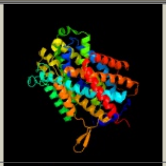
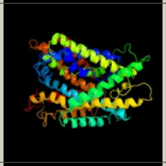
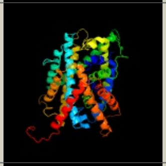
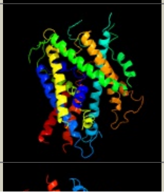
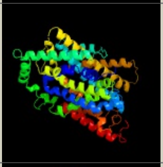
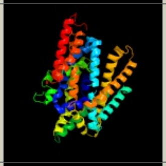
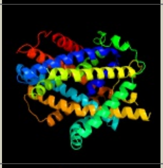
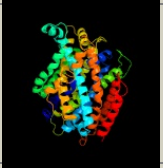
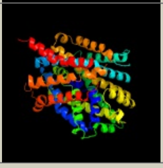
Email	mdejesus@rockefeller.edu
Description	RVBD2320c_(rocE)_2592733_2594163
Date	Mon Aug 5 13:25:47 BST 2019
Unique Job ID	3ab3edbf5785bc00

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oqtA_	Alignment		100.0	43	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**amino acid transporter; **PDBTitle:** crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
2	c6f2wA_	Alignment		100.0	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative amino acid/polyamine transport protein; **PDBTitle:** bacterial asc transporter crystal structure in open to in conformation
3	c4djiA_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable glutamate/gamma-aminobutyrate antiporter; **PDBTitle:** structure of glutamate-gaba antiporter gadc
4	c6nplA_	Alignment		100.0	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**solute carrier family 12 (sodium/potassium/chloride **PDBTitle:** cryo-em structure of nkcc1
5	c6irtB_	Alignment		100.0	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**large neutral amino acids transporter small subunit 1; **PDBTitle:** human lat1-4f2hc complex bound with bch
6	c3giaA_	Alignment		100.0	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**uncharacterized protein mj0609; **PDBTitle:** crystal structure of apct transporter
7	c6jmqA_	Alignment		100.0	23	**PDB header:**membrane protein/immune system **Chain:** A: **PDB Molecule:**large neutral amino acids transporter small subunit 1; **PDBTitle:** lat1-cd98hc complex bound to mem-108 fab
8	c3lrcC_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
9	c6csfC_	Alignment		100.0	12	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**sodium/alanine symporter agcs; **PDBTitle:** crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
10	c2jlnA_	Alignment		100.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
11	c6c08F_	Alignment		99.8	13	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**sodium-coupled neutral amino acid transporter 9; **PDBTitle:** zebrafish slc38a9 with arginine bound in the cytosol open state

12	c6c08C_	Alignment		99.5	13	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**sodium-coupled neutral amino acid transporter 9; **PDBTitle:** zebrafish slc38a9 with arginine bound in the cytosol open state
13	c5nvaA_	Alignment		99.4	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative sodium:solute symporter; **PDBTitle:** substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site
14	c3dh4A_	Alignment		99.1	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
15	c2xq2A_	Alignment		99.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
16	c4wgwA_	Alignment		98.9	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**divalent metal cation transporter mnth; **PDBTitle:** staphylococcus capitis divalent metal ion transporter (dmt) in complex2 with manganese
17	c4wgvC_	Alignment		98.9	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**divalent metal cation transporter mnth; **PDBTitle:** crystal structure of staphylococcus capitis divalent metal ion2 transporter (dmt) in complex with nanobody
18	c5m87A_	Alignment		98.3	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**divalent metal cation transporter mnth; **PDBTitle:** crystal structure of eremococcus coleocola manganese transporter
19	c4us3A_	Alignment		97.3	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transporter; **PDBTitle:** crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
20	c4m48A_	Alignment		97.3	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transporter; **PDBTitle:** x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
21	c5i6xA_	Alignment	not modelled	97.1	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sodium-dependent serotonin transporter; **PDBTitle:** x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
22	c4ainB_	Alignment	not modelled	97.0	11	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glycine betaine transporter betp; **PDBTitle:** crystal structure of betp with asymmetric protomers.
23	d2a65a1	Alignment	not modelled	96.9	13	**Fold:**SNF-like **Superfamily:**SNF-like **Family:**SNF-like
24	c2w8aC_	Alignment	not modelled	94.4	11	**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
25	c5kteA_	Alignment	not modelled	92.4	12	**PDB header:**transport protein/immune system **Chain:** A: **PDB Molecule:**divalent metal cation transporter mnth; **PDBTitle:** crystal structure of deinococcus radiodurans mnth, an nramp-family2 transition metal transporter
26	c3hfxA_	Alignment	not modelled	91.3	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter; **PDBTitle:** crystal structure of carnitine transporter
27	d1fftb2	Alignment	not modelled	34.4	12	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
28	c5ogeE_	Alignment	not modelled	30.1	7	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**gdp-mannose transporter 1; **PDBTitle:** crystal structure of a nucleotide sugar transporter
						PDB header:membrane protein

29	c2lowA_	Alignment	not modelled	29.3	7	**Chain:** A: **PDB Molecule:**apelin receptor; **PDBTitle:** solution structure of ar55 in 50% hfip
30	c6dt0D_	Alignment	not modelled	21.7	24	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mitochondrial calcium uniporter; **PDBTitle:** cryo-em structure of a mitochondrial calcium uniporter
31	c2micA_	Alignment	not modelled	18.0	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily member 16; **PDBTitle:** nmr structure of p75 transmembrane domain in dpc micelles
32	c2micB_	Alignment	not modelled	18.0	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**tumor necrosis factor receptor superfamily member 16; **PDBTitle:** nmr structure of p75 transmembrane domain in dpc micelles
33	c4x5mB_	Alignment	not modelled	16.4	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of semisweet in the inward-open conformation
34	c6hwhL_	Alignment	not modelled	13.6	7	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**cytochrome c oxidase subunit 2; **PDBTitle:** structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
35	c2jwaA_	Alignment	not modelled	13.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
36	c2ks1A_	Alignment	not modelled	13.4	14	**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
37	c6c14A_	Alignment	not modelled	12.7	4	**PDB header:**membrane protein, metal transport **Chain:** A: **PDB Molecule:**protocadherin-15; **PDBTitle:** cryoem structure of mouse pcdh15-1ec-lhfpl5 complex
38	c1ujlA_	Alignment	not modelled	12.6	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily h **PDBTitle:** solution structure of the herg k+ channel s5-p2 extracellular linker
39	c6e9oA_	Alignment	not modelled	12.5	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**d-galactonate transport; **PDBTitle:** e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
40	d2iuba2	Alignment	not modelled	11.9	9	**Fold:**Transmembrane helix hairpin **Superfamily:**Magnesium transport protein CorA, transmembrane region **Family:**Magnesium transport protein CorA, transmembrane region
41	c4n7wA_	Alignment	not modelled	11.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transporter, sodium/bile acid symporter family; **PDBTitle:** crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
42	c2rddB_	Alignment	not modelled	11.1	28	**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.
43	c2m67A_	Alignment	not modelled	10.6	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** full-length mercury transporter protein merf in lipid bilayer2 membranes
44	c4kppA_	Alignment	not modelled	9.9	5	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of h+/ca2+ exchanger cax
45	c5v2sA_	Alignment	not modelled	9.7	4	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein b; **PDBTitle:** crystal structure of glycoprotein b from herpes simplex virus type i
46	c6p2rB_	Alignment	not modelled	8.9	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dolichyl-phosphate-mannose--protein mannosyltransferase 2; **PDBTitle:** structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
47	c2yevB_	Alignment	not modelled	8.9	17	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c oxidase subunit 2; **PDBTitle:** structure of caa3-type cytochrome oxidase
48	c6agfB_	Alignment	not modelled	8.9	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
49	c2kluA_	Alignment	not modelled	8.8	7	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
50	c1qa4A_	Alignment	not modelled	8.5	35	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hiv-1 nef anchor domain (2-57)); **PDBTitle:** hiv-1 nef anchor domain, nmr, 2 structures
51	c2bbjB_	Alignment	not modelled	8.4	9	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
52	c2ndjA_	Alignment	not modelled	8.4	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e member 3; **PDBTitle:** structural basis for kcne3 and estrogen modulation of the kcnq12 channel
53	c5oonA_	Alignment	not modelled	8.2	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**undecaprenyl-diphosphatase; **PDBTitle:** structure of undecaprenyl-pyrophosphate phosphatase, baca

54	c2kogA_	Alignment	not modelled	8.1	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** lipid-bound synaptobrevin solution nmr structure
55	c2n2aA_	Alignment	not modelled	8.0	14	**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
56	c5xamA_	Alignment	not modelled	8.0	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein translocase subunit secd; **PDBTitle:** crystal structure of secdf in i form at 4 a resolution
57	c3arct_	Alignment	not modelled	8.0	16	**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
58	c6h8qH_	Alignment	not modelled	7.8	36	**PDB header:**cell cycle **Chain:** H: **PDB Molecule:**sister chromatid cohesion protein 1; **PDBTitle:** structural basis for scc3-dependent cohesin recruitment to chromatin
59	c1pjnA_	Alignment	not modelled	7.7	36	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**histone-binding protein n1/n2; **PDBTitle:** mouse importin alpha-bipartite nls n1n2 from xenopus laevis2 phosphoprotein complex
60	c2na6B_	Alignment	not modelled	7.5	4	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** transmembrane domain of mouse fas/cd95 death receptor
61	c2na6C_	Alignment	not modelled	7.5	4	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** transmembrane domain of mouse fas/cd95 death receptor
62	c2na6A_	Alignment	not modelled	7.5	4	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily member 6; **PDBTitle:** transmembrane domain of mouse fas/cd95 death receptor
63	c5u1dB_	Alignment	not modelled	7.5	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**antigen peptide transporter 2; **PDBTitle:** cryo-em structure of the human tap atp-binding cassette transporter
64	c3mk7F_	Alignment	not modelled	7.5	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
65	c5ochF_	Alignment	not modelled	7.4	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atp-binding cassette sub-family b member 8, mitochondrial; **PDBTitle:** the crystal structure of human abcb8 in an outward-facing state
66	c5xpdA_	Alignment	not modelled	7.3	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar transporter; **PDBTitle:** sugar transporter of atsweet13 in inward-facing state with a substrate2 analog
67	c3v5uA_	Alignment	not modelled	7.3	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**uncharacterized membrane protein mj0091; **PDBTitle:** structure of sodium/calcium exchanger from methanocaldococcus2 jannaschii dsm 2661
68	c6iu3A_	Alignment	not modelled	7.2	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**vit1; **PDBTitle:** crystal structure of iron transporter vit1 with zinc ions
69	c3qf4B_	Alignment	not modelled	7.2	8	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**uncharacterized abc transporter atp-binding protein **PDBTitle:** crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
70	c5jnqA_	Alignment	not modelled	6.9	13	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**phospho-n-acetylmuramoyl-pentapeptide-transferase; **PDBTitle:** mray tunicamycin complex
71	c4ry2A_	Alignment	not modelled	6.8	8	**PDB header:**transport protein/hydrolase **Chain:** A: **PDB Molecule:**abc-type bacteriocin transporter; **PDBTitle:** crystal structure of the peptidase-containing abc transporter pcat1
72	c5zlgA_	Alignment	not modelled	6.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome b reductase 1; **PDBTitle:** human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
73	c2gfpA_	Alignment	not modelled	6.7	7	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
74	c3j46n_	Alignment	not modelled	6.7	33	**PDB header:**ribosome/protein transport **Chain:** N: **PDB Molecule:** **PDBTitle:** structure of the secy protein translocation channel in action
75	c6ajjA_	Alignment	not modelled	6.7	11	**PDB header:**membrane protein, hydrolase **Chain:** A: **PDB Molecule:**drug exporters of the rnd superfamily-like protein, **PDBTitle:** crystal structure of mycolic acid transporter mmpl3 from mycobacterium2 smegmatis complexed with ica38
76	c2momB_	Alignment	not modelled	6.6	27	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lysosome-associated membrane glycoprotein 2; **PDBTitle:** structural insights of tm domain of lamp-2a in dpc micelles
77	c2momC_	Alignment	not modelled	6.6	27	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**lysosome-associated membrane glycoprotein 2; **PDBTitle:** structural insights of tm domain of lamp-2a in dpc

						micelles
78	c5i20C_	Alignment	not modelled	6.6	6	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein
79	d1ks9a1	Alignment	not modelled	6.4	11	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Ketopantoate reductase PanE
80	c6h8qG_	Alignment	not modelled	6.4	31	**PDB header:**cell cycle **Chain:** G: **PDB Molecule:**sister chromatid cohesion protein 1; **PDBTitle:** structural basis for scc3-dependent cohesin recruitment to chromatin
81	c3qf4A_	Alignment	not modelled	6.3	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, atp-binding protein; **PDBTitle:** crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
82	c5xsyB_	Alignment	not modelled	6.3	17	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**voltage-gated sodium channel beta subunit 1; **PDBTitle:** structure of the nav1.4-beta1 complex from electric eel
83	c2k21A_	Alignment	not modelled	6.3	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
84	c4qtnB_	Alignment	not modelled	6.2	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**nicotinamide riboside transporter pnuc; **PDBTitle:** crystal structure of the vitamin b3 transporter pnuc
85	c2n28A_	Alignment	not modelled	6.1	7	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein vpu; **PDBTitle:** solid-state nmr structure of vpu
86	c6f0gD_	Alignment	not modelled	6.0	38	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**ip3; **PDBTitle:** crystal structure asf1-ip3
87	c6f0gC_	Alignment	not modelled	6.0	38	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**ip3; **PDBTitle:** crystal structure asf1-ip3
88	c2kloA_	Alignment	not modelled	5.9	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna replication factor cdt1; **PDBTitle:** structure of the cdt1 c-terminal domain
89	c5wb5B_	Alignment	not modelled	5.7	33	**PDB header:**translation **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** leishmania if4e-1 bound to leishmania 4e-ip1
90	c5lc5A_	Alignment	not modelled	5.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-ubiquinone oxidoreductase chain 3; **PDBTitle:** structure of mammalian respiratory complex i, class2
91	c2yl4A_	Alignment	not modelled	5.7	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 10, **PDBTitle:** structure of the human mitochondrial abc transporter, abcb10
92	c1fftG_	Alignment	not modelled	5.6	12	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
93	c4dncD_	Alignment	not modelled	5.6	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**male-specific lethal 1 homolog; **PDBTitle:** crystal structure of human mof in complex with msl1
94	c3jcut_	Alignment	not modelled	5.5	16	**PDB header:**membrane protein **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein tc; **PDBTitle:** cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
95	c3jcuT_	Alignment	not modelled	5.5	16	**PDB header:**membrane protein **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein tc; **PDBTitle:** cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
96	c2k1aA_	Alignment	not modelled	5.5	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
97	c4fbyT_	Alignment	not modelled	5.4	15	**PDB header:**photosynthesis **Chain:** T: **PDB Molecule:**photosystem ii reaction center protein t; **PDBTitle:** fs x-ray diffraction of photosystem ii
98	c4tnjT_	Alignment	not modelled	5.4	15	**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
99	c4tnhT_	Alignment	not modelled	5.4	15	**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