
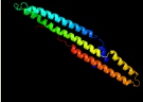

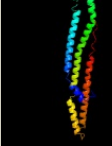

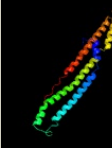



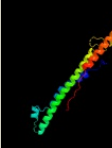

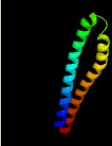

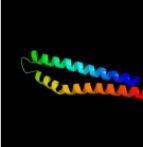

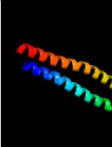

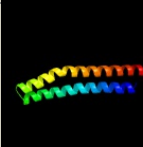

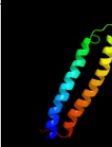

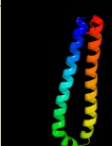


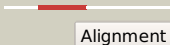
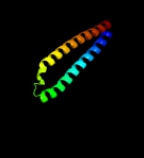
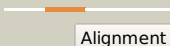
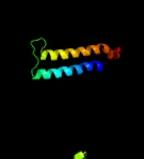

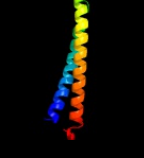


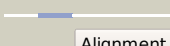

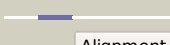
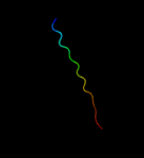



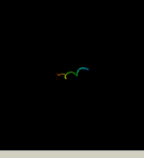
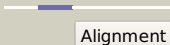



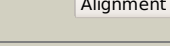
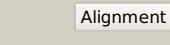
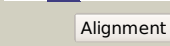
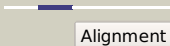
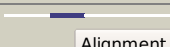


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1706c_(PPE23)_1932701_1933885
 Date Fri Aug 2 13:30:30 BST 2019
 Unique Job ID 040ac9c73a32ca4a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	61	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	32	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	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
4	c4xy3A_	 Alignment		100.0	21	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		98.5	15	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.6	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.4	16	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c4iogD_	 Alignment		97.4	15	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
9	c3zbhC_	 Alignment		97.2	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.5	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.2	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	 Alignment		94.8	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	 Alignment		94.3	18	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c2kg7B	 Alignment		86.4	15	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
15	c4i0xA	 Alignment		85.7	18	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
16	c4i0xJ	 Alignment		53.9	20	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		21.0	63	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		18.0	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvC	 Alignment		17.3	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
20	c1bkvB	 Alignment		17.3	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
21	c4bz4D	 Alignment	not modelled	16.7	58	PDB header: copper-binding protein Chain: D: PDB Molecule: copper-repressible polypeptide; PDBTitle: cora is a surface-associated copper-binding protein2 important in methylomicrobium album bg8 copper acquisition
22	c2ke4A	 Alignment	not modelled	14.0	63	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	d1ui5a2	 Alignment	not modelled	11.8	19	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
24	c5h9xA	 Alignment	not modelled	10.8	30	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,3-glucanase; PDBTitle: crystal structure of gh family 64 laminaripentaose-producing beta-1,3-2 glucanase from paenibacillus barengoltzii
25	c5vzmB	 Alignment	not modelled	10.4	63	PDB header: protein binding Chain: B: PDB Molecule: dna repair protein rev1; PDBTitle: solution nmr structure of human rev1 (932-1039) in complex with2 ubiquitin
26	c4lzxB	 Alignment	not modelled	9.7	31	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
27	d2fcla1	 Alignment	not modelled	9.4	28	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: TM1012-like
28	c4m1IB	 Alignment	not modelled	8.2	36	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-bound cam
						Fold: Tetracyclin repressor-like, C-terminal domain

