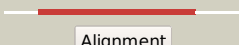

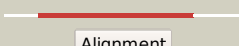

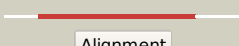

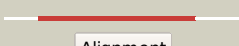




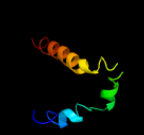




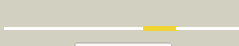
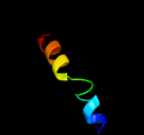



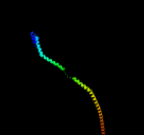
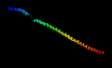







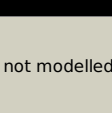


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2287_(yjcE)_2559713_2561341
Date	Mon Aug 5 13:25:42 BST 2019
Unique Job ID	0a91b3e1f9743528

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4czbB_	 Alignment		100.0	18	PDB header: membrane protein Chain: B: PDB Molecule: na(+)/h(+) antiporter 1; PDBTitle: structure of the sodium proton antiporter mjnhap1 from2 methanocaldococcus jannaschii at ph 8.
2	c4cz8A_	 Alignment		100.0	24	PDB header: membrane protein Chain: A: PDB Molecule: na+/h+ antiporter, putative; PDBTitle: structure of the sodium proton antiporter panhap from2 pyrococcus abyssii at ph 8.
3	c5bz3A_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of sodium proton antiporter napa in outward-facing2 conformation.
4	c4bwzA_	 Alignment		100.0	18	PDB header: transport protein Chain: A: PDB Molecule: na(+)/h(+) antiporter; PDBTitle: crystal structure of the sodium proton antiporter, napa
5	c1zcdA_	 Alignment		99.9	11	PDB header: membrane protein Chain: A: PDB Molecule: na(+)/h(+) antiporter 1; PDBTitle: crystal structure of the na+/h+ antiporter nhaa
6	c2mdfA_	 Alignment		98.8	27	PDB header: proton transport Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: nmr structure of a two-transmembrane segment tm vi-vii of nhe1
7	c4n7wA_	 Alignment		97.5	11	PDB header: transport protein Chain: A: PDB Molecule: transporter, sodium/bile acid symporter family; PDBTitle: crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
8	c210eA_	 Alignment		90.0	21	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: structural and functional analysis of tm vi of the nhe1 isoform of the2 na+/h+ exchanger
9	c2kbvA_	 Alignment		79.0	17	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: structural and functional analysis of tm xi of the nhe12 isoform of the na+/h+ exchanger
10	c6nd1E_	 Alignment		77.2	14	PDB header: protein transport Chain: E: PDB Molecule: translocation protein sec66; PDBTitle: cryoem structure of the sec complex from yeast
11	c6b8hb_	 Alignment		75.0	11	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer

12	c6j5ib_	Alignment		59.0	13	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase
13	c6n3qE_	Alignment		58.9	17	PDB header: transport protein Chain: E: PDB Molecule: translocation protein sec66; PDBTitle: cryo-em structure of the yeast sec complex
14	c6iu3A_	Alignment		51.3	13	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
15	c4k1cB_	Alignment		50.1	12	PDB header: membrane protein/metal transport Chain: B: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
16	c4k1cA_	Alignment		48.6	13	PDB header: membrane protein/metal transport Chain: A: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
17	d1vqop1	Alignment		45.7	17	Fold: Ribosomal protein L19 (L19e) Superfamily: Ribosomal protein L19 (L19e) Family: Ribosomal protein L19 (L19e)
18	c5l0wA_	Alignment		45.4	20	PDB header: membrane protein Chain: A: PDB Molecule: sec71; PDBTitle: structure of post-translational translocation sec71/sec72 complex
19	c2htgA_	Alignment		41.2	33	PDB header: membrane protein Chain: A: PDB Molecule: nhe1 isoform of na+/h+ exchanger 1; PDBTitle: structural and functional characterization of tm vii of the2 nhe1 isoform of the na+/h+ exchanger
20	c3j2lO_	Alignment		40.3	19	PDB header: ribosome Chain: Q: PDB Molecule: 50s ribosomal protein l19e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
21	c4a1cO_	Alignment	not modelled	39.8	14	PDB header: ribosome Chain: O: PDB Molecule: rpl19; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
22	c2k3cA_	Alignment	not modelled	37.9	31	PDB header: metal transport Chain: A: PDB Molecule: tmix peptide; PDBTitle: structural and functional characterization of tm ix of the2 nhe1 isoform of the na+/h+ exchanger
23	c4a17O_	Alignment	not modelled	37.4	14	PDB header: ribosome Chain: O: PDB Molecule: rpl19; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
24	d1f6ga_	Alignment	not modelled	35.4	11	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
25	c3j39R_	Alignment	not modelled	34.9	15	PDB header: ribosome Chain: R: PDB Molecule: 60s ribosomal protein l19; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
26	c2zkrp_	Alignment	not modelled	34.3	14	PDB header: ribosomal protein/rna Chain: P: PDB Molecule: rna expansion segment es31 part i; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
27	d2csba1	Alignment	not modelled	32.6	5	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Topoisomerase V repeat domain
28	c5a1cB_	Alignment	not modelled	31.5	17	PDB header: transport protein Chain: B: PDB Molecule: citrate-sodium symporter;

