



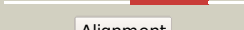

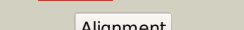
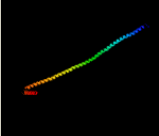
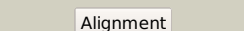
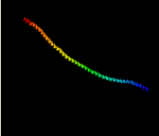
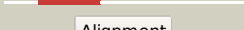
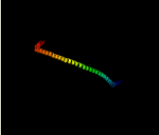







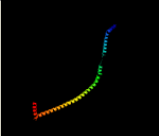
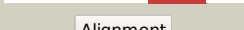





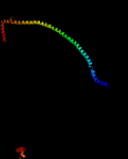
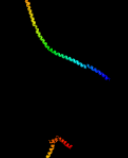
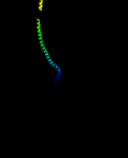
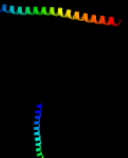
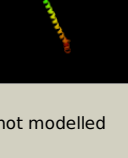


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1307_(atpH)_1461849_1463189
 Date Wed Jul 31 22:05:40 BST 2019
 Unique Job ID 2586795499152071

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fkfd_	 Alignment		100.0	18	PDB header: membrane protein Chain: D: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 1
2	c6rdlp_	 Alignment		100.0	23	PDB header: proton transport Chain: P: PDB Molecule: mitochondrial atp synthase subunit oscp; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1b,2 monomer-masked refinement
3	c5t4oL_	 Alignment		100.0	19	PDB header: hydrolase Chain: L: PDB Molecule: atp synthase subunit delta; PDBTitle: autoinhibited e. coli atp synthase state 1
4	c6fkib_	 Alignment		100.0	11	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit beta, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
5	c5t4oJ_	 Alignment		99.9	26	PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
6	c6fkjp_	 Alignment		99.9	11	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
7	c6b8ho_	 Alignment		99.9	21	PDB header: membrane protein Chain: O: PDB Molecule: atp synthase subunit 5, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
8	c2wssS_	 Alignment		99.9	22	PDB header: hydrolase Chain: S: PDB Molecule: atp synthase subunit o, mitochondrial; PDBTitle: the structure of the membrane extrinsic region of bovine atp synthase
9	c5lqzU_	 Alignment		99.9	17	PDB header: hydrolase Chain: U: PDB Molecule: atp synthase oscp subunit; PDBTitle: structure of f-atpase from pichia angusta, state1
10	c6b8hb_	 Alignment		99.9	13	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: mosaic model of yeast mitochondrial atp synthase monomer
11	c5dn6H_	 Alignment		99.8	17	PDB header: hydrolase Chain: H: PDB Molecule: atp synthase subunit delta; PDBTitle: atp synthase from paracoccus denitrificans

12	c2jmxA	Alignment		99.7	23	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase o subunit, mitochondrial; PDBTitle: oscp-nt (1-120) in complex with n-terminal (1-25) alpha2 subunit from f1-atpase
13	c6rdvP	Alignment		99.7	22	PDB header: proton transport Chain: P: PDB Molecule: mitochondrial atp synthase subunit oscp; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 focussed refinement of f1 head and rotor
14	d1abva	Alignment		99.7	13	Fold: ATPD N-terminal domain-like Superfamily: N-terminal domain of the delta subunit of the F1F0-ATP synthase Family: N-terminal domain of the delta subunit of the F1F0-ATP synthase
15	c2a7uB	Alignment		99.7	13	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase delta chain; PDBTitle: nmr solution structure of the e.coli f-atpase delta subunit n-terminal2 domain in complex with alpha subunit n-terminal 22 residues
16	c6j5ib	Alignment		99.5	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
17	c5lqvV	Alignment		98.5	18	PDB header: hydrolase Chain: V: PDB Molecule: atp synthase subunit b; PDBTitle: structure of f-atpase from pichia angusta, in state2
18	c5arhT	Alignment		98.5	11	PDB header: hydrolase Chain: T: PDB Molecule: atp synthase f(0) complex subunit b1, mitochondrial; PDBTitle: bovine mitochondrial atp synthase state 2a
19	d1l2pa	Alignment		98.4	27	Fold: Single transmembrane helix Superfamily: F1F0 ATP synthase subunit B, membrane domain Family: F1F0 ATP synthase subunit B, membrane domain
20	c4dt0A	Alignment		97.6	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
21	c3k5bE	Alignment	not modelled	97.5	19	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
22	c1b9uA	Alignment	not modelled	97.0	21	PDB header: hydrolase Chain: A: PDB Molecule: protein (atp synthase); PDBTitle: membrane domain of the subunit b of the e.coli atp synthase
23	c4dl0J	Alignment	not modelled	97.0	7	PDB header: hydrolase Chain: J: PDB Molecule: v-type proton atpase subunit e; PDBTitle: crystal structure of the heterotrimeric egchead peripheral stalk2 complex of the yeast vacuolar atpase
24	c2khkA	Alignment	not modelled	95.1	34	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
25	c5b0oG	Alignment	not modelled	94.9	8	PDB header: hydrolase/motor protein Chain: G: PDB Molecule: flagellar assembly protein flih; PDBTitle: structure of the flih-flii complex
26	d2dm9a1	Alignment	not modelled	93.6	15	Fold: FwdE/GAPDH domain-like Superfamily: V-type ATPase subunit E-like Family: V-type ATPase subunit E
27	c2dm9B	Alignment	not modelled	93.6	15	PDB header: hydrolase Chain: B: PDB Molecule: v-type atp synthase subunit e; PDBTitle: crystal structure of ph1978 from pyrococcus horikoshii ot3
28	c5b0oH	Alignment	not modelled	92.7	10	PDB header: hydrolase/motor protein Chain: H: PDB Molecule: flagellar assembly protein flih; PDBTitle: structure of the flih-flii complex
						PDB header: membrane protein

29	c2oarA	Alignment	not modelled	92.4	13	Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
30	c3uz0A	Alignment	not modelled	91.4	16	PDB header: transport protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: crystal structure of spoiiiah and spoiiq complex
31	c6b2zb	Alignment	not modelled	91.2	20	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
32	c3vkqA	Alignment	not modelled	90.6	16	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
33	c3lg8B	Alignment	not modelled	90.2	13	PDB header: hydrolase Chain: B: PDB Molecule: a-type atp synthase subunit e; PDBTitle: crystal structure of the c-terminal part of subunit e (e101-206) from <i>Methanocaldococcus jannaschii</i> of a1ao atp synthase
34	d2oara1	Alignment	not modelled	89.9	16	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
35	c1y4cA	Alignment	not modelled	88.6	18	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp
36	c2k88A	Alignment	not modelled	88.0	28	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 <i>Saccharomyces cerevisiae</i> v1vo atpase
37	c3tufA	Alignment	not modelled	87.5	16	PDB header: signaling protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: structure of the spoiiq-spoiiiah pore forming complex.
38	c2zv40	Alignment	not modelled	86.4	10	PDB header: structural protein Chain: O: PDB Molecule: major vault protein; PDBTitle: the structure of rat liver vault at 3.5 angstrom resolution
39	c4y7jE	Alignment	not modelled	84.8	30	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
40	c3k5bB	Alignment	not modelled	84.1	15	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
41	c4dl0G	Alignment	not modelled	83.3	19	PDB header: hydrolase Chain: G: PDB Molecule: v-type proton atpase subunit g; PDBTitle: crystal structure of the heterotrimeric eghead peripheral stalk2 complex of the yeast vacuolar atpase
42	c6fnE	Alignment	not modelled	83.3	13	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
43	c3hzqA	Alignment	not modelled	82.9	22	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: structure of a tetrameric mscl in an expanded intermediate state
44	c4cg4D	Alignment	not modelled	71.9	7	PDB header: actin-binding protein Chain: D: PDB Molecule: pyrin; PDBTitle: crystal structure of the chs-b30.2 domains of trim20
45	c3wo1B	Alignment	not modelled	65.5	9	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl aminopeptidase bii; PDBTitle: crystal structure of the dap bii dipeptide complex i
46	c2kk7A	Alignment	not modelled	63.8	34	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 <i>Methanocaldococcus jannaschii</i>
47	c2rddB	Alignment	not modelled	63.6	6	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.
48	c5jxfA	Alignment	not modelled	63.5	12	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
49	c2ayaA	Alignment	not modelled	62.0	25	PDB header: transferase Chain: A: PDB Molecule: dna polymerase iii subunit tau; PDBTitle: solution structure of the c-terminal 14 kda domain of the2 tau subunit from <i>Escherichia coli</i> dna polymerase iii
50	c4nqjB	Alignment	not modelled	57.3	8	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase trim69; PDBTitle: structure of coiled-coil domain
51	c3ojaB	Alignment	not modelled	57.2	11	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
52	c6qajB	Alignment	not modelled	51.7	12	PDB header: nuclear protein Chain: B: PDB Molecule: endolysin,transcription intermediary factor 1-beta; PDBTitle: structure of the tripartite motif of kap1/trim28
53	c4xtbA	Alignment	not modelled	44.9	23	PDB header: transport protein Chain: A: PDB Molecule: calcium uniporter protein, mitochondrial; PDBTitle: crystal structure of the n-terminal domain of the human mitochondrial2 calcium uniporter
54	c1ncrD	Alignment	not modelled	42.4	12	PDB header: oxidoreductase Chain: D: PDB Molecule: ubiquinol cytochrome c oxidoreductase;

54	c1qclD	Alignment	not modelled	42.4	12	PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only PDB header: electron transport, oxidoreductase Chain: A: PDB Molecule: monothiol glutaredoxin-s14, chloroplastic; PDBTitle: crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
55	c3ipzA	Alignment	not modelled	40.9	16	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
56	c3vkhA	Alignment	not modelled	39.4	12	Fold: TerB-like Superfamily: TerB-like Family: COG3793-like
57	d2ou3a1	Alignment	not modelled	39.0	14	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
58	c2lseA	Alignment	not modelled	32.4	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)
59	c4kqtA	Alignment	not modelled	30.6	11	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
60	c2k6iA	Alignment	not modelled	30.3	31	PDB header: hydrolase Chain: T: PDB Molecule: atp synthase subunit b, mitochondrial; PDBTitle: model of the yeast f1fo-atp synthase dimer based on subtomogram2 average
61	c4b2qt	Alignment	not modelled	30.1	10	PDB header: chaperone Chain: C: PDB Molecule: histone-like protein hlp-1; PDBTitle: crystal structure of skp
62	c1u2mC	Alignment	not modelled	29.0	8	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
63	c6b2zL	Alignment	not modelled	28.1	21	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
64	c6b2zA	Alignment	not modelled	28.1	21	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
65	d2al1a2	Alignment	not modelled	27.8	42	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
66	d2uubc1	Alignment	not modelled	27.2	19	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
67	c1ei3E	Alignment	not modelled	26.4	11	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: Nip7p homolog, N-terminal domain
68	d1sqwa2	Alignment	not modelled	24.8	13	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
69	d2np5a2	Alignment	not modelled	24.2	15	PDB header: oxidoreductase Chain: I: PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
70	c3rfrI	Alignment	not modelled	24.1	12	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
71	c3ghgl	Alignment	not modelled	24.0	5	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: solution structure of integrin b2 monomer tranmembrane domain in2 bicelle
72	c5zazA	Alignment	not modelled	23.9	15	PDB header: metal transport Chain: A: PDB Molecule: piezo-type mechanosensitive ion channel component 1; PDBTitle: cryo-em study of a channel
73	c3jacA	Alignment	not modelled	22.9	20	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis sensory transducer; PDBTitle: periplasmic sensor domain of chemotaxis protein, adeh_3718
74	c4k08A	Alignment	not modelled	22.7	17	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
75	c3lvgD	Alignment	not modelled	22.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of an osmc-like hydroperoxide resistance protein2 (jann_2040) from jannaschia sp. ccs1 at 1.70 a resolution
76	c3cjeA	Alignment	not modelled	21.9	22	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
77	c4pd3B	Alignment	not modelled	21.7	8	PDB header: transferase Chain: A: PDB Molecule: hexokinase-1; PDBTitle: arabidopsis hexokinase 1 (athxk1) mutant s177a structure in glucose-2 bound form
78	c4qs9A	Alignment	not modelled	21.2	12	PDB header: electron transport

