
















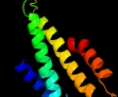




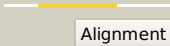

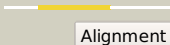

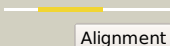


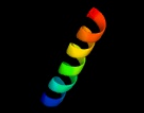

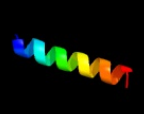
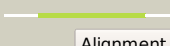

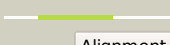




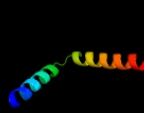
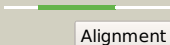
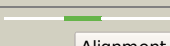
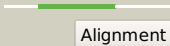
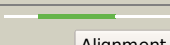
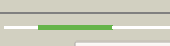
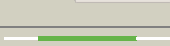
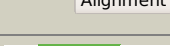
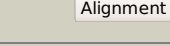


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1111c_(-) _1237214_1238197
Date	Wed Jul 31 22:05:19 BST 2019
Unique Job ID	00d74a247cf93a98

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ht2B_	 Alignment		93.3	12	PDB header: membrane protein Chain: B; PDB Molecule: h(+)/cl(-) exchange transporter clca; PDBTitle: structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
2	d1otsa_	 Alignment		91.9	12	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
3	d1kpla_	 Alignment		88.2	11	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
4	c3nd0A_	 Alignment		87.2	11	PDB header: transport protein Chain: A; PDB Molecule: sli0855 protein; PDBTitle: x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
5	c5oqtA_	 Alignment		84.9	15	PDB header: transport protein Chain: A; PDB Molecule: amino acid transporter; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
6	c3giaA_	 Alignment		81.4	14	PDB header: transport protein Chain: A; PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
7	c5d92B_	 Alignment		78.0	16	PDB header: membrane protein Chain: B; PDB Molecule: af2299 protein,phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
8	c2ksfA_	 Alignment		75.9	15	PDB header: transferase Chain: A; PDB Molecule: sensor protein kdpd; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor kdpd, center for structures of membrane proteins (csm)3 target 4312c
9	c4m5bA_	 Alignment		75.9	17	PDB header: membrane protein Chain: A; PDB Molecule: cobalamin biosynthesis protein cbim; PDBTitle: crystal structure of an truncated transition metal transporter
10	c4m5cA_	 Alignment		75.9	17	PDB header: membrane protein Chain: A; PDB Molecule: cobalamin biosynthesis protein cbim; PDBTitle: crystal structure of an truncated transition metal transporter
11	c3k07A_	 Alignment		74.7	12	PDB header: transport protein Chain: A; PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa

12	c4px7A_	 Alignment		73.5	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pggp
13	c6d0nA_	 Alignment		70.9	15	PDB header: transport protein Chain: A: PDB Molecule: clc-type fluoride/proton antiporter; PDBTitle: crystal structure of a clc-type fluoride/proton antiporter, v319g2 mutant
14	c4k5yA_	 Alignment		70.2	18	PDB header: membrane protein, receptor Chain: A: PDB Molecule: corticotropin-releasing factor receptor 1, t4-lysozyme PDBTitle: crystal structure of human corticotropin-releasing factor receptor 12 (crf1r) in complex with the antagonist cp-376395
15	c3jcuJ_	 Alignment		66.2	43	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
16	c5xnmj_	 Alignment		66.0	33	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: structure of unstacked c2s2m2-type psii-lhcii supercomplex from pismus2 sativum
17	c4djiA_	 Alignment		65.1	15	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
18	c5ws4A_	 Alignment		62.3	11	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
19	c4hg6A_	 Alignment		62.3	15	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase subunit a; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
20	c5v2sA_	 Alignment		61.6	15	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
21	c6exsA_	 Alignment	not modelled	59.7	13	PDB header: membrane protein Chain: A: PDB Molecule: peptide abc transporter permease; PDBTitle: crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
22	d1cola_	 Alignment	not modelled	59.0	27	Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin
23	c4ikyA_	 Alignment	not modelled	58.8	12	PDB header: transport protein Chain: A: PDB Molecule: di-tripeptide abc transporter (permease); PDBTitle: crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
24	c5mg3D_	 Alignment	not modelled	57.9	9	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secd; PDBTitle: em fitted model of bacterial holo-translocon
25	c2v50A_	 Alignment	not modelled	56.8	10	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb
26	c6nbxG_	 Alignment	not modelled	56.1	13	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
27	d1wpga4	 Alignment	not modelled	55.6	11	Fold: Calcium ATPase, transmembrane domain M Superfamily: Calcium ATPase, transmembrane domain M Family: Calcium ATPase, transmembrane domain M
28	c6irtB_	 Alignment	not modelled	54.3	11	PDB header: membrane protein Chain: B: PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: human lat1-4f2hc complex bound with bch PDB header: membrane protein

29	c4o9uB_	Alignment	not modelled	54.2	14	Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
30	c5lq3F_	Alignment	not modelled	54.1	16	PDB header: transport protein Chain: F: PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
31	c5n6mA_	Alignment	not modelled	54.0	13	PDB header: membrane protein Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: structure of the membrane integral lipoprotein n-acyltransferase Int2 from p. aeruginosa
32	c6csxA_	Alignment	not modelled	53.1	11	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
33	c6f2wA_	Alignment	not modelled	52.7	10	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
34	c6ajjA_	Alignment	not modelled	52.5	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 mmp13 from mycobacterium2 smegmatis complexed with ica38
35	c6nt5B_	Alignment	not modelled	50.4	23	PDB header: immune system Chain: B: PDB Molecule: stimulator of interferon protein; PDBTitle: cryo-em structure of full-length human sting in the apo state
36	c4b03A_	Alignment	not modelled	50.4	30	PDB header: virus Chain: A: PDB Molecule: dengue virus 1 e protein; PDBTitle: 6a electron cryomicroscopy structure of immature dengue virus serotype2 1
37	c5lj7B_	Alignment	not modelled	48.8	14	PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
38	c3javD_	Alignment	not modelled	47.8	8	PDB header: transport protein Chain: D: PDB Molecule: inositol 1,4,5-trisphosphate receptor type 1; PDBTitle: structure of full-length ip3r1 channel in the apo-state determined by2 single particle cryo-em
39	c5m87A_	Alignment	not modelled	47.3	15	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mnth; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
40	c6fj3A_	Alignment	not modelled	47.2	13	PDB header: membrane protein Chain: A: PDB Molecule: parathyroid hormone/parathyroid hormone-related peptide PDBTitle: high resolution crystal structure of parathyroid hormone 1 receptor in2 complex with a peptide agonist.
41	c5kzoA_	Alignment	not modelled	47.1	37	PDB header: transcription Chain: A: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: notch1 transmembrane and associated juxtamembrane segment
42	c4apsB_	Alignment	not modelled	45.4	11	PDB header: transport protein Chain: B: PDB Molecule: di-or tripeptide h+ symporter; PDBTitle: crystal structure of a pot family peptide transporter in an inward2 open conformation.
43	c4k0eA_	Alignment	not modelled	45.4	13	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	c3wo6A_	Alignment	not modelled	45.0	10	PDB header: membrane protein Chain: A: PDB Molecule: membrane protein insertase yidc 2; PDBTitle: crystal structure of yidc from bacillus halodurans (form i)
45	c3b8eC_	Alignment	not modelled	44.2	7	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
46	c1p58C_	Alignment	not modelled	44.2	36	PDB header: virus Chain: C: PDB Molecule: major envelope protein e; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction
47	c4ky0B_	Alignment	not modelled	44.0	20	PDB header: transport protein, membrane protein Chain: B: PDB Molecule: proton/glutamate symporter, sdf family; PDBTitle: crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
48	c6o7ua_	Alignment	not modelled	43.3	8	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
49	c5ireA_	Alignment	not modelled	42.0	24	PDB header: virus Chain: A: PDB Molecule: e protein; PDBTitle: the cryo-em structure of zika virus
50	c6an7D_	Alignment	not modelled	41.9	8	PDB header: transport protein Chain: D: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
51	c2yevC_	Alignment	not modelled	40.9	17	PDB header: electron transport Chain: C: PDB Molecule: caa3-type cytochrome oxidase subunit iv; PDBTitle: structure of caa3-type cytochrome oxidase
52	c5h36E_	Alignment	not modelled	40.6	17	PDB header: membrane protein Chain: E: PDB Molecule: uncharacterized protein tric; PDBTitle: crystal structures of the tric trimeric intracellular cation channel2 orthologue from rhodobacter sphaeroides
53	c2lowA_	Alignment	not modelled	40.5	15	PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfip

54	c1oy8A_	Alignment	not modelled	40.3	11	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
55	c5wudA_	Alignment	not modelled	39.5	17	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structural basis for conductance through tric cation channels
56	c5tfyj_	Alignment	not modelled	39.1	17	PDB header: cell adhesion Chain: J: PDB Molecule: flagellin; PDBTitle: the archaeal flagellum of methanospirillum hungatei strain jf1.
57	c6e59A_	Alignment	not modelled	38.8	16	PDB header: signaling protein Chain: A: PDB Molecule: substance-p receptor, glga glycogen synthase, substance-p PDBTitle: crystal structure of the human nk1 tachykinin receptor
58	c1mhsA_	Alignment	not modelled	37.0	6	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
59	d2axtj1	Alignment	not modelled	37.0	24	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
60	c3a0hj_	Alignment	not modelled	37.0	24	PDB header: electron transport Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
61	c5wsnC_	Alignment	not modelled	36.8	25	PDB header: virus Chain: C: PDB Molecule: e protein; PDBTitle: structure of japanese encephalitis virus
62	d2nr9a1	Alignment	not modelled	36.8	8	Fold: Rhomboid-like Superfamily: Rhomboid-like Family: Rhomboid-like
63	c5a1sB_	Alignment	not modelled	35.9	19	PDB header: transport protein Chain: B: PDB Molecule: citrate-sodium symporter; PDBTitle: crystal structure of the sodium-dependent citrate symporter secits2 form salmonella enterica.
64	c4iu8A_	Alignment	not modelled	35.1	18	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
65	c5x3xm_	Alignment	not modelled	34.9	11	PDB header: transport protein Chain: M: PDB Molecule: cobalt transport protein cbim; PDBTitle: 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo
66	d1o0la_	Alignment	not modelled	34.6	10	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
67	c4cl5B_	Alignment	not modelled	34.5	11	PDB header: transport protein Chain: B: PDB Molecule: nitrate transporter 1.1; PDBTitle: crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
68	c6an7C_	Alignment	not modelled	34.2	12	PDB header: transport protein Chain: C: PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
69	c5i6cB_	Alignment	not modelled	33.0	14	PDB header: transport protein Chain: B: PDB Molecule: uric acid-xanthine permease; PDBTitle: the structure of the eukaryotic purine/h+ symporter, uapa, in complex2 with xanthine
70	c4k0eC_	Alignment	not modelled	32.9	14	PDB header: transport protein Chain: C: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii
71	c5h35C_	Alignment	not modelled	32.5	19	PDB header: immune system/membrane protein Chain: C: PDB Molecule: membrane protein tric; PDBTitle: crystal structures of the tric trimeric intracellular cation channel2 orthologue from sulfolobus solfataricus
72	c5zihA_	Alignment	not modelled	32.1	10	PDB header: membrane protein Chain: A: PDB Molecule: sensory opsin a,chrimson; PDBTitle: crystal structure of the red light-activated channelrhodopsin2 chrimson.
73	c5nikK_	Alignment	not modelled	31.9	15	PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump
74	c6qvcB_	Alignment	not modelled	30.9	14	PDB header: membrane protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: cryoem structure of the human clc-1 chloride channel, cbs state 1
75	c4mt1A_	Alignment	not modelled	30.8	9	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
76	c3keyA_	Alignment	not modelled	30.1	20	PDB header: structural protein Chain: A: PDB Molecule: protein stn1; PDBTitle: crystal structure of s. cerevisiae stn1 c-terminal
77	c6p2rB_	Alignment	not modelled	29.6	14	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
78	c1z65A_	Alignment	not modelled	28.9	46	PDB header: unknown function Chain: A: PDB Molecule: prion-like protein doppel; PDBTitle: mouse doppel 1-30 peptide
79	c5khpB_	Alignment	not modelled	28.2	14	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter;

79	c3kmb_	Alignment	not modelled	28.2	14	PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn PDB header: membrane protein Chain: A; PDB Molecule: soluble cytochrome b562 and glucagon receptor chimera; PDBTitle: structure of the class b human glucagon g protein coupled receptor
80	c4l6rA_	Alignment	not modelled	27.8	13	PDB header: membrane protein Chain: A; PDB Molecule: dipeptide and tripeptide permease a; PDBTitle: crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
81	c6gs7A_	Alignment	not modelled	27.4	10	PDB header: membrane protein Chain: A; PDB Molecule: proton-dependent oligopeptide transporter family protein; PDBTitle: crystal structure of auto inhibited pot family peptide transporter
82	c6ei3A_	Alignment	not modelled	26.2	14	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
83	c3a0bx_	Alignment	not modelled	26.2	25	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
84	c3a0bX_	Alignment	not modelled	26.2	25	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of br-substituted photosystem ii complex
85	c3a0hx_	Alignment	not modelled	26.2	25	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
86	c3a0hX_	Alignment	not modelled	26.2	25	PDB header: electron transport Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: crystal structure of i-substituted photosystem ii complex
87	c3jd8A_	Alignment	not modelled	26.1	10	PDB header: membrane protein Chain: A; PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom
88	c6gifA_	Alignment	not modelled	25.9	20	PDB header: toxin Chain: A; PDB Molecule: aapa1; PDBTitle: aapa1 v26a toxin from helicobacter pylori 26695
89	c1s5lx_	Alignment	not modelled	25.7	23	PDB header: photosynthesis Chain: X; PDB Molecule: photosystem ii psbx protein; PDBTitle: architecture of the photosynthetic oxygen evolving center
90	c5gasN_	Alignment	not modelled	25.6	13	PDB header: hydrolase Chain: N; PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
91	c2b5fD_	Alignment	not modelled	25.3	10	PDB header: transport protein,membrane protein Chain: D; PDB Molecule: aquaporin; PDBTitle: crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
92	c1qleB_	Alignment	not modelled	25.0	14	PDB header: oxidoreductase/immune system Chain: B; PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: cryo-structure of the paracoccus denitrificans four-subunit cytochrome2 c oxidase in the completely oxidized state complexed with an antibody3 fv fragment
93	c5do7A_	Alignment	not modelled	24.9	7	PDB header: transport protein Chain: A; PDB Molecule: atp-binding cassette sub-family g member 5; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
94	c5azcA_	Alignment	not modelled	24.5	13	PDB header: transferase Chain: A; PDB Molecule: prolipoprotein diacylglyceryl transferase; PDBTitle: crystal structure of escherichia coli lgt in complex with2 phosphatidylglycerol
95	c3sviA_	Alignment	not modelled	24.1	27	PDB header: signaling protein Chain: A; PDB Molecule: type iii effector hopab2; PDBTitle: structure of the pto-binding domain of hoppmal generated by limited2 thermolysin digestion
96	c2m59B_	Alignment	not modelled	23.4	20	PDB header: transferase Chain: B; PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
97	c2m59A_	Alignment	not modelled	23.4	20	PDB header: transferase Chain: A; PDB Molecule: vascular endothelial growth factor receptor 2; PDBTitle: spatial structure of dimeric vegfr2 membrane domain in dpc micelles
98	c5o4uK_	Alignment	not modelled	23.3	27	PDB header: cell adhesion Chain: K; PDB Molecule: flagellin; PDBTitle: the flagellin of pyrococcus furiosus
99	c5fgnA_	Alignment	not modelled	23.2	11	PDB header: transferase,hydrolase Chain: A; PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
100	c6n52B_	Alignment	not modelled	23.0	8	PDB header: membrane protein Chain: B; PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
101	c5z1lL_	Alignment	not modelled	22.8	24	PDB header: protein fibril Chain: L; PDB Molecule: flagellin; PDBTitle: cryo-em structure of methanoccus maripaludis archaellum
102	c6f7hA_	Alignment	not modelled	22.6	10	PDB header: transport protein Chain: A; PDB Molecule: aquaporin-10; PDBTitle: crystal structure of human aqp10
103	c5voxb_	Alignment	not modelled	22.5	11	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)

104	c6hwhX_	Alignment	not modelled	22.3	22	PDB header: electron transport Chain: X; PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
105	c3lrcC_	Alignment	not modelled	22.3	12	PDB header: transport protein Chain: C; PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
106	c3orgB_	Alignment	not modelled	22.3	14	PDB header: transport protein Chain: B; PDB Molecule: cmclC; PDBTitle: crystal structure of a eukaryotic clc transporter
107	c6csmC_	Alignment	not modelled	22.2	10	PDB header: membrane protein Chain: C; PDB Molecule: gtacr1; PDBTitle: crystal structure of the natural light-gated anion channel gtacr1
108	c1ciiA_	Alignment	not modelled	22.2	19	PDB header: transmembrane protein Chain: A; PDB Molecule: colicin ia; PDBTitle: colicin ia
109	c3wdoA_	Alignment	not modelled	21.9	17	PDB header: transport protein Chain: A; PDB Molecule: mfs transporter; PDBTitle: structure of e. coli yajr transporter
110	c6hu9s_	Alignment	not modelled	21.7	19	PDB header: oxidoreductase/electron transport Chain: S; PDB Molecule: cytochrome b-c1 complex subunit 8; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
111	c6hu9g_	Alignment	not modelled	21.7	19	PDB header: oxidoreductase/electron transport Chain: G; PDB Molecule: cytochrome b-c1 complex subunit 7; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
112	c6owsB_	Alignment	not modelled	21.5	6	PDB header: membrane protein Chain: B; PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
113	c6ithA_	Alignment	not modelled	21.2	17	PDB header: membrane protein Chain: A; PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
114	c5oc0A_	Alignment	not modelled	20.9	18	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome b561; PDBTitle: structure of e. coli superoxide oxidase
115	c5cgaC_	Alignment	not modelled	20.4	25	PDB header: transferase Chain: C; PDB Molecule: hydroxyethylthiazole kinase; PDBTitle: structure of hydroxyethylthiazole kinase thim from staphylococcus2 aureus in complex with substrate analog 2-(1,3,5-trimethyl-1h-3 pyrazole-4-yl)ethanol