
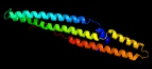

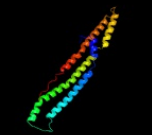

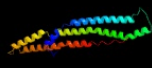

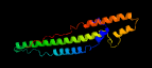

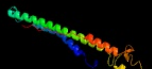











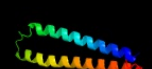
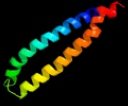










Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2892c_(PPE45)_3200804_3202030
 Date Thu Aug 8 16:20:04 BST 2019
 Unique Job ID cf6cd08eb1fa848a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	64	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	d2g38b1	 Alignment		100.0	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	34	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c4xy3A_	 Alignment		100.0	18	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		98.4	17	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.7	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.6	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		97.6	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
9	c3zbhC_	 Alignment		97.4	13	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		95.5	18	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		95.1	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		94.9	15	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		94.1	16	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		88.5	12	PDB header: unknown function Chain: B; PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ	Alignment		71.6	23	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	d1ui5a2	Alignment		29.0	22	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c1bkvA	Alignment		17.0	56	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvB	Alignment		16.2	56	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvC	Alignment		16.2	56	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
21	c5frgA	Alignment	not modelled	10.9	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
22	c2lkqA	Alignment	not modelled	8.3	44	PDB header: immune system Chain: A; PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
23	c1vytF	Alignment	not modelled	8.0	25	PDB header: transport protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
24	c4xb6D	Alignment	not modelled	7.5	22	PDB header: transferase Chain: D; PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
25	c2nvjA	Alignment	not modelled	7.4	40	PDB header: hydrolase Chain: A; PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
26	c2iu1A	Alignment	not modelled	7.4	22	PDB header: transcription Chain: A; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
27	c5lzkB	Alignment	not modelled	7.3	4	PDB header: structural genomics Chain: B; PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
28	c2kg7A	Alignment	not modelled	7.1	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
29	c6nbiP	Alignment	not modelled	6.9	80	PDB header: signaling protein Chain: P: PDB Molecule: long-acting parathyroid hormone analog; PDBTitle: cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
30	c2fulE	Alignment	not modelled	6.7	22	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
31	c4lzxB	Alignment	not modelled	6.3	31	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
32	c2jtwA	Alignment	not modelled	6.0	50	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
33	c2kc5A	Alignment	not modelled	5.9	28	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase-2 operon protein hybe; PDBTitle: solution structure of hybe from escherichia coli
34	c6aokA	Alignment	not modelled	5.9	38	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
35	c1vytE	Alignment	not modelled	5.8	25	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
36	c6cgjA	Alignment	not modelled	5.7	38	PDB header: hydrolase Chain: A: PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
37	c2ke4A	Alignment	not modelled	5.7	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 cjp4
38	c4i6jB	Alignment	not modelled	5.5	44	PDB header: transcription Chain: B: PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
39	c4dexB	Alignment	not modelled	5.5	25	PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent n-type calcium channel subunit alpha-1b; PDBTitle: crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav2.2 i-ii linker.
40	c3trhI	Alignment	not modelled	5.5	19	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
41	c6et5X	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: X: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
42	c6et5v	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: V: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
43	c6et5s	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: S: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
44	c6et5j	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: J: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
45	c6et55	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: 5: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
46	c6et5l	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: I: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
47	c6et5R	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: R: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
48	c6et5y	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: Y: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
49	c6et5d	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: D: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
50	c6et52	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: 2: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
51	c6et5g	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: G: PDB Molecule: light-harvesting protein b-1015 beta chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
52	c6et5p	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: P: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
53	c6et5m	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: M: PDB Molecule: reaction center protein m chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
54	c6et5O	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: O: PDB Molecule: light-harvesting protein b-1015 gamma chain;

						PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
55	c6et5a_	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: A: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
56	c6et5U_	Alignment	not modelled	5.5	42	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
57	c3sjrB_	Alignment	not modelled	5.2	6	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknown function protein cv 1783 from <i>Chromobacterium violaceum</i> atcc 12472
58	c4m1IB_	Alignment	not modelled	5.1	36	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca ²⁺ -bound cam
59	c5uc0B_	Alignment	not modelled	5.1	60	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of 2 cog5400 from <i>Brucella abortus</i>
60	c6dzsD_	Alignment	not modelled	5.0	38	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp