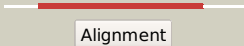

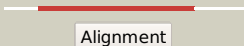

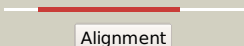



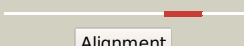

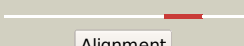

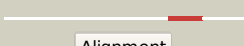









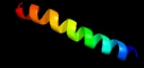
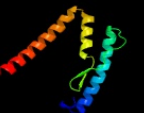


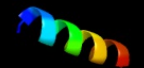



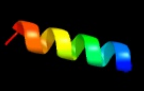


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0985c_(mscL)_1101029_1101484
 Date Wed Jul 31 22:05:05 BST 2019
 Unique Job ID e9dcfa598f16004e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oarA_	 Alignment		100.0	100	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
2	d2oara1	 Alignment		100.0	100	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
3	c4y7jE_	 Alignment		100.0	34	PDB header: membrane protein,transport protein Chain: E: PDB Molecule: large-conductance mechanosensitive channel protein, PDBTitle: structure of an archaeal mechanosensitive channel in expanded state
4	c3hzqA_	 Alignment		100.0	40	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of a tetrameric mscL in an expanded intermediate state
5	c4lkuA_	 Alignment		97.4	42	PDB header: transport protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
6	c4lkuB_	 Alignment		97.4	42	PDB header: transport protein Chain: B: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
7	c4lkuD_	 Alignment		97.2	50	PDB header: transport protein Chain: D: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
8	c4lkuC_	 Alignment		97.1	52	PDB header: transport protein Chain: C: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
9	c4lkuE_	 Alignment		96.8	55	PDB header: transport protein Chain: E: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of the c-terminal domain of the e. coli mechanosensitive2 channel of large conductance
10	c6fkiB_	 Alignment		82.5	16	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
11	c6fkiP_	 Alignment		80.8	16	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3

12	c5t4oJ_	Alignment		78.3	25	PDB header: hydrolase Chain: J; PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
13	c4rp9A_	Alignment		78.0	13	PDB header: membrane protein Chain: A; PDB Molecule: ascorbate-specific permease iic component ulaa; PDBTitle: bacterial vitamin c transporter ulaa/sgat in c2 form
14	c2rddB_	Alignment		72.9	16	PDB header: membrane protein/transport protein Chain: B; PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
15	c3qngD_	Alignment		70.1	17	PDB header: membrane protein, transport protein Chain: D; PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
16	c4uotE_	Alignment		49.6	50	PDB header: de novo protein Chain: E; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
17	c4uotC_	Alignment		49.6	50	PDB header: de novo protein Chain: C; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
18	c4uotA_	Alignment		49.6	50	PDB header: de novo protein Chain: A; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
19	c4uotD_	Alignment		49.6	50	PDB header: de novo protein Chain: D; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
20	c4uotB_	Alignment		49.6	50	PDB header: de novo protein Chain: B; PDB Molecule: designed helical bundle 5h2l; PDBTitle: thermodynamic hyperstability in parametrically designed2 helical bundles
21	c3t98C_	Alignment	not modelled	46.7	38	PDB header: protein transport Chain: C; PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
22	c5v2sA_	Alignment	not modelled	32.4	25	PDB header: viral protein Chain: A; PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
23	d1q1va_	Alignment	not modelled	31.1	29	Fold: Another 3-helical bundle Superfamily: DEK C-terminal domain Family: DEK C-terminal domain
24	c3t98A_	Alignment	not modelled	30.6	38	PDB header: protein transport Chain: A; PDB Molecule: nuclear pore complex protein nup54; PDBTitle: molecular architecture of the transport channel of the nuclear pore2 complex: nup54/nup58
25	c1vdfB_	Alignment	not modelled	27.5	38	PDB header: extracellular matrix protein Chain: B; PDB Molecule: cartilage oligomeric matrix protein; PDBTitle: assembly domain of cartilage oligomeric matrix protein
26	c4kjsB_	Alignment	not modelled	27.4	11	PDB header: transport protein Chain: B; PDB Molecule: cation exchanger yfke; PDBTitle: structure of native yfke
27	c2l35B_	Alignment	not modelled	26.0	40	PDB header: protein binding Chain: B; PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer
28	c2lseA_	Alignment	not modelled	25.6	37	PDB header: de novo protein Chain: A; PDB Molecule: four helix bundle protein; PDBTitle: solution nmr structure of de novo designed four helix bundle protein,2 northeast structural genomics consortium (nsg)

						target or188
29	c4wo1A_	Alignment	not modelled	24.9	40	PDB header: signaling protein Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
30	c2l34A_	Alignment	not modelled	24.9	40	PDB header: protein binding Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
31	c2l34B_	Alignment	not modelled	24.9	40	PDB header: protein binding Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: structure of the dap12 transmembrane homodimer
32	c4wo1D_	Alignment	not modelled	24.3	40	PDB header: signaling protein Chain: D: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
33	c4wo1A_	Alignment	not modelled	24.3	40	PDB header: signaling protein Chain: A: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
34	c4wo1B_	Alignment	not modelled	24.3	40	PDB header: signaling protein Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
35	c4wo1C_	Alignment	not modelled	24.3	40	PDB header: signaling protein Chain: C: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipid cubic2 phase
36	c4wo1B_	Alignment	not modelled	23.6	40	PDB header: signaling protein Chain: B: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
37	c4wo1C_	Alignment	not modelled	23.6	40	PDB header: signaling protein Chain: C: PDB Molecule: tyro protein tyrosine kinase-binding protein; PDBTitle: crystal structure of the dap12 transmembrane domain in lipidic cubic2 phase
38	c6g6hA_	Alignment	not modelled	22.7	44	PDB header: de novo protein Chain: A: PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
39	c6g6hB_	Alignment	not modelled	22.7	44	PDB header: de novo protein Chain: B: PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
40	c6g6hC_	Alignment	not modelled	22.7	44	PDB header: de novo protein Chain: C: PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
41	c6g6hE_	Alignment	not modelled	22.7	44	PDB header: de novo protein Chain: E: PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
42	c6g6hD_	Alignment	not modelled	22.7	44	PDB header: de novo protein Chain: D: PDB Molecule: 5h2l_2.1-i9l; PDBTitle: crystal structure of an antiparallel five-helix coiled coil 5h2l_2.1-2 i9l
43	d2ctda1	Alignment	not modelled	19.6	24	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
44	c5xugB_	Alignment	not modelled	17.6	45	PDB header: hydrolase Chain: B: PDB Molecule: endo-1,4-beta-mannanase; PDBTitle: complex structure(rmman134a-m5).
45	c4k1cB_	Alignment	not modelled	15.2	29	PDB header: membrane protein/metal transport Chain: B: PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
46	c4jd9B_	Alignment	not modelled	14.7	27	PDB header: protein binding Chain: B: PDB Molecule: 14.5 kda salivary protein; PDBTitle: contact pathway inhibitor from a sand fly
47	d2b3wa1	Alignment	not modelled	14.6	43	Fold: YbiA-like Superfamily: YbiA-like Family: YbiA-like
48	c4z3pA_	Alignment	not modelled	13.8	26	PDB header: transport protein Chain: A: PDB Molecule: putative drug/sodium antiporter; PDBTitle: mate transporter clbm in complex with rb+
49	d1sh0a_	Alignment	not modelled	12.9	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
50	c5zovA_	Alignment	not modelled	12.3	11	PDB header: transport protein Chain: A: PDB Molecule: pts ascorbate-specific subunit iibc; PDBTitle: inward-facing conformation of l-ascorbate transporter ulaa
51	c5lnk2_	Alignment	not modelled	12.3	29	PDB header: oxidoreductase Chain: 2: PDB Molecule: mitochondrial complex i, 24 kda subunit; PDBTitle: entire ovine respiratory complex i
52	c4zrkH_	Alignment	not modelled	11.8	63	PDB header: signaling protein/transferase Chain: H: PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex
						PDB header: signaling protein/transferase

53	c4zrkE	Alignment	not modelled	11.8	63	Chain: E: PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex
54	c4zrkF	Alignment	not modelled	11.8	63	PDB header: signaling protein/transferase Chain: F: PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex
55	c4zrkG	Alignment	not modelled	11.8	63	PDB header: signaling protein/transferase Chain: G: PDB Molecule: serine/threonine-protein kinase lats1; PDBTitle: merlin-ferm and lats1 complex
56	c2l35A	Alignment	not modelled	11.1	40	PDB header: protein binding Chain: A: PDB Molecule: dap12-nkg2c_tm; PDBTitle: structure of the dap12-nkg2c transmembrane heterotrimer
57	c2uutA	Alignment	not modelled	11.1	29	PDB header: hydrolase Chain: A: PDB Molecule: rna-directed rna polymerase; PDBTitle: the 2.4 angstrom resolution structure of the d346g mutant of the2 sapporo virus rdrp polymerase
58	c2b43D	Alignment	not modelled	10.3	18	PDB header: viral protein Chain: D: PDB Molecule: non-structural polyprotein; PDBTitle: crystal structure of the norwalk virus rna dependent rna polymerase2 from strain hu/nlv/dresden174/1997/ge
59	c2yubA	Alignment	not modelled	10.0	20	PDB header: transferase Chain: A: PDB Molecule: lim domain kinase 2; PDBTitle: solution structure of the pdz domain from mouse lim domain2 kinase
60	c1c94B	Alignment	not modelled	9.7	45	PDB header: gene regulation Chain: B: PDB Molecule: retro-gcn4 leucine zipper; PDBTitle: reversing the sequence of the gcn4 leucine zipper does not affect its2 fold.
61	c6a6iG	Alignment	not modelled	9.7	19	PDB header: hydrolase Chain: G: PDB Molecule: excision repair cross-complementing rodent repair PDBTitle: crystal structure of the winged-helix domain of cockayne syndrome2 group b protein in complex with ubiquitin
62	c4g9iA	Alignment	not modelled	9.6	18	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation protein hypf; PDBTitle: crystal structure of t.kodakarensis hypf
63	c3vthB	Alignment	not modelled	9.4	24	PDB header: transferase Chain: B: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
64	c2jpnA	Alignment	not modelled	8.5	67	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase uvsw; PDBTitle: solution structure of t4 bacteriophage helicase uvsw.1
65	d1khva	Alignment	not modelled	8.4	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
66	d1lm8v	Alignment	not modelled	8.4	19	Fold: Prealbumin-like Superfamily: VHL Family: VHL
67	c3m91B	Alignment	not modelled	8.0	46	PDB header: hydrolase regulator Chain: B: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa
68	c3m91D	Alignment	not modelled	8.0	46	PDB header: hydrolase regulator Chain: D: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa
69	c3vthA	Alignment	not modelled	7.8	19	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
70	c2n28A	Alignment	not modelled	7.7	21	PDB header: viral protein Chain: A: PDB Molecule: protein vpu; PDBTitle: solid-state nmr structure of vpu
71	c5jtsA	Alignment	not modelled	7.0	55	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,4-mannanase; PDBTitle: structure of a beta-1,4-mannanase, ssg134.
72	c5yxwA	Alignment	not modelled	7.0	25	PDB header: viral protein Chain: A: PDB Molecule: glycoprotein f2; PDBTitle: crystal structure of the prefusion form of measles virus fusion2 protein
73	c4rfsS	Alignment	not modelled	6.9	14	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: substrate binding prtein s; PDBTitle: structure of a pantothenate energy coupling factor transporter
74	c5sy1A	Alignment	not modelled	6.8	36	PDB header: membrane protein/calcium binding protein Chain: A: PDB Molecule: stra6; PDBTitle: structure of the stra6 receptor for retinol uptake in complex with2 calmodulin
75	c6fddC	Alignment	not modelled	6.7	33	PDB header: structural protein Chain: C: PDB Molecule: whirlin; PDBTitle: crystal structure of the hhd2 domain of whirlin
76	c4f0qA	Alignment	not modelled	6.7	14	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease; PDBTitle: mspji restriction endonuclease - p21 form
77	c2hdeA	Alignment	not modelled	6.6	15	PDB header: transcription Chain: A: PDB Molecule: histone deacetylase complex subunit sap18; PDBTitle: solution structure of human sap18
78	c3m9dR	Alignment	not modelled	6.5	29	PDB header: chaperone Chain: R: PDB Molecule: prokaryotic ubiquitin-like protein pup; PDBTitle: crystal structure of the prokaryotic ubiquitin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter

						domain
79	c2j5dA_	Alignment	not modelled	6.5	25	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting protein 3; PDBTitle: nmr structure of bnip3 transmembrane domain in lipid bicelles
80	c4g29A_	Alignment	not modelled	6.3	12	PDB header: protein binding Chain: A: PDB Molecule: secreted effector protein ssei; PDBTitle: structure of the catalytic domain of the salmonella virulence factor2 ssei
81	c4bl0B_	Alignment	not modelled	6.2	33	PDB header: cell cycle Chain: B: PDB Molecule: checkpoint serine/threonine-protein kinase bub1; PDBTitle: crystal structure of yeast bub3-bub1 bound to phospho-spc105
82	c4f0qC_	Alignment	not modelled	6.2	12	PDB header: hydrolase Chain: C: PDB Molecule: restriction endonuclease; PDBTitle: mspji restriction endonuclease - p21 form
83	c5o9zH_	Alignment	not modelled	6.0	26	PDB header: splicing Chain: H: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp31; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
84	c3nahC_	Alignment	not modelled	5.9	24	PDB header: transferase Chain: C: PDB Molecule: rna dependent rna polymerase; PDBTitle: crystal structures and functional analysis of murine norovirus rna-2 dependent rna polymerase
85	d1xr6a_	Alignment	not modelled	5.8	24	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
86	c2ka1A_	Alignment	not modelled	5.8	25	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
87	c2ka2B_	Alignment	not modelled	5.8	25	PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
88	c2ka1B_	Alignment	not modelled	5.8	25	PDB header: membrane protein Chain: B: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
89	c2ka2A_	Alignment	not modelled	5.8	25	PDB header: membrane protein Chain: A: PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting PDBTitle: solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
90	d1g8eb_	Alignment	not modelled	5.8	44	Fold: Flagellar transcriptional activator FlhD Superfamily: Flagellar transcriptional activator FlhD Family: Flagellar transcriptional activator FlhD
91	c6c90B_	Alignment	not modelled	5.7	44	PDB header: hydrolase/rna binding protein Chain: B: PDB Molecule: zinc finger cchc domain-containing protein 8; PDBTitle: human mtr4 helicase in complex with zcchc8-ctd
92	c3iv0A_	Alignment	not modelled	5.7	13	PDB header: sugar binding protein Chain: A: PDB Molecule: susd homolog; PDBTitle: crystal structure of susd homolog (np_809186.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.35 a resolution
93	c2lnaA_	Alignment	not modelled	5.7	31	PDB header: hydrolase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: solution nmr structure of the mitochondrial inner membrane domain2 (residues 164-251), fts_h_ext, from the paraplegin-like protein afg3l23 from homo sapiens, northeast structural genomics consortium target4 hr6741a
94	c5edlA_	Alignment	not modelled	5.7	12	PDB header: transport protein Chain: A: PDB Molecule: putative hmp/thiamine permease protein ykoe; PDBTitle: crystal structure of an s-component of ecf transporter
95	c2m0oA_	Alignment	not modelled	5.6	44	PDB header: peptide binding protein Chain: A: PDB Molecule: phd finger protein 1; PDBTitle: the solution structure of human phf1 in complex with h3k36me3
96	d1nara_	Alignment	not modelled	5.6	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
97	d1u09a_	Alignment	not modelled	5.5	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
98	d1xpja_	Alignment	not modelled	5.5	33	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein VC0232
99	c3si5X_	Alignment	not modelled	5.4	38	PDB header: cell cycle Chain: X: PDB Molecule: protein casc5; PDBTitle: kinetochore-bub1 kinase complex