


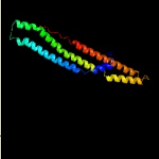

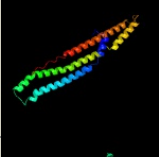

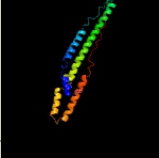

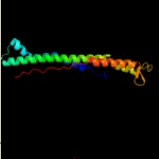

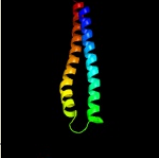

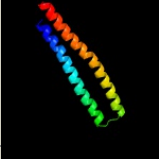

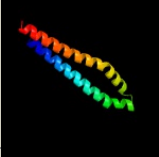

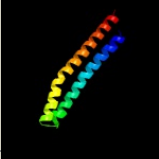

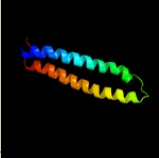

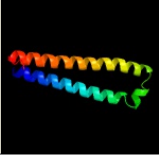
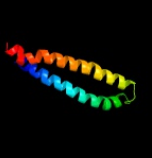

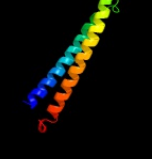
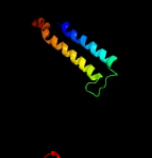
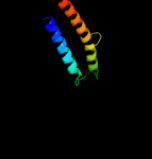
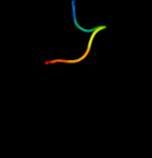
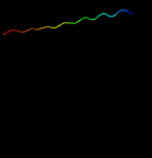

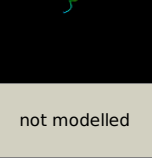


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1787_(PPE25)_2025308_2026405
 Date Fri Aug 2 13:30:39 BST 2019
 Unique Job ID 6099185555e5b4c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	62	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
2	c2g38B_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	32	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	16	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		98.8	16	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.8	14	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.7	14	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
8	c3gvmA_	 Alignment		97.7	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
9	c3zbhC_	 Alignment		97.5	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.7	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.9	17	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		95.3	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		95.3	19	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		94.1	12	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
15	c2kg7B	Alignment		89.6	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
16	c4i0xJ	Alignment		66.2	22	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
17	c5frgA	Alignment		18.9	75	PDB header: protein binding Chain: A; PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
18	c1bkvA	Alignment		15.2	50	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvC	Alignment		14.5	50	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvB	Alignment		14.5	50	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
21	d1ui5a2	Alignment	not modelled	13.8	22	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
22	c2ke4A	Alignment	not modelled	12.2	75	PDB header: membrane protein Chain: A; PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
23	d1zeeal	Alignment	not modelled	11.3	32	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
24	c2iu1A	Alignment	not modelled	9.6	28	PDB header: transcription Chain: A; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
25	c2fulE	Alignment	not modelled	8.9	39	PDB header: translation Chain: E; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
26	c2kg7A	Alignment	not modelled	7.7	35	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
27	c3h6pB	Alignment	not modelled	7.5	24	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
28	c2lkqA	Alignment	not modelled	7.0	33	PDB header: immune system Chain: A; PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide

29	c1vytF_	Alignment	not modelled	7.0	50	PDB header: transport protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
30	c4lzxB_	Alignment	not modelled	6.8	41	PDB header: metal binding protein Chain: B; PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
31	d1fcdA3	Alignment	not modelled	6.6	46	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
32	c2i94B_	Alignment	not modelled	6.4	67	PDB header: protein binding Chain: B; PDB Molecule: rhodopsin kinase; PDBTitle: nmr structure of recoverin bound to rhodopsin kinase
33	c4m1iB_	Alignment	not modelled	6.2	50	PDB header: metal binding protein Chain: B; PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-bound cam
34	c3juiA_	Alignment	not modelled	5.8	23	PDB header: translation Chain: A; PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
35	c5ucOB_	Alignment	not modelled	5.5	40	PDB header: hydrolase Chain: B; PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
36	d1khba2	Alignment	not modelled	5.5	20	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
37	c2i5bA_	Alignment	not modelled	5.4	44	PDB header: apoptosis Chain: A; PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
38	c1paqA_	Alignment	not modelled	5.4	24	PDB header: translation Chain: A; PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
39	d1paqa_	Alignment	not modelled	5.4	24	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
40	c1vytE_	Alignment	not modelled	5.4	50	PDB header: transport protein Chain: E; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
41	c6q5iA_	Alignment	not modelled	5.2	27	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-i24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-i24h
42	c4i6jB_	Alignment	not modelled	5.2	44	PDB header: transcription Chain: B; PDB Molecule: tf-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
43	c6q5iB_	Alignment	not modelled	5.2	27	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-i24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-i24h
44	c6q5hA_	Alignment	not modelled	5.2	27	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-i24d; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-i24d
45	c6q5mB_	Alignment	not modelled	5.1	27	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-i24dab; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-i24dab
46	c6q5iB_	Alignment	not modelled	5.1	27	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-i24e; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-i24e
47	c6q5kA_	Alignment	not modelled	5.1	27	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-i24k; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-i24k