28	c9d1sb	Alignment	not modelled	31.5	17	PDBTitle: crystal structure of the sodium-dependent citrate symporter sec2ts2 from salmonella enterica. PDB header: ribosome
29	c3iz5T	Alignment	not modelled	30.7	11	Chain: T; PDB Molecule: 60s ribosomal protein l19 (l19e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
30	c2zv4O	Alignment	not modelled	29.8	13	PDB header: structural protein Chain: O; PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
31	c4b6aR	Alignment	not modelled	29.4	20	PDB header: ribosome Chain: R; PDB Molecule: 60s ribosomal protein l19-b; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
32	c4a1eO	Alignment	not modelled	29.0	14	PDB header: ribosome Chain: O; PDB Molecule: rpl19; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
33	c3zf7T	Alignment	not modelled	28.6	23	PDB header: ribosome Chain: T; PDB Molecule: 60s ribosomal protein l19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
34	c6fkip	Alignment	not modelled	27.9	7	PDB header: membrane protein Chain: P; PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
35	c3hzaA	Alignment	not modelled	27.9	13	PDB header: transferase Chain: A; PDB Molecule: monofunctional glycosyltransferase; PDBTitle: s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
36	c6b3rE	Alignment	not modelled	27.7	5	PDB header: transport protein Chain: E; PDB Molecule: piezo-type mechanosensitive ion channel component 1; PDBTitle: structure of the mechanosensitive channel piezo1
37	d2nwwa1	Alignment	not modelled	27.1	14	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
38	c2m7xA	Alignment	not modelled	25.1	11	PDB header: membrane protein Chain: A; PDB Molecule: na(+)/h(+) antiporter; PDBTitle: structural and functional analysis of transmembrane segment iv of the2 salt tolerance protein sod2
39	c6epgD	Alignment	not modelled	25.0	13	PDB header: toxin Chain: D; PDB Molecule: zeta_1 toxin; PDBTitle: structure of the epsilon_1 / zeta_1 antitoxin / toxin system from2 neisseria gonorrhoeae.
40	c3f0cA	Alignment	not modelled	24.3	6	PDB header: transcription regulator Chain: A; PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
41	c5nugB	Alignment	not modelled	20.3	8	PDB header: motor protein Chain: B; PDB Molecule: cytoplasmic dynein 1 heavy chain 1; PDBTitle: motor domains from human cytoplasmic dynein-1 in the phi-particle2 conformation
42	c5arhT	Alignment	not modelled	20.2	14	PDB header: hydrolase Chain: T; PDB Molecule: atp synthase f(0) complex subunit b1, mitochondrial; PDBTitle: bovine mitochondrial atp synthase state 2a
43	c6eznH	Alignment	not modelled	19.6	16	PDB header: membrane protein Chain: H; PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
44	c4l6rA	Alignment	not modelled	19.2	16	PDB header: membrane protein Chain: A; PDB Molecule: soluble cytochrome b562 and glucagon receptor chimera; PDBTitle: structure of the class b human glucagon g protein coupled receptor
45	c6iiuA	Alignment	not modelled	19.1	19	PDB header: signaling protein Chain: A; PDB Molecule: soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, PDBTitle: crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
46	c1y4cA	Alignment	not modelled	17.1	9	PDB header: de novo protein Chain: A; PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
47	c5lqvV	Alignment	not modelled	16.8	14	PDB header: hydrolase Chain: V; PDB Molecule: atp synthase subunit b; PDBTitle: structure of f-atpase from pichia angusta, in state2
48	d2bfdal	Alignment	not modelled	16.8	7	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
49	c3aaqB	Alignment	not modelled	16.7	21	PDB header: membrane protein Chain: B; PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
50	c5z96C	Alignment	not modelled	16.6	11	PDB header: membrane protein Chain: C; PDB Molecule: short transient receptor potential channel 4; PDBTitle: structure of the mouse trpc4 ion channel
51	d1umda	Alignment	not modelled	16.3	6	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
52	c5mqfQ	Alignment	not modelled	15.2	9	PDB header: splicing Chain: Q; PDB Molecule: protein bud31 homolog; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
53	c5xamA	Alignment	not modelled	14.6	18	PDB header: membrane protein Chain: A; PDB Molecule: protein translocase subunit secd;

						PDBTitle: crystal structure of secdf in i form at 4 a resolution
54	c2yicC	Alignment	not modelled	14.4	16	PDB header: lyase Chain: C: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
55	c3vugD	Alignment	not modelled	13.2	10	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (tetr/acrr family); PDBTitle: crystal structure of ttha0167, a transcriptional regulator, tetr/acrr2 family from thermus thermophilus hb8
56	c4gctA	Alignment	not modelled	13.1	8	PDB header: dna binding protein/dna Chain: A: PDB Molecule: nucleoid occlusion factor slma; PDBTitle: structure of no factor protein-dna complex
57	c4q28B	Alignment	not modelled	12.5	25	PDB header: structural protein Chain: B: PDB Molecule: periplakin; PDBTitle: crystal structure of the plectin 1 and 2 repeats of the human2 periplakin. northeast structural genomics consortium (nesg) target3 hr9083a
58	c3aygA	Alignment	not modelled	12.0	6	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno
59	c5t4oj	Alignment	not modelled	11.9	13	PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
60	c3exmA	Alignment	not modelled	11.8	8	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase sc4828; PDBTitle: crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
61	c3thzA	Alignment	not modelled	11.7	12	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna mismatch repair protein msh2; PDBTitle: human mutsbeta complexed with an idl of 6 bases (loop6) and adp
62	c6flnE	Alignment	not modelled	11.6	11	PDB header: protein binding Chain: E: PDB Molecule: e3 ubiquitin/isg15 ligase trim25; PDBTitle: crystal structure of the human trim25 coiled-coil and pryspy domains
63	c6c9aB	Alignment	not modelled	11.6	12	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
64	c4jkvA	Alignment	not modelled	11.2	16	PDB header: membrane protein Chain: A: PDB Molecule: soluble cytochrome b562, smoothed homolog; PDBTitle: structure of the human smoothed 7tm receptor in complex with an2 antitumor agent
65	c4k0eA	Alignment	not modelled	10.7	13	PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
66	c4cg4D	Alignment	not modelled	10.7	7	PDB header: actin-binding protein Chain: D: PDB Molecule: pyrin; PDBTitle: crystal structure of the chs-b30.2 domains of trim20
67	c1y4eA	Alignment	not modelled	10.4	24	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: nmr structure of transmembrane segment iv of the nhe12 isoform of the na+/h+ exchanger
68	c2i10A	Alignment	not modelled	10.3	10	PDB header: transcription Chain: A: PDB Molecule: putative tetr transcriptional regulator; PDBTitle: putative tetr transcriptional regulator from rhodococcus sp. rha1
69	d2oeza1	Alignment	not modelled	10.2	24	Fold: YacF-like Superfamily: YacF-like Family: YacF-like
70	c4n6hA	Alignment	not modelled	9.9	16	PDB header: signaling protein Chain: A: PDB Molecule: soluble cytochrome b562, delta-type opioid receptor PDBTitle: 1.8 a structure of the human delta opioid 7tm receptor (psi community2 target)
71	d2c0sa1	Alignment	not modelled	9.7	6	Fold: ROP-like Superfamily: BAS1536-like Family: BAS1536-like
72	c5c4iC	Alignment	not modelled	9.2	18	PDB header: oxidoreductase Chain: C: PDB Molecule: oxalate oxidoreductase subunit beta; PDBTitle: structure of an oxalate oxidoreductase
73	c6cnmA	Alignment	not modelled	9.1	8	PDB header: membrane protein Chain: A: PDB Molecule: intermediate conductance calcium-activated potassium PDBTitle: cryo-em structure of the human sk4/calmodulin channel complex
74	c5zdnA	Alignment	not modelled	9.1	3	PDB header: hydrolase Chain: A: PDB Molecule: fomd; PDBTitle: the complex structure of fomd with cdp
75	c4dncD	Alignment	not modelled	9.0	29	PDB header: transcription Chain: D: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of human mof in complex with msl1
76	c2lx0A	Alignment	not modelled	9.0	15	PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
77	c6fkib	Alignment	not modelled	8.9	12	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
						Fold: Lysozyme-like

78	d2oqoa1	Alignment	not modelled	8.6	13	Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
79	c6b87C	Alignment	not modelled	8.5	23	PDB header: membrane protein Chain: C: PDB Molecule: tmhc2_e; PDBTitle: crystal structure of transmembrane protein tmhc2_e
80	c3kitB	Alignment	not modelled	8.5	18	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of a vimentin fragment
81	c2my1A	Alignment	not modelled	8.4	13	PDB header: splicing Chain: A: PDB Molecule: pre-mrna-splicing factor bud31; PDBTitle: solution structure of bud31p
82	c2g7sA	Alignment	not modelled	8.4	6	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens
83	c5eulE	Alignment	not modelled	8.4	17	PDB header: protein transport Chain: E: PDB Molecule: preprotein translocase sece subunit; PDBTitle: structure of the seca-secy complex with a translocating polypeptide2 substrate
84	c3vmtA	Alignment	not modelled	8.4	13	PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: crystal structure of staphylococcus aureus membrane-bound2 transglycosylase in complex with a lipid ii analog
85	c2l2lA	Alignment	not modelled	8.3	28	PDB header: transferase Chain: A: PDB Molecule: transcriptional repressor p66-alpha; PDBTitle: solution structure of the coiled-coil complex between mbd2 and2 p66alpha
86	c6qajB	Alignment	not modelled	8.3	10	PDB header: nuclear protein Chain: B: PDB Molecule: endolysin,transcription intermediary factor 1-beta; PDBTitle: structure of the tripartite motif of kap1/trim28
87	c5dkaA	Alignment	not modelled	8.2	18	PDB header: replication Chain: A: PDB Molecule: cell division protein zapd; PDBTitle: the structure of escherichia coli zapd
88	d1w85a	Alignment	not modelled	8.2	5	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Branched-chain alpha-keto acid dehydrogenase PP module
89	c3t57A	Alignment	not modelled	8.1	11	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine o-acyltransferase domain-containing PDBTitle: activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase
90	c6ayiA	Alignment	not modelled	8.1	8	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator uidr; PDBTitle: escherichia coli gusr
91	c5j3nA	Alignment	not modelled	8.0	11	PDB header: hydrolase Chain: A: PDB Molecule: green fluorescent protein,hsdr; PDBTitle: c-terminal domain of ecor124i hsdR subunit fused with the ph-sensitive2 gfp variant ratiometric phluorin
92	d1zk8a2	Alignment	not modelled	8.0	10	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
93	c5cbfA	Alignment	not modelled	7.8	14	PDB header: transport protein Chain: A: PDB Molecule: ion transport 2 domain protein; PDBTitle: structural and functional characterization of a calcium-activated2 cation channel from tsukamurella paurometabola
94	c1vi0B	Alignment	not modelled	7.8	10	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
95	c3jb9e	Alignment	not modelled	7.7	16	PDB header: rna binding protein/rna Chain: E: PDB Molecule: small nuclear ribonucleoprotein-associated protein b; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
96	c1yo7A	Alignment	not modelled	7.7	11	PDB header: replication regulator Chain: A: PDB Molecule: regulatory protein rop; PDBTitle: re-engineering topology of the homodimeric rop protein into a single-2 chain 4-helix bundle
97	d1i0aa	Alignment	not modelled	7.7	9	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
98	c5hg1A	Alignment	not modelled	7.7	22	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hexokinase-2; PDBTitle: crystal structure of human hexokinase 2 with cmpd 1, a c-2-substituted2 glucosamine
99	c5frgA	Alignment	not modelled	7.6	10	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1