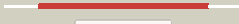
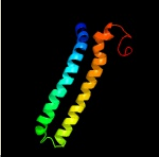

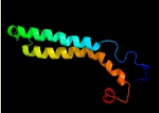
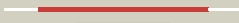
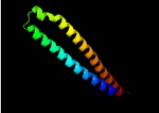



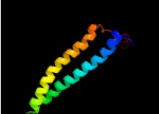















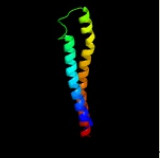





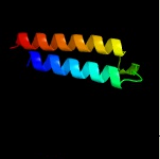

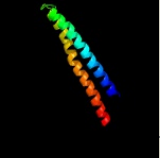
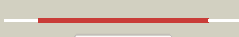
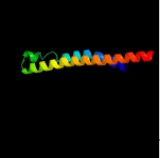

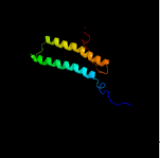

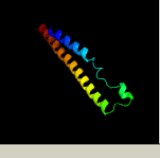


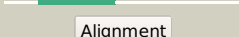
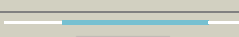

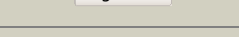
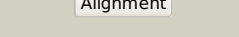
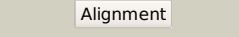


Phyre2

Email mdejesus@rockefeller.edu
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 Date Sat Aug 10 22:05:06 BST 2019
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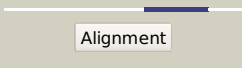
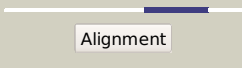
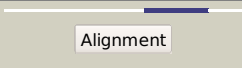
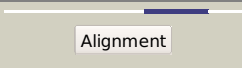
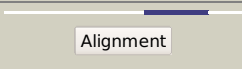
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wa8b1	 Alignment		99.9	100	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
2	c2kg7B	 Alignment		99.9	21	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
3	c4lwsA	 Alignment		99.9	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
4	c3gvmA	 Alignment		99.8	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
5	d1wa8a1	 Alignment		99.8	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	c4iogD	 Alignment		99.8	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	c4lwsB	 Alignment		99.8	23	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
8	c3zbhC	 Alignment		99.8	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
9	c2vs0B	 Alignment		99.8	13	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
10	c4i0xl	 Alignment		98.9	24	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
11	c4i0xA	 Alignment		98.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex

12	c3q4hB_	 Alignment		98.5	24	PDB header: metal transport Chain: B: PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esxg complex2 (msmeg_0620-msmeg_0621)
13	d2g38b1	 Alignment		97.7	21	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
14	c2g38B_	 Alignment		97.7	21	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	12	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
16	c3h6pD_	 Alignment		97.1	26	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 esp5 from m.2 tuberculosis
18	c4wj2A_	 Alignment		93.7	12	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
19	c2kg7A_	 Alignment		93.5	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		87.4	9	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	80.2	19	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	c4nj1A_	 Alignment	not modelled	51.3	15	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
23	c5wlqA_	 Alignment	not modelled	48.6	8	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
24	c1ls4A_	 Alignment	not modelled	38.7	14	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein-iii; PDBTitle: nmr structure of apolipoprotein-iii from locusta migratoria
25	c1wdfA_	 Alignment	not modelled	38.6	13	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of mhv spike protein fusion core
26	c3ogiC_	 Alignment	not modelled	38.4	15	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	d1st6a6	 Alignment	not modelled	38.0	13	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
28	d2j0na1	 Alignment	not modelled	37.4	24	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like

29	c4qzrA	Alignment	not modelled	37.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esoxp2 (rv2346c-rv2347c) complex in space group c2221
30	c1p68A	Alignment	not modelled	33.4	24	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	30.7	13	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
32	c3kltB	Alignment	not modelled	29.6	19	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of a vimentin fragment
33	d1h6ga1	Alignment	not modelled	29.3	15	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
34	c1qu7A	Alignment	not modelled	28.4	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
35	d1aepa	Alignment	not modelled	26.1	15	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
36	c5uxtA	Alignment	not modelled	23.0	16	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
37	c6nb3B	Alignment	not modelled	22.7	15	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing Ica60 antibody fab fragment2 (state 1)
38	c5x5fC	Alignment	not modelled	22.5	15	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
39	c2bezC	Alignment	not modelled	21.4	15	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
40	c6nzkB	Alignment	not modelled	20.8	13	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
41	c5i08A	Alignment	not modelled	19.2	19	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
42	d1h6gb1	Alignment	not modelled	18.6	15	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
43	c4y66D	Alignment	not modelled	17.9	9	PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
44	c3jclC	Alignment	not modelled	16.6	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
45	c6h9mA	Alignment	not modelled	15.0	10	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
46	c4modB	Alignment	not modelled	14.8	17	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
47	c5wrgB	Alignment	not modelled	14.5	15	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
48	c5xlrC	Alignment	not modelled	13.7	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
49	c3g67A	Alignment	not modelled	13.5	8	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
50	c1zv8I	Alignment	not modelled	12.0	16	PDB header: viral protein Chain: I: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
51	c3iv1F	Alignment	not modelled	11.8	5	PDB header: hydrolase Chain: F: PDB Molecule: tumor susceptibility gene 101 protein; PDBTitle: coiled-coil domain of tumor susceptibility gene 101
52	c2d1IA	Alignment	not modelled	11.0	12	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)
53	c4ug1A	Alignment	not modelled	10.8	3	PDB header: cell cycle Chain: A: PDB Molecule: cell cycle protein gpsb; PDBTitle: gpsb n-terminal domain
54	c5ijnS	Alignment	not modelled	10.8	13	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)
						PDB header: cell invasion

55	c2ym0B_	Alignment	not modelled	10.5	21	Chain: B: PDB Molecule: cell invasion protein sipd; PDBTitle: truncated sipd from salmonella typhimurium
56	c6cs2A_	Alignment	not modelled	10.5	15	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
57	c5x5bB_	Alignment	not modelled	10.4	15	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
58	d2j0oa1	Alignment	not modelled	10.1	22	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
59	c2j0oA_	Alignment	not modelled	10.1	22	PDB header: cell invasion Chain: A: PDB Molecule: invasin ipad; PDBTitle: shigella flexneri ipad
60	c1wncE_	Alignment	not modelled	9.5	16	PDB header: viral protein Chain: E: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of the sars-cov spike protein fusion core
61	c3vp8B_	Alignment	not modelled	9.2	16	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
62	c6cv0C_	Alignment	not modelled	8.6	11	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
63	c1nohB_	Alignment	not modelled	8.6	14	PDB header: viral protein Chain: B: PDB Molecule: head morphogenesis protein; PDBTitle: the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
64	c3viqC_	Alignment	not modelled	8.5	9	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
65	c6gqaD_	Alignment	not modelled	8.4	11	PDB header: cell cycle Chain: D: PDB Molecule: cell cycle protein gpsb; PDBTitle: cell division regulator s. pneumoniae gpsb
66	c2kbbA_	Alignment	not modelled	8.2	10	PDB header: structural protein Chain: A: PDB Molecule: taln-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
67	c3n8uB_	Alignment	not modelled	8.0	18	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
68	c5zhyA_	Alignment	not modelled	7.7	10	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
69	c2wukD_	Alignment	not modelled	7.7	6	PDB header: cell cycle Chain: D: PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant
70	c3ci9B_	Alignment	not modelled	6.4	13	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
71	c6ckoC_	Alignment	not modelled	6.3	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
72	c6ckoD_	Alignment	not modelled	6.3	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
73	c3oa7A_	Alignment	not modelled	6.2	10	PDB header: structural protein Chain: A: PDB Molecule: head morphogenesis protein, chaotic nuclear migration PDBTitle: structure of the c-terminal domain of cnm67, a core component of the2 spindle pole body of saccharomyces cerevisiae
74	c1avyA_	Alignment	not modelled	5.8	15	PDB header: coiled coil Chain: A: PDB Molecule: fibrinin; PDBTitle: fibrinin deletion mutant m (bacteriophage t4)
75	c2c6rA_	Alignment	not modelled	5.8	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
76	c2oszA_	Alignment	not modelled	5.6	14	PDB header: structural protein Chain: A: PDB Molecule: nucleoporin p58/p45; PDBTitle: structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
77	c2pnvA_	Alignment	not modelled	5.5	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
78	c6gajA_	Alignment	not modelled	5.3	11	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
79	c1mg1A_	Alignment	not modelled	5.1	14	PDB header: viral protein Chain: A: PDB Molecule: protein (htlv-1 gp21 ectodomain/maltose-binding protein PDBTitle: htlv-1 gp21 ectodomain/maltose-binding protein chimera
80	c4pnaB_	Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: B: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept

81	c4pnaG_	 Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
82	c4pnaA_	 Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: A: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
83	c4pnaC_	 Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: C: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
84	c4pnaD_	 Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: D: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
85	c4pnaF_	 Alignment	not modelled	5.0	26	PDB header: de novo protein Chain: F: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept