










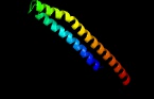


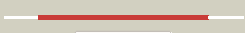









Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3445c_esxU_3863126_3863443
 Date Fri Aug 9 18:20:11 BST 2019
 Unique Job ID 5392a24c800ae3d8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4lwsA_	 Alignment		99.9	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
2	d1wa8b1	 Alignment		99.8	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
3	d1wa8a1	 Alignment		99.8	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
4	c3gvmA_	 Alignment		99.7	14	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	c4lwsB_	 Alignment		99.7	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
6	c3zbcC_	 Alignment		99.7	12	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
7	c2kg7B_	 Alignment		99.7	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
8	c2vs0B_	 Alignment		99.6	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
9	c4iogD_	 Alignment		99.6	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
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	20	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	c3q4hB_	Alignment		97.4	18	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		97.0	18	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
14	c2g38B_	Alignment		97.0	18	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		96.9	12	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
16	c5xfsB_	Alignment		95.8	13	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
17	c3h6pD_	Alignment		93.0	13	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	c2kg7A_	Alignment		89.2	15	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
19	c4nj1A_	Alignment		89.1	15	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
20	c6b3oB_	Alignment		87.9	17	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
21	c1wdfA_	Alignment	not modelled	87.5	17	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of mhv spike protein fusion core
22	c2bezC_	Alignment	not modelled	83.6	19	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
23	c4wj2A_	Alignment	not modelled	78.6	12	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
24	c3h6pB_	Alignment	not modelled	74.7	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
25	c1wyvB_	Alignment	not modelled	72.7	19	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
26	d1hy5a_	Alignment	not modelled	65.5	16	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
27	c3iv1F_	Alignment	not modelled	64.5	5	PDB header: hydrolase Chain: F: PDB Molecule: tumor susceptibility gene 101 protein; PDBTitle: coiled-coil domain of tumor susceptibility gene 101
28	c3jclC_	Alignment	not modelled	60.9	17	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
						PDB header: viral protein

29	c6nzkB_	Alignment	not modelled	58.8	19	Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
30	c5i08A_	Alignment	not modelled	56.1	20	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
31	c5x5fC_	Alignment	not modelled	55.4	15	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
32	c5zuvB_	Alignment	not modelled	55.3	17	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
33	c3ogiD_	Alignment	not modelled	53.2	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative esat-6-like protein 7; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esop2 complex (rv2346c-rv2347c)
34	c6cs2A_	Alignment	not modelled	52.4	19	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
35	c5xlrC_	Alignment	not modelled	50.0	19	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
36	c4qzrA_	Alignment	not modelled	49.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esop2 (rv2346c-rv2347c) complex in space group c2221
37	c6nb3B_	Alignment	not modelled	49.1	15	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing Ica60 antibody fab fragment2 (state 1)
38	c4xy3A_	Alignment	not modelled	47.6	17	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
39	c3ogiC_	Alignment	not modelled	46.2	17	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative esat-6-like protein 6; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esop2 complex (rv2346c-rv2347c)
40	c6b7nC_	Alignment	not modelled	43.8	13	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
41	c5wrgB_	Alignment	not modelled	40.4	19	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
42	c2ieqC_	Alignment	not modelled	33.2	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
43	c6cv0C_	Alignment	not modelled	32.3	19	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
44	c5x5bB_	Alignment	not modelled	32.0	19	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
45	d1st6a6	Alignment	not modelled	31.1	8	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
46	d1h6gb1	Alignment	not modelled	29.8	11	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
47	c1ls4A_	Alignment	not modelled	29.3	16	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein-iii; PDBTitle: nmr structure of apolipoprotein-iii from locusta migratoria
48	d2j0na1	Alignment	not modelled	27.3	10	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
49	d1h6ga1	Alignment	not modelled	27.3	11	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
50	c2ym0B_	Alignment	not modelled	24.5	14	PDB header: cell invasion Chain: B: PDB Molecule: cell invasion protein sipd; PDBTitle: truncated sipd from salmonella typhimurium
51	d1aepa_	Alignment	not modelled	23.7	16	Fold: Apolipoprotein-III Superfamily: Apolipoprotein-III Family: Apolipoprotein-III
52	c1zv8l_	Alignment	not modelled	23.7	21	PDB header: viral protein Chain: I: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
53	d1g4us1	Alignment	not modelled	20.7	15	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
54	c4modB_	Alignment	not modelled	20.3	19	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
55	c1wncE_	Alianment	not modelled	20.1	21	PDB header: viral protein Chain: E: PDB Molecule: e2 glycoprotein;

						PDBTitle: crystal structure of the sars-cov spike protein fusion core
56	c5szsC	Alignment	not modelled	18.9	22	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
57	c3g67A	Alignment	not modelled	15.4	4	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
58	d1he1a	Alignment	not modelled	13.9	17	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
59	c5zhyA	Alignment	not modelled	13.7	15	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
60	d2j0oa1	Alignment	not modelled	13.7	10	Fold: IpaD-like Superfamily: IpaD-like Family: IpaD-like
61	c2j0oA	Alignment	not modelled	13.7	10	PDB header: cell invasion Chain: A: PDB Molecule: invasin ipad; PDBTitle: shigella flexneri ipad
62	c2yy0D	Alignment	not modelled	13.4	13	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
63	c3ci9B	Alignment	not modelled	12.0	9	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
64	d1vhba	Alignment	not modelled	11.8	7	Fold: Globin-like Superfamily: Globin-like Family: Globins
65	c3ls1A	Alignment	not modelled	11.0	11	PDB header: photosynthesis Chain: A: PDB Molecule: sll1638 protein; PDBTitle: crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
66	c3cazA	Alignment	not modelled	10.3	18	PDB header: signaling protein Chain: A: PDB Molecule: bar protein; PDBTitle: crystal structure of a bar protein from galdieria sulphuraria
67	c2kbbA	Alignment	not modelled	9.4	7	PDB header: structural protein Chain: A: PDB Molecule: talin-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
68	c5wlqA	Alignment	not modelled	8.8	18	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
69	c4f7gB	Alignment	not modelled	8.1	7	PDB header: cell adhesion Chain: B: PDB Molecule: talin-1; PDBTitle: crystal structure of talin autoinhibition complex
70	c1qu7A	Alignment	not modelled	7.8	12	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
71	c2wtgA	Alignment	not modelled	7.0	15	PDB header: oxygen transport Chain: A: PDB Molecule: globin-like protein; PDBTitle: high resolution 3d structure of c.elegans globin-like2 protein glb-1
72	d1cqxa1	Alignment	not modelled	6.6	9	Fold: Globin-like Superfamily: Globin-like Family: Globins
73	c4pnaD	Alignment	not modelled	6.3	19	PDB header: de novo protein Chain: D: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
74	c4pnaA	Alignment	not modelled	6.3	19	PDB header: de novo protein Chain: A: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
75	c4pnaB	Alignment	not modelled	6.3	19	PDB header: de novo protein Chain: B: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
76	c4pnaC	Alignment	not modelled	6.3	19	PDB header: de novo protein Chain: C: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
77	c4pnaG	Alignment	not modelled	6.3	19	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
78	c4pnaF	Alignment	not modelled	6.3	19	PDB header: de novo protein Chain: F: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
79	c4pnaE	Alignment	not modelled	6.3	19	PDB header: de novo protein Chain: E: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
80	c3wfwA	Alignment	not modelled	6.2	6	PDB header: oxygen transport Chain: A: PDB Molecule: hemoglobin-like flavoprotein fused to roadblock/lc7 domain; PDBTitle: crystal structure of the closed form of the hgbrl's globin domain
81	c3dyjA	Alignment	not modelled	5.7	10	PDB header: structural protein Chain: A: PDB Molecule: talin-1; PDBTitle: crystal structure a talin rod fragment

82	c6eikC_	Alignment	not modelled	5.5	22	PDB header: de novo protein Chain: C: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
83	c6eikG_	Alignment	not modelled	5.5	22	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
84	c6eikD_	Alignment	not modelled	5.5	22	PDB header: de novo protein Chain: D: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
85	c6eikB_	Alignment	not modelled	5.5	22	PDB header: de novo protein Chain: B: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
86	c6eikF_	Alignment	not modelled	5.5	22	PDB header: de novo protein Chain: F: PDB Molecule: cc-hept-i24e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i24e
87	c5uxtA_	Alignment	not modelled	5.3	14	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
88	c2zxeG_	Alignment	not modelled	5.3	20	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+ .pi2 state