














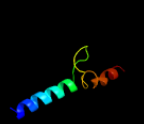






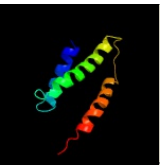
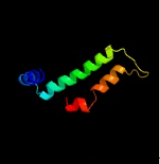
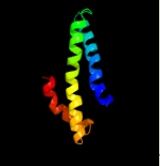
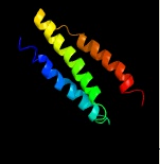
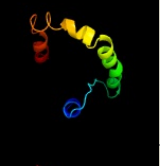
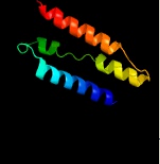
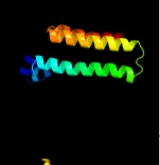
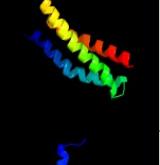



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0497 (-)_587380_588312
Date	Fri Jul 26 01:50:04 BST 2019
Unique Job ID	8d93d4d3cae96cdf

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r6gf1	 Alignment		94.5	5	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
2	c3jd8A_	 Alignment		94.0	16	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
3	c2lopA_	 Alignment		93.9	17	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 14a; PDBTitle: backbone structure of human membrane protein tmem14a
4	c3aqpB_	 Alignment		93.4	21	PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
5	c5khnB_	 Alignment		91.6	17	PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
6	c2losA_	 Alignment		90.6	17	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 14c; PDBTitle: backbone structure of human membrane protein tmem14c
7	c5mg3D_	 Alignment		90.5	13	PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
8	c6o7ua_	 Alignment		86.4	29	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
9	c5mg3F_	 Alignment		86.3	9	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
10	c4k0eC_	 Alignment		85.2	18	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
11	c6p25A_	 Alignment		84.4	10	PDB header: transferase Chain: A: PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor

12	d1iwga7	Alignment		83.6	20	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
13	c6p2rB_	Alignment		82.5	13	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
14	c6owsB_	Alignment		82.1	11	PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump
15	d1iwga8	Alignment		81.2	10	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
16	c5l25A_	Alignment		81.0	26	PDB header: transport protein Chain: A: PDB Molecule: boron transporter 1; PDBTitle: crystal structure of arabidopsis thaliana bor1
17	c6dmoA_	Alignment		80.5	19	PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
18	c4od5C_	Alignment		80.2	16	PDB header: transferase Chain: C: PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1
19	c6ajjA_	Alignment		80.0	13	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
20	c6iu3A_	Alignment		78.7	10	PDB header: metal transport Chain: A: PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
21	c5ir6B_	Alignment	not modelled	77.5	8	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
22	c5da0A_	Alignment	not modelled	76.4	11	PDB header: transport protein Chain: A: PDB Molecule: sulphate transporter; PDBTitle: structure of the the slc26 transporter slc26dg in complex with a2 nanobody
23	c5zbgC_	Alignment	not modelled	76.0	22	PDB header: membrane protein Chain: C: PDB Molecule: short transient receptor potential channel 3; PDBTitle: cryo-em structure of human trpc3 at 4.36a resolution
24	c5fgnA_	Alignment	not modelled	74.9	6	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
25	c4mt1A_	Alignment	not modelled	74.8	11	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
26	c5nf8A_	Alignment	not modelled	74.4	16	PDB header: membrane protein Chain: A: PDB Molecule: respiratory supercomplex factor 1, mitochondrial; PDBTitle: solution structure of detergent-solubilized rcf1, a yeast2 mitochondrial inner membrane protein involved in respiratory complex3 iii/iv supercomplex formation
27	c2kncA_	Alignment	not modelled	73.9	9	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaiiB-beta3 transmembrane-cytoplasmic2 heterocomplex

28	c2yvxD_	Alignment	not modelled	73.3	18	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
29	c6csfC_	Alignment	not modelled	73.1	9	PDB header: membrane protein Chain: C: PDB Molecule: sodium/alanine symporter agcs; PDBTitle: crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
30	c1oy8A_	Alignment	not modelled	72.8	17	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
31	c1m57H_	Alignment	not modelled	72.4	13	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)
32	c3qe7A_	Alignment	not modelled	70.7	20	PDB header: transport protein Chain: A: PDB Molecule: uracil permease; PDBTitle: crystal structure of uracil transporter--uraa
33	c6csxA_	Alignment	not modelled	70.2	18	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
34	c5xu1M_	Alignment	not modelled	69.8	14	PDB header: transport protein Chain: M: PDB Molecule: abc transporter permease; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
35	c6bwiA_	Alignment	not modelled	68.8	21	PDB header: membrane protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of full length human trpm4
36	c6bwdC_	Alignment	not modelled	67.7	16	PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of truncated mouse trpm7
37	c6bwdB_	Alignment	not modelled	67.7	16	PDB header: membrane protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of truncated mouse trpm7
38	c6bwdD_	Alignment	not modelled	67.7	16	PDB header: membrane protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of truncated mouse trpm7
39	c6bwdA_	Alignment	not modelled	67.7	16	PDB header: membrane protein Chain: A: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of truncated mouse trpm7
40	c5xamA_	Alignment	not modelled	67.3	16	PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secd; PDBTitle: crystal structure of secdf in i form at 4 a resolution
41	c6nbxG_	Alignment	not modelled	66.0	18	PDB header: oxidoreductase Chain: G: PDB Molecule: ndh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
42	c6bwiB_	Alignment	not modelled	65.8	21	PDB header: membrane protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of full length human trpm4
43	c6bwiD_	Alignment	not modelled	65.8	21	PDB header: membrane protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of full length human trpm4
44	c6bwiC_	Alignment	not modelled	65.8	21	PDB header: membrane protein Chain: C: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.7 angstrom cryoem structure of full length human trpm4
45	c5do7B_	Alignment	not modelled	64.9	11	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
46	c5lq3F_	Alignment	not modelled	64.4	13	PDB header: transport protein Chain: F: PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb
47	c6eznH_	Alignment	not modelled	64.4	16	PDB header: membrane protein Chain: H: PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
48	c3rceA_	Alignment	not modelled	64.3	18	PDB header: transferase/peptide Chain: A: PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
49	c3k07A_	Alignment	not modelled	63.6	16	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
50	c6gctA_	Alignment	not modelled	63.5	28	PDB header: membrane protein Chain: A: PDB Molecule: neutral amino acid transporter b(0); PDBTitle: cryo-em structure of the human neutral amino acid transporter asct2
51	c6nd1D_	Alignment	not modelled	63.2	33	PDB header: protein transport Chain: D: PDB Molecule: protein transport protein sbh1; PDBTitle: cryoem structure of the sec complex from yeast

52	c2v50A	Alignment	not modelled	62.8	17	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
53	c4ky0B	Alignment	not modelled	61.6	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
54	c3fewX	Alignment	not modelled	61.2	21	PDB header: immune system Chain: X: PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a duplicated2 receptor binding domain
55	c5vkgC	Alignment	not modelled	61.1	18	PDB header: membrane protein Chain: C: PDB Molecule: no mechanoreceptor potential c isoform l; PDBTitle: structure of a mechanotransduction ion channel drosophila nompc in2 nanodisc
56	d2nwwa1	Alignment	not modelled	60.6	12	Fold: Proton glutamate symport protein Superfamily: Proton glutamate symport protein Family: Proton glutamate symport protein
57	c5z96C	Alignment	not modelled	60.4	27	PDB header: membrane protein Chain: C: PDB Molecule: short transient receptor potential channel 4; PDBTitle: structure of the mouse trpc4 ion channel
58	c3kp9A	Alignment	not modelled	59.2	8	PDB header: blood coagulation,oxidoreductase Chain: A: PDB Molecule: vkorc1/thioredoxin domain protein; PDBTitle: structure of a bacterial homolog of vitamin k epoxide reductase
59	c4rfsS	Alignment	not modelled	59.2	17	PDB header: hydrolase, transport protein Chain: S: PDB Molecule: substrate binding protein s; PDBTitle: structure of a pantothenate energy coupling factor transporter
60	c5zx5D	Alignment	not modelled	59.1	15	PDB header: transferase Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.3 angstrom structure of mouse trpm7 with edta
61	c6bcoD	Alignment	not modelled	59.0	16	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with short coiled coil2 at 2.9 angstrom resolution
62	c3rfuC	Alignment	not modelled	58.6	18	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
63	c2ht2B	Alignment	not modelled	58.6	18	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
64	c4l6rA	Alignment	not modelled	58.2	11	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
65	c5oonA	Alignment	not modelled	57.4	18	PDB header: membrane protein Chain: A: PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, baca
66	c4a01B	Alignment	not modelled	56.9	9	PDB header: hydrolase Chain: B: PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase
67	c6r6bl	Alignment	not modelled	56.4	15	PDB header: protein transport Chain: I: PDB Molecule: surface presentation of antigens protein spaq; PDBTitle: structure of the core shigella flexneri type iii secretion system2 export gate complex sctrst (spa24/spa9/spa29).
68	c6buhH	Alignment	not modelled	56.0	13	PDB header: membrane protein Chain: H: PDB Molecule: d-alanyl transfer protein dlbt; PDBTitle: crystal structure of a membrane protein, crystal form ii
69	c6f2dj	Alignment	not modelled	55.6	13	PDB header: protein transport Chain: J: PDB Molecule: flagellar biosynthetic protein fliq; PDBTitle: a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
70	c6f2dl	Alignment	not modelled	55.6	13	PDB header: protein transport Chain: I: PDB Molecule: flagellar biosynthetic protein fliq; PDBTitle: a flipqr complex forms the core of the salmonella type iii secretion2 system export apparatus.
71	c4k0eA	Alignment	not modelled	55.6	22	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
72	c2n7iA	Alignment	not modelled	55.5	39	PDB header: hormone receptor Chain: A: PDB Molecule: prolactin receptor; PDBTitle: nmr structure of the prolactin receptor transmembrane domain
73	c1ijjA	Alignment	not modelled	55.0	25	PDB header: signaling protein Chain: A: PDB Molecule: erbB-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbB-2 membrane spanning2 segment
74	c6nhwA	Alignment	not modelled	54.6	19	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
75	c6nhwF	Alignment	not modelled	54.6	19	PDB header: immune system Chain: F: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
						PDB header: immune system Chain: D: PDB Molecule: tumor necrosis factor receptor

76	c6nhwD_	Alignment	not modelled	54.6	19	superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
77	c4wgvC_	Alignment	not modelled	54.3	22	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
78	c1xl6B_	Alignment	not modelled	54.2	10	PDB header: metal transport Chain: B: PDB Molecule: inward rectifier potassium channel; PDBTitle: intermediate gating structure 2 of the inwardly rectifying k+ channel2 kirbac3.1
79	c6nhwB_	Alignment	not modelled	53.6	19	PDB header: immune system Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
80	c6hwhX_	Alignment	not modelled	53.6	19	PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
81	c3mk7K_	Alignment	not modelled	52.4	8	PDB header: oxidoreductase Chain: K: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit n; PDBTitle: the structure of cbb3 cytochrome oxidase
82	c4wgvA_	Alignment	not modelled	52.3	15	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
83	c5i6cB_	Alignment	not modelled	52.3	18	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
84	c5nj3B_	Alignment	not modelled	52.1	9	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
85	c3nd0A_	Alignment	not modelled	52.0	13	PDB header: transport protein Chain: A: PDB Molecule: sll0855 protein; PDBTitle: x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
86	c5ldwZ_	Alignment	not modelled	51.5	38	PDB header: oxidoreductase Chain: Z: PDB Molecule: nahd dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class1
87	c5lc5Z_	Alignment	not modelled	51.5	38	PDB header: oxidoreductase Chain: Z: PDB Molecule: nahd dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class2
88	c5ldxZ_	Alignment	not modelled	51.5	38	PDB header: oxidoreductase Chain: Z: PDB Molecule: nahd dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class3.
89	c5voxb_	Alignment	not modelled	51.1	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)
90	d1y5ic1	Alignment	not modelled	51.0	15	Fold: Heme-binding four-helical bundle Superfamily: Respiratory nitrate reductase 1 gamma chain Family: Respiratory nitrate reductase 1 gamma chain
91	c2k1aA_	Alignment	not modelled	50.9	10	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: bicelle-embedded integrin alpha(iiB) transmembrane segment
92	c2kr6A_	Alignment	not modelled	50.7	16	PDB header: hydrolase Chain: A: PDB Molecule: presenilin-1; PDBTitle: solution structure of presenilin-1 ctf subunit
93	c5vrhA_	Alignment	not modelled	50.4	23	PDB header: transferase Chain: A: PDB Molecule: apolipoprotein n-acyltransferase; PDBTitle: apolipoprotein n-acyltransferase c387s active site mutant
94	c5tcxA_	Alignment	not modelled	50.1	9	PDB header: cell invasion Chain: A: PDB Molecule: cd81 antigen; PDBTitle: crystal structure of human tetraspanin cd81
95	c5y6rA_	Alignment	not modelled	50.0	22	PDB header: transferase Chain: A: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of csfv ns5b
96	c6humG_	Alignment	not modelled	49.8	13	PDB header: proton transport Chain: G: PDB Molecule: nahd dehydrogenase subunit 6; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
97	c5lj7B_	Alignment	not modelled	49.7	19	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)
98	c6nhwC_	Alignment	not modelled	49.4	19	PDB header: immune system Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
99	d2pila_	Alignment	not modelled	48.0	12	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
100	c6navl_	Alignment	not modelled	47.8	42	PDB header: structural protein Chain: I: PDB Molecule: m9ud72; PDBTitle: cryo-em reconstruction of sulfolobus islandicus la14/1 pilus
101	c1fftG_	Alignment	not modelled	47.8	20	PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase;

						PDBTitle: the structure of ubiquinol oxidase from escherichia coli
102	c6nhwE_	Alignment	not modelled	47.7	19	PDB header: immune system Chain: E: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
103	c6mhvD_	Alignment	not modelled	47.6	14	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel subfamily v PDBTitle: structure of human trpv3 in the presence of 2-apb in c4 symmetry
104	c5oqtC_	Alignment	not modelled	47.0	25	PDB header: transport protein Chain: C: PDB Molecule: uncharacterized protein ynem; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
105	c6f34C_	Alignment	not modelled	47.0	25	PDB header: membrane protein Chain: C: PDB Molecule: mgts; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue bound to arginine.
106	c2jp3A_	Alignment	not modelled	47.0	15	PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
107	c6k1hF_	Alignment	not modelled	46.9	8	PDB header: protein transport Chain: F: PDB Molecule: pts system mannose-specific eiid component; PDBTitle: structure of membrane protein
108	c6n52B_	Alignment	not modelled	46.9	13	PDB header: membrane protein Chain: B: PDB Molecule: metabotropic glutamate receptor 5; PDBTitle: metabotropic glutamate receptor 5 apo form
109	c4hg6B_	Alignment	not modelled	46.7	10	PDB header: transferase Chain: B: PDB Molecule: cellulose synthase subunit b; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
110	c2lomA_	Alignment	not modelled	46.7	12	PDB header: membrane protein Chain: A: PDB Molecule: hig1 domain family member 1a; PDBTitle: backbone structure of human membrane protein higd1a
111	c5lm4A_	Alignment	not modelled	45.9	24	PDB header: transport protein Chain: A: PDB Molecule: excitatory amino acid transporter 1,neutral amino acid PDBTitle: structure of the thermostalilized eaat1 cryst-ii mutant in complex2 with l-asp and the allosteric inhibitor ucph101
112	d1kpla_	Alignment	not modelled	45.9	17	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
113	d1oqwa_	Alignment	not modelled	45.2	16	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
114	c2kv5A_	Alignment	not modelled	45.2	38	PDB header: toxin Chain: A: PDB Molecule: putative uncharacterized protein rna; PDBTitle: solution structure of the par toxin fst in dpc micelles
115	c4o9tH_	Alignment	not modelled	44.9	22	PDB header: membrane protein Chain: H: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
116	c6bccqB_	Alignment	not modelled	44.8	16	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: cryo-em structure of trpm4 in atp bound state with long coiled coil at2 3.3 angstrom resolution
117	c6hwhB_	Alignment	not modelled	44.8	9	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
118	c2cpbA_	Alignment	not modelled	44.3	23	PDB header: viral protein Chain: A: PDB Molecule: m13 major coat protein; PDBTitle: solution nmr structures of the major coat protein of2 filamentous bacteriophage m13 solubilized in3 dodecylphosphocholine micelles, 25 lowest energy structures
119	c6hu9n_	Alignment	not modelled	43.7	18	PDB header: oxidoreductase/electron transport Chain: N: PDB Molecule: cytochrome b; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
120	c2l8sA_	Alignment	not modelled	43.1	13	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles