
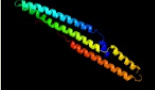
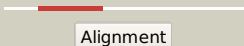

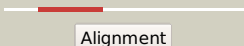




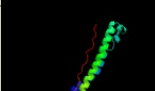
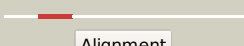

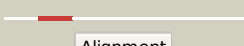











Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0256c_(PPE2)_307877_309547
 Date Tue Jul 23 14:50:31 BST 2019
 Unique Job ID 1132be5d6fd175ec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	35	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	26	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	26	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		98.2	18	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.7	10	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.5	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
8	c3gvmA_	 Alignment		97.5	18	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	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.9	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		95.6	19	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	Alignment		95.4	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		95.2	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		94.6	15	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		90.0	20	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ_	Alignment		56.9	26	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	d1ui5a2	Alignment		28.2	17	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	c2kg7A_	Alignment		15.4	26	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
19	d1xkna_	Alignment		15.2	11	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
20	c4xb6D_	Alignment		15.0	16	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
21	c6et5I_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: I: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
22	c6et5R_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: R: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
23	c6et5s_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: S: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
24	c6et5U_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
25	c6et5O_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: O: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
26	c6et5d_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: D: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
27	c6et5j_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: J: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
28	c6et5y_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: Y: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
						PDB header: photosynthesis

29	c6et5g_	Alignment	not modelled	14.4	44	Chain: G: PDB Molecule: light-harvesting protein b-1015 beta chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
30	c6et5m_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: M: PDB Molecule: reaction center protein m chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
31	c6et5a_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: A: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
32	c6et52_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: 2: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
33	c6et5v_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: V: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
34	c6et55_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: 5: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
35	c6et5x_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: X: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
36	c6et5p_	Alignment	not modelled	14.4	44	PDB header: photosynthesis Chain: P: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
37	c4el8A_	Alignment	not modelled	13.9	33	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.bescii cela gh48 module
38	d1zeea1	Alignment	not modelled	13.4	30	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
39	c2nvjA_	Alignment	not modelled	12.4	30	PDB header: hydrolase Chain: A: PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
40	c5l85B_	Alignment	not modelled	11.9	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 nufip12 proteins
41	c1l2aD_	Alignment	not modelled	11.8	18	PDB header: hydrolase Chain: D: PDB Molecule: cellobiohydrolase; PDBTitle: the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
42	d1l1ya_	Alignment	not modelled	11.8	18	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
43	c4fusA_	Alignment	not modelled	10.9	27	PDB header: hydrolase Chain: A: PDB Molecule: rtx toxins and related ca2+-binding protein; PDBTitle: the x-ray structure of hahella chejuensis family 48 glycosyl hydrolase
44	c4kkkA_	Alignment	not modelled	10.8	27	PDB header: hydrolase Chain: A: PDB Molecule: exoglucanase s; PDBTitle: complex structure of catalytic domain of clostridium cellulovorans2 exgs and cellotetraose
45	c4jjiA_	Alignment	not modelled	10.4	20	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of t. fusca gh48 d224n mutant
46	c3h6pB_	Alignment	not modelled	10.3	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein exxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
47	c1bkvA_	Alignment	not modelled	9.9	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
48	c6aokA_	Alignment	not modelled	9.5	33	PDB header: hydrolase Chain: A: PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
49	c1bkvC_	Alignment	not modelled	9.5	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
50	c1bkvB_	Alignment	not modelled	9.5	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
51	c6cgiA_	Alignment	not modelled	9.2	33	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
52	d1dmua_	Alignment	not modelled	9.1	56	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease BglI
53	c2iu1A_	Alignment	not modelled	9.0	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
54	d1g9ga_	Alignment	not modelled	8.9	23	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain

55	c1bzgA	Alignment	not modelled	8.8	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
56	c3sjrB	Alignment	not modelled	8.6	20	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
57	c3zfsA	Alignment	not modelled	8.6	28	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
58	c2fulE	Alignment	not modelled	8.5	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
59	c1vytF	Alignment	not modelled	8.4	63	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
60	c2lkqA	Alignment	not modelled	7.9	56	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
61	d1vfn1	Alignment	not modelled	7.5	100	Fold: Prealbumin-like Superfamily: Cna protein B-type domain Family: Cna protein B-type domain
62	c4deyB	Alignment	not modelled	7.3	29	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 l-ii linker.
63	c5bv9A	Alignment	not modelled	6.9	33	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: the structure of bacillus pumilus gh48 in complex with cellobiose
64	c2jtwA	Alignment	not modelled	6.7	38	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane helix 7 of yeast vatpase; PDBTitle: solution structure of tm7 bound to dpc micelles
65	c4c47B	Alignment	not modelled	6.6	25	PDB header: cell adhesion Chain: B: PDB Molecule: inner membrane lipoprotein; PDBTitle: salmonella enterica trimeric lipoprotein sadb
66	c5i4rA	Alignment	not modelled	6.5	43	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
67	c1t0jC	Alignment	not modelled	6.4	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
68	c2i5bA	Alignment	not modelled	6.0	35	PDB header: apoptosis Chain: A: PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
69	d1dlpa1	Alignment	not modelled	6.0	18	Fold: beta-Prism II Superfamily: alpha-D-mannose-specific plant lectins Family: alpha-D-mannose-specific plant lectins
70	d3e46a1	Alignment	not modelled	6.0	40	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
71	c4gyxC	Alignment	not modelled	5.9	50	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
72	c5hl8B	Alignment	not modelled	5.8	23	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein I; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
73	c5u31A	Alignment	not modelled	5.8	27	PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated endonuclease c2c1; PDBTitle: crystal structure of aacc2c1-sgrna-8mer substrate dna ternary complex
74	c5wqeA	Alignment	not modelled	5.8	27	PDB header: rna binding protein Chain: A: PDB Molecule: crispr-associated endonuclease c2c1; PDBTitle: crystal structure of alicyclobacillus acidoterrestris c2c1 in complex2 with single-guide rna at 3.1 angstrom resolution
75	d2fgga1	Alignment	not modelled	5.7	15	Fold: dsRBD-like Superfamily: Rv2632c-like Family: Rv2632c-like
76	c4f3fC	Alignment	not modelled	5.7	38	PDB header: immune system Chain: C: PDB Molecule: mesothelin; PDBTitle: crystal structure of msln7-64 morab-009 fab complex
77	c6nbiP	Alignment	not modelled	5.7	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
78	c4u39O	Alignment	not modelled	5.6	45	PDB header: cell cycle Chain: Q: PDB Molecule: cell division factor; PDBTitle: crystal structure of ftsz:mciz complex from bacillus subtilis
						PDB header: photosynthesis

79	c2wseE_	Alignment	not modelled	5.5	35	Chain: E: PDB Molecule: photosystem i reaction center subunit iv a, chloroplastic; PDBTitle: improved model of plant photosystem i
80	c2vwaE_	Alignment	not modelled	5.5	25	PDB header: unknown function Chain: E: PDB Molecule: putative uncharacterized protein pf13_0012; PDBTitle: crystal structure of a sporozoite protein essential for2 liver stage development of malaria parasite
81	c4dmtA_	Alignment	not modelled	5.4	46	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
82	c4dmtC_	Alignment	not modelled	5.4	46	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
83	c4dmtB_	Alignment	not modelled	5.4	46	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
84	c5ucOB_	Alignment	not modelled	5.3	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
85	d1fcda3	Alignment	not modelled	5.3	31	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
86	c2rpwX_	Alignment	not modelled	5.3	38	PDB header: transport protein Chain: X: PDB Molecule: 25 meric peptide from v-type proton atpase PDBTitle: structure of a peptide derived from h+-v-atpase subunit a
87	c4mveB_	Alignment	not modelled	5.3	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcur_1030 protein from thermomonospora curvata
88	c4wpyA_	Alignment	not modelled	5.2	15	PDB header: de novo protein Chain: A: PDB Molecule: protein dl-rv1738; PDBTitle: racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
89	c3lgeG_	Alignment	not modelled	5.2	42	PDB header: lyase/protein binding Chain: G: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
90	c3lgeF_	Alignment	not modelled	5.2	42	PDB header: lyase/protein binding Chain: F: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
91	c1nauA_	Alignment	not modelled	5.2	17	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon; PDBTitle: nmr solution structure of the glucagon antagonist [deshis1,2 desphe6, glu9]glucagon amide in the presence of3 perdeuterated dodecylphosphocholine micelles
92	c4gyxB_	Alignment	not modelled	5.1	55	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
93	c4gyxA_	Alignment	not modelled	5.1	55	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
94	d1paqa_	Alignment	not modelled	5.0	18	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like