29	d2np5a2	Alignment	not modelled	7.7	30	Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
30	d1khba2	Alignment	not modelled	7.7	20	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
31	c2iu1A_	Alignment	not modelled	7.6	22	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
32	c4is4G_	Alignment	not modelled	7.3	8	PDB header: ligase Chain: G: PDB Molecule: glutamine synthetase; PDBTitle: the glutamine synthetase from the dicotyledonous plant m. truncatula2 is a decamer
33	c1vytF_	Alignment	not modelled	7.2	13	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
34	c6rlxA_	Alignment	not modelled	6.9	71	PDB header: hormone(muscle relaxant) Chain: A: PDB Molecule: relaxin, a-chain; PDBTitle: x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
35	c6rlxC_	Alignment	not modelled	6.9	71	PDB header: hormone(muscle relaxant) Chain: C: PDB Molecule: relaxin, a-chain; PDBTitle: x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
36	c2mv1A_	Alignment	not modelled	6.9	71	PDB header: signaling protein Chain: A: PDB Molecule: relaxin a chain; PDBTitle: solution nmr structure of human relaxin-2
37	c2v36D_	Alignment	not modelled	6.8	35	PDB header: transferase Chain: D: PDB Molecule: gamma-glutamyltranspeptidase small chain; PDBTitle: crystal structure of gamma-glutamyl transferase from bacillus subtilis
38	c2fulE_	Alignment	not modelled	6.8	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
39	c1bcvA_	Alignment	not modelled	6.6	44	PDB header: synthetic peptide Chain: A: PDB Molecule: peptide corresponding to the major immunogen site of fmd PDBTitle: synthetic peptide corresponding to the major immunogen site of fmd2 virus, nmr, 10 structures
40	c3ibzA_	Alignment	not modelled	6.4	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative tellurium resistant like protein terd; PDBTitle: crystal structure of putative tellurium resistant like protein (terd)2 from streptomyces coelicolor a3(2)
41	c2k6tA_	Alignment	not modelled	6.3	71	PDB header: hormone Chain: A: PDB Molecule: insulin-like 3 a chain; PDBTitle: solution structure of the relaxin-like factor
42	c2h8bA_	Alignment	not modelled	6.3	71	PDB header: hormone/growth factor Chain: A: PDB Molecule: insulin-like 3; PDBTitle: solution structure of insl3
43	c4baxH_	Alignment	not modelled	6.3	8	PDB header: ligase Chain: H: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from streptomyces2 coelicolor
44	c2d3aj_	Alignment	not modelled	6.2	17	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
45	c4i6jB_	Alignment	not modelled	6.1	33	PDB header: transcription Chain: B: PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
46	c2k6uA_	Alignment	not modelled	6.1	71	PDB header: hormone Chain: A: PDB Molecule: insulin-like 3 a chain; PDBTitle: the solution structure of a conformationally restricted2 fully active derivative of the human relaxin-like factor3 (rlf)
47	c3fkyD_	Alignment	not modelled	6.0	8	PDB header: ligase Chain: D: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
48	d1kshb_	Alignment	not modelled	5.9	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
49	c5uc0B_	Alignment	not modelled	5.9	60	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
50	d1k47a1	Alignment	not modelled	5.7	13	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
51	c3r5zB_	Alignment	not modelled	5.6	19	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
52	c1t0jC_	Alignment	not modelled	5.5	14	PDB header: signaling protein Chain: C: PDB Molecule: voltage-dependent l-type calcium channel alpha-1c subunit; PDBTitle: crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
53	c4deyB_	Alignment	not modelled	5.5	6	PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: crystal structure of the voltage dependent calcium

						channel beta-22 subunit in complex with the cav1.2 I-II linker.
54	c2lkqA_	Alignment	not modelled	5.5	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
55	d2q09a1	Alignment	not modelled	5.4	30	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: !imidazolonepropionase-like
56	c4hppA_	Alignment	not modelled	5.4	17	PDB header: ligase Chain: A: PDB Molecule: probable glutamine synthetase; PDBTitle: crystal structure of novel glutamine synthase homolog
57	c2le2B_	Alignment	not modelled	5.2	60	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: p56; PDBTitle: novel dimeric structure of phage phi29-encoded protein p56: insights2 into uracil-dna glycosylase inhibition
58	c3ng0A_	Alignment	not modelled	5.2	33	PDB header: ligase Chain: A: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
59	c2y5tG_	Alignment	not modelled	5.2	83	PDB header: immune system Chain: G: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
60	c4ndvB_	Alignment	not modelled	5.2	63	PDB header: sugar binding protein Chain: B: PDB Molecule: alpha-galactosyl-binding lectin; PDBTitle: crystal structure of l. decastes alpha-galactosyl-binding lectin in2 complex with globotriose
61	c6cgvW_	Alignment	not modelled	5.2	31	PDB header: virus Chain: W: PDB Molecule: pre-protein vi; PDBTitle: revised crystal structure of human adenovirus
62	c3j2i_	Alignment	not modelled	5.2	31	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
63	c3izrm_	Alignment	not modelled	5.1	31	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein I23 (I14p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
64	c1htoB_	Alignment	not modelled	5.1	25	PDB header: ligase Chain: B: PDB Molecule: glutamine synthetase; PDBTitle: crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
65	c2qsrA_	Alignment	not modelled	5.1	38	PDB header: transcription Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of c-terminal domain of transcription-repair2 coupling factor
66	d1xdpa4	Alignment	not modelled	5.1	25	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
67	c5craB_	Alignment	not modelled	5.1	45	PDB header: hydrolase Chain: B: PDB Molecule: sdea; PDBTitle: structure of the sdea dub domain