

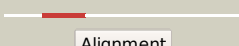
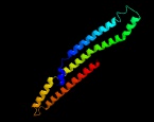
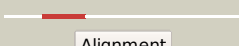
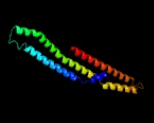
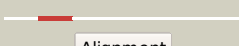
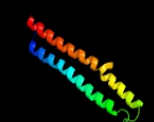





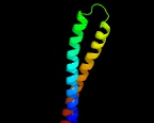

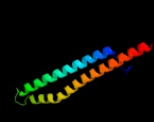
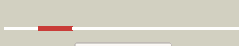


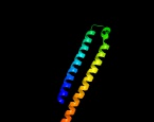

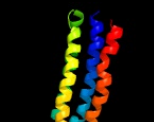


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3903c_(-)_4388070_4390610
Date	Sat Aug 10 22:05:09 BST 2019
Unique Job ID	3b80d6d62dd878a9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4qlpB_	 Alignment		100.0	98	PDB header: hydrolase/protein binding Chain: B: PDB Molecule: alanine and proline rich protein, tuberculosis necrotizing PDBTitle: atomic structure of tuberculosis necrotizing toxin (tnt) complexed2 with its immunity factor ift
2	c2g38B_	 Alignment		97.0	13	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		97.0	13	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4iogD_	 Alignment		95.6	20	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
5	c5xfsB_	 Alignment		94.0	14	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
6	c3zbhC_	 Alignment		93.6	8	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
7	c2vs0B_	 Alignment		93.4	12	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	c3gvmA_	 Alignment		93.2	15	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	d1wa8a1	 Alignment		93.0	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
10	c4lwsA_	 Alignment		91.1	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
11	d1eq1a_	 Alignment		82.5	13	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III

12	c4b1vN_	Alignment		69.6	73	PDB header: structural protein Chain: N: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpe1-n domain bound to g-actin
13	c4b1vM_	Alignment		69.6	73	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpe1-n domain bound to g-actin
14	c4b1uM_	Alignment		67.7	73	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpe1 domain and rpe1 motif directed2 assemblies with g-actin reveal the molecular basis for actin binding3 cooperativity.
15	c4lwsB_	Alignment		67.2	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
16	c2kg7B_	Alignment		64.7	10	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
17	d1g4us1	Alignment		54.0	11	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
18	d1wa8b1	Alignment		49.5	5	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
19	c4wj2A_	Alignment		46.7	11	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
20	c6b7nC_	Alignment		45.0	10	PDB header: viral protein Chain: C: PDB Molecule: spike protein; PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
21	c4xy3A_	Alignment	not modelled	40.1	13	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
22	c3mhsE_	Alignment	not modelled	20.7	15	PDB header: hydrolase/transcription regulator/protei Chain: E: PDB Molecule: saga-associated factor 73; PDBTitle: structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
23	c2mn4A_	Alignment	not modelled	20.4	70	PDB header: de novo protein Chain: A: PDB Molecule: computational designed protein based on structure template PDBTitle: nmr solution structure of a computational designed protein based on2 structure template 1cy5
24	c1rh1A_	Alignment	not modelled	19.6	12	PDB header: antibiotic Chain: A: PDB Molecule: colicin b; PDBTitle: crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
25	c6cv0C_	Alignment	not modelled	19.2	14	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
26	c6nzkB_	Alignment	not modelled	19.2	15	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
27	c4i0xA_	Alignment	not modelled	16.9	13	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
28	c2vxzA_	Alignment	not modelled	16.5	7	PDB header: viral protein Chain: A: PDB Molecule: pyrsv_gp04; PDBTitle: crystal structure of hypothetical protein pyrsv_gp04 from pyrobaculum2 spherical virus

29	c2lo3A	Alignment	not modelled	14.4	15	PDB header: transcription Chain: A: PDB Molecule: saga-associated factor 73; PDBTitle: solution structure of sgf73(59-102) zinc finger domain
30	c1qu7A	Alignment	not modelled	12.9	6	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
31	c2zp2B	Alignment	not modelled	12.6	13	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
32	c3jclC	Alignment	not modelled	12.5	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
33	c5x5bB	Alignment	not modelled	12.2	15	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
34	c3g67A	Alignment	not modelled	11.9	5	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
35	c5x5fC	Alignment	not modelled	11.6	10	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
36	c5i08A	Alignment	not modelled	10.9	15	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
37	c5xlrC	Alignment	not modelled	10.7	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
38	c1ei3E	Alignment	not modelled	10.3	5	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
39	c5o9eB	Alignment	not modelled	10.3	41	PDB header: ribosome Chain: B: PDB Molecule: putative u3 small nucleolar ribonucleoprotein protein; PDBTitle: crystal structure of the imp4-mpp10 complex from chaetomium2 thermophilum
40	c6nb3B	Alignment	not modelled	9.6	10	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
41	c3ghgK	Alignment	not modelled	9.5	8	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
42	c5szsC	Alignment	not modelled	9.1	14	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
43	c4i0xl	Alignment	not modelled	9.1	9	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex
44	d2gqba1	Alignment	not modelled	9.1	17	Fold: RPA2825-like Superfamily: RPA2825-like Family: RPA2825-like
45	c5wrgB	Alignment	not modelled	8.5	15	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
46	d1he1a	Alignment	not modelled	8.5	9	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
47	c6n1fD	Alignment	not modelled	8.2	22	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, 2og-fe(ii) oxygenase family; PDBTitle: crystal structure of oxidoreductase, 2og-fe(ii) oxygenase family, from2 burkholderia pseudomallei
48	c2ieqC	Alignment	not modelled	8.1	14	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
49	c3qflA	Alignment	not modelled	8.0	13	PDB header: protein binding Chain: A: PDB Molecule: mia10; PDBTitle: coiled-coil domain-dependent homodimerization of intracellular mia2 immune receptors defines a minimal functional module for triggering3 cell death
50	c6akmA	Alignment	not modelled	8.0	13	PDB header: protein binding Chain: A: PDB Molecule: suppressor of ikbke 1; PDBTitle: crystal structure of slmap-sike1 complex
51	c2jv4A	Alignment	not modelled	7.9	45	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis/trans isomerase; PDBTitle: structure characterisation of pina ww domain and comparison2 with other group iv ww domains, pin1 and ess1
52	c6cs2A	Alignment	not modelled	7.4	15	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrinin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
53	c6dmaD	Alignment	not modelled	6.8	19	PDB header: de novo protein Chain: D: PDB Molecule: dhd15_closed_b; PDBTitle: dhd15_closed
54	c3lnrA	Alignment	not modelled	6.8	16	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p.

						aeruginosa soluble2 receptor aer2 PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
55	c4e40A_	Alignment	not modelled	6.7	12	
56	d1khia2	Alignment	not modelled	6.6	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
57	c4ut1A_	Alignment	not modelled	6.4	17	PDB header: motor protein Chain: A: PDB Molecule: flagellar hook-associated protein; PDBTitle: the structure of the flagellar hook junction protein flgk2 from burkholderia pseudomallei
58	c1sfcD_	Alignment	not modelled	6.3	9	PDB header: transport protein Chain: D: PDB Molecule: protein (snap-25b); PDBTitle: neuronal synaptic fusion complex
59	c1deqO_	Alignment	not modelled	6.3	6	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
60	c2d4yA_	Alignment	not modelled	6.1	12	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
61	c3ivrA_	Alignment	not modelled	6.1	21	PDB header: ligase Chain: A: PDB Molecule: putative long-chain-fatty-acid coa ligase; PDBTitle: crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
62	d1owaa_	Alignment	not modelled	6.1	7	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
63	c3gw6F_	Alignment	not modelled	6.0	14	PDB header: chaperone Chain: F: PDB Molecule: endo-n-acetylneuraminidase; PDBTitle: intramolecular chaperone
64	d1fx7a3	Alignment	not modelled	6.0	35	Fold: SH3-like barrel Superfamily: C-terminal domain of transcriptional repressors Family: FeoA-like
65	c1ei3C_	Alignment	not modelled	6.0	9	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
66	c6ozvA_	Alignment	not modelled	5.9	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: txo1; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
67	c2i56A_	Alignment	not modelled	5.8	15	PDB header: isomerase, metal-binding protein Chain: A: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
68	c2choA_	Alignment	not modelled	5.7	13	PDB header: hydrolase Chain: A: PDB Molecule: glucosaminidase; PDBTitle: bacteroides thetaiotaomicron hexosaminidase with o-2 glcnacase activity
69	c4nl6C_	Alignment	not modelled	5.7	15	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
70	d1z6ra1	Alignment	not modelled	5.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
71	d2p0va1	Alignment	not modelled	5.5	20	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
72	c2p0vA_	Alignment	not modelled	5.5	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bt3781; PDBTitle: crystal structure of bt3781 protein from bacteroides thetaiotaomicron,2 northeast structural genomics target btr58
73	c2l0gA_	Alignment	not modelled	5.4	33	PDB header: protein binding Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution nmr structure of ubiquitin-binding motif (ubm2) of human2 polymerase iota
74	d1lm5a_	Alignment	not modelled	5.3	9	Fold: beta-hairpin-alpha-hairpin repeat Superfamily: Plakin repeat Family: Plakin repeat
75	d1szia_	Alignment	not modelled	5.3	13	Fold: Four-helical up-and-down bundle Superfamily: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain Family: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
76	c2k4vA_	Alignment	not modelled	5.1	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1076; PDBTitle: solution structure of uncharacterized protein pa1076 from pseudomonas2 aeruginosa. northeast structural genomics consortium (nesg) target3 pat3, ontario center for structural proteomics target pa1076 .
77	c4qmdB_	Alignment	not modelled	5.1	9	PDB header: cell adhesion Chain: B: PDB Molecule: envoplakin; PDBTitle: crystal structure of human envoplakin plakin repeat domain
78	c2n03A_	Alignment	not modelled	5.0	15	PDB header: structural protein Chain: A: PDB Molecule: plectin; PDBTitle: solution nmr structure plectin repeat domain 6 (4403-4606) of plectin2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr6354e