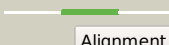

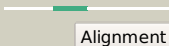

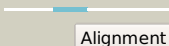
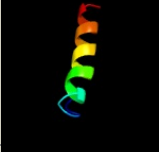
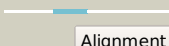
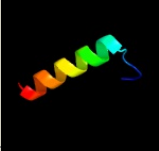
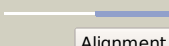
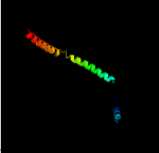
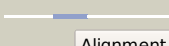
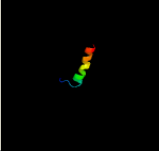
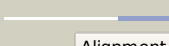
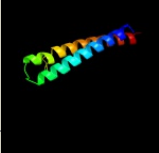

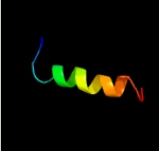

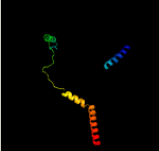

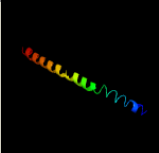

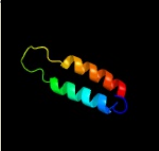


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1231c_(-)_1374328_1374870
Date	Wed Jul 31 22:05:32 BST 2019
Unique Job ID	07e8543a74835045

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6cfwA_	 Alignment		51.5	18	PDB header: membrane protein Chain: A: PDB Molecule: monovalent cation/h+ antiporter subunit e; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
2	c4cbfE_	 Alignment		44.5	23	PDB header: virus Chain: E: PDB Molecule: envelope protein e; PDBTitle: near-atomic resolution cryo-em structure of dengue serotype 4 virus
3	c5ireA_	 Alignment		34.6	27	PDB header: virus Chain: A: PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus
4	c5o6vC_	 Alignment		32.3	32	PDB header: virus Chain: C: PDB Molecule: envelope protein; PDBTitle: the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
5	c6bwiA_	 Alignment		28.0	8	PDB header: membrane protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of full length human trpm4
6	c5wsnC_	 Alignment		27.8	23	PDB header: virus Chain: C: PDB Molecule: e protein; PDBTitle: structure of japanese encephalitis virus
7	d1k4ta1	 Alignment		26.0	18	Fold: Long alpha-hairpin Superfamily: Eukaryotic DNA topoisomerase I, dispensable insert domain Family: Eukaryotic DNA topoisomerase I, dispensable insert domain
8	c4b03A_	 Alignment		20.4	32	PDB header: virus Chain: A: PDB Molecule: dengue virus 1 e protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
9	c6co7C_	 Alignment		18.2	9	PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; PDBTitle: structure of the nvtrpm2 channel in complex with ca2+
10	c4ltpC_	 Alignment		17.9	16	PDB header: transport protein Chain: C: PDB Molecule: ion transport protein; PDBTitle: bacterial sodium channel in high calcium, i222 space group, crystal 2
11	c1p58C_	 Alignment		17.1	24	PDB header: virus Chain: C: PDB Molecule: major envelope protein e; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction

12	c6rdu9_	Alignment		17.1	17	PDB header: proton transport Chain: 9: PDB Molecule: asa-9: polytomella f-atp synthase associated subunit 9; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
13	c2mxbA_	Alignment		16.9	22	PDB header: membrane protein Chain: A: PDB Molecule: erythropoietin receptor; PDBTitle: structure of the transmembrane domain of the mouse erythropoietin2 receptor
14	c2w2eA_	Alignment		15.7	17	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin pip2-7 7; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin, aqy1, in a2 closed conformation at ph 3.5
15	c4ev6E_	Alignment		15.6	11	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
16	c3m9bk_	Alignment		15.4	19	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
17	d1dfma_	Alignment		15.2	40	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease BgIII
18	c2m6xC_	Alignment		14.0	20	PDB header: membrane protein Chain: C: PDB Molecule: p7; PDBTitle: structure of the p7 channel of hepatitis c virus, genotype 5a
19	c2kn8A_	Alignment		11.4	20	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: dna cleavage and packaging protein large subunit, ul89; PDBTitle: nmr structure of the c-terminal domain of pul89
20	c6bwiB_	Alignment		10.5	16	PDB header: membrane protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of full length human trpm4
21	c6bwiD_	Alignment	not modelled	10.5	16	PDB header: membrane protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of full length human trpm4
22	c6bwiC_	Alignment	not modelled	10.5	16	PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of full length human trpm4
23	c6bcqB_	Alignment	not modelled	10.3	14	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with long coiled coil at2 3.3 angstrom resolution
24	c1ci6A_	Alignment	not modelled	10.0	20	PDB header: transcription Chain: A: PDB Molecule: transcription factor atf-4; PDBTitle: transcription factor atf4-c/ebp beta bzip heterodimer
25	c5zx5D_	Alignment	not modelled	9.6	13	PDB header: transferase Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.3 angstrom structure of mouse trpm7 with edta
26	d2i7pa1	Alignment	not modelled	9.6	56	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
27	c2mv6A_	Alignment	not modelled	9.2	29	PDB header: membrane protein Chain: A: PDB Molecule: erythropoietin receptor; PDBTitle: solution structure of the transmembrane domain and the juxta-membrane2 domain of the erythropoietin receptor in micelles
28	c4uicA_	Alignment	not modelled	8.4	23	PDB header: sugar binding protein Chain: A: PDB Molecule: surface layer protein; PDBTitle: crystal structure of the s-layer protein rsbsc(31-844)

29	c5fv8A_	Alignment	not modelled	8.4	33	PDB header: structural protein Chain: A: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
30	c1d7mA_	Alignment	not modelled	8.1	30	PDB header: contractile protein Chain: A: PDB Molecule: cortexillin i; PDBTitle: coiled-coil dimerization domain from cortexillin i
31	d2i7na2	Alignment	not modelled	8.0	56	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
32	c3hd6A_	Alignment	not modelled	8.0	17	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
33	c2bbjB_	Alignment	not modelled	7.9	10	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
34	c2lifA_	Alignment	not modelled	7.7	38	PDB header: viral protein, membrane protein Chain: A: PDB Molecule: core protein p21; PDBTitle: solution structure of kkgf
35	c2rsmA_	Alignment	not modelled	7.6	26	PDB header: translation Chain: A: PDB Molecule: probable peptide chain release factor c12orf65 homolog, PDBTitle: solution structure and sirna-mediated knockdown analysis of the2 mitochondrial disease-related protein c12orf65 (ict2)
36	c5fv8B_	Alignment	not modelled	7.2	35	PDB header: structural protein Chain: B: PDB Molecule: fosw; PDBTitle: structure of cjun-fosw coiled coil complex.
37	c3a5tB_	Alignment	not modelled	7.1	22	PDB header: transcription regulator/dna Chain: B: PDB Molecule: transcription factor mafg; PDBTitle: crystal structure of mafg-dna complex
38	c3vjjA_	Alignment	not modelled	6.9	50	PDB header: viral protein Chain: A: PDB Molecule: p9-1; PDBTitle: crystal structure analysis of the p9-1
39	d2f9wa2	Alignment	not modelled	6.6	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
40	c2js5B_	Alignment	not modelled	6.5	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
41	c3vviB_	Alignment	not modelled	6.3	40	PDB header: transport protein Chain: B: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
42	c3vviF_	Alignment	not modelled	6.3	40	PDB header: transport protein Chain: F: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
43	c3vviC_	Alignment	not modelled	6.3	40	PDB header: transport protein Chain: C: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
44	c3vviG_	Alignment	not modelled	6.3	40	PDB header: transport protein Chain: G: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
45	c3vviA_	Alignment	not modelled	6.3	40	PDB header: transport protein Chain: A: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
46	c3vviE_	Alignment	not modelled	6.3	40	PDB header: transport protein Chain: E: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
47	c3vviH_	Alignment	not modelled	6.3	40	PDB header: transport protein Chain: H: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
48	c3vviD_	Alignment	not modelled	6.3	40	PDB header: transport protein Chain: D: PDB Molecule: non selective cation channel homologous to trp channel; PDBTitle: crystal structure of the coiled-coil domain of the transient receptor2 potential channel from gibberella zeae (trpgz)
49	d2a65a1	Alignment	not modelled	6.2	12	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
50	c2kl5A_	Alignment	not modelled	6.2	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yutd; PDBTitle: solution nmr structure of protein yutd from b.subtilis, northeast2 structural genomics consortium target sr232
51	c6b2zA_	Alignment	not modelled	6.1	29	PDB header: membrane protein Chain: A: PDB Molecule: atp synthase protein 8; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
52	c6b2zL_	Alignment	not modelled	6.1	29	PDB header: membrane protein Chain: L: PDB Molecule: atp synthase protein 8; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
						PDB header: dna binding protein

53	c5gpdB_	Alignment	not modelled	6.0	33	Chain: B: PDB Molecule: sterol regulatory element-binding protein 1; PDBTitle: crystal structure of the binding domain of srebp from fission yeast
54	c5khtD_	Alignment	not modelled	5.9	32	PDB header: actin-binding protein Chain: D: PDB Molecule: tropomyosin alpha-1 chain,general control protein gcn4; PDBTitle: crystal structure of the n-terminal fragment of tropomyosin isoform2 tpm1.1 at 1.5 a resolution
55	c3iyqQ_	Alignment	not modelled	5.7	17	PDB header: virus Chain: Q: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
56	c5nikK_	Alignment	not modelled	5.6	24	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
57	c5b7iA_	Alignment	not modelled	5.6	10	PDB header: hydrolase/unknown function Chain: A: PDB Molecule: crispr-associated nuclease/helicase cas3 subtype i-f/ypest; PDBTitle: cas3-acrf3 complex
58	c1wq6A_	Alignment	not modelled	5.5	19	PDB header: oncprotein Chain: A: PDB Molecule: aml1-eto; PDBTitle: the tetramer structure of the neryv homolgy two (nhr2) domain of aml1-2 eto is critical for aml1-eto's activity
59	c5ey2A_	Alignment	not modelled	5.5	22	PDB header: transcription Chain: A: PDB Molecule: gtp-sensing transcriptional pleiotropic repressor cody; PDBTitle: crystal structure of cody from bacillus cereus
60	c5ed9A_	Alignment	not modelled	5.4	28	PDB header: transport protein Chain: A: PDB Molecule: sun domain-containing protein 2; PDBTitle: crystal structure of cc1 of mouse sun2
61	c5l75F_	Alignment	not modelled	5.2	16	PDB header: transport protein Chain: F: PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
62	c6c9aB_	Alignment	not modelled	5.2	14	PDB header: membrane protein Chain: B: PDB Molecule: two pore calcium channel protein 1; PDBTitle: cryo-em structure of mouse tpc1 channel in the ptdins(3,5)p2-bound2 state
63	c6e3yE_	Alignment	not modelled	5.1	10	PDB header: signaling protein Chain: E: PDB Molecule: receptor activity-modifying protein 1; PDBTitle: cryo-em structure of the active, gs-protein complexed, human cgrp2 receptor
64	d2vbuA1	Alignment	not modelled	5.1	40	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: CTP-dependent riboflavin kinase-like
65	c5aoqA_	Alignment	not modelled	5.0	63	PDB header: transferase Chain: A: PDB Molecule: torso; PDBTitle: structural basis of neurohormone perception by the receptor tyrosine2 kinase torso
66	d1u7ga_	Alignment	not modelled	5.0	15	Fold: Ammonium transporter Superfamily: Ammonium transporter Family: Ammonium transporter