






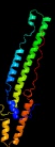





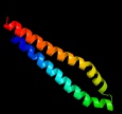











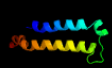



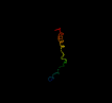



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3018c_(PPE46)_3376949_3378253
 Date Thu Aug 8 16:20:18 BST 2019
 Unique Job ID 8830b71c601ff116

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	39	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	29	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	29	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		97.9	21	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.6	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.5	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	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
9	c3zbhC_	 Alignment		97.2	16	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.3	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		94.1	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		93.3	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
13	c4lwsA	Alignment		92.9	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA	Alignment		91.5	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
15	c2kg7B	Alignment		86.3	17	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		80.6	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	c1nayC	Alignment		47.9	26	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
18	d1lui5a2	Alignment		46.9	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
19	c5ctdA	Alignment		19.2	18	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-1(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
20	d1zeeA1	Alignment		18.9	37	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
21	c1bkvA	Alignment	not modelled	18.7	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
22	c1bkvB	Alignment	not modelled	17.9	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
23	c1bkvC	Alignment	not modelled	17.9	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
24	d1dlpa1	Alignment	not modelled	16.6	18	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
25	c5ctdB	Alignment	not modelled	15.7	18	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-2(i) chain,collagen alpha-2(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
26	c5ctiC	Alignment	not modelled	12.5	21	PDB header: structural protein Chain: C: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-3(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
27	c4xb6D	Alignment	not modelled	11.5	33	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 PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar ato svnphase

28	c2nvjA_	Alignment	not modelled	10.3	40	subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
29	d1vfn1	Alignment	not modelled	9.7	100	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
30	c1bzgA_	Alignment	not modelled	9.6	14	PDB header: hormone Chain: A: PDB Molecule: parathyroid hormone-related protein; PDBTitle: the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
31	c6aokA_	Alignment	not modelled	8.8	25	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
32	c6qpiA_	Alignment	not modelled	8.6	16	PDB header: membrane protein Chain: A: PDB Molecule: anoctamin-6; PDBTitle: cryo-em structure of calcium-free mtmem16f lipid scramblase in2 nanodisc
33	c3sjrB_	Alignment	not modelled	8.6	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknwn function protein cv_1783 from2 chromobacterium violaceum atcc 12472
34	c4gyxC_	Alignment	not modelled	8.5	45	PDB header: structural protein, blood clotting Chain: C: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
35	c6cgjA_	Alignment	not modelled	8.2	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
36	c2kg7A_	Alignment	not modelled	8.2	47	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
37	c2iu1A_	Alignment	not modelled	8.2	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
38	c2y5tG_	Alignment	not modelled	7.7	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
39	c3h6pB_	Alignment	not modelled	7.7	47	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
40	c1vytF_	Alignment	not modelled	7.6	50	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
41	c6nbiP_	Alignment	not modelled	7.5	60	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
42	c5I85B_	Alignment	not modelled	7.5	36	PDB header: signaling protein Chain: B: PDB Molecule: nuclear fragile x mental retardation-interacting protein 1; PDBTitle: solution structure of the complex between human znhit3 and nupif12 proteins
43	c2fulE_	Alignment	not modelled	7.4	28	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
44	c2lkqA_	Alignment	not modelled	7.3	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
45	c2y5tE_	Alignment	not modelled	7.3	83	PDB header: immune system Chain: E: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
46	d1fcda3	Alignment	not modelled	7.0	23	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
47	c5ucOB_	Alignment	not modelled	7.0	100	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
48	c3a1hF_	Alignment	not modelled	6.7	29	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
49	c2f6aj_	Alignment	not modelled	6.6	71	PDB header: cell adhesion/structural protein Chain: J: PDB Molecule: collagen; PDBTitle: collagen adhesin and collagen complex structure
50	c2wuhD_	Alignment	not modelled	6.4	83	PDB header: receptor/peptide Chain: D: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
51	c3qi7A_	Alignment	not modelled	6.3	44	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
52	c5h18B_	Alignment	not modelled	6.2	25	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein I; PDBTitle: 1.93 angstrom resolution crystal structure of a

52	c2iunB	Alignment	not modelled	6.2	49	pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
53	c2iunD	Alignment	not modelled	6.2	50	PDB header: viral protein Chain: D: PDB Molecule: avian adenovirus celo long fibre; PDBTitle: structure of the c-terminal head domain of the avian adenovirus celo2 long fibre (p21 crystal form)
54	c2wuhB	Alignment	not modelled	6.2	83	PDB header: receptor/peptide Chain: B: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
55	c2wuhC	Alignment	not modelled	6.2	83	PDB header: receptor/peptide Chain: C: PDB Molecule: collagen peptide; PDBTitle: crystal structure of the ddr2 discoidin domain bound to a2 triple-helical collagen peptide
56	c3ah9D	Alignment	not modelled	6.1	26	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
57	c1vytE	Alignment	not modelled	6.0	50	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
58	c3zfsA	Alignment	not modelled	5.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: f420-reducing hydrogenase, subunit alpha; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
59	c1t0jC	Alignment	not modelled	5.6	43	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
60	c5vmoB	Alignment	not modelled	5.6	50	PDB header: viral protein/apoptosis Chain: B: PDB Molecule: bcl-2 interacting mediator of cell death; PDBTitle: crystal structure of grouper iridovirus glv66:bim complex
61	d1nkt4	Alignment	not modelled	5.5	67	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
62	c3ah9F	Alignment	not modelled	5.5	25	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
63	c3pobB	Alignment	not modelled	5.5	55	PDB header: hydrolase Chain: B: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
64	c3ponB	Alignment	not modelled	5.5	55	PDB header: unknown function Chain: B: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of mbl collagen-like peptide
65	c3ponA	Alignment	not modelled	5.5	55	PDB header: unknown function Chain: A: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of mbl collagen-like peptide
66	c3pobC	Alignment	not modelled	5.5	55	PDB header: hydrolase Chain: C: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
67	c3pobD	Alignment	not modelled	5.5	55	PDB header: hydrolase Chain: D: PDB Molecule: mbl collagen-like peptide; PDBTitle: crystal structure of masp-1 cub2 domain in complex with the collagen-2 like domain of mbl
68	c2drtA	Alignment	not modelled	5.4	83	PDB header: structural protein Chain: A: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
69	c2drtB	Alignment	not modelled	5.4	83	PDB header: structural protein Chain: B: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
70	c4dexB	Alignment	not modelled	5.4	38	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.
71	c2jtwA	Alignment	not modelled	5.4	50	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
72	c1qsuC	Alignment	not modelled	5.3	83	PDB header: structural protein Chain: C: PDB Molecule: protein ((pro-hyp-gly)4- glu-lys-gly(pro-hyp-gly)5); PDBTitle: crystal structure of the triple-helical collagen-like peptide, (pro-2 hyp-gly)4-glu-lys-gly(pro-hyp-gly)5
73	c2drtC	Alignment	not modelled	5.3	83	PDB header: structural protein Chain: C: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
74	c4y9iA	Alignment	not modelled	5.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
75	c3ah9A	Alignment	not modelled	5.3	26	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
76	c1cagA	Alignment	not modelled	5.2	83	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
77	c1cagC	Alignment	not modelled	5.2	83	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like

						peptide2 at 1.9 angstrom resolution
78	c2drxB_	Alignment	not modelled	5.1	67	PDB header: structural protein Chain: B: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4
79	c1k6fB_	Alignment	not modelled	5.1	22	PDB header: structural protein Chain: B: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
80	c1k6fD_	Alignment	not modelled	5.1	22	PDB header: structural protein Chain: D: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
81	c1k6fE_	Alignment	not modelled	5.1	22	PDB header: structural protein Chain: E: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
82	c1k6fC_	Alignment	not modelled	5.1	22	PDB header: structural protein Chain: C: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
83	c1k6fF_	Alignment	not modelled	5.1	22	PDB header: structural protein Chain: F: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
84	c1k6fA_	Alignment	not modelled	5.1	22	PDB header: structural protein Chain: A: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
85	c2drxA_	Alignment	not modelled	5.1	67	PDB header: structural protein Chain: A: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4
86	c1cagB_	Alignment	not modelled	5.0	83	PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal and molecular structure of a collagen-like peptide2 at 1.9 angstrom resolution
87	c1cgdC_	Alignment	not modelled	5.0	83	PDB header: collagen Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
88	c1cgdA_	Alignment	not modelled	5.0	83	PDB header: collagen Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide
89	c1cgdB_	Alignment	not modelled	5.0	83	PDB header: collagen Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: hydration structure of a collagen peptide