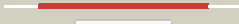



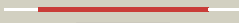




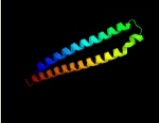

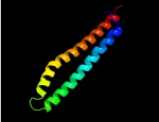





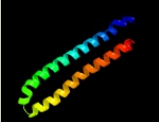

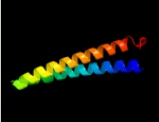

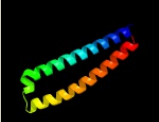


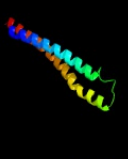

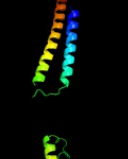


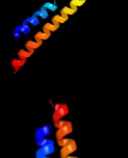
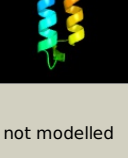


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3874_(esxB)_4352452_4352754
 Date Sat Aug 10 22:05:05 BST 2019
 Unique Job ID 49fde18c8da3e1f6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wa8a1	 Alignment		99.9	100	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
2	c3gvmA	 Alignment		99.8	13	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
3	c4iogD	 Alignment		99.8	29	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
4	c3zbc	 Alignment		99.8	17	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
5	c4lwsA	 Alignment		99.8	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
6	c2vs0B	 Alignment		99.8	14	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	d1wa8b1	 Alignment		99.7	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
8	c2kg7B	 Alignment		99.6	16	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
9	c4lwsB	 Alignment		99.6	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c4i0xA	 Alignment		98.8	16	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		98.4	27	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	d2gtsa1	Alignment		98.3	15	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
13	d2g38b1	Alignment		97.9	16	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
14	c2g38B_	Alignment		97.9	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
15	c5xfsB_	Alignment		97.6	18	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	c3ogiD_	Alignment		95.6	18	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)
17	c4wj2A_	Alignment		94.2	13	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
18	c3q4hB_	Alignment		93.1	17	PDB header: metal transport Chain: B: PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esxhg complex2 (msmeg_0620-msmeg_0621)
19	c4xy3A_	Alignment		90.2	15	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
20	c3h6pD_	Alignment		89.2	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
21	c2kg7A_	Alignment	not modelled	83.3	29	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	c3h6pB_	Alignment	not modelled	58.5	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
23	c3ogiC_	Alignment	not modelled	51.2	14	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)
24	c4qzrA_	Alignment	not modelled	50.0	14	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
25	c3n8uB_	Alignment	not modelled	47.8	12	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
26	c3iv1F_	Alignment	not modelled	25.4	5	PDB header: hydrolase Chain: F: PDB Molecule: tumor susceptibility gene 101 protein; PDBTitle: coiled-coil domain of tumor susceptibility gene 101
27	c3g67A_	Alignment	not modelled	25.3	2	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
28	c2ym9C_	Alignment	not modelled	24.7	5	PDB header: cell invasion Chain: C: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium

29	c1qu7A	Alignment	not modelled	22.8	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
30	c2of5K	Alignment	not modelled	22.6	9	PDB header: apoptosis Chain: K: PDB Molecule: leucine-rich repeat and death domain-containing protein; PDBTitle: oligomeric death domain complex
31	c3viqC	Alignment	not modelled	22.5	14	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
32	c1ls4A	Alignment	not modelled	21.9	16	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein-iii; PDBTitle: nmr structure of apolipoprotein-iii from locusta migratoria
33	c1ichA	Alignment	not modelled	20.7	13	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor-1; PDBTitle: solution structure of the tumor necrosis factor receptor-12 death domain
34	d1icha	Alignment	not modelled	20.7	13	Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
35	c3kdgB	Alignment	not modelled	19.2	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of a functionally unknown conserved2 protein from corynebacterium diphtheriae.
36	d1g4us1	Alignment	not modelled	19.1	22	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
37	d2c2aa1	Alignment	not modelled	18.7	13	Fold: ROP-like Superfamily: Homodimeric domain of signal transducing histidine kinase Family: Homodimeric domain of signal transducing histidine kinase
38	d2p90a1	Alignment	not modelled	18.7	15	Fold: Phosphorylase/hydrolase-like Superfamily: Cgl1923-like Family: Cgl1923-like
39	c3ci9B	Alignment	not modelled	18.6	26	PDB header: transcription Chain: B: PDB Molecule: heat shock factor-binding protein 1; PDBTitle: crystal structure of the human hsbp1
40	c3kitB	Alignment	not modelled	17.2	17	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of a vimentin fragment
41	d1aepa	Alignment	not modelled	16.0	16	Fold: Apolipoprotein-III Superfamily: Apolipoprotein-III Family: Apolipoprotein-III
42	c6f1ux	Alignment	not modelled	14.9	16	PDB header: motor protein Chain: X: PDB Molecule: bicd family-like cargo adapter 1; PDBTitle: n terminal region of dynein tail domains in complex with dynactin2 filament and bicdr-1
43	c4kp4B	Alignment	not modelled	14.6	10	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.
44	c3uunA	Alignment	not modelled	14.4	14	PDB header: structural protein Chain: A: PDB Molecule: dystrophin; PDBTitle: crystal structure of n-terminal first spectrin repeat of dystrophin
45	c6e6aB	Alignment	not modelled	14.0	12	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
46	c2i10A	Alignment	not modelled	12.4	21	PDB header: structural protein Chain: A: PDB Molecule: talin-1; PDBTitle: structure of the talin rod residues, domain c
47	c3d1nK	Alignment	not modelled	12.1	10	PDB header: transcription regulator/dna Chain: K: PDB Molecule: pou domain, class 6, transcription factor 1; PDBTitle: structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
48	c2oqgA	Alignment	not modelled	11.8	23	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, arsr family protein; PDBTitle: arsr-like transcriptional regulator from rhodococcus sp. rha1
49	d2j0oa1	Alignment	not modelled	11.8	19	Fold: IpaD-like Superfamily: IpaD-like Family: IpaD-like
50	c2j0oA	Alignment	not modelled	11.8	19	PDB header: cell invasion Chain: A: PDB Molecule: invasin ipad; PDBTitle: shigella flexneri ipad
51	c1zxbB	Alignment	not modelled	11.2	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein mg377 homolog; PDBTitle: crystal structure of the hypothetical mycoplasma protein, mpn555
52	d1st6a6	Alignment	not modelled	11.0	16	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
53	c2p90B	Alignment	not modelled	10.4	12	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
54	c3vp8B	Alignment	not modelled	10.3	10	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

