6	PDB header: cell invasion Chain: D: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium
73	c5x5bB_	Alignment	not modelled	10.3	6	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
74	c4y66D_	Alignment	not modelled	10.1	10	PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
75	c2p90B_	Alignment	not modelled	9.8	10	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
76	c1kmiZ_	Alignment	not modelled	8.7	9	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
77	c6cfzC_	Alignment	not modelled	8.6	19	PDB header: nuclear protein Chain: C: PDB Molecule: dad2; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
78	c2yjkF_	Alignment	not modelled	8.6	19	PDB header: metal-binding protein Chain: F: PDB Molecule: afp; PDBTitle: structure of dps from microbacterium arborescens in the2 high iron form
79	d2p90a1	Alignment	not modelled	8.4	13	Fold: Phosphorylase/hydrolase-like Superfamily: Cgl1923-like Family: Cgl1923-like
80	c2d11A_	Alignment	not modelled	8.3	11	PDB header: protein binding Chain: A: PDB Molecule: metastasis suppressor protein 1; PDBTitle: structure of f-actin binding domain imd of mim (missing in metastasis)

81	c2l10A_	Alignment	not modelled	8.2	11	PDB header: structural protein Chain: A; PDB Molecule: talain-1; PDBTitle: structure of the talin rod residues, domain c
82	c6cv0C_	Alignment	not modelled	8.1	14	PDB header: viral protein Chain: C; PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
83	d1lvfa_	Alignment	not modelled	7.6	10	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
84	c5azpA_	Alignment	not modelled	7.6	12	PDB header: membrane protein Chain: A; PDB Molecule: multidrug efflux outer membrane protein oprn; PDBTitle: crystal structure of a membrane protein from pseudomonas aeruginosa
85	c5uxtA_	Alignment	not modelled	7.5	26	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
86	d2c2aa1	Alignment	not modelled	7.1	11	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
87	c1dkgB_	Alignment	not modelled	7.1	13	PDB header: complex (hsp24/hsp70) Chain: B; PDB Molecule: nucleotide exchange factor grpe; PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
88	c2kbbA_	Alignment	not modelled	6.9	16	PDB header: structural protein Chain: A; PDB Molecule: talain-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
89	d1eq1a_	Alignment	not modelled	6.9	13	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
90	c2pnvA_	Alignment	not modelled	6.7	15	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
91	c4egwB_	Alignment	not modelled	6.7	4	PDB header: metal transport Chain: B; PDB Molecule: magnesium transport protein cora; PDBTitle: the structure of the soluble domain of cora from methanocaldococcus2 jannaschii
92	c1ls4A_	Alignment	not modelled	6.6	20	PDB header: lipid transport Chain: A; PDB Molecule: apolipoporphin-iii; PDBTitle: nmr structure of apolipoporphin-iii from locusta migratoria
93	c1sfcl_	Alignment	not modelled	6.6	12	PDB header: transport protein Chain: J; PDB Molecule: protein (syntaxin 1a); PDBTitle: neuronal synaptic fusion complex
94	d1g4us1	Alignment	not modelled	6.5	16	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
95	c2npsB_	Alignment	not modelled	6.5	16	PDB header: transport protein Chain: B; PDB Molecule: syntaxin 13; PDBTitle: crystal structure of the early endosomal snare complex
96	c6e6aB_	Alignment	not modelled	6.3	12	PDB header: protein binding Chain: B; PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
97	c2l16A_	Alignment	not modelled	6.1	7	PDB header: protein transport Chain: A; PDB Molecule: sec-independent protein translocase protein tatad; PDBTitle: solution structure of bacillus subtilis tatad protein in dpc micelles
98	c4ev6E_	Alignment	not modelled	5.7	5	PDB header: metal transport Chain: E; PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
99	d1tjoa_	Alignment	not modelled	5.5	15	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin