
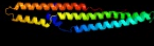

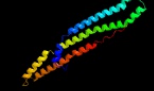



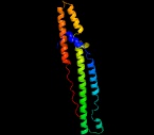

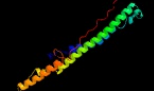














# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0387c_(-)_466673_468004
Date	Tue Jul 23 14:50:46 BST 2019
Unique Job ID	eea19b8362c14a5d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	61	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein ppe15; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	<a href="#">d2g38b1</a>	 Alignment		100.0	36	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
3	<a href="#">c2g38B_</a>	 Alignment		100.0	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ppe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> esx-1 secretion-associated protein espb; <b>PDBTitle:</b> structure of esx-1 secreted protein espb
5	<a href="#">c4wj2A_</a>	 Alignment		98.6	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> antigen mtb48; <b>PDBTitle:</b> mycobacterial protein
6	<a href="#">c2vs0B_</a>	 Alignment		97.9	9	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	<a href="#">c4iogD_</a>	 Alignment		97.8	14	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
8	<a href="#">c3gvmA_</a>	 Alignment		97.7	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	<a href="#">c3zbhC_</a>	 Alignment		97.6	15	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
10	<a href="#">d1wa8a1</a>	 Alignment		97.0	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsB_</a>	 Alignment		96.2	13	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	<a href="#">c4lwsA_</a>	Alignment		96.1	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	<a href="#">d1wa8b1</a>	Alignment		95.9	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		94.7	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein mab_3112; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	<a href="#">c2kg7B_</a>	Alignment		91.0	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6-like protein eshx; <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	<a href="#">c4i0xJ_</a>	Alignment		85.9	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> J: <b>PDB Molecule:</b> esat-6-like protein mab_3113; <b>PDBTitle:</b> crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	<a href="#">d1ui5a2</a>	Alignment		25.0	20	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
18	<a href="#">c1bkvA_</a>	Alignment		12.3	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
19	<a href="#">c5frgA_</a>	Alignment		11.9	75	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> formin-binding protein 1-like; <b>PDBTitle:</b> the nmr structure of the cdc42-interacting region of toca1
20	<a href="#">c1bkvB_</a>	Alignment		11.7	50	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
21	<a href="#">c1bkvC_</a>	Alignment	not modelled	11.7	50	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
22	<a href="#">c2iu1A_</a>	Alignment	not modelled	8.7	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of eif5 c-terminal domain
23	<a href="#">c2fulE_</a>	Alignment	not modelled	7.9	22	<b>PDB header:</b> translation <b>Chain:</b> E: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5; <b>PDBTitle:</b> crystal structure of the c-terminal domain of s. cerevisiae eif5
24	<a href="#">c1vytF_</a>	Alignment	not modelled	7.8	25	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
25	<a href="#">c4xb6D_</a>	Alignment	not modelled	7.6	33	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; <b>PDBTitle:</b> structure of the e. coli c-p lyase core complex
26	<a href="#">c3sjrB_</a>	Alignment	not modelled	6.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of conserved unknwn function protein cv_1783 from2 chromobacterium violaceum atcc 12472
27	<a href="#">c3zfsA_</a>	Alignment	not modelled	6.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> f420-reducing hydrogenase, subunit alpha; <b>PDBTitle:</b> cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
28	<a href="#">c1bzgA_</a>	Alignment	not modelled	6.1	0	<b>PDB header:</b> hormone <b>Chain:</b> A: <b>PDB Molecule:</b> parathyroid hormone-related protein; <b>PDBTitle:</b> the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures

29	<a href="#">c6aokA</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ceg4; <b>PDBTitle:</b> crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
30	<a href="#">c2nviA</a>	Alignment	not modelled	5.8	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 25mer peptide from vacuolar atp synthase subunit <b>PDBTitle:</b> nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
31	<a href="#">d1vifn1</a>	Alignment	not modelled	5.7	80	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Cna protein B-type domain <b>Family:</b> Cna protein B-type domain
32	<a href="#">c2ke4A</a>	Alignment	not modelled	5.6	75	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cdc42-interacting protein 4; <b>PDBTitle:</b> the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
33	<a href="#">c6cgiA</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein lem4 (lpg1101); <b>PDBTitle:</b> structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
34	<a href="#">c5l85B</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear fragile x mental retardation-interacting protein 1; <b>PDBTitle:</b> solution structure of the complex between human znhit3 and nufip12 proteins
35	<a href="#">c2lkqA</a>	Alignment	not modelled	5.5	44	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin lambda-like polypeptide 1; <b>PDBTitle:</b> nmr structure of the lambda 5 22-45 peptide
36	<a href="#">c6et5m</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> M: <b>PDB Molecule:</b> reaction center protein m chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
37	<a href="#">c6et55</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> 5: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
38	<a href="#">c6et5y</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> Y: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
39	<a href="#">c6et5l</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> I: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
40	<a href="#">c6et5O</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> O: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
41	<a href="#">c6et5g</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> light-harvesting protein b-1015 beta chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
42	<a href="#">c6et5R</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> R: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
43	<a href="#">c6et5p</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> P: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
44	<a href="#">c6et52</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> 2: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
45	<a href="#">c6et5d</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> D: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
46	<a href="#">c6et5X</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
47	<a href="#">c6et5v</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> V: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
48	<a href="#">c6et5s</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> S: <b>PDB Molecule:</b> light-harvesting protein b-1015 alpha chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
49	<a href="#">c6et5U</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> U: <b>PDB Molecule:</b> light-harvesting protein b-1015 gamma chain; <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
50	<a href="#">c6et5a</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
51	<a href="#">c6et5j</a>	Alignment	not modelled	5.4	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> J: <b>PDB Molecule:</b> <b>PDBTitle:</b> reaction centre light harvesting complex 1 from blc. viridis
52	<a href="#">c1vytE</a>	Alignment	not modelled	5.4	25	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel <b>PDBTitle:</b> beta3 subunit complexed with aid
53	<a href="#">c3trhl</a>	Alignment	not modelled	5.2	14	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase <b>PDBTitle:</b> structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
54	<a href="#">c4dexB</a>	Alignment	not modelled	5.2	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent n-type calcium channel subunit alpha-1b;

			<p><b>PDBTitle:</b> crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav2.2 i-ii linker.</p>
55 <a href="#">c4mveB_</a>	<div style="border: 1px solid black; padding: 2px; display: inline-block;">Alignment</div>	not modelled	<p><b>PDB header:</b> structural genomics, unknown function  <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein;  <b>PDBTitle:</b> crystal structure of tcur_1030 protein from thermomonospora curvata</p>