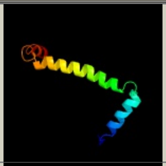
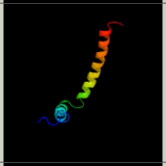
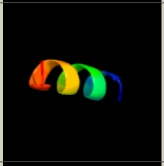
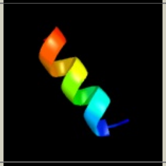
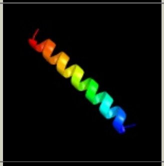
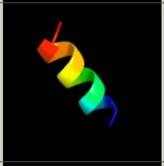
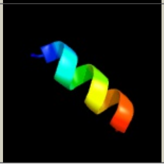
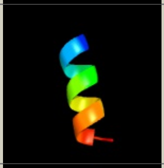
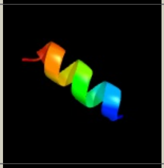
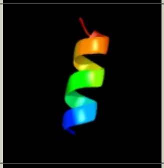
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2094c_(tatA)_2353054_2353305
Date	Mon Aug 5 13:25:21 BST 2019
Unique Job ID	65ac4ee844921925

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2mi2A_	Alignment		99.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatb; **PDBTitle:** solution structure of the e. coli tatb protein in dpc micelles
2	c2l16A_	Alignment		99.8	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatad; **PDBTitle:** solution structure of bacillus subtilits tatad protein in dpc micelles
3	c2lzsE_	Alignment		99.7	38	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**sec-independent protein translocase protein tata; **PDBTitle:** tata oligomer
4	c4pj0l_	Alignment		22.1	8	**PDB header:**oxidoreductase, electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
5	c4pj0L_	Alignment		22.1	8	**PDB header:**oxidoreductase, electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
6	c3a0hi_	Alignment		22.0	23	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**photosystem ii reaction center protein i; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
7	d2axti1	Alignment		22.0	23	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
8	c6dlmA_	Alignment		22.0	35	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**dhd127_a; **PDBTitle:** dhd127
9	c4il6l_	Alignment		21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** structure of sr-substituted photosystem ii
10	c1s5ll_	Alignment		21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
11	c3bz1L_	Alignment		21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer

12	c4il6L_	Alignment		21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** structure of sr-substituted photosystem ii
13	c3arcL_	Alignment		21.7	8	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
14	d2axtl1	Alignment		21.7	8	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
15	c3kziL_	Alignment		21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
16	c5e7cL_	Alignment		21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** macromolecular diffractive imaging using imperfect crystals - bragg2 data
17	c5e7cl_	Alignment		21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** macromolecular diffractive imaging using imperfect crystals - bragg2 data
18	c3a0hL_	Alignment		21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
19	c4ub8L_	Alignment		21.7	8	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
20	c4tnjL_	Alignment		21.7	8	**PDB header:**electron transport,photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
21	c3prqL_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
22	c4ixqL_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt fs x-ray diffraction of photosystem ii, dark state
23	c4tnjl_	Alignment	not modelled	21.7	8	**PDB header:**electron transport,photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
24	c3prrL_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
25	c2axtl_	Alignment	not modelled	21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
26	c3wu2l_	Alignment	not modelled	21.7	8	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure analysis of photosystem ii complex
27	c4ixrL_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt fs x-ray diffraction of photosystem ii, first illuminated state
28	c1s5lL_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center

29	c3a0bL_	Alignment	not modelled	21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
30	c3wu2L_	Alignment	not modelled	21.7	8	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure analysis of photosystem ii complex
31	c4ixql_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt fs x-ray diffraction of photosystem ii, dark state
32	c4rvyL_	Alignment	not modelled	21.7	8	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
33	c3bz2L_	Alignment	not modelled	21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer
34	c4ixrl_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt fs x-ray diffraction of photosystem ii, first illuminated state
35	c4rvyl_	Alignment	not modelled	21.7	8	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
36	c4fbyd_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**photosystem ii d2 protein; **PDBTitle:** fs x-ray diffraction of photosystem ii
37	c2axtL_	Alignment	not modelled	21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
38	c4tnkL_	Alignment	not modelled	21.7	8	**PDB header:**electron transport,photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
39	c3a0hl_	Alignment	not modelled	21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
40	c4ub6l_	Alignment	not modelled	21.7	8	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
41	c4fbyL_	Alignment	not modelled	21.7	8	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** fs x-ray diffraction of photosystem ii
42	c4tnhL_	Alignment	not modelled	21.7	8	**PDB header:**electron transport,photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
43	c4ub8l_	Alignment	not modelled	21.7	8	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
44	c4ub6L_	Alignment	not modelled	21.7	8	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
45	c4tnhl_	Alignment	not modelled	21.7	8	**PDB header:**electron transport,photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
46	c4tnil_	Alignment	not modelled	21.7	8	**PDB header:**electron transport,photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
47	c3a0bl_	Alignment	not modelled	21.7	8	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
48	c4tnkl_	Alignment	not modelled	21.7	8	**PDB header:**electron transport,photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
49	c4tniL_	Alignment	not modelled	21.7	8	**PDB header:**electron transport,photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
50	c3jcuI_	Alignment	not modelled	21.5	23	**PDB header:**membrane protein **Chain:** I: **PDB Molecule:**protein photosystem ii reaction center protein i; **PDBTitle:** cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
51	c2o0cB_	Alignment	not modelled	20.9	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**alr2278 protein; **PDBTitle:** crystal structure of the h-nox domain from nostoc sp. pcc 71202 complexed to no
52	c3arcl_	Alignment	not modelled	20.3	8	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
53	c2kdcC_	Alignment	not modelled	16.3	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
54	c3jcul_	Alignment	not modelled	13.9	15	**PDB header:**membrane protein **Chain:** L: **PDB Molecule:**protein photosystem ii reaction center protein l; **PDBTitle:** cryo-em structure of spinach psii-lhcii supercomplex at

						3.2 angstrom2 resolution
55	d2ffha2	Alignment	not modelled	12.0	10	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
56	c1by0A_	Alignment	not modelled	11.9	37	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
57	d1hq1a_	Alignment	not modelled	11.6	7	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
58	c4ue4C_	Alignment	not modelled	11.5	13	**PDB header:**translation **Chain:** C: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** structural basis for targeting and elongation arrest of bacillus2 signal recognition particle
59	d2cqqa1	Alignment	not modelled	11.3	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
60	c6fkip_	Alignment	not modelled	10.7	16	**PDB header:**membrane protein **Chain:** P: **PDB Molecule:**atp synthase subunit c, chloroplastic; **PDBTitle:** chloroplast f1fo conformation 3
61	d1dula_	Alignment	not modelled	10.7	7	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
62	c1a92B_	Alignment	not modelled	10.2	30	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
63	d2f2ea1	Alignment	not modelled	9.8	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**HxlR-like
64	c3a0hJ_	Alignment	not modelled	9.7	21	**PDB header:**electron transport **Chain:** J: **PDB Molecule:**photosystem ii reaction center protein j; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
65	d2axtj1	Alignment	not modelled	9.7	21	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein J, PsbJ **Family:**PsbJ-like
66	d1m56d_	Alignment	not modelled	9.0	24	**Fold:**Single transmembrane helix **Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV **Family:**Bacterial aa3 type cytochrome c oxidase subunit IV
67	c5ndaA_	Alignment	not modelled	8.0	21	**PDB header:**protein **Chain:** A: **PDB Molecule:**rsp-c33leu -recombinant pulmonary surfactant-associated **PDBTitle:** nmr structural characterisation of pharmaceutically relevant proteins2 obtained through a novel recombinant production: the case of the3 pulmonary surfactant polypeptide c analogue rsp-c33leu.
68	c5hs9A_	Alignment	not modelled	7.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator yodb; **PDBTitle:** crystal structure of the quinone-bound yodb from b. subtilis
69	c5xnmj_	Alignment	not modelled	7.0	8	**PDB header:**membrane protein **Chain:** J: **PDB Molecule:**photosystem ii reaction center protein j; **PDBTitle:** structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
70	c5ireD_	Alignment	not modelled	6.5	25	**PDB header:**virus **Chain:** D: **PDB Molecule:**m protein; **PDBTitle:** the cryo-em structure of zika virus
71	d1qzxa2	Alignment	not modelled	6.5	10	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
72	d1qb2a_	Alignment	not modelled	6.4	14	**Fold:**Signal peptide-binding domain **Superfamily:**Signal peptide-binding domain **Family:**Signal peptide-binding domain
73	c3jcuj_	Alignment	not modelled	6.3	21	**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
74	c5wdaL_	Alignment	not modelled	6.2	21	**PDB header:**protein transport **Chain:** L: **PDB Molecule:**general secretion pathway protein g; **PDBTitle:** structure of the pulg pseudopilus
75	c2jqeA_	Alignment	not modelled	6.2	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** soution structure of af54 m-domain
76	c5hk1A_	Alignment	not modelled	5.6	28	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sigma non-opioid intracellular receptor 1; **PDBTitle:** human sigma-1 receptor bound to pd144418
77	c6c4zD_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
78	c6c4yJ_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** J: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
79	c6c4zA_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
80	c6c4yM_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** M: **PDB Molecule:**cross-alpha amyloid-like structure

		Alignment				alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
81	c6c4zB_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
82	c6c4yB_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
83	c6c4yQ_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** Q: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
84	c6c4zQ_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** Q: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
85	c6c4zL_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** L: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
86	c6c4yD_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
87	c6c4zG_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** G: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
88	c6c4zC_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
89	c6c4yN_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** N: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
90	c6c4yR_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** R: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
91	c6c4yE_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
92	c6c4yH_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** H: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
93	c6c4yI_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** I: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
94	c6c4zI_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** I: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
95	c6c4yO_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** O: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
96	c6c4yF_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** F: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
97	c6c4zP_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** P: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution
98	c6c4yL_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** L: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg; **PDBTitle:** cross-alpha amyloid-like structure alphaamg
99	c6c4zK_	Alignment	not modelled	5.5	38	**PDB header:**de novo protein **Chain:** K: **PDB Molecule:**cross-alpha amyloid-like structure alphaamg - low **PDBTitle:** cross-alpha amyloid-like structure alphaamg - low resolution