
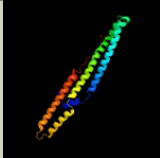

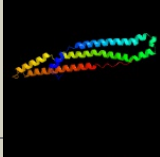

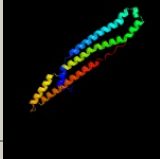

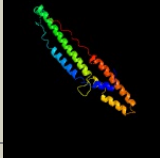

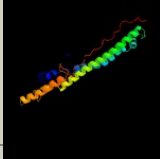

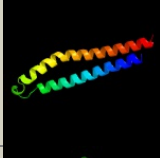

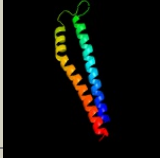

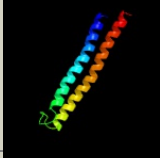

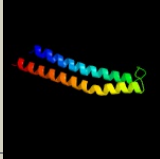

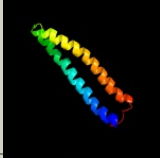

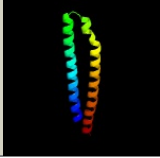


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0878c\_(PPE13)\_976875\_978206  
 Date Fri Jul 26 01:50:47 BST 2019  
 Unique Job ID 9a5774eb6d88fe80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xfsB_</a>	 Alignment		100.0	54	<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="#">c2g38B_</a>	 Alignment		100.0	34	<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
3	<a href="#">d2g38b1</a>	 Alignment		100.0	34	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PPE
4	<a href="#">c4xy3A_</a>	 Alignment		100.0	16	<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		99.0	16	<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		98.0	10	<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="#">c3gvmA_</a>	 Alignment		97.8	10	<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
8	<a href="#">c4iogD_</a>	 Alignment		97.7	19	<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
9	<a href="#">c3zbhC_</a>	 Alignment		97.7	14	<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		97.2	20	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
11	<a href="#">c4lwsA_</a>	 Alignment		96.3	19	<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

12	<a href="#">c4lwsB_</a>	Alignment		96.2	12	<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
13	<a href="#">d1wa8b1</a>	Alignment		95.9	18	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
14	<a href="#">c4i0xA_</a>	Alignment		95.5	21	<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		93.5	22	<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		88.7	25	<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		53.2	24	<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		21.6	50	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
19	<a href="#">c1bkvC_</a>	Alignment		20.3	50	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
20	<a href="#">c1bkvB_</a>	Alignment		20.3	50	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> t3-785; <b>PDBTitle:</b> collagen
21	<a href="#">c2iu1A_</a>	Alignment	not modelled	19.8	33	<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
22	<a href="#">c5frgA_</a>	Alignment	not modelled	19.1	63	<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
23	<a href="#">c2fulE_</a>	Alignment	not modelled	16.5	33	<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="#">d1xkna_</a>	Alignment	not modelled	16.3	13	<b>Fold:</b> Pentelin, beta/alpha-propeller <b>Superfamily:</b> Pentelin <b>Family:</b> Porphyromonas-type peptidylarginine deiminase
25	<a href="#">c2ke4A_</a>	Alignment	not modelled	10.9	63	<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
26	<a href="#">c1paqA_</a>	Alignment	not modelled	10.0	18	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor eif-2b epsilon <b>PDBTitle:</b> crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
27	<a href="#">d1paqa_</a>	Alignment	not modelled	10.0	18	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> MIF4G domain-like
28	<a href="#">c2kp7A_</a>	Alignment	not modelled	10.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> crossover junction endonuclease mus81; <b>PDBTitle:</b> solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
						<b>PDB header:</b> translation

29	<a href="#">c3juiA_</a>	Alignment	not modelled	9.5	23	<b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor eif-2b subunit epsilon; <b>PDBTitle:</b> crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
30	<a href="#">c5lc5a_</a>	Alignment	not modelled	9.3	63	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase chain 3; <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
31	<a href="#">c2l5bA_</a>	Alignment	not modelled	8.0	50	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> activator of apoptosis harakiri; <b>PDBTitle:</b> solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
32	<a href="#">c3h6pB_</a>	Alignment	not modelled	8.0	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> esat-6 like protein exs; <b>PDBTitle:</b> crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
33	<a href="#">c4oanB_</a>	Alignment	not modelled	7.9	18	<b>PDB header:</b> membrane protein/protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> trap dicarboxylate transporter dctp subunit; <b>PDBTitle:</b> crystal structure of a trap periplasmic solute binding protein from2 rhodospseudomonas palustris haa2 (rpb_2686), target efi-510221, with3 density modeled as (s)-2-hydroxy-2-methyl-3-oxobutanoate ((s)-2-4 acetolactate)
34	<a href="#">c2kg7A_</a>	Alignment	not modelled	7.4	32	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein exsg (pe family protein); <b>PDBTitle:</b> structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
35	<a href="#">c4jijA_</a>	Alignment	not modelled	7.4	43	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose 1,4-beta-cellobiosidase; <b>PDBTitle:</b> the structure of t. fusca gh48 d224n mutant
36	<a href="#">c4el8A_</a>	Alignment	not modelled	7.3	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 48; <b>PDBTitle:</b> the unliganded structure of c.bescii cela gh48 module
37	<a href="#">c5hl8B_</a>	Alignment	not modelled	7.0	33	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> type ii secretion system protein i; <b>PDBTitle:</b> 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspl3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
38	<a href="#">d1luaa2</a>	Alignment	not modelled	6.8	29	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Methylene-tetrahydromethanopterin dehydrogenase
39	<a href="#">c4deyB_</a>	Alignment	not modelled	6.7	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> voltage-dependent l-type calcium channel subunit alpha-1c; <b>PDBTitle:</b> crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker.
40	<a href="#">c4i6jB_</a>	Alignment	not modelled	6.6	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tf-box/lrr-repeat protein 3; <b>PDBTitle:</b> a ubiquitin ligase-substrate complex
41	<a href="#">c4yk3B_</a>	Alignment	not modelled	6.5	29	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bepe protein; <b>PDBTitle:</b> crystal structure of the bid domain of bepe from bartonella henselae
42	<a href="#">c3h96B_</a>	Alignment	not modelled	6.5	8	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> f420-h2 dependent reductase a; <b>PDBTitle:</b> msmeq_3358 f420 reductase
43	<a href="#">c3n6xA_</a>	Alignment	not modelled	6.5	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glutathionylspermidine synthase; <b>PDBTitle:</b> crystal structure of a putative glutathionylspermidine synthase2 (mfla_0391) from methylobacillus flagellatus kt at 2.35 a resolution
44	<a href="#">c3r5zB_</a>	Alignment	not modelled	6.3	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
45	<a href="#">c3jywF_</a>	Alignment	not modelled	6.1	52	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 60s ribosomal protein l7(a); <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
46	<a href="#">d1saza2</a>	Alignment	not modelled	6.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
47	<a href="#">d1l1ya_</a>	Alignment	not modelled	5.9	19	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
48	<a href="#">c1l2aD_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cellobiohydrolase; <b>PDBTitle:</b> the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
49	<a href="#">c4yk2B_</a>	Alignment	not modelled	5.8	19	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> bartonella effector protein (bep) substrate of virb t4ss; <b>PDBTitle:</b> crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
50	<a href="#">c5i4rA_</a>	Alignment	not modelled	5.7	71	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> contact-dependent inhibitor a; <b>PDBTitle:</b> contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
51	<a href="#">c4kkkA_</a>	Alignment	not modelled	5.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exoglucanase s; <b>PDBTitle:</b> complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
						<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> rtx toxins and related ca2+-binding

52	<a href="#">c4fusA_</a>	Alignment	not modelled	5.7	38	protein; <b>PDBTitle:</b> the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
53	<a href="#">c5lzkB_</a>	Alignment	not modelled	5.3	9	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> protein fam83b; <b>PDBTitle:</b> structure of the domain of unknown function duf1669 from human fam83b
54	<a href="#">c3rhtB_</a>	Alignment	not modelled	5.2	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> (gatase1)-like protein; <b>PDBTitle:</b> crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
55	<a href="#">c3j3bF_</a>	Alignment	not modelled	5.2	31	<b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> 60s ribosomal protein l7; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
56	<a href="#">c2ahmG_</a>	Alignment	not modelled	5.1	22	<b>PDB header:</b> viral protein, replication <b>Chain:</b> G: <b>PDB Molecule:</b> replicase polyprotein 1ab, heavy chain; <b>PDBTitle:</b> crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
57	<a href="#">d1g9ga_</a>	Alignment	not modelled	5.1	31	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Cellulases catalytic domain
58	<a href="#">d1fcda3</a>	Alignment	not modelled	5.1	23	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain