
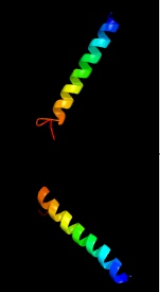

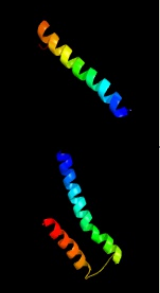
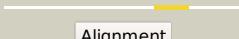
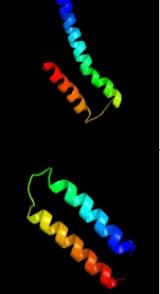
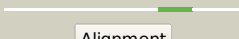
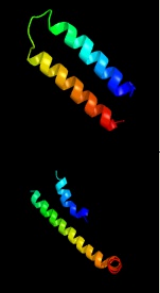
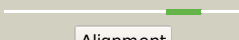
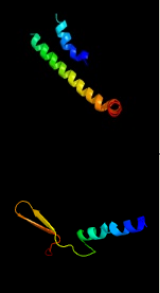
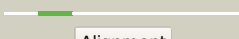
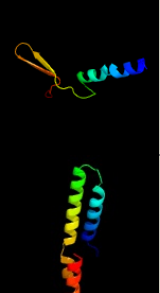

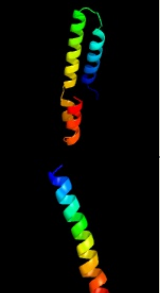

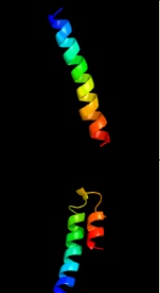

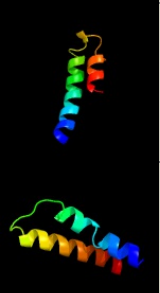

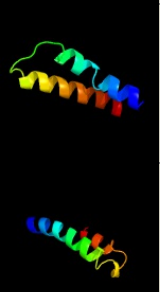

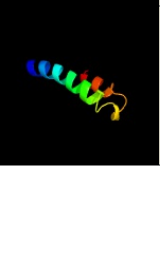

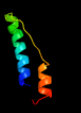




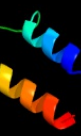




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0996 (-)_1112388_1113464
Date	Wed Jul 31 22:05:06 BST 2019
Unique Job ID	ca74ffe216ed40b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jwaA_	 Alignment		85.3	25	PDB header: transferase Chain: A; PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: erbB2 transmembrane segment dimer spatial structure
2	c2ks1A_	 Alignment		83.7	25	PDB header: transferase Chain: A; PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: heterodimeric association of transmembrane domains of erbB1 and erbB22 receptors enabling kinase activation
3	c5n9yB_	 Alignment		74.3	15	PDB header: membrane protein Chain: B; PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
4	c4kppA_	 Alignment		58.6	9	PDB header: membrane protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
5	c4k1cA_	 Alignment		57.4	12	PDB header: membrane protein/metal transport Chain: A; PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
6	c1eysH_	 Alignment		56.4	22	PDB header: electron transport Chain: H; PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
7	c5zihA_	 Alignment		54.8	12	PDB header: membrane protein Chain: A; PDB Molecule: sensory opsin a,chrmsn; PDBTitle: crystal structure of the red light-activated channelrhodopsin2 chrmsn.
8	c6hu9u_	 Alignment		53.4	11	PDB header: oxidoreductase/electron transport Chain: U; PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
9	c2mpnB_	 Alignment		53.4	5	PDB header: membrane protein Chain: B; PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
10	c4ev6E_	 Alignment		49.6	18	PDB header: metal transport Chain: E; PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
11	c2mpnA_	 Alignment		49.4	5	PDB header: membrane protein Chain: A; PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli

12	c2m20B_	Alignment		45.0	16	PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
13	c6cfwD_	Alignment		42.0	27	PDB header: membrane protein Chain: D: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
14	c5v2sA_	Alignment		36.8	15	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
15	c4zyoA_	Alignment		36.3	2	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase; PDBTitle: crystal structure of human integral membrane stearyl-coa desaturase2 with substrate
16	c6humQ_	Alignment		35.1	9	PDB header: proton transport Chain: Q: PDB Molecule: proton-translocating nadh-quinone dehydrogenase subunit q PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
17	d2iuba2	Alignment		34.9	15	Fold: Transmembrane helix hairpin Superfamily: Magnesium transport protein CorA, transmembrane region Family: Magnesium transport protein CorA, transmembrane region
18	c1ciiA_	Alignment		34.1	27	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
19	c6g2jI_	Alignment		33.8	13	PDB header: oxidoreductase Chain: J: PDB Molecule: nadh-ubiquinone oxidoreductase chain 6; PDBTitle: mouse mitochondrial complex i in the active state
20	c5xtdm_	Alignment		32.5	16	PDB header: oxidoreductase/electron transport Chain: M: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: cryo-em structure of human respiratory complex i
21	c5d92B_	Alignment	not modelled	31.8	15	PDB header: membrane protein Chain: B: PDB Molecule: af2299 protein,phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
22	c5mx2T_	Alignment	not modelled	31.4	18	PDB header: oxidoreductase Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
23	c2n2aA_	Alignment	not modelled	30.7	15	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
24	c6dt0D_	Alignment	not modelled	30.2	14	PDB header: transport protein Chain: D: PDB Molecule: mitochondrial calcium uniporter; PDBTitle: cryo-em structure of a mitochondrial calcium uniporter
25	c5lnkr_	Alignment	not modelled	29.2	24	PDB header: oxidoreductase Chain: R: PDB Molecule: PDBTitle: entire ovine respiratory complex i
26	c4tnjT_	Alignment	not modelled	28.7	18	PDB header: electron transport,photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
27	c4ixqt_	Alignment	not modelled	28.7	18	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state
28	c4ixqT_	Alignment	not modelled	28.7	18	PDB header: photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state

29	c4tnjt_	Alignment	not modelled	28.7	18	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution
30	c4tnkT_	Alignment	not modelled	28.7	18	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
31	c4fbyT_	Alignment	not modelled	28.7	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: fs x-ray diffraction of photosystem ii
32	c3bz1T_	Alignment	not modelled	28.7	18	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer
33	c3prqT_	Alignment	not modelled	28.7	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
34	c3bz2T_	Alignment	not modelled	28.7	18	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer
35	c3prrT_	Alignment	not modelled	28.7	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
36	c4fbyg_	Alignment	not modelled	28.7	18	PDB header: photosynthesis Chain: G; PDB Molecule: photosystem q(b) protein 1; PDBTitle: fs x-ray diffraction of photosystem ii
37	c4tnkt_	Alignment	not modelled	28.7	18	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution
38	c4tnit_	Alignment	not modelled	28.7	18	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
39	c4ixrt_	Alignment	not modelled	28.7	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state
40	c4tniT_	Alignment	not modelled	28.7	18	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution
41	c4ixrT_	Alignment	not modelled	28.7	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state
42	c4tnht_	Alignment	not modelled	28.7	18	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
43	c4tnhT_	Alignment	not modelled	28.7	18	PDB header: electron transport,photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution
44	c5mx2t_	Alignment	not modelled	28.4	18	PDB header: oxidoreductase Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
45	c4pj0T_	Alignment	not modelled	28.4	18	PDB header: oxidoreductase, electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
46	c4pj0t_	Alignment	not modelled	28.4	18	PDB header: oxidoreductase, electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
47	c1s5IT_	Alignment	not modelled	28.4	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii psbt protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
48	c1s5It_	Alignment	not modelled	28.4	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii psbt protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
49	c5ldwj_	Alignment	not modelled	28.2	13	PDB header: oxidoreductase Chain: J; PDB Molecule: nadh-ubiquinone oxidoreductase chain 6; PDBTitle: structure of mammalian respiratory complex i, class1
50	c5e7ct_	Alignment	not modelled	28.0	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: macromolecular diffractive imaging using imperfect crystals - bragg2 data
51	c3a0ht_	Alignment	not modelled	28.0	18	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of i-substituted photosystem ii complex
52	c5e79t_	Alignment	not modelled	28.0	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: macromolecular diffractive imaging using imperfect crystals
53	c3a0hT_	Alignment	not modelled	28.0	18	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of i-substituted photosystem ii complex
54	c4rvyt_	Alignment	not modelled	28.0	18	PDB header: oxidoreductase Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: serial time resolved crystallography of photosystem ii

						using a2 femtosecond x-ray laser. the s state after two flashes (s3)
55	c3a0bt_	Alignment	not modelled	28.0	18	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of br-substituted photosystem ii complex
56	c2axtT_	Alignment	not modelled	28.0	18	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center t protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
57	c4rvyT_	Alignment	not modelled	28.0	18	PDB header: oxidoreductase Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: serial time resolved crystallography of photosystem ii using a2 femtosecond x-ray laser. the s state after two flashes (s3)
58	d2axtt1	Alignment	not modelled	28.0	18	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein T, PsbT Family: PsbT-like
59	c3arcT_	Alignment	not modelled	28.0	18	PDB header: electron transport, photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
60	c5e79T_	Alignment	not modelled	28.0	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: macromolecular diffractive imaging using imperfect crystals
61	c5e7cT_	Alignment	not modelled	28.0	18	PDB header: photosynthesis Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: macromolecular diffractive imaging using imperfect crystals - bragg2 data
62	c3kziT_	Alignment	not modelled	28.0	18	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii
63	c2axtt_	Alignment	not modelled	28.0	18	PDB header: electron transport Chain: T; PDB Molecule: photosystem ii reaction center t protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
64	d2axtm1	Alignment	not modelled	27.5	54	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein M, PsbM Family: PsbM-like
65	c4ymkA_	Alignment	not modelled	26.4	4	PDB header: oxidoreductase Chain: A; PDB Molecule: acyl-coa desaturase 1; PDBTitle: crystal structure of stearoyl-coenzyme a desaturase 1
66	c4k1cB_	Alignment	not modelled	26.4	9	PDB header: membrane protein/metal transport Chain: B; PDB Molecule: vacuolar calcium ion transporter; PDBTitle: vcx1 calcium/proton exchanger
67	c6hwhX_	Alignment	not modelled	25.7	18	PDB header: electron transport Chain: X; PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
68	c6d80A_	Alignment	not modelled	24.7	18	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
69	c6c5wA_	Alignment	not modelled	24.7	20	PDB header: membrane protein Chain: A; PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the mitochondrial calcium uniporter
70	c5xtdb_	Alignment	not modelled	24.6	38	PDB header: oxidoreductase/electron transport Chain: B; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: cryo-em structure of human respiratory complex i
71	d1e12a_	Alignment	not modelled	24.2	18	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
72	c3a0hm_	Alignment	not modelled	22.6	46	PDB header: electron transport Chain: M; PDB Molecule: photosystem ii reaction center protein m; PDBTitle: crystal structure of i-substituted photosystem ii complex
73	c2voyB_	Alignment	not modelled	21.3	14	PDB header: hydrolase Chain: B; PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
74	c5o6vC_	Alignment	not modelled	21.0	14	PDB header: virus Chain: C; PDB Molecule: envelope protein; PDBTitle: the cryo-em structure of tick-borne encephalitis virus complexed with2 fab fragment of neutralizing antibody 19/1786
75	c5dgoA_	Alignment	not modelled	20.9	36	PDB header: cell cycle Chain: A; PDB Molecule: cell division control protein 45 homolog; PDBTitle: crystal structure of cell division cycle protein 45 (cdc45)
76	c2na9A_	Alignment	not modelled	19.5	25	PDB header: signaling protein Chain: A; PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the p441a mutant of the cytokine receptor2 common subunit beta
77	c2na8A_	Alignment	not modelled	19.3	25	PDB header: membrane protein Chain: A; PDB Molecule: cytokine receptor common subunit beta; PDBTitle: transmembrane structure of the cytokine receptor common subunit beta
78	c4b03A_	Alignment	not modelled	18.3	11	PDB header: virus Chain: A; PDB Molecule: dengue virus 1 e protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
79	c2jagA_	Alignment	not modelled	18.2	19	PDB header: membrane protein Chain: A; PDB Molecule: halorhodopsin; PDBTitle: i1-intermediate of halorhodopsin t203v
80	c5by1A_	Alignment	not modelled	18.0	17	PDB header: viral protein Chain: A; PDB Molecule: non-structural protein 1; PDBTitle: h18 bat influenza ns1 rna binding domain

81	c5ireA_	Alignment	not modelled	17.6	8	PDB header: virus Chain: A: PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus
82	c1rh1A_	Alignment	not modelled	16.9	11	PDB header: antibiotic Chain: A: PDB Molecule: colicin b; PDBTitle: crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
83	c3jc6E_	Alignment	not modelled	16.2	27	PDB header: replication Chain: E: PDB Molecule: cell division control protein 45; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
84	c3a0bT_	Alignment	not modelled	16.2	21	PDB header: electron transport Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of br-substituted photosystem ii complex
85	c6bm8A_	Alignment	not modelled	16.2	16	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
86	c3ipdB_	Alignment	not modelled	15.6	6	PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
87	c2n1pA_	Alignment	not modelled	15.2	18	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
88	d2r6gf1	Alignment	not modelled	15.1	7	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
89	c6eyuA_	Alignment	not modelled	15.0	23	PDB header: membrane protein Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of the inward h(+) pump xenorhodopsin
90	c2bbjB_	Alignment	not modelled	14.9	20	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
91	c2lcoA_	Alignment	not modelled	14.6	24	PDB header: membrane protein Chain: A: PDB Molecule: walp19-p8 peptide; PDBTitle: 1h and 15n assignments of walp19-p8 peptide in sds micelles
92	c4zr0A_	Alignment	not modelled	14.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ceramide very long chain fatty acid hydroxylase scs7; PDBTitle: full length scs7p (only hydroxylase domain visible)
93	c3arct_	Alignment	not modelled	14.3	18	PDB header: electron transport, photosynthesis Chain: T: PDB Molecule: photosystem ii reaction center protein t; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
94	c6j9mA_	Alignment	not modelled	14.3	41	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: nmebh+acriic2
95	c6qpbB_	Alignment	not modelled	14.0	8	PDB header: membrane protein Chain: B: PDB Molecule: anoctamin-6; PDBTitle: cryo-em structure of calcium-free mtmem16f lipid scramblase in2 digitonin
96	c5wsnC_	Alignment	not modelled	13.2	19	PDB header: virus Chain: C: PDB Molecule: e protein; PDBTitle: structure of japanese encephalitis virus
97	d1aila_	Alignment	not modelled	13.0	33	Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: N-terminal, RNA-binding domain of nonstructural protein NS1
98	c6agfB_	Alignment	not modelled	12.7	8	PDB header: membrane protein Chain: B: PDB Molecule: sodium channel subunit beta-1; PDBTitle: structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
99	c5xnlM_	Alignment	not modelled	12.5	38	PDB header: membrane protein Chain: M: PDB Molecule: photosystem ii reaction center protein m; PDBTitle: structure of stacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum