
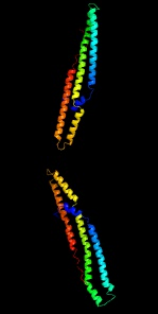

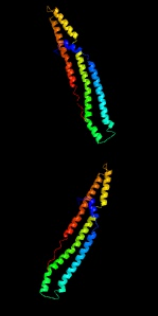

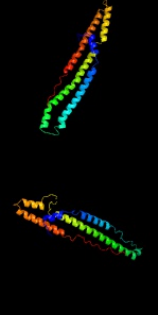

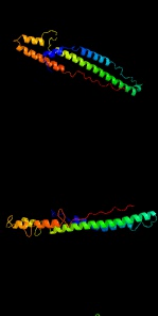

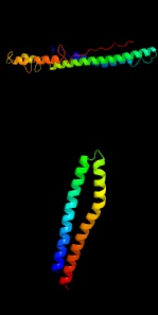

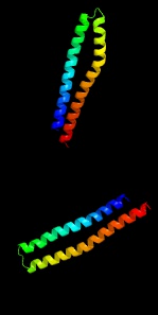

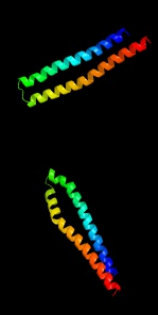

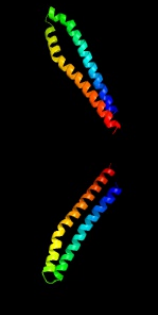
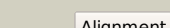
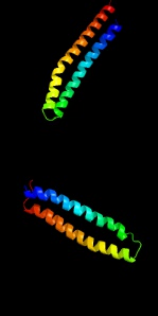

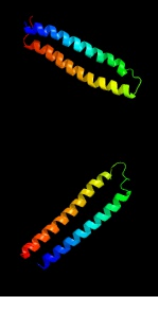




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2770c_(PPE44)_3079319_3080467
 Date Wed Aug 7 12:50:43 BST 2019
 Unique Job ID 0be612ee8f7229b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	68	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	19	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	17	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.7	13	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	13	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		97.5	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
9	c3zbhC_	 Alignment		97.4	18	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.7	19	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.4	9	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	Alignment		94.5	16	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		93.9	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		91.9	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		86.1	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		54.1	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	c1bkvA_	Alignment		22.9	31	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
18	c1bkvB_	Alignment		21.9	31	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
19	c1bkvC_	Alignment		21.9	31	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
20	c5frgA_	Alignment		19.0	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
21	c2ke4A_	Alignment	not modelled	12.1	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
22	c3a1iA_	Alignment	not modelled	11.1	43	PDB header: hydrolase Chain: A; PDB Molecule: amidase; PDBTitle: crystal structure of rhodococcus sp. n-771 amidase complexed2 with benzamide
23	c3a2qA_	Alignment	not modelled	8.7	29	PDB header: hydrolase Chain: A; PDB Molecule: 6-aminohexanoate-cyclic-dimer hydrolase; PDBTitle: structure of 6-aminohexanoate cyclic dimer hydrolase complexed with2 substrate
24	d1mt5a_	Alignment	not modelled	8.5	43	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
25	c2iu1A_	Alignment	not modelled	8.4	17	PDB header: transcription Chain: A; PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
26	d1ui5a2	Alignment	not modelled	8.3	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
27	c1vytF_	Alignment	not modelled	8.0	50	PDB header: transport protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
28	d1zeeal	Alignment	not modelled	7.9	36	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
29	c2fu1F_	Alignment	not modelled	7.8	28	PDB header: translation Chain: E; PDB Molecule: eukaryotic translation initiation factor 5;

29	c2lruE_	Alignment	not modelled	7.8	48	PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
30	c4lzxB_	Alignment	not modelled	7.7	38	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-free cam
31	c3trhl_	Alignment	not modelled	7.6	21	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
32	c3sjrB_	Alignment	not modelled	7.2	6	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved unknow function protein cv_1783 from2 chromobacterium violaceum atcc 12472
33	c2lkqA_	Alignment	not modelled	7.1	44	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
34	c2y5tG_	Alignment	not modelled	6.7	33	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
35	c4issA_	Alignment	not modelled	6.7	29	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: semet-substituted kluveromyces lactis allophanate hydrolase
36	c3kfuE_	Alignment	not modelled	6.7	43	PDB header: ligase/rna Chain: E: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: crystal structure of the transamidosome
37	c4gyxC_	Alignment	not modelled	6.6	27	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
38	c4gyxB_	Alignment	not modelled	6.6	27	PDB header: structural protein, blood clotting Chain: B: 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
39	c4gyxA_	Alignment	not modelled	6.6	27	PDB header: structural protein, blood clotting Chain: A: 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
40	c4dmtB_	Alignment	not modelled	6.6	23	PDB header: structural protein Chain: B: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
41	c4dmtA_	Alignment	not modelled	6.6	23	PDB header: structural protein Chain: A: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
42	c4dmtC_	Alignment	not modelled	6.6	23	PDB header: structural protein Chain: C: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
43	c4gysA_	Alignment	not modelled	6.6	36	PDB header: hydrolase Chain: A: PDB Molecule: allophanate hydrolase; PDBTitle: granulibacter bethedsensis allophanate hydrolase co-crystallized with2 malonate
44	d1ocka_	Alignment	not modelled	6.5	29	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
45	c1vytE_	Alignment	not modelled	6.5	50	PDB header: transport protein Chain: E: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
46	c2y5tE_	Alignment	not modelled	6.4	33	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
47	c4m1lB_	Alignment	not modelled	6.3	43	PDB header: metal binding protein Chain: B: PDB Molecule: iq domain-containing protein g; PDBTitle: complex of iqcg and ca2+-bound cam
48	c2kg7A_	Alignment	not modelled	6.2	24	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
49	d2gi3a1	Alignment	not modelled	6.2	36	Fold: Amidase signature (AS) enzymes Superfamily: Amidase signature (AS) enzymes Family: Amidase signature (AS) enzymes
50	c4dexB_	Alignment	not modelled	6.1	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 l-ii linker.
51	c4i6jB_	Alignment	not modelled	6.0	33	PDB header: transcription Chain: B: PDB Molecule: rf-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
52	c6dzsD_	Alignment	not modelled	6.0	38	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
53	c4mveB_	Alignment	not modelled	6.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcur_1030 protein from thermomonospora curvata
54	c5h6cB_	Alignment	not modelled	6.0	21	PDB header: hydrolase Chain: B: PDB Molecule: amidase;

54	c1n0sB	Alignment	not modelled	5.9	41	PDBTitle: crystal structure of hydrazidase s179a mutant complexed with a2 substrate
55	d1vfn1	Alignment	not modelled	5.9	60	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
56	c2y5tF	Alignment	not modelled	5.8	33	PDB header: immune system Chain: F: PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
57	c4grdA	Alignment	not modelled	5.7	32	PDB header: lyase, isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
58	c1bzgA	Alignment	not modelled	5.6	0	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
59	c6a0aA	Alignment	not modelled	5.6	25	PDB header: structural protein Chain: A: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
60	c2wuhD	Alignment	not modelled	5.6	33	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
61	c2vyaB	Alignment	not modelled	5.6	43	PDB header: hydrolase Chain: B: PDB Molecule: fatty-acid amide hydrolase 1; PDBTitle: crystal structure of fatty acid amide hydrolase conjugated2 with the drug-like inhibitor pf-750
62	c3h0rP	Alignment	not modelled	5.6	36	PDB header: ligase Chain: P: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit a; PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
63	c3juia	Alignment	not modelled	5.5	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
64	c6nbiP	Alignment	not modelled	5.5	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
65	c2i94B	Alignment	not modelled	5.4	67	PDB header: protein binding Chain: B: PDB Molecule: rhodopsin kinase; PDBTitle: nmr structure of recoverin bound to rhodopsin kinase
66	c2dc0A	Alignment	not modelled	5.4	29	PDB header: hydrolase Chain: A: PDB Molecule: probable amidase; PDBTitle: crystal structure of amidase
67	c5l85B	Alignment	not modelled	5.4	9	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 nufip12 proteins
68	c2wuhC	Alignment	not modelled	5.4	33	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
69	c2wuhB	Alignment	not modelled	5.4	33	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
70	c4auoE	Alignment	not modelled	5.4	33	PDB header: hydrolase/peptide Chain: E: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
71	c4auoH	Alignment	not modelled	5.4	33	PDB header: hydrolase/peptide Chain: H: PDB Molecule: triple-helical collagen peptide; PDBTitle: crystal structure of mmp-1(e200a) in complex with a triple-2 helical collagen peptide
72	c1t0jC	Alignment	not modelled	5.3	57	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
73	c6a0cB	Alignment	not modelled	5.3	25	PDB header: structural protein Chain: B: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
74	c6c6gA	Alignment	not modelled	5.3	29	PDB header: hydrolase Chain: A: PDB Molecule: biuret hydrolase; PDBTitle: an unexpected vestigial protein complex reveals the evolutionary2 origins of an s-triazine catabolic enzyme. inhibitor bound complex.
75	d1khba2	Alignment	not modelled	5.2	30	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
76	c5lzkB	Alignment	not modelled	5.2	4	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
77	c6q5lA	Alignment	not modelled	5.1	18	PDB header: de novo protein Chain: A: PDB Molecule: cc-hex*-l24h; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-l24h
						PDB header: structural protein Chain: C: PDB Molecule: protein ((pro-hyp-gly)4- glu-lys-gly(pro-

78	c1qsuC_	Alignment	not modelled	5.1	25	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
79	c1paqA_	Alignment	not modelled	5.1	12	PDB header: translation Chain: A; PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
80	d1paqa_	Alignment	not modelled	5.1	12	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
81	c6q5hA_	Alignment	not modelled	5.1	18	PDB header: de novo protein Chain: A; PDB Molecule: cc-hex*-I24d; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24d
82	c6q5iB_	Alignment	not modelled	5.0	18	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-I24e; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24e
83	c6q5mB_	Alignment	not modelled	5.0	18	PDB header: de novo protein Chain: B; PDB Molecule: cc-hex*-I24dab; PDBTitle: crystal structure of a cc-hex mutant that forms an antiparallel four-2 helix coiled coil cc-hex*-I24dab
84	c2drxB_	Alignment	not modelled	5.0	33	PDB header: structural protein Chain: B; PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-(log)2-(pog)4