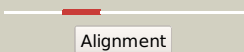
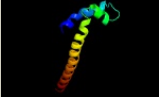
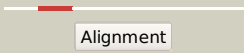

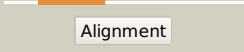
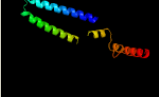

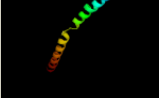


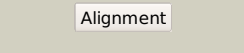

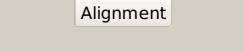


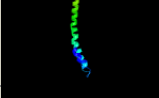
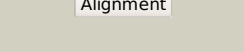

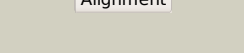
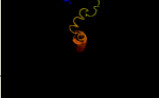
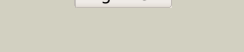



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3604c_(-)_4046482_4047675
Date	Fri Aug 9 18:20:28 BST 2019
Unique Job ID	7d8a2126649bb2e7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pjwH_	 Alignment		96.2	9	PDB header: endocytosis/exocytosis Chain: H; PDB Molecule: uncharacterized protein yhI002w; PDBTitle: the vps27/hse1 complex is a gat domain-based scaffold for ubiquitin-2 dependent sorting
2	d2r6gf1	 Alignment		91.3	13	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
3	c6dt0D_	 Alignment		89.9	19	PDB header: transport protein Chain: D; PDB Molecule: mitochondrial calcium uniporter; PDBTitle: cryo-em structure of a mitochondrial calcium uniporter
4	c5d3aA_	 Alignment		87.4	17	PDB header: motor protein Chain: A; PDB Molecule: kinesin-like protein kif21a; PDBTitle: kif21a regulatory coiled coil
5	c6iedA_	 Alignment		86.5	11	PDB header: membrane protein Chain: A; PDB Molecule: heme a synthase; PDBTitle: crystal structure of heme a synthase from bacillus subtilis
6	c6iu3A_	 Alignment		84.3	9	PDB header: metal transport Chain: A; PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
7	c4clvB_	 Alignment		76.2	16	PDB header: metal binding protein Chain: B; PDB Molecule: nickel-cobalt-cadmium resistance protein nccx; PDBTitle: crystal structure of dodecylphosphocholine-solubilized nccx2 from cupriavidus metallidurans 31a
8	c5u0pG_	 Alignment		72.2	22	PDB header: transcription Chain: G; PDB Molecule: mediator complex subunit 7; PDBTitle: cryo-em structure of the transcriptional mediator
9	c6mjpG_	 Alignment		71.9	15	PDB header: lipid transport Chain: G; PDB Molecule: lps export abc transporter permease lptg; PDBTitle: lptb(e163q)fgc from vibrio cholerae
10	c6d80A_	 Alignment		70.4	17	PDB header: transport protein Chain: A; PDB Molecule: mitochondrial calcium uniporter; PDBTitle: cryo-em structure of the mitochondrial calcium uniporter from n.2 fischeri bound to saposin
11	c3tnuA_	 Alignment		68.4	17	PDB header: cytosolic protein Chain: A; PDB Molecule: keratin, type i cytoskeletal 14; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)

12	c3m9bK_	Alignment		67.1	34	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
13	c4akkA_	Alignment		63.9	24	PDB header: transcription Chain: A: PDB Molecule: nitrate regulatory protein; PDBTitle: structure of the nasr transcription antiterminator
14	c5nf8A_	Alignment		62.3	16	PDB header: membrane protein Chain: A: PDB Molecule: respiratory supercomplex factor 1, mitochondrial; PDBTitle: solution structure of detergent-solubilized rcf1, a yeast2 mitochondrial inner membrane protein involved in respiratory complex3 iii/iv supercomplex formation
15	c4o9uB_	Alignment		61.3	29	PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
16	c3k8vB_	Alignment		60.2	17	PDB header: structural protein Chain: B: PDB Molecule: flagellin homolog; PDBTitle: crysatl structure of a bacterial cell-surface flagellin n20c20
17	c6c5wA_	Alignment		59.2	18	PDB header: membrane protein Chain: A: PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the mitochondrial calcium uniporter
18	c5kw2A_	Alignment		59.2	30	PDB header: fatty acid binding protein/hydrolase Chain: A: PDB Molecule: free fatty acid receptor 1,lysozyme,free fatty acid PDBTitle: the extra-helical binding site of gpr40 and the structural basis for2 allosteric agonism and incretin stimulation
19	d2pila_	Alignment		58.6	31	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
20	c6hu9U_	Alignment		58.1	27	PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
21	c5x5yG_	Alignment	not modelled	58.0	10	PDB header: membrane protein Chain: G: PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
22	c6mquC_	Alignment	not modelled	57.4	28	PDB header: de novo protein Chain: C: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
23	c3sokB_	Alignment	not modelled	57.3	25	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
24	c6mquA_	Alignment	not modelled	57.1	28	PDB header: de novo protein Chain: A: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
25	c6mquH_	Alignment	not modelled	57.1	28	PDB header: de novo protein Chain: H: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
26	c6mquG_	Alignment	not modelled	57.0	28	PDB header: de novo protein Chain: G: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
27	c6mquB_	Alignment	not modelled	57.0	28	PDB header: de novo protein Chain: B: PDB Molecule: pl5, designed tm pentamer; PDBTitle: pl5, synthetic transmembrane domain variant of human phospholamban
28	c4mt1A_	Alignment	not modelled	56.9	8	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
29	c6mquI_	Alignment	not modelled	56.1	28	PDB header: de novo protein Chain: I: PDB Molecule: pl5, designed tm pentamer;

29	c6mquI_	Alignment	not modelled	56.1	28	PDBTitle: p15, synthetic transmembrane domain variant of human phospholamban PDB header: de novo protein
30	c6mquF_	Alignment	not modelled	56.1	28	Chain: F: PDB Molecule: p15, designed tm pentamer; PDBTitle: p15, synthetic transmembrane domain variant of human phospholamban
31	c6mquD_	Alignment	not modelled	56.1	28	PDB header: de novo protein Chain: D: PDB Molecule: p15, designed tm pentamer; PDBTitle: p15, synthetic transmembrane domain variant of human phospholamban
32	c5wosA_	Alignment	not modelled	55.7	11	PDB header: viral protein Chain: A: PDB Molecule: cnpv058 bcl-2 like protein; PDBTitle: structural and functional insights into canarypox virus cnp0582 regulation of apoptosis
33	c4dveA_	Alignment	not modelled	55.1	8	PDB header: transport protein Chain: A: PDB Molecule: biotin transporter bioy; PDBTitle: crystal structure at 2.1 a of the s-component for biotin from an ecf-2 type abc transporter
34	c3k8wA_	Alignment	not modelled	55.0	17	PDB header: structural protein Chain: A: PDB Molecule: flagellin homolog; PDBTitle: crysatl structure of a bacterial cell-surface flagellin n20c45
35	c4uicA_	Alignment	not modelled	54.7	20	PDB header: sugar binding protein Chain: A: PDB Molecule: surface layer protein; PDBTitle: crystal structure of the s-layer protein rsbsc(31-844)
36	c6mquE_	Alignment	not modelled	54.3	28	PDB header: de novo protein Chain: E: PDB Molecule: p15, designed tm pentamer; PDBTitle: p15, synthetic transmembrane domain variant of human phospholamban
37	c6mquJ_	Alignment	not modelled	54.3	28	PDB header: de novo protein Chain: J: PDB Molecule: p15, designed tm pentamer; PDBTitle: p15, synthetic transmembrane domain variant of human phospholamban
38	c3u5eh_	Alignment	not modelled	54.0	30	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l9-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
39	c2a3dA_	Alignment	not modelled	52.5	28	PDB header: three-helix bundle Chain: A: PDB Molecule: protein (de novo three-helix bundle); PDBTitle: solution structure of a de novo designed single chain three-2 helix bundle (a3d)
40	c4o9tH_	Alignment	not modelled	52.4	23	PDB header: membrane protein Chain: H: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
41	c6j5ib_	Alignment	not modelled	51.7	15	PDB header: membrane protein Chain: B: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: cryo-em structure of the mammalian dp-state atp synthase
42	c3wajA_	Alignment	not modelled	50.6	11	PDB header: transferase Chain: A: PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
43	c4k0eA_	Alignment	not modelled	50.4	9	PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
44	c6o58C_	Alignment	not modelled	50.0	16	PDB header: transport protein Chain: C: PDB Molecule: calcium uniporter protein, mitochondrial; PDBTitle: human mcv-emre complex, dimer of channel
45	c3tnuB_	Alignment	not modelled	49.2	18	PDB header: cytosolic protein Chain: B: PDB Molecule: keratin, type ii cytoskeletal 5; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
46	c5t4oJ_	Alignment	not modelled	49.0	15	PDB header: hydrolase Chain: J: PDB Molecule: atp synthase subunit b; PDBTitle: autoinhibited e. coli atp synthase state 1
47	c5ua4A_	Alignment	not modelled	47.7	10	PDB header: apoptosis Chain: A: PDB Molecule: 5-hl; PDBTitle: crystal structure of a179l:bid bh3 complex
48	c6o7ua_	Alignment	not modelled	47.1	10	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
49	c2kncB_	Alignment	not modelled	46.9	36	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaib-beta3 transmembrane-cytoplasmic2 heterocomplex
50	c4o7oB_	Alignment	not modelled	46.6	22	PDB header: transferase Chain: B: PDB Molecule: maltokinase; PDBTitle: crystal structure of mycobacterium tuberculosis maltose kinase mak
51	c1gk4A_	Alignment	not modelled	45.6	13	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 2b fragment (cys2)
52	c3j3bh_	Alignment	not modelled	44.9	25	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l9; PDBTitle: structure of the human 60s ribosomal proteins
53	c3j39h_	Alignment	not modelled	44.8	25	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l9; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
54	c2lw9A_	Alignment	not modelled	44.6	22	PDB header: motor protein Chain: A: PDB Molecule: unconventionnal myosin-x; PDBTitle: nmr solution structure of myo10 anti-cc

55	c2w8aC	Alignment	not modelled	44.6	14	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
56	c5voxb	Alignment	not modelled	43.8	8	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
57	c5hzpA	Alignment	not modelled	43.5	37	PDB header: immune system Chain: A: PDB Molecule: m protein, serotype 49; PDBTitle: structure of human c4b-binding protein alpha chain ccp domains 1 and 22 in complex with the hypervariable region of group a streptococcus m493 protein.
58	c2jlnA	Alignment	not modelled	43.3	17	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
59	c1kqfB	Alignment	not modelled	43.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
60	c2ks1B	Alignment	not modelled	42.9	32	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
61	c5ideA	Alignment	not modelled	42.8	15	PDB header: signaling protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: cryo-em structure of glua2/3 ampa receptor heterotetramer (model i)
62	c3kg2A	Alignment	not modelled	41.5	6	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: glutamate receptor 2; PDBTitle: ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
63	c3kl4B	Alignment	not modelled	41.5	29	PDB header: hydrolase Chain: B: PDB Molecule: signal peptide of yeast dipeptidyl aminopeptidase b; PDBTitle: recognition of a signal peptide by the signal recognition particle
64	c5tzipA	Alignment	not modelled	41.3	18	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein fpv039; PDBTitle: crystal structure of fpv039:bik bh3 complex
65	c6mjpF	Alignment	not modelled	40.9	24	PDB header: lipid transport Chain: F: PDB Molecule: fig000988: predicted permease; PDBTitle: lptb(e163q)fgc from vibrio cholerae
66	c5x5yF	Alignment	not modelled	40.3	22	PDB header: membrane protein Chain: F: PDB Molecule: uncharacterized protein; PDBTitle: a membrane protein complex
67	c3lrcC	Alignment	not modelled	39.6	9	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
68	c4wd7A	Alignment	not modelled	39.0	15	PDB header: membrane protein Chain: A: PDB Molecule: bestrophin domain protein; PDBTitle: crystal structure of a bacterial bestrophin homolog from klebsiella2 pneumoniae by zn-sad phasing
69	c3r4hD	Alignment	not modelled	38.5	42	PDB header: de novo protein Chain: D: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
70	c2uuiA	Alignment	not modelled	38.5	23	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
71	c6f0kA	Alignment	not modelled	38.1	13	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
72	c2yevB	Alignment	not modelled	37.9	16	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
73	c6owsB	Alignment	not modelled	37.8	17	PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
74	c3r4aA	Alignment	not modelled	37.5	42	PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix cc-tet; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet
75	c5v8kA	Alignment	not modelled	37.0	27	PDB header: photosynthesis Chain: A: PDB Molecule: p800 reaction center core protein; PDBTitle: homodimeric reaction center of h. modesticaldum
76	c6cfwA	Alignment	not modelled	36.9	11	PDB header: membrane protein Chain: A: PDB Molecule: monovalent cation/h+ antiporter subunit e; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
77	c3r4aB	Alignment	not modelled	36.9	42	PDB header: de novo protein Chain: B: PDB Molecule: coiled coil helix cc-tet; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet
78	c3j9tZ	Alignment	not modelled	36.7	15	PDB header: hydrolase Chain: Z: PDB Molecule: v-type proton atpase subunit c; PDBTitle: yeast v-atpase state 1
79	c3r4hB	Alignment	not modelled	36.6	42	PDB header: de novo protein Chain: B: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
80	c3r4hC	Alignment	not modelled	36.6	42	PDB header: de novo protein Chain: C: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22

81	c3r4hA_	Alignment	not modelled	36.4	42	PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
82	c5lq3F_	Alignment	not modelled	36.4	9	PDB header: transport protein Chain: F: PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
83	c2mc7A_	Alignment	not modelled	36.3	53	PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgrtr
84	c5lc5c_	Alignment	not modelled	36.2	25	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, PDBTitle: structure of mammalian respiratory complex i, class2
85	c5wdaL_	Alignment	not modelled	36.1	15	PDB header: protein transport Chain: L: PDB Molecule: general secretion pathway protein g; PDBTitle: structure of the pulg pseudopilus
86	c1s1iX_	Alignment	not modelled	36.1	36	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l35; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
87	c4a1eU_	Alignment	not modelled	35.9	27	PDB header: ribosome Chain: U: PDB Molecule: rpl35; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
88	c3iynQ_	Alignment	not modelled	35.2	23	PDB header: virus Chain: Q: PDB Molecule: hexon-associated protein; PDBTitle: 3.6-angstrom cryoem structure of human adenovirus type 5
89	c4p6vC_	Alignment	not modelled	35.2	14	PDB header: oxidoreductase Chain: C: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit c; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
90	c3rkoM_	Alignment	not modelled	35.1	18	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit m; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
91	c4zryA_	Alignment	not modelled	35.1	15	PDB header: protein fibril Chain: A: PDB Molecule: keratin, type i cytoskeletal 10; PDBTitle: crystal structure of the heterocomplex between coil 2b domains of2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
92	c2lw1A_	Alignment	not modelled	34.8	19	PDB header: dna binding protein Chain: A: PDB Molecule: abc transporter atp-binding protein uup; PDBTitle: the c-terminal domain of the uup protein is a dna-binding coiled coil2 motif
93	c4hg6A_	Alignment	not modelled	34.2	11	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
94	c6dnfA_	Alignment	not modelled	34.0	18	PDB header: membrane protein Chain: A: PDB Molecule: mitochondrial calcium uniporter mcu; PDBTitle: cryo-em structure of the mitochondrial calcium uniporter mcu from the2 fungus cyphellophora europaea
95	c4hg6B_	Alignment	not modelled	33.9	24	PDB header: transferase Chain: B: PDB Molecule: cellulose synthase subunit b; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
96	c6gcs6_	Alignment	not modelled	33.9	22	PDB header: oxidoreductase Chain: 6: PDB Molecule: nd6 subunit (nu6m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
97	c5u5aA_	Alignment	not modelled	33.5	50	PDB header: de novo protein Chain: A: PDB Molecule: designed dimeric coiled coil peptide with two terpyridine PDBTitle: coiled coil peptide metal coordination framework: dimer fold
98	c5u59A_	Alignment	not modelled	33.5	50	PDB header: de novo protein Chain: A: PDB Molecule: designed dimeric coiled coil peptide with two terpyridine PDBTitle: coiled coil peptide metal coordination framework: dimer fold grown2 with citrate
99	c2wt7B_	Alignment	not modelled	33.2	19	PDB header: transcription Chain: B: PDB Molecule: transcription factor mafb; PDBTitle: crystal structure of the bzip heterodimeric complex mafb:cfos bound to2 dna
100	c3hd7A_	Alignment	not modelled	32.9	8	PDB header: exocytosis Chain: A: PDB Molecule: vesicle-associated membrane protein 2; PDBTitle: helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
101	c4pe5A_	Alignment	not modelled	32.6	20	PDB header: transport protein Chain: A: PDB Molecule: glutamate receptor ionotropic, nmda 1; PDBTitle: crystal structure of glun1a/glun2b nmda receptor ion channel
102	c1xrdA_	Alignment	not modelled	32.1	35	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, alpha chain; PDBTitle: light-harvesting complex 1 alfa subunit from wild-type2 rhodospirillum rubrum
103	d1xrd1	Alignment	not modelled	32.1	35	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
104	c3movB_	Alignment	not modelled	32.0	20	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of human lamin-b1 coil 2 segment

105	c4rhpB_	Alignment	not modelled	31.9	10	PDB header: biosynthetic protein Chain: B: PDB Molecule: ubiquinone biosynthesis protein coq9, mitochondrial; PDBTitle: crystal structure of human coq9 in complex with a phospholipid,2 northeast structural genomics consortium target hr5043
106	c4cfiA_	Alignment	not modelled	31.3	19	PDB header: structural protein Chain: A: PDB Molecule: flagellin; PDBTitle: 3d structure of flag from burkholderia pseudomallei
107	c6co7C_	Alignment	not modelled	31.3	16	PDB header: membrane protein Chain: C: PDB Molecule: predicted protein; PDBTitle: structure of the nvtprm2 channel in complex with ca2+
108	c6fkip_	Alignment	not modelled	31.2	11	PDB header: membrane protein Chain: P: PDB Molecule: atp synthase subunit c, chloroplastic; PDBTitle: chloroplast f1fo conformation 3
109	c2ifmA_	Alignment	not modelled	31.2	24	PDB header: virus Chain: A: PDB Molecule: pf1 filamentous bacteriophage; PDBTitle: pf1 filamentous bacteriophage: refinement of a molecular2 model by simulated annealing using 3.3 angstroms3 resolution x-ray fibre diffraction data
110	c1ql1A_	Alignment	not modelled	31.2	24	PDB header: virus Chain: A: PDB Molecule: pf1 bacteriophage coat protein b; PDBTitle: inovirus (filamentous bacteriophage) strain pf1 major coat2 protein assembly
111	c5garX_	Alignment	not modelled	31.2	14	PDB header: hydrolase Chain: X: PDB Molecule: vacuolar type atp synthase subunit; PDBTitle: thermus thermophilus v/a-atpase, conformation 1
112	c3r4hE_	Alignment	not modelled	31.2	47	PDB header: de novo protein Chain: E: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
113	c6csxA_	Alignment	not modelled	31.1	8	PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
114	c3jcuJ_	Alignment	not modelled	31.1	5	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
115	c4gx2B_	Alignment	not modelled	30.9	12	PDB header: transport protein Chain: B: PDB Molecule: trka domain protein; PDBTitle: gsuk channel bound to nad
116	c3j21W_	Alignment	not modelled	30.6	23	PDB header: ribosome Chain: W: PDB Molecule: 50s ribosomal protein l29p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
117	c4e17B_	Alignment	not modelled	30.6	25	PDB header: cell adhesion Chain: B: PDB Molecule: catenin alpha-1; PDBTitle: alpha-e-catenin is an autoinhibited molecule that co-activates2 vinculin
118	c6btmA_	Alignment	not modelled	30.4	24	PDB header: membrane protein Chain: A: PDB Molecule: alternative complex iii subunit a; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
119	c3r4hF_	Alignment	not modelled	29.8	47	PDB header: de novo protein Chain: F: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
120	c6gv9K_	Alignment	not modelled	29.5	13	PDB header: protein fibril Chain: K: PDB Molecule: prepilin peptidase-dependent protein d; PDBTitle: structure of the type iv pilus from enterohemorrhagic escherichia coli2 (ehc)