79	c3gx8A_	Alignment	not modelled	20.8	25	Chain: A; PDB Molecule: monothiol glutaredoxin-5, mitochondrial; PDBTitle: structural and biochemical characterization of yeast2 monothiol glutaredoxin grx5
80	c1deqF_	Alignment	not modelled	20.7	10	PDB header: blood clotting Chain: F; PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
81	c3vkhB_	Alignment	not modelled	20.1	13	PDB header: motor protein Chain: B; PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
82	c5mlc9_	Alignment	not modelled	19.3	13	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
83	c5xauD_	Alignment	not modelled	18.5	18	PDB header: cell adhesion Chain: D; PDB Molecule: laminin subunit alpha-5; PDBTitle: crystal structure of integrin binding fragment of laminin-511
84	d1bg3a2	Alignment	not modelled	18.2	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
85	c3jacC_	Alignment	not modelled	18.2	20	PDB header: metal transport Chain: C; PDB Molecule: piezo-type mechanosensitive ion channel component 1; PDBTitle: cryo-em study of a channel
86	c2qzvB_	Alignment	not modelled	17.5	10	PDB header: structural protein Chain: B; PDB Molecule: major vault protein; PDBTitle: draft crystal structure of the vault shell at 9 angstroms2 resolution
87	c2jacA_	Alignment	not modelled	17.3	10	PDB header: electron transport Chain: A; PDB Molecule: glutaredoxin-1; PDBTitle: glutaredoxin grx1p c30s mutant from yeast
88	c3spuB_	Alignment	not modelled	16.8	22	PDB header: hydrolase Chain: B; PDB Molecule: beta-lactamase ndm-1; PDBTitle: apo ndm-1 crystal structure
89	c3ghgK_	Alignment	not modelled	16.7	8	PDB header: blood clotting Chain: K; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
90	c3n5iC_	Alignment	not modelled	16.6	11	PDB header: hydrolase Chain: C; PDB Molecule: beta-peptidyl aminopeptidase; PDBTitle: crystal structure of the precursor (s250a mutant) of the n-terminal2 beta-aminopeptidase bapa
91	c5ew5C_	Alignment	not modelled	16.5	9	PDB header: hydrolase Chain: C; PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
92	c3c1sA_	Alignment	not modelled	15.9	10	PDB header: oxidoreductase Chain: A; PDB Molecule: glutaredoxin-1; PDBTitle: crystal structure of grx1 in glutathionylated form
93	c2kz9A_	Alignment	not modelled	15.8	8	PDB header: proton transport Chain: A; PDB Molecule: v-type proton atpase subunit e; PDBTitle: structure of e1-69 of yeast v-atpase
94	d1ts9a_	Alignment	not modelled	15.5	24	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: RNase P subunit p29-like
95	c2rmzA_	Alignment	not modelled	15.4	13	PDB header: cell adhesion Chain: A; PDB Molecule: integrin beta-3; PDBTitle: bicelle-embedded integrin beta3 transmembrane segment
96	d2akza2	Alignment	not modelled	15.4	23	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
97	c5nugB_	Alignment	not modelled	15.2	14	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
98	c5t77A_	Alignment	not modelled	15.1	17	PDB header: transport protein Chain: A; PDB Molecule: putative lipid ii flippase murj; PDBTitle: crystal structure of the mop flippase murj
99	c2k1aA_	Alignment	not modelled	15.1	20	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iib; PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment