


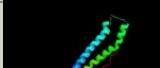

















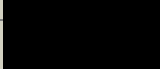



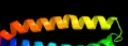


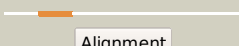

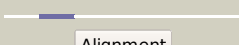

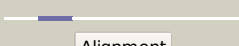

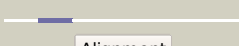





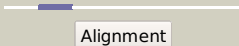
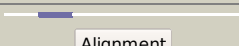
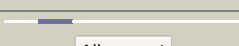
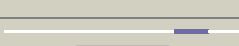
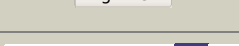
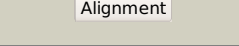
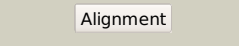




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1809_(PPE33)_2051289_2052695
 Date Fri Aug 2 13:30:42 BST 2019
 Unique Job ID 2ef91d047f8de4cf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	56	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	c2g38B_	 Alignment		100.0	36	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	36	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	14	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		98.1	21	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.3	8	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		96.9	9	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		96.9	12	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		96.8	10	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.0	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsB_	 Alignment		91.8	12	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsA_	 Alignment		91.5	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	 Alignment		90.2	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	 Alignment		84.9	12	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		82.3	23	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	d1ui5a2	 Alignment		18.1	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
17	c4i0xJ_	 Alignment		18.0	17	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
18	c5frgA_	 Alignment		15.5	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
19	c3mmyF_	 Alignment		15.5	36	PDB header: nuclear protein Chain: F: PDB Molecule: nuclear pore complex protein nup98; PDBTitle: structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
20	d1xkna_	 Alignment		15.4	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
21	c1bkvA_	 Alignment	not modelled	11.5	50	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
22	c1bkvB_	 Alignment	not modelled	10.9	50	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
23	c1bkvC_	 Alignment	not modelled	10.9	50	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
24	c5c5zA_	 Alignment	not modelled	10.3	18	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl-trna amidotransferase; PDBTitle: crystal structure analysis of c4763, a uropathogenic e. coli-specific2 protein
25	c5c3lA_	 Alignment	not modelled	9.8	32	PDB header: transport protein Chain: A: PDB Molecule: nup54; PDBTitle: structure of the metazoan nup62.nup58.nup54 nucleoporin complex.
26	d2cyya2	 Alignment	not modelled	9.4	28	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
27	d1nmpa_	 Alignment	not modelled	8.8	9	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
28	c2i94B_	 Alignment	not modelled	8.5	67	PDB header: protein binding Chain: B: PDB Molecule: rhodopsin kinase; PDBTitle: nmr structure of recoverin bound to rhodopsin kinase
29	d1mtyg_	 Alignment	not modelled	8.5	50	Fold: Open three-helical up-and-down bundle Superfamily: Methane monooxygenase hydrolase, gamma subunit

						Family: Methane monooxygenase hydrolase, gamma subunit
30	c2zbcH_	Alignment	not modelled	8.1	31	PDB header: transcription Chain: H: PDB Molecule: 83aa long hypothetical transcriptional regulator asnc; PDBTitle: crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
31	c2ke4A_	Alignment	not modelled	8.1	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
32	c2w6jH_	Alignment	not modelled	8.0	43	PDB header: hydrolase Chain: H: PDB Molecule: f1-atpase delta subunit; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 5.
33	c2kg7A_	Alignment	not modelled	7.7	30	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
34	d2cfxa2	Alignment	not modelled	7.6	21	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
35	c3q94B_	Alignment	not modelled	7.5	18	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
36	c4xb6D_	Alignment	not modelled	7.3	40	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
37	c2cfxD_	Alignment	not modelled	7.3	18	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
38	d2jdih2	Alignment	not modelled	7.2	36	Fold: Epsilon subunit of F1F0-ATP synthase N-terminal domain Superfamily: Epsilon subunit of F1F0-ATP synthase N-terminal domain Family: Epsilon subunit of F1F0-ATP synthase N-terminal domain
39	c6ff48_	Alignment	not modelled	7.1	33	PDB header: splicing Chain: 8: PDB Molecule: splicing factor 3b subunit 2; PDBTitle: human bact spliceosome core structure
40	d1a0ia1	Alignment	not modelled	7.1	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
41	d2cg4a2	Alignment	not modelled	7.1	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
42	d1khba2	Alignment	not modelled	7.1	10	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain
43	c4pcqC_	Alignment	not modelled	6.9	9	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
44	d1stza1	Alignment	not modelled	6.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
45	c6fjID_	Alignment	not modelled	6.6	15	PDB header: metal binding protein Chain: D: PDB Molecule: abc-type fe3+ transport system, periplasmic component; PDBTitle: structure of ibps from dickeya dadantii
46	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
47	c6cslA_	Alignment	not modelled	6.6	27	PDB header: metal binding protein Chain: A: PDB Molecule: histidine triad protein d; PDBTitle: pneumococcal phtd protein 269-339 fragment with bound zn(ii)
48	c3b42B_	Alignment	not modelled	6.6	15	PDB header: signaling protein Chain: B: PDB Molecule: methyl-accepting chemotaxis protein, putative; PDBTitle: periplasmic sensor domain of chemotaxis protein gsu0935
49	c4hobC_	Alignment	not modelled	6.3	40	PDB header: dna binding protein Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of the alpha domain from cyprinid herpes virus2 3
50	c3df0C_	Alignment	not modelled	6.3	47	PDB header: hydrolase Chain: C: PDB Molecule: calpastatin; PDBTitle: calcium-dependent complex between m-calpain and calpastatin
51	c2dbbA_	Alignment	not modelled	6.2	14	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
52	c5yz4A_	Alignment	not modelled	6.2	41	PDB header: hydrolase Chain: A: PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
53	c3r9IA_	Alignment	not modelled	6.2	11	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of nucleoside diphosphate kinase from giardia2 lamblia featuring a disordered dinucleotide binding site
54	c5jpdq_	Alignment	not modelled	6.1	37	PDB header: ribosome Chain: D: PDB Molecule: wd40 domain proteins;

						PDBTitle: cryo-em structure of the 90s pre-ribosome
55	d1fcda3	Alignment	not modelled	6.0	27	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
56	d1i1ga2	Alignment	not modelled	5.9	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
57	c6nbiP_	Alignment	not modelled	5.9	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
58	c4ep0E_	Alignment	not modelled	5.9	18	PDB header: structural protein, viral protein Chain: E: PDB Molecule: major tail protein; PDBTitle: structure of the bacteriophage c1 tail knob protein, gp12
59	c1unvA_	Alignment	not modelled	5.9	31	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces of four2 helix bundles
60	c4el8A_	Alignment	not modelled	5.9	40	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 48; PDBTitle: the unliganded structure of c.bescii cela gh48 module
61	c2a02A_	Alignment	not modelled	5.8	16	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: ferric-pseudobactin 358 receptor; PDBTitle: solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter pupa from3 pseudomonas putida.
62	c1u9fA_	Alignment	not modelled	5.8	31	PDB header: transcription Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-p1i based coiled2 coils: replacement of k(15) (16)
63	c5b3zB_	Alignment	not modelled	5.8	13	PDB header: isomerase,sugar binding protein Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase nima-interacting 1, PDBTitle: crystal structure of hpin1 ww domain (5-39) fused with maltose-binding2 protein
64	c4mj7B_	Alignment	not modelled	5.7	22	PDB header: rna binding protein Chain: B: PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
65	c1bzgA_	Alignment	not modelled	5.7	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
66	c3c52B_	Alignment	not modelled	5.7	22	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolhydroxamic acid, a competitive3 inhibitor
67	c4i6jB_	Alignment	not modelled	5.6	33	PDB header: transcription Chain: B: PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
68	c1u9fC_	Alignment	not modelled	5.6	31	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-p1i based coiled2 coils: replacement of k(15) (16)
69	c1u9fB_	Alignment	not modelled	5.6	31	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-p1i based coiled2 coils: replacement of k(15) (16)
70	c1unuB_	Alignment	not modelled	5.5	31	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces of four2 helix bundles
71	c1unuA_	Alignment	not modelled	5.5	31	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces of four2 helix bundles
72	c1uo5A_	Alignment	not modelled	5.5	31	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces of four2 helix bundles
73	d1iyjb4	Alignment	not modelled	5.4	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
74	c2nviA_	Alignment	not modelled	5.4	40	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
75	d1gvfa_	Alignment	not modelled	5.4	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
76	c3j3bF_	Alignment	not modelled	5.4	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
77	c1u9fD_	Alignment	not modelled	5.3	31	PDB header: transcription Chain: D: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-p1i based coiled2 coils: replacement of k(15) (16)
78	c2nqcA_	Alignment	not modelled	5.3	24	PDB header: immune system Chain: A: PDB Molecule: filamin-c; PDBTitle: crystal structure of ig-like domain 23 from human filamin c

79	d2nqca1	Alignment	not modelled	5.3	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
80	c2e1aD	Alignment	not modelled	5.3	12	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
81	c1gclA	Alignment	not modelled	5.3	31	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
82	c1gclB	Alignment	not modelled	5.3	31	PDB header: leucine zipper Chain: B: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
83	c1gclC	Alignment	not modelled	5.3	31	PDB header: leucine zipper Chain: C: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
84	c1gclD	Alignment	not modelled	5.3	31	PDB header: leucine zipper Chain: D: PDB Molecule: gcn4; PDBTitle: gcn4 leucine zipper core mutant p-li
85	c1untA	Alignment	not modelled	5.2	31	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces of four2 helix bundles
86	c4gyxC	Alignment	not modelled	5.2	64	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
87	c1uo2A	Alignment	not modelled	5.1	31	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces of four2 helix bundles
88	c1w5iA	Alignment	not modelled	5.1	31	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: aba does not affect topology of pli.
89	c5lzkB	Alignment	not modelled	5.1	9	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
90	d1ygya3	Alignment	not modelled	5.1	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
91	d2e9xc2	Alignment	not modelled	5.1	23	Fold: GINS/PriA/YqbF domain Superfamily: PriA/YqbF domain Family: PSF3 N-terminal domain-like