55	d1eq1a_	Alignment	not modelled	10.3	22	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III
56	c6ckoC_	Alignment	not modelled	10.2	22	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
57	c6ckoD_	Alignment	not modelled	10.2	22	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
58	c3sjbC_	Alignment	not modelled	10.0	8	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
59	c5zhyA_	Alignment	not modelled	9.3	7	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
60	c3layF_	Alignment	not modelled	8.8	18	PDB header: metal binding protein Chain: F: PDB Molecule: zinc resistance-associated protein; PDBTitle: alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
61	c4modB_	Alignment	not modelled	8.2	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
62	c4pnaB_	Alignment	not modelled	8.1	15	PDB header: de novo protein Chain: B: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
63	c4pnaG_	Alignment	not modelled	8.1	15	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
64	c4pnaD_	Alignment	not modelled	8.1	15	PDB header: de novo protein Chain: D: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
65	c4pnaA_	Alignment	not modelled	8.1	15	PDB header: de novo protein Chain: A: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
66	c4pnaC_	Alignment	not modelled	8.1	15	PDB header: de novo protein Chain: C: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
67	c4pnaE_	Alignment	not modelled	8.1	15	PDB header: de novo protein Chain: E: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
68	c4pnaF_	Alignment	not modelled	8.1	15	PDB header: de novo protein Chain: F: PDB Molecule: cc-hept; PDBTitle: a de novo designed heptameric coiled coil cc-hept
69	d2j0na1	Alignment	not modelled	7.9	19	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
70	d1iwga5	Alignment	not modelled	7.9	12	Fold: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains
71	c6b7nC_	Alignment	not modelled	7.7	16	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
72	c3myfB_	Alignment	not modelled	7.5	9	PDB header: transferase Chain: B: PDB Molecule: sensor protein; PDBTitle: the crystal structure of the hpt domain from the hpt sensor hybrid2 histidine kinase from shewanella to 1.80a
73	c3whIB_	Alignment	not modelled	7.4	16	PDB header: hydrolase/chaperone Chain: B: PDB Molecule: probable 26s proteasome regulatory subunit p27; PDBTitle: crystal structure of nas2 n-terminal domain complexed with pan-rpt5c2 chimera
74	c5zuvB_	Alignment	not modelled	7.4	10	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
75	c1sj8A_	Alignment	not modelled	7.4	17	PDB header: structural protein Chain: A: PDB Molecule: talain 1; PDBTitle: crystal structure of talin residues 482-789
76	d1yvia1	Alignment	not modelled	7.0	8	Fold: Four-helical up-and-down bundle Superfamily: Histidine-containing phosphotransfer domain, HPT domain Family: Phosphorelay protein-like
77	d1e3oc2	Alignment	not modelled	7.0	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
78	d1he1a_	Alignment	not modelled	6.9	9	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
79	c2r47C_	Alignment	not modelled	6.8	11	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein mth_862; PDBTitle: crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
80	c6mtkA_	Alignment	not modelled	6.7	9	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from

					elizabethkingia2 anophelis nuhp1
81	c1p68A_	Alignment	not modelled	6.6	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
82	c3lnrA_	Alignment	not modelled	6.4	9 PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
83	c2l16A_	Alignment	not modelled	6.3	13 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
84	c5j0hA_	Alignment	not modelled	6.3	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
85	c2ym0B_	Alignment	not modelled	6.2	16 PDB header: cell invasion Chain: B: PDB Molecule: cell invasion protein sipd; PDBTitle: truncated sipd from salmonella typhimurium
86	c2ym9D_	Alignment	not modelled	6.1	3 PDB header: cell invasion Chain: D: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium
87	d1i0aa_	Alignment	not modelled	6.1	10 Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
88	d1h6gb1	Alignment	not modelled	6.1	13 Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
89	c4y66D_	Alignment	not modelled	6.0	6 PDB header: cell cycle Chain: D: PDB Molecule: putative tbpip family protein; PDBTitle: crystal structure of giardia lamblia hop2-mnd1 complex
90	c3vjfA_	Alignment	not modelled	6.0	19 PDB header: de novo protein Chain: A: PDB Molecule: wa20; PDBTitle: crystal structure of de novo 4-helix bundle protein wa20
91	d1wn0a1	Alignment	not modelled	5.9	8 Fold: Four-helical up-and-down bundle Superfamily: Histidine-containing phosphotransfer domain, HPT domain Family: Phosphorelay protein-like
92	d1vcsa1	Alignment	not modelled	5.8	9 Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
93	c3wz2C_	Alignment	not modelled	5.7	16 PDB header: chaperone Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbaa, an archaeal homolog of2 proteasome-assembly chaperone
94	c1wdfA_	Alignment	not modelled	5.6	10 PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of mhv spike protein fusion core
95	c6cfzC_	Alignment	not modelled	5.4	10 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
96	c5uxtA_	Alignment	not modelled	5.2	20 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
97	c2ld3A_	Alignment	not modelled	5.2	10 PDB header: motor protein Chain: A: PDB Molecule: myosin vi; PDBTitle: solution structure of myosin vi lever arm extension
98	d1cuna2	Alignment	not modelled	5.1	9 Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat