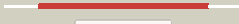
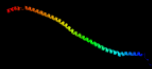

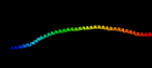
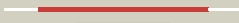
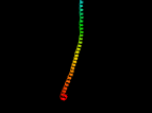

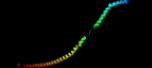

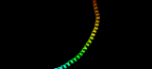

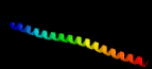

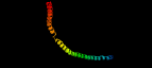



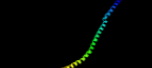

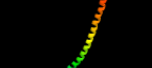

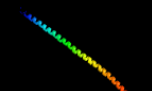
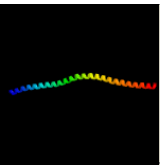
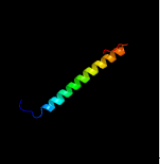
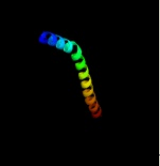

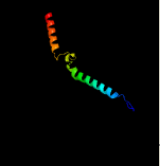
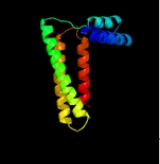
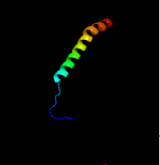
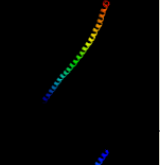
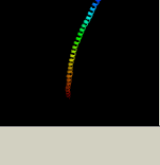


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1306_(atpF)_1461327_1461842
 Date Wed Jul 31 22:05:40 BST 2019
 Unique Job ID bc873d31b9648860

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fkip_	 Alignment		100.0	17	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
2	c5t4oj_	 Alignment		100.0	19	PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
3	c6fkib_	 Alignment		100.0	14	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
4	c6b8hb_	 Alignment		99.8	13	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
5	c6j5ib_	 Alignment		99.4	9	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase
6	d1l2pa_	 Alignment		98.1	20	Fold: Single transmembrane helix Superfamily: F1F0 ATP synthase subunit B, membrane domain Family: F1F0 ATP synthase subunit B, membrane domain
7	c5arhT_	 Alignment		98.0	12	PDB header: hydrolase Chain: T: PDB Molecule: atp synthase f(0) complex subunit b1, mitochondrial; PDBTitle: bovine mitochondrial atp synthase state 2a
8	c1b9uA_	 Alignment		97.8	20	PDB header: hydrolase Chain: A: PDB Molecule: protein (atp synthase); PDBTitle: membrane domain of the subunit b of the e.coli atp synthase
9	c5lqyV_	 Alignment		97.5	15	PDB header: hydrolase Chain: V: PDB Molecule: atp synthase subunit b; PDBTitle: structure of f-atpase from pichia angusta, in state2
10	c4dt0A_	 Alignment		97.2	20	PDB header: hydrolase Chain: A: PDB Molecule: v-type atp synthase subunit e; PDBTitle: the structure of the peripheral stalk subunit e from pyrococcus2 horikoshii
11	c3k5bE_	 Alignment		96.5	13	PDB header: hydrolase Chain: E: PDB Molecule: v-type atp synthase subunit e; PDBTitle: crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase

12	c4dl0J_	Alignment		95.6	6	PDB header: hydrolase Chain: J: PDB Molecule: v-type proton atpase subunit e; PDBTitle: crystal structure of the heterotrimeric egthead peripheral stalk2 complex of the yeast vacuolar atpase
13	c2khkA_	Alignment		93.7	19	PDB header: transport protein Chain: A: PDB Molecule: atp synthase subunit b; PDBTitle: nmr solution structure of the b30-82 domain of subunit b of2 escherichia coli f1fo atp synthase
14	c6b2zb_	Alignment		93.6	15	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit c, mitochondrial; PDBTitle: cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
15	c4dl0G_	Alignment		92.7	12	PDB header: hydrolase Chain: G: PDB Molecule: v-type proton atpase subunit g; PDBTitle: crystal structure of the heterotrimeric egthead peripheral stalk2 complex of the yeast vacuolar atpase
16	c2oarA_	Alignment		92.4	14	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
17	c1y4cA_	Alignment		92.1	11	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
18	d2oara1	Alignment		90.5	15	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
19	c3k5bB_	Alignment		88.6	21	PDB header: hydrolase Chain: B: PDB Molecule: v-type atp synthase, subunit (vapc-therm); PDBTitle: crystal structure of the peripheral stalk of thermus thermophilus h+-2 atpase/synthase
20	c4cg4D_	Alignment		87.4	16	PDB header: actin-binding protein Chain: D: PDB Molecule: pyrin; PDBTitle: crystal structure of the chs-b30.2 domains of trim20
21	c4y7jE_	Alignment	not modelled	83.3	13	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
22	c4nqjB_	Alignment	not modelled	80.6	9	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase trim69; PDBTitle: structure of coiled-coil domain
23	c6flnE_	Alignment	not modelled	79.3	9	PDB header: protein binding Chain: E: PDB Molecule: e3 ubiquitin/isg15 ligase trim25; PDBTitle: crystal structure of the human trim25 coiled-coil and pryspry domains
24	c3hzqA_	Alignment	not modelled	78.3	18	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of a tetrameric mscl in an expanded intermediate state
25	c3cwbO_	Alignment	not modelled	77.5	8	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
26	c2k88A_	Alignment	not modelled	75.8	16	PDB header: hydrolase Chain: A: PDB Molecule: vacuolar proton pump subunit g; PDBTitle: association of subunit d (vma6p) and e (vma4p) with g2 (vma10p) and the nmr solution structure of subunit g (g1-3 59) of the saccharomyces cerevisiae v1vo atpase
27	c5b0oH_	Alignment	not modelled	74.4	13	PDB header: hydrolase/motor protein Chain: H: PDB Molecule: flagellar assembly protein flih; PDBTitle: structure of the flih-flii complex
						PDB header: oxidoreductase

28	c1p84D_	Alignment	not modelled	74.4	12	Chain: D; PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
29	c5b0oG_	Alignment	not modelled	74.3	14	PDB header: hydrolase/motor protein Chain: G; PDB Molecule: flagellar assembly protein flih; PDBTitle: structure of the flih-flii complex
30	c2rddB_	Alignment	not modelled	72.0	10	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.
31	c6b2zA_	Alignment	not modelled	64.1	16	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
32	c6b2zL_	Alignment	not modelled	64.1	16	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
33	c1qcrD_	Alignment	not modelled	62.3	4	PDB header: oxidoreductase Chain: D; PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
34	c2kncB_	Alignment	not modelled	62.0	5	PDB header: cell adhesion Chain: B; PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
35	c1zrtD_	Alignment	not modelled	54.8	20	PDB header: oxidoreductase/metal transport Chain: D; PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
36	c2kk7A_	Alignment	not modelled	41.1	26	PDB header: hydrolase Chain: A; PDB Molecule: v-type atp synthase subunit e; PDBTitle: nmr solution structure of the n terminal domain of subunit e2 (e1-52) of a1ao atp synthase from methanocaldococcus3 jannaschii
37	c6mu1C_	Alignment	not modelled	39.7	17	PDB header: membrane protein Chain: C; PDB Molecule: inositol 1,4,5-trisphosphate receptor type 1; PDBTitle: structure of full-length ip3r1 channel bound with adenophostin a
38	c2rmzA_	Alignment	not modelled	38.8	5	PDB header: cell adhesion Chain: A; PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
39	c1ei3E_	Alignment	not modelled	32.5	11	PDB header: blood clotting Chain: E; PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
40	c5j8vD_	Alignment	not modelled	31.1	14	PDB header: transport protein Chain: D; PDB Molecule: ryanodine receptor 1; PDBTitle: structure of rabbit ryanodine receptor ryr1 open state activated by2 calcium ion
41	d2axtz1	Alignment	not modelled	30.0	24	Fold: Transmembrane helix hairpin Superfamily: PsbZ-like Family: PsbZ-like
42	c1deqO_	Alignment	not modelled	28.1	10	PDB header: blood clotting Chain: O; PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
43	c5zazA_	Alignment	not modelled	25.4	10	PDB header: cell adhesion Chain: A; PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
44	c3zc4G_	Alignment	not modelled	24.4	26	PDB header: immune system Chain: G; PDB Molecule: isso1398; PDBTitle: the structure of csa5 from sulfolobus solfataricus.
45	c6qajB_	Alignment	not modelled	23.8	7	PDB header: nuclear protein Chain: B; PDB Molecule: endolysin,transcription intermediary factor 1-beta; PDBTitle: structure of the tripartite motif of kap1/trim28
46	c4gn0D_	Alignment	not modelled	22.9	10	PDB header: signaling protein Chain: D; PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
47	c3lvgD_	Alignment	not modelled	22.2	15	PDB header: structural protein Chain: D; PDB Molecule: clathrin light chain b; PDBTitle: crystal structure of a clathrin heavy chain and clathrin light chain2 complex
48	c3ghgK_	Alignment	not modelled	21.3	8	PDB header: blood clotting Chain: K; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
49	c3errB_	Alignment	not modelled	21.1	14	PDB header: ligase Chain: B; PDB Molecule: fusion protein of microtubule binding domain from mouse PDBTitle: microtubule binding domain from mouse cytoplasmic dynein as a fusion2 with seryl-trna synthetase
50	c1u2mC_	Alignment	not modelled	20.4	10	PDB header: chaperone Chain: C; PDB Molecule: histone-like protein hlp-1; PDBTitle: crystal structure of skp
51	d1u00a1	Alignment	not modelled	20.0	13	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
52	c2fyfH_	Alignment	not modelled	18.8	22	PDB header: oxidoreductase Chain: H; PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
53	c1u00A_	Alignment	not modelled	18.2	8	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein hsca; PDBTitle: hsca substrate binding domain complexed with the iscu2

						recognition peptide elppvkihc PDB header: transport protein Chain: E: PDB Molecule: piezo-type mechanosensitive ion channel component 1; PDBTitle: structure of the mechanosensitive channel piezo1
54	c6b3rE_	Alignment	not modelled	17.8	7	PDB header: ribosome Chain: 9: PDB Molecule: ribosome-recycling factor, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
55	c5mlc9_	Alignment	not modelled	16.6	8	PDB header: transport protein/isomerase Chain: G: PDB Molecule: ryanodine receptor 1; PDBTitle: cryo-em structure of ryanodine receptor/calstabin-2 complex
56	c3j8eG_	Alignment	not modelled	16.5	13	PDB header: chaperone Chain: A: PDB Molecule: putative outer membrane chaperone (omph-like); PDBTitle: crystal structure of a putative outer membrane chaperone (omph-like)2 (cc_1914) from caulobacter crescentus cb15 at 2.83 a resolution (psi3 community target, shapiro)
57	c4kqtA_	Alignment	not modelled	16.4	7	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
58	c2yiuE_	Alignment	not modelled	16.4	29	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
59	c3qnqD_	Alignment	not modelled	16.3	18	PDB header: membrane protein Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: lipid-bound synaptobrevin solution nmr structure
60	c2kogA_	Alignment	not modelled	15.9	10	PDB header: structural protein Chain: E: PDB Molecule: clathrin light chain b; PDBTitle: crystal structure of a clathrin heavy chain and clathrin light chain2 complex
61	c3lvqE_	Alignment	not modelled	15.4	15	PDB header: membrane protein Chain: W: PDB Molecule: photosystem ii reaction center w protein, chloroplastic; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
62	c3jcuw_	Alignment	not modelled	14.9	12	PDB header: structural protein Chain: E: PDB Molecule: clathrin light chain b; PDBTitle: crystal structure of a clathrin heavy chain and clathrin light chain2 complex
63	c3lvhE_	Alignment	not modelled	14.3	15	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like
64	d2qzga1	Alignment	not modelled	13.4	21	PDB header: photoreceptor Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: three-dimensional structure of proteolytic fragment 163-2312 of bacterioopsin determined from nuclear magnetic3 resonance data in solution
65	c1bctA_	Alignment	not modelled	12.7	33	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
66	c3ghgl_	Alignment	not modelled	12.1	11	PDB header: transport protein Chain: D: PDB Molecule: inositol 1,4,5-trisphosphate receptor type 1; PDBTitle: structure of full-length ip3r1 channel in the apo-state determined by2 single particle cryo-em
67	c3javD_	Alignment	not modelled	11.6	13	PDB header: transferase Chain: E: PDB Molecule: protein kinase c-binding protein 1; PDBTitle: crystal structure of the leucine zipper of human prkcbp1
68	c5mq4E_	Alignment	not modelled	11.6	13	PDB header: membrane protein Chain: E: PDB Molecule: complexin i snare-complex binding region; PDBTitle: three-dimensional structure of the complexin/snare complex
69	c1kilE_	Alignment	not modelled	11.5	19	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfaib-beta3 transmembrane-cytoplasmic2 heterocomplex
70	c2kncA_	Alignment	not modelled	10.9	19	PDB header: chaperone Chain: A: PDB Molecule: prefoldin subunit beta; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
71	c2zdiA_	Alignment	not modelled	10.9	10	PDB header: protein transport Chain: L: PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus
72	c5wdaL_	Alignment	not modelled	10.6	17	PDB header: viral protein Chain: A: PDB Molecule: protein vpu; PDBTitle: solid-state nmr structure of vpu
73	c2n28A_	Alignment	not modelled	10.3	27	PDB header: contractile protein Chain: B: PDB Molecule: nonmuscle myosin heavy chain b, alpha-actinin a chimera PDBTitle: crystal structure of rigor-like human nonmuscle myosin-2b
74	c4pd3B_	Alignment	not modelled	9.9	8	PDB header: structural protein Chain: F: PDB Molecule: clathrin light chain b; PDBTitle: crystal structure of a clathrin heavy chain and clathrin light chain2 complex
75	c3lvqF_	Alignment	not modelled	9.7	14	PDB header: structural protein Chain: O: PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
76	c2zv4O_	Alignment	not modelled	9.7	13	PDB header: membrane protein Chain: C: PDB Molecule: piezo-type mechanosensitive ion channel
77	c5z10C_	Alignment	not modelled	9.4	7	

77	c2z1vC_	Alignment	not modelled	9.4	7	component 1; PDBTitle: structure of the mechanosensitive piezo1 channel
78	d1oqwa_	Alignment	not modelled	9.3	13	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
79	d2qsba1	Alignment	not modelled	9.2	16	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like
80	c6nrc6_	Alignment	not modelled	8.7	5	PDB header: chaperone Chain: 6: PDB Molecule: prefoldin subunit 6; PDBTitle: htric-hpfd class3
81	c6hu9e_	Alignment	not modelled	8.6	12	PDB header: oxidoreductase/electron transport Chain: E: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
82	c3rfrl_	Alignment	not modelled	8.5	12	PDB header: oxidoreductase Chain: I: PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
83	c3vkhA_	Alignment	not modelled	8.1	11	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
84	c2mc7A_	Alignment	not modelled	8.0	21	PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgrtr
85	c4ltpC_	Alignment	not modelled	7.6	10	PDB header: transport protein Chain: C: PDB Molecule: ion transport protein; PDBTitle: bacterial sodium channel in high calcium, i222 space group, crystal 2
86	c2y69Q_	Alignment	not modelled	6.9	18	PDB header: electron transport Chain: Q: PDB Molecule: cytochrome c oxidase subunit 4 isoform 1; PDBTitle: bovine heart cytochrome c oxidase re-refined with molecular oxygen
87	d1v54d_	Alignment	not modelled	6.9	18	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit IV Family: Mitochondrial cytochrome c oxidase subunit IV
88	c5nugB_	Alignment	not modelled	6.8	9	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
89	d1gs9a_	Alignment	not modelled	6.6	17	Fold: Four-helical up-and-down bundle Superfamily: Apolipoprotein Family: Apolipoprotein
90	c3wxxF_	Alignment	not modelled	6.5	18	PDB header: membrane protein/chaperone Chain: F: PDB Molecule: aopb; PDBTitle: crystal structure of a t3ss complex from aeromonas hydrophila
91	c2k6iA_	Alignment	not modelled	6.5	21	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein mj0223; PDBTitle: the domain features of the peripheral stalk subunit h of the2 methanogenic a1ao atp synthase and the nmr solution3 structure of h1-47
92	c1usdA_	Alignment	not modelled	6.5	14	PDB header: signaling protein Chain: A: PDB Molecule: vasodilator-stimulated phosphoprotein; PDBTitle: human vasp tetramerisation domain l352m
93	c5v2sA_	Alignment	not modelled	6.5	16	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
94	d3c07a2	Alignment	not modelled	6.3	9	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
95	c3lvhD_	Alignment	not modelled	6.3	15	PDB header: structural protein Chain: D: PDB Molecule: clathrin light chain b; PDBTitle: crystal structure of a clathrin heavy chain and clathrin light chain2 complex
96	d1xlya_	Alignment	not modelled	6.3	12	Fold: RNA-binding protein She2p Superfamily: RNA-binding protein She2p Family: RNA-binding protein She2p
97	c2kz9A_	Alignment	not modelled	6.2	12	PDB header: proton transport Chain: A: PDB Molecule: v-type proton atpase subunit e; PDBTitle: structure of e1-69 of yeast v-atpase
98	c2rifA_	Alignment	not modelled	5.8	13	PDB header: proton transport Chain: A: PDB Molecule: matrix protein 2; PDBTitle: proton channel m2 from influenza a in complex with2 inhibitor rimantadine
99	c5hvdA_	Alignment	not modelled	5.6	6	PDB header: transport protein Chain: A: PDB Molecule: ion transport protein; PDBTitle: full length open-form sodium channel navms i218c