

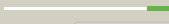
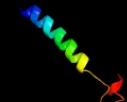

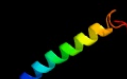

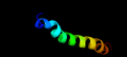

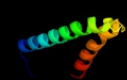







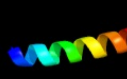






Phyre2


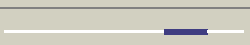

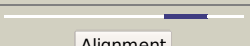
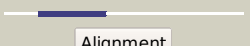
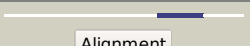
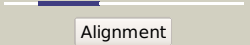
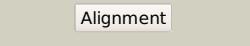
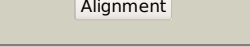
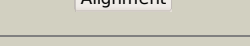



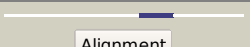

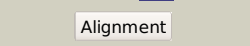
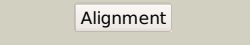
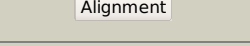
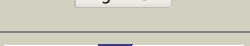






Email	mdejesus@rockefeller.edu
Description	RVBD3669_(-)_4111005_4111523
Date	Fri Aug 9 18:20:36 BST 2019
Unique Job ID	5010a68521e447f5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5x5yF_	 Alignment		75.5	8	PDB header: membrane protein Chain: F; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
2	c4kt0F_	 Alignment		59.6	16	PDB header: electron transport Chain: F; PDB Molecule: photosystem i subunit iii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
3	d1jb0F_	 Alignment		56.3	16	Fold: Single transmembrane helix Superfamily: Subunit III of photosystem I reaction centre, PsaF Family: Subunit III of photosystem I reaction centre, PsaF
4	c2kncA_	 Alignment		54.7	25	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
5	c5x5yG_	 Alignment		54.7	15	PDB header: membrane protein Chain: G; PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
6	c6mjpG_	 Alignment		54.4	16	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
7	c6fosF_	 Alignment		53.0	13	PDB header: photosynthesis Chain: F; PDB Molecule: photosystem i reaction center subunit ii; PDBTitle: cyanidioschyzon merolae photosystem i
8	c5z1lL_	 Alignment		52.6	47	PDB header: protein fibril Chain: L; PDB Molecule: flagellin; PDBTitle: cryo-em structure of methanococcus maripaludis archaeum
9	c5tfyL_	 Alignment		51.6	29	PDB header: cell adhesion Chain: J; PDB Molecule: flagellin; PDBTitle: the archaeal flagellum of methanospirillum hungatei strain jf1.
10	c6mjpF_	 Alignment		51.2	11	PDB header: lipid transport Chain: F; PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
11	c5o4uK_	 Alignment		48.8	47	PDB header: cell adhesion Chain: K; PDB Molecule: flagellin; PDBTitle: the flagellin of pyrococcus furiosus

12	c6igzF_	Alignment		48.6	16	PDB header: plant protein Chain: F; PDB Molecule: psaf; PDBTitle: structure of psi-lhci
13	c2jp3A_	Alignment		46.6	32	PDB header: transcription Chain: A; PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
14	c5xu1M_	Alignment		42.9	14	PDB header: transport protein Chain: M; PDB Molecule: abc transporter permeae; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
15	c6ijjF_	Alignment		40.9	13	PDB header: membrane protein Chain: F; PDB Molecule: psaf; PDBTitle: photosystem i of chlamydomonas reinhardtii
16	c4hb1A_	Alignment		31.9	29	PDB header: designed helical bundle Chain: A; PDB Molecule: dhp1; PDBTitle: a designed four helix bundle protein.
17	d2in1a1	Alignment		29.2	24	Fold: UBC-like Superfamily: UBC-like Family: UFC1-like
18	c5ws4A_	Alignment		28.7	8	PDB header: membrane protein Chain: A; PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
19	c3kpaB_	Alignment		27.6	10	PDB header: ligase Chain: B; PDB Molecule: probable ubiquitin fold modifier conjugating enzyme; PDBTitle: ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable)
20	c2zxeG_	Alignment		26.7	32	PDB header: hydrolase/transport protein Chain: G; PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
21	c3fewX_	Alignment	not modelled	25.4	11	PDB header: immune system Chain: X; PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a duplicated2 receptor binding domain
22	c2oarA_	Alignment	not modelled	24.1	14	PDB header: membrane protein Chain: A; PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
23	c2jo1A_	Alignment	not modelled	21.7	11	PDB header: hydrolase regulator Chain: A; PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
24	c2mkvA_	Alignment	not modelled	21.2	14	PDB header: transport protein Chain: A; PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
25	c6mctJ_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: J; PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
26	c6mctN_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: N; PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
27	c6mq2D_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: D; PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
28	c6mctB_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: B; PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by

						van der waals2 interaction
29	c6mctG_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: G: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
30	c6mpwA_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: A: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
31	c6mctA_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: A: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
32	c6mctl_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: I: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
33	c6mctD_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
34	c6mctE_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: E: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
35	c6mctH_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: H: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
36	c6mctl_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: L: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
37	c6mctC_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: C: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
38	c6mctM_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: M: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
39	c6mctF_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: F: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
40	c6mctO_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: O: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
41	c6mctK_	Alignment	not modelled	20.4	32	PDB header: de novo protein Chain: K: PDB Molecule: mini-evgl membrane protein; PDBTitle: a designed pentameric membrane protein stabilized by van der waals2 interaction
42	c2kdcC_	Alignment	not modelled	17.4	14	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
43	c5n9yB_	Alignment	not modelled	17.2	12	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
44	c5I75G_	Alignment	not modelled	15.7	18	PDB header: transport protein Chain: G: PDB Molecule: fig000906: predicted permease; PDBTitle: a protein structure
45	c2o01F_	Alignment	not modelled	14.1	15	PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit iii, chloroplast; PDBTitle: the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
46	c5I75F_	Alignment	not modelled	13.5	2	PDB header: transport protein Chain: F: PDB Molecule: fig000988: predicted permease; PDBTitle: a protein structure
47	c5nikK_	Alignment	not modelled	13.2	17	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
48	c6hwhX_	Alignment	not modelled	12.1	16	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
49	c3d36C_	Alignment	not modelled	11.5	13	PDB header: transferase/transferase inhibitor Chain: C: PDB Molecule: sporulation kinase inhibitor sda; PDBTitle: how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
50	c5vhxE_	Alignment	not modelled	10.7	15	PDB header: transport protein Chain: E: PDB Molecule: glutamate receptor 2,germ cell-specific gene 1-like PDBTitle: glua2-1xgsg1l bound to zk
51	d1e7la1	Alignment	not modelled	10.5	23	Fold: LEM/SAP HeH motif Superfamily: Recombination endonuclease VII, C-terminal and dimerization domains Family: Recombination endonuclease VII, C-terminal and dimerization domains
52	d1k46a_	Alignment	not modelled	10.2	40	Fold: YopH tyrosine phosphatase N-terminal domain Superfamily: YopH tyrosine phosphatase N-terminal domain Family: YopH tyrosine phosphatase N-terminal domain
53	c4ev6E_	Alignment	not modelled	10.2	14	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii

54	c2l16A_		Alignment	not modelled	8.7	19	PDB header: protein transport Chain: A: PDB Molecule: sec-independent protein translocase protein tatad; PDBTitle: solution structure of bacillus subtilis tatad protein in dpc micelles
55	c1tnuL_		Alignment	not modelled	8.3	9	PDB header: transferase Chain: L: PDB Molecule: geranylgeranyl transferase type i beta subunit; PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a gcinckvl peptide derived from rhob
56	d1pv0a_		Alignment	not modelled	8.3	13	Fold: Long alpha-hairpin Superfamily: Sporulation inhibitor Sda Family: Sporulation inhibitor Sda
57	d1n4qb_		Alignment	not modelled	8.3	9	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases
58	c4l6rA_		Alignment	not modelled	7.9	15	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
59	c2lzsE_		Alignment	not modelled	7.6	20	PDB header: protein transport Chain: E: PDB Molecule: sec-independent protein translocase protein tata; PDBTitle: tata oligomer
60	c5fcmB_		Alignment	not modelled	7.5	13	PDB header: cell cycle Chain: B: PDB Molecule: basal body protein; PDBTitle: crbld10-n 1-70
61	c6c5wA_		Alignment	not modelled	7.4	9	PDB header: membrane protein Chain: A: PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the mitochondrial calcium uniporter
62	c2k1aA_		Alignment	not modelled	6.6	22	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment
63	c6mq2A_		Alignment	not modelled	6.5	30	PDB header: de novo protein Chain: A: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
64	c6mpwD_		Alignment	not modelled	6.5	30	PDB header: de novo protein Chain: D: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
65	c6mq2E_		Alignment	not modelled	6.5	30	PDB header: de novo protein Chain: E: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
66	c6mpwB_		Alignment	not modelled	6.5	30	PDB header: de novo protein Chain: B: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
67	c6mq2C_		Alignment	not modelled	6.5	30	PDB header: de novo protein Chain: C: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
68	c6mpwE_		Alignment	not modelled	6.5	30	PDB header: de novo protein Chain: E: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
69	c6mpwC_		Alignment	not modelled	6.5	30	PDB header: de novo protein Chain: C: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-1
70	c6mq2B_		Alignment	not modelled	6.5	30	PDB header: de novo protein Chain: B: PDB Molecule: mini-evgl membrane protein; PDBTitle: de novo design of membrane protein--mini-evgl membrane protein, c22212 form-2
71	c4rndB_		Alignment	not modelled	6.5	16	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit f; PDBTitle: crystal structure of the subunit df-assembly of the eukaryotic v-2 atpase.
72	d1sjpa3		Alignment	not modelled	6.4	39	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: GroEL-like chaperone, intermediate domain
73	c5m87A_		Alignment	not modelled	6.4	12	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
74	c6ithA_		Alignment	not modelled	6.3	22	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
75	c4p79A_		Alignment	not modelled	6.3	5	PDB header: cell adhesion Chain: A: PDB Molecule: claudin-15; PDBTitle: crystal structure of mouse claudin-15
76	c5lj7B_		Alignment	not modelled	6.2	6	PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
77	c2wsfF_		Alignment	not modelled	5.9	15	PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit iii, chloroplastic; PDBTitle: improved model of plant photosystem i
78	c3jbrE_		Alignment	not modelled	5.9	14	PDB header: membrane protein Chain: E: PDB Molecule: voltage-dependent calcium channel gamma-1 subunit; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom

79	c5nnpG_	Alignment	not modelled	5.8	35	PDB header: transferase Chain: G: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of naa15/naa10 bound to hypk-thb
80	c2l27B_	Alignment	not modelled	5.7	46	PDB header: membrane protein, peptide binding protei Chain: B: PDB Molecule: peptide agonist; PDBTitle: nmr structure of the ecd1 of crf-r1 in complex with a peptide agonist
81	c3n23E_	Alignment	not modelled	5.7	25	PDB header: hydrolase Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the e2p form of the sodium-potassium pump
82	c6c3oE_	Alignment	not modelled	5.6	11	PDB header: transport protein Chain: E: PDB Molecule: atp-binding cassette sub-family c member 8; PDBTitle: cryo-em structure of human katp bound to atp and adp in quatrefoil2 form
83	c5b2gG_	Alignment	not modelled	5.5	7	PDB header: membrane protein Chain: G: PDB Molecule: endolysin,claudin-4; PDBTitle: crystal structure of human claudin-4 in complex with c-terminal2 fragmrnt of clostridium perfringens enterotoxin
84	c5xnlX_	Alignment	not modelled	5.5	20	PDB header: membrane protein Chain: X: PDB Molecule: photosystem ii reaction center protein x; PDBTitle: structure of stacked c2s2m2-type psii-lhcii supercomplex from pismus2 sativum
85	c2kluA_	Alignment	not modelled	5.4	19	PDB header: immune system, membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
86	c6roiC_	Alignment	not modelled	5.4	14	PDB header: lipid transport Chain: C: PDB Molecule: cell division control protein 50; PDBTitle: cryo-em structure of the partially activated drs2p-cdc50p
87	c2ww9B_	Alignment	not modelled	5.4	11	PDB header: ribosome Chain: B: PDB Molecule: protein transport protein sss1; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
88	c2bbjB_	Alignment	not modelled	5.3	23	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter