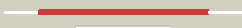
































Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2936_(drrA)_3272224_3273219
 Date Thu Aug 8 16:20:09 BST 2019
 Unique Job ID c56db64e307ac1a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xjyA_	 Alignment		100.0	27	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
2	c1q1bD_	 Alignment		100.0	29	PDB header: transport protein Chain: D: PDB Molecule: maltose/maltodextrin transport atp-binding protein malk; PDBTitle: crystal structure of e. coli malk in the nucleotide-free form
3	c2yyzA_	 Alignment		100.0	29	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
4	c2it1B_	 Alignment		100.0	28	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
5	c4rvcA_	 Alignment		100.0	30	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
6	c4tqvO_	 Alignment		100.0	27	PDB header: transport protein Chain: O: PDB Molecule: algs; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
7	c1oxtB_	 Alignment		100.0	31	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, atp binding protein; PDBTitle: crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
8	c3fvqB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: fe(3+) ions import atp-binding protein fbpc; PDBTitle: crystal structure of the nucleotide binding domain fbpc complexed with2 atp
9	c2olkD_	 Alignment		100.0	27	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
10	c1z47B_	 Alignment		100.0	31	PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative sulfate atp-2 binding cassette (abc) transporter from alicyclobacillus3 acidocaldarius
11	d1oxk2	 Alignment		100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like

12	c3dhwC	Alignment		100.0	28	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
13	d3dhw1	Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
14	d1g2912	Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
15	c5ws4A	Alignment		100.0	26	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
16	c4yerB	Alignment		100.0	40	PDB header: hydrolase Chain: B: PDB Molecule: abc transporter atp-binding protein; PDBTitle: crystal structure of an abc transporter atp-binding protein (tm_1403)2 from thermotoga maritima msb8 at 2.35 a resolution
17	d1vpla	Alignment		100.0	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
18	c5x5yB	Alignment		100.0	30	PDB header: membrane protein Chain: B: PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex
19	c4u02C	Alignment		100.0	25	PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein; PDBTitle: crystal structure of apo-ttha1159
20	c4p31B	Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: lipopolysaccharide export system atp-binding protein lptb; PDBTitle: crystal structure of a selenomethionine derivative of e. coli lptb in2 complex with adp-magnesium
21	c1vciA	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: A: PDB Molecule: sugar-binding transport atp-binding protein; PDBTitle: crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
22	c4wbsA	Alignment	not modelled	100.0	35	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from2 burkholderia phymatum
23	c5x40A	Alignment	not modelled	100.0	31	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
24	c5lj7B	Alignment	not modelled	100.0	24	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)
25	c3gfoA	Alignment	not modelled	100.0	27	PDB header: atp binding protein Chain: A: PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from clostridium perfringens: part of the abc2 transporter complex cbionq.
26	c4ymuj	Alignment	not modelled	100.0	30	PDB header: protein binding/transport protein Chain: J: PDB Molecule: abc-type polar amino acid transport system, atpase PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps
27	c5nikK	Alignment	not modelled	100.0	27	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

28	c6ic4I_	Alignment	not modelled	100.0	27	PDB header: protein transport Chain: I: PDB Molecule: abc transporter atp-binding protein; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
29	c2d62A_	Alignment	not modelled	100.0	28	PDB header: sugar binding protein Chain: A: PDB Molecule: multiple sugar-binding transport atp-binding PDBTitle: crystal structure of multiple sugar binding transport atp-2 binding protein
30	d3d31a2	Alignment	not modelled	100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
31	c4fwiB_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: B: PDB Molecule: abc-type dipeptide/oligopeptide/nickel transport system, PDBTitle: crystal structure of the nucleotide-binding domain of a dipeptide abc2 transporter
32	d1b0ua_	Alignment	not modelled	100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
33	d1v43a3	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
34	c5d3mF_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: F: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
35	c3d31B_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding protein; PDBTitle: modbc from methanosarcina acetivorans
36	c4mkiB_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: cobalt transporter atp-binding subunit
37	d1ji0a_	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
38	c6c0vA_	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance protein 1; PDBTitle: molecular structure of human p-glycoprotein in the atp-bound, outward-2 facing conformation
39	c2pcjB_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein lold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
40	d1g6ha_	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
41	c5xu1A_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
42	c3g5uB_	Alignment	not modelled	100.0	26	PDB header: membrane protein Chain: B: PDB Molecule: multidrug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
43	c4hluC_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp
44	d2pmka1	Alignment	not modelled	100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
45	c6amxA_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
46	c5ykfH_	Alignment	not modelled	100.0	21	PDB header: membrane protein Chain: H: PDB Molecule: atp-binding cassette sub-family c member 8 isoform x2; PDBTitle: structure of pancreatic atp-sensitive potassium channel bound with2 glibenclamide and atpgammas (3d class1 at 4.33a)
47	c5ujaA_	Alignment	not modelled	100.0	21	PDB header: protein transport Chain: A: PDB Molecule: bovine multidrug resistance protein 1 (mrp1),multidrug PDBTitle: cryo-em structure of bovine multidrug resistance protein 1 (mrp1)2 bound to leukotriene c4
48	c5uj9A_	Alignment	not modelled	100.0	21	PDB header: transport protein Chain: A: PDB Molecule: bovine multidrug resistance protein 1 (mrp1),multidrug PDBTitle: cryo-em structure of bovine multidrug resistance protein 1 (mrp1)
49	c4f4cA_	Alignment	not modelled	100.0	28	PDB header: hydrolase,protein transport Chain: A: PDB Molecule: multidrug resistance protein pgp-1; PDBTitle: the crystal structure of the multi-drug transporter
50	c6c3oE_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: E: PDB Molecule: atp-binding cassette sub-family c member 8; PDBTitle: cryo-em structure of human katp bound to atp and adp in quatrefoil2 form
51	c4huqB_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfa PDBTitle: crystal structure of a transporter
						PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding

52	c2yz2B_	Alignment	not modelled	100.0	24	protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
53	c4hzuB_	Alignment	not modelled	100.0	28	PDB header: hydrolase, transport protein Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfA PDBTitle: structure of a bacterial energy-coupling factor transporter
54	c5x7kB_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: B: PDB Molecule: lipase b; PDBTitle: crystal structure of the nucleotide-binding domain (nbd) of lipb, a2 abc transporter subunit of a type i secretion system
55	d1mv5a_	Alignment	not modelled	100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
56	c6bhuA_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: cryo-em structure of atp-bound, outward-facing bovine multidrug2 resistance protein 1 (mrp1)
57	c5d3mA_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
58	d3b60a1	Alignment	not modelled	100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
59	c4g1uD_	Alignment	not modelled	100.0	26	PDB header: transport protein/hydrolase Chain: D: PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
60	d1l2ta_	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
61	c4hziA_	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: crystal structure of the leptospira interrogans atpase subunit of an2 orphan abc transporter
62	c5do7B_	Alignment	not modelled	100.0	25	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
63	c5u71A_	Alignment	not modelled	100.0	22	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: structure of human cystic fibrosis transmembrane conductance regulator2 (cftr)
64	c3gd7C_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: C: PDB Molecule: fusion complex of cystic fibrosis transmembrane conductance PDBTitle: crystal structure of human nbd2 complexed with n6-phenylethyl-atp (p-2 atp)
65	c6bzfA_	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd2 in adp-bound state
66	d1jj7a_	Alignment	not modelled	100.0	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
67	c5do7A_	Alignment	not modelled	100.0	28	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
68	c5tsiA_	Alignment	not modelled	100.0	20	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: structure of the cystic fibrosis transmembrane conductance regulator2 (cftr) from zebrafish
69	c2nq2C_	Alignment	not modelled	100.0	24	PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter.
70	c3vx4D_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: D: PDB Molecule: putative abc transporter, atp-binding protein coma; PDBTitle: crystal structure of the nucleotide-binding domain of s. mutans coma,2 a bifunctional atp-binding cassette transporter involved in the3 quorum-sensing pathway
71	c5wuaF_	Alignment	not modelled	100.0	19	PDB header: transport protein Chain: F: PDB Molecule: sur1; PDBTitle: structure of a pancreatic atp-sensitive potassium channel
72	c5idvA_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: structure of the nucleotide binding domain of an abc transporter msba2 from acinetobacter baumannii
73	c2d2fA_	Alignment	not modelled	100.0	22	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufC from thermus2 thermophilus hb8
74	d2onka1	Alignment	not modelled	100.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
75	d2hyda1	Alignment	not modelled	100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like

76	c5nj3B_	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
77	c3nhaA_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 6, mitochondrial; PDBTitle: nucleotide binding domain of human abcb6 (adp mg bound structure)
78	c5l22B_	Alignment	not modelled	100.0	24	PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prtd t1ss abc transporter
79	c4p10B_	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: B: PDB Molecule: microcin-j25 export atp-binding/permease protein mcjd; PDBTitle: crystal structure of the antibacterial peptide abc transporter mcjd in2 an outward occluded state
80	c6bzsA_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd1 in apo state
81	c4mycC_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: C: PDB Molecule: iron-sulfur clusters transporter atm1, mitochondrial; PDBTitle: structure of the mitochondrial abc transporter, atm1
82	c2d3wB_	Alignment	not modelled	100.0	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufC; PDBTitle: crystal structure of escherichia coli sufC, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
83	c2cbzA_	Alignment	not modelled	100.0	22	PDB header: transport Chain: A: PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: structure of the human multidrug resistance protein 12 nucleotide binding domain 1
84	c4ry2A_	Alignment	not modelled	100.0	22	PDB header: transport protein/hydrolase Chain: A: PDB Molecule: abc-type bacteriocin transporter; PDBTitle: crystal structure of the peptidase-containing abc transporter pcat1
85	c4mrnB_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: B: PDB Molecule: abc transporter related protein; PDBTitle: structure of a bacterial atm1-family abc transporter
86	c2hydB_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
87	c3qf4A_	Alignment	not modelled	100.0	28	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
88	c3wmeA_	Alignment	not modelled	100.0	21	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette, sub-family b, member 1; PDBTitle: crystal structure of an inward-facing eukaryotic abc multidrug2 transporter
89	c2ihyB_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter
90	c5mkkA_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
91	c5ochH_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: H: PDB Molecule: atp-binding cassette sub-family b member 8, mitochondrial; PDBTitle: the crystal structure of human abcb8 in an outward-facing state
92	c5u1dA_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: A: PDB Molecule: antigen peptide transporter 1; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
93	c5mkkB_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance abc transporter atp-binding and PDBTitle: crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
94	c2yl4A_	Alignment	not modelled	100.0	25	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
95	d1pf4a1	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
96	c2pzfB_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
97	c5ochF_	Alignment	not modelled	100.0	25	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
98	c3qf4B_	Alignment	not modelled	100.0	22	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
99	c3b5xB_	Alignment	not modelled	100.0	28	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba;

						PDBTitle: crystal structure of msba from vibrio cholerae
100	d1xmia_	Alignment	not modelled	100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
101	c1yqtA_	Alignment	not modelled	100.0	27	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
102	c2pjzA_	Alignment	not modelled	100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st1066; PDBTitle: the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066
103	c3b5wE_	Alignment	not modelled	100.0	24	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
104	d2awna2	Alignment	not modelled	100.0	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
105	c3ozxA_	Alignment	not modelled	100.0	25	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
106	d1r0wa_	Alignment	not modelled	100.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
107	c5b57D_	Alignment	not modelled	100.0	24	PDB header: metal transport Chain: D: PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: inward-facing conformation of abc heme importer bhuv from2 burkholderia cenocepacia
108	d1l7vc_	Alignment	not modelled	100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
109	c5dgxA_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: 1.73 angstrom resolution crystal structure of the abc-atpase domain2 (residues 357-609) of lipid a transport protein (msba) from3 francisella tularensis subsp. tularensis schu s4 in complex with adp
110	c4aa3A_	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter,2 abcb10 (plate form)
111	c2ghID_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance protein 2
112	c5c76D_	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: D: PDB Molecule: wlab protein; PDBTitle: atp-driven lipid-linked oligosaccharide flippase pgkI in apo-inward2 facing state (2)
113	d1sgwa_	Alignment	not modelled	100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
114	c5u1dB_	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: B: PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
115	c3bk7A_	Alignment	not modelled	100.0	26	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-I inhibitor protein from2 pyrococcus abyssi
116	c4finA_	Alignment	not modelled	100.0	27	PDB header: atp-binding protein Chain: A: PDB Molecule: etta (yijk) abcf family protein; PDBTitle: crystal structure of etta (formerly yijk) - an e. coli abc-type atpase
117	c5zxdB_	Alignment	not modelled	100.0	22	PDB header: translation Chain: B: PDB Molecule: atp-binding cassette sub-family f member 1; PDBTitle: crystal structure of atp-bound human abcf1
118	c6n9IA_	Alignment	not modelled	100.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp
119	c3j16B_	Alignment	not modelled	100.0	20	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
120	c2r6fA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra