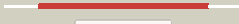


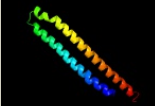
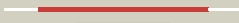






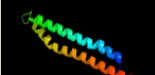



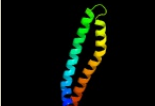





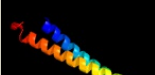


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3444c_esxT_3862803_3863105
 Date Fri Aug 9 18:20:11 BST 2019
 Unique Job ID 19cfa4cebdf47d5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wa8b1	 Alignment		99.9	24	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
2	c4lwsA_	 Alignment		99.9	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
3	c2kg7B_	 Alignment		99.9	20	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
4	c4lwsB_	 Alignment		99.9	24	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
5	d1wa8a1	 Alignment		99.8	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
6	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
7	c3zbhC_	 Alignment		99.7	11	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
8	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
9	c4iogD_	 Alignment		99.7	16	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	c4i0xl_	 Alignment		99.0	29	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		98.6	18	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		97.9	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		97.2	9	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
14	c2g38B_	Alignment		97.2	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
15	c3h6pD_	Alignment		96.3	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
16	c5xfsB_	Alignment		95.6	17	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	c2kg7A_	Alignment		92.4	19	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
18	d2gtsa1	Alignment		91.9	7	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
19	c4wj2A_	Alignment		86.6	12	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
20	c3h6pB_	Alignment		77.1	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
21	d2j0na1	Alignment	not modelled	74.8	10	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
22	d1aepa_	Alignment	not modelled	68.8	16	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
23	c1ls4A_	Alignment	not modelled	67.9	21	PDB header: lipid transport Chain: A: PDB Molecule: apolipoporphin-iii; PDBTitle: nmr structure of apolipoporphin-iii from locusta migratoria
24	c5wlqA_	Alignment	not modelled	67.3	19	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
25	c2ym0B_	Alignment	not modelled	62.9	19	PDB header: cell invasion Chain: B: PDB Molecule: cell invasion protein sipd; PDBTitle: truncated sipd from salmonella typhimurium
26	c4xy3A_	Alignment	not modelled	52.6	14	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
27	c1p68A_	Alignment	not modelled	47.7	21	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
28	c2j0oA_	Alignment	not modelled	33.3	10	PDB header: cell invasion Chain: A: PDB Molecule: invasin ipad; PDBTitle: shigella flexneri ipad
						Fold: lpaD-like

29	d2j0oa1	Alignment	not modelled	33.3	10	Superfamily: lpaD-like Family: lpaD-like
30	c4y66D	Alignment	not modelled	30.7	6	PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
31	c2kbbA	Alignment	not modelled	21.4	21	PDB header: structural protein Chain: A: PDB Molecule: talin-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
32	c3ogiD	Alignment	not modelled	21.3	12	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative esat-6-like protein 7; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxp2 complex (rv2346c-rv2347c)
33	d1h6ga1	Alignment	not modelled	21.1	13	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
34	c3vp8B	Alignment	not modelled	17.3	12	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
35	c4qzrA	Alignment	not modelled	17.2	14	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
36	c3ogiC	Alignment	not modelled	16.9	13	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)
37	d1st6a6	Alignment	not modelled	15.6	13	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
38	c2izpB	Alignment	not modelled	15.0	13	PDB header: toxin Chain: B: PDB Molecule: putative membrane antigen; PDBTitle: bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.
39	c2ym9C	Alignment	not modelled	13.9	19	PDB header: cell invasion Chain: C: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium
40	d1h6gb1	Alignment	not modelled	13.5	13	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
41	d2izpa1	Alignment	not modelled	12.8	13	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
42	c5uxtA	Alignment	not modelled	11.3	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
43	c2p7nA	Alignment	not modelled	11.2	12	PDB header: cell invasion Chain: A: PDB Molecule: pathogenicity island 1 effector protein; PDBTitle: crystal structure of the pathogenicity island 1 effector protein from2 chromobacterium violaceum. northeast structural genomics consortium3 (nesgc) target cvr69.
44	c4zrjB	Alignment	not modelled	10.7	26	PDB header: signaling protein Chain: B: PDB Molecule: merlin; PDBTitle: structure of merlin-ferm and ctd
45	c5t58N	Alignment	not modelled	10.3	9	PDB header: cell cycle Chain: N: PDB Molecule: klla0c15939p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
46	c5xefA	Alignment	not modelled	9.5	5	PDB header: chaperone Chain: A: PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of flagellar chaperone from bacteria
47	c2d1lA	Alignment	not modelled	9.3	13	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)
48	c6h9mA	Alignment	not modelled	8.9	18	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
49	c5lkdB	Alignment	not modelled	8.5	6	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
50	d1orjb	Alignment	not modelled	8.5	15	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone FliS Family: Flagellar export chaperone FliS
51	c3swfA	Alignment	not modelled	7.9	13	PDB header: transport protein Chain: A: PDB Molecule: cgmp-gated cation channel alpha-1; PDBTitle: cnga1 621-690 containing clz domain
52	d1orja	Alignment	not modelled	6.9	17	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone FliS Family: Flagellar export chaperone FliS
53	c3tnuA	Alignment	not modelled	6.9	18	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)
54	d1pzqa	Alignment	not modelled	6.7	14	Fold: Dimerisation interlock Superfamily: Docking domain A of the erythromycin polyketide synthase (DEBS) Family: Docking domain A of the erythromycin polyketide synthase (DEBS) PDB header: cell invasion

55	c3nzzA_	Alignment	not modelled	6.4	18	Chain: A; PDB Molecule: cell invasion protein sipd; PDBTitle: crystal structure of the salmonella type iii secretion system tip2 protein sipd
56	c6cfzC_	Alignment	not modelled	6.3	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
57	c1wdfA_	Alignment	not modelled	6.1	15	PDB header: viral protein Chain: A; PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of mhv spike protein fusion core
58	c3dyjA_	Alignment	not modelled	5.6	18	PDB header: structural protein Chain: A; PDB Molecule: talin-1; PDBTitle: crystal structure a talin rod fragment
59	c3iynQ_	Alignment	not modelled	5.6	19	PDB header: virus Chain: Q; PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
60	c3ok8A_	Alignment	not modelled	5.4	13	PDB header: protein binding Chain: A; PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: i-bar of pinkbar
61	c6nd1E_	Alignment	not modelled	5.4	15	PDB header: protein transport Chain: E; PDB Molecule: translocation protein sec66; PDBTitle: cryoem structure of the sec complex from yeast