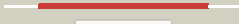



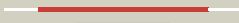












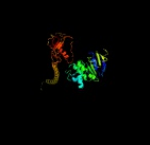



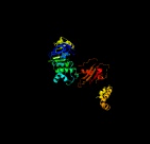


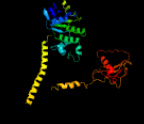

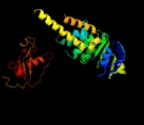
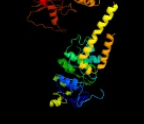





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1668c_(-)_1894231_1895349
Date	Fri Aug 2 13:30:26 BST 2019
Unique Job ID	d16a4795efc5f35d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4finA_</a>	 Alignment		100.0	35	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> etta (yjjk) abcf family protein; <b>PDBTitle:</b> crystal structure of etta (formerly yjjk) - an e. coli abc-type atpase
2	<a href="#">c1yqtA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A; <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> rnase-I inhibitor
3	<a href="#">c2iw3B_</a>	 Alignment		100.0	23	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor 3a; <b>PDBTitle:</b> elongation factor 3 in complex with adp
4	<a href="#">c5zxdB_</a>	 Alignment		100.0	31	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> atp-binding cassette sub-family f member 1; <b>PDBTitle:</b> crystal structure of atp-bound human abcf1
5	<a href="#">c4f4cA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase,protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> multidrug resistance protein pgp-1; <b>PDBTitle:</b> the crystal structure of the multi-drug transporter
6	<a href="#">c3ozxA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase, translation <b>Chain:</b> A; <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
7	<a href="#">c3bk7A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A; <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abce1/rnaase-I inhibitor protein from2 pyrococcus abyssi
8	<a href="#">c3j16B_</a>	 Alignment		100.0	23	<b>PDB header:</b> ribosome <b>Chain:</b> B; <b>PDB Molecule:</b> rli1p; <b>PDBTitle:</b> models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
9	<a href="#">c6c3oE_</a>	 Alignment		100.0	25	<b>PDB header:</b> transport protein <b>Chain:</b> E; <b>PDB Molecule:</b> atp-binding cassette sub-family c member 8; <b>PDBTitle:</b> cryo-em structure of human katp bound to atp and adp in quatrefoil2 form
10	<a href="#">c3g5uB_</a>	 Alignment		100.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> multidrug resistance protein 1a; <b>PDBTitle:</b> structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
11	<a href="#">c6c0vA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> multidrug resistance protein 1; <b>PDBTitle:</b> molecular structure of human p-glycoprotein in the atp-bound, outward-2 facing conformation

12	<a href="#">c4tqvO_</a>	Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> O: <b>PDB Molecule:</b> algs; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
13	<a href="#">c5uj9A_</a>	Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> bovine multidrug resistance protein 1 (mrp1),multidrug <b>PDBTitle:</b> cryo-em structure of bovine multidrug resistance protein 1 (mrp1)
14	<a href="#">c5ujaA_</a>	Alignment		100.0	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> bovine multidrug resistance protein 1 (mrp1),multidrug <b>PDBTitle:</b> cryo-em structure of bovine multidrug resistance protein 1 (mrp1)2 bound to leukotriene c4
15	<a href="#">c6bhuA_</a>	Alignment		100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance-associated protein 1; multidrug2 resistance protein 1 (mrp1) <b>PDBTitle:</b> cryo-em structure of atp-bound, outward-facing bovine multidrug2 resistance protein 1 (mrp1)
16	<a href="#">c5ykhH_</a>	Alignment		100.0	25	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> atp-binding cassette sub-family c member 8 isoform x2; <b>PDBTitle:</b> structure of pancreatic atp-sensitive potassium channel bound with2 glibenclamide and atpgammas (3d class1 at 4.33a)
17	<a href="#">c5wuaF_</a>	Alignment		100.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> sur1; <b>PDBTitle:</b> structure of a pancreatic atp-sensitive potassium channel
18	<a href="#">c5xjyA_</a>	Alignment		100.0	27	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family a member 1; <b>PDBTitle:</b> cryo-em structure of human abca1
19	<a href="#">c5tsiaA_</a>	Alignment		100.0	23	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cystic fibrosis transmembrane conductance regulator; <b>PDBTitle:</b> structure of the cystic fibrosis transmembrane conductance regulator2 (cftr) from zebrafish
20	<a href="#">c2yyzA_</a>	Alignment		100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of sugar abc transporter, atp-binding protein
21	<a href="#">c5u71A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cystic fibrosis transmembrane conductance regulator; <b>PDBTitle:</b> structure of human cystic fibrosis transmembrane conductance regulator2 (cftr)
22	<a href="#">c1oxtB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp binding protein; <b>PDBTitle:</b> crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
23	<a href="#">c1q1bD_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> maltose/maltodextrin transport atp-binding protein malk; <b>PDBTitle:</b> crystal structure of e. coli malk in the nucleotide-free form
24	<a href="#">c2olkD_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> amino acid abc transporter; <b>PDBTitle:</b> abc protein artp in complex with adp-beta-s
25	<a href="#">c2it1B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> 362aa long hypothetical maltose/maltodextrin <b>PDBTitle:</b> structure of ph0203 protein from pyrococcus horikoshii
26	<a href="#">c3fvqB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fe(3+) ions import atp-binding protein fbpc; <b>PDBTitle:</b> crystal structure of the nucleotide binding domain fbpc complexed with2 atp
27	<a href="#">c2d62A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multiple sugar-binding transport atp-binding <b>PDBTitle:</b> crystal structure of multiple sugar binding transport atp-2 binding protein
						<b>PDB header:</b> transport protein

28	<a href="#">c4u02C_</a>	Alignment	not modelled	100.0	23	<b>Chain:</b> C: <b>PDB Molecule:</b> amino acid abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of apo-ttha1159
29	<a href="#">c3dhwC_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> membrane protein/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> methionine import atp-binding protein metn; <b>PDBTitle:</b> crystal structure of methionine importer metni
30	<a href="#">d1g2912</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
31	<a href="#">c5lj7B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
32	<a href="#">c5ws4A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
33	<a href="#">c1z47B_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc-transporter atp-binding protein; <b>PDBTitle:</b> structure of the atpase subunit cysa of the putative sulfate atp-2 binding cassette (abc) transporter from alicyclobacillus3 acidocaldarius
34	<a href="#">c1vciA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transport atp-binding protein; <b>PDBTitle:</b> crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
35	<a href="#">c5nikK_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of the macab-tolc abc-type tripartite multidrug efflux pump
36	<a href="#">c4ymuJ_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> protein binding/transport protein <b>Chain:</b> J: <b>PDB Molecule:</b> abc-type polar amino acid transport system, atpase <b>PDBTitle:</b> crystal structure of an amino acid abc transporter complex with2 arginines and atps
37	<a href="#">c4rvcA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of atp binding subunit of abc transporter
38	<a href="#">c5x40A_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cobalt abc transporter atp-binding protein; <b>PDBTitle:</b> structure of a cbio dimer bound with amppcp
39	<a href="#">d1oxk2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
40	<a href="#">d3dhwC1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
41	<a href="#">c4wbsA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter related; <b>PDBTitle:</b> crystal structure of an abc transporter related protein from2 burkholderia phymatum
42	<a href="#">c2pcjB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system atp-binding protein lold; <b>PDBTitle:</b> crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
43	<a href="#">d3d31a2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
44	<a href="#">c5x5yB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-binding component of abc transporter; <b>PDBTitle:</b> a membrane protein complex
45	<a href="#">c3d31B_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, atp-binding protein; <b>PDBTitle:</b> modbc from methanosarcina acetivorans
46	<a href="#">d1b0ua_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
47	<a href="#">c3gfoA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> atp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cobalt import atp-binding protein cbio 1; <b>PDBTitle:</b> structure of cbio1 from clostridium perfringens: part of the abc2 transporter complex cbionq.
48	<a href="#">d1g6ha_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
49	<a href="#">d1v43a3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
50	<a href="#">c4fwiB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc-type dipeptide/oligopeptide/nickel transport system, <b>PDBTitle:</b> crystal structure of the nucleotide-binding domain of a dipeptide abc2 transporter
51	<a href="#">c4p31B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide export system atp-binding protein lptb; <b>PDBTitle:</b> crystal structure of a selenomethionine derivative of e. coli lptb in2 complex with adp-magnesium

52	<a href="#">c6ic4l_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
53	<a href="#">c2nq2C_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical abc transporter atp-binding protein <b>PDBTitle:</b> an inward-facing conformation of a putative metal-chelate2 type abc transporter.
54	<a href="#">d1ji0a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
55	<a href="#">c4yerB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> crystal structure of an abc transporter atp-binding protein (tm_1403)2 from thermotoga maritima msb8 at 2.35 a resolution
56	<a href="#">d1vp1a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
57	<a href="#">c6n91A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> crystal structure of t. maritima uvra d117-399 with adp
58	<a href="#">c4g1uD_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transport protein/hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> hemin import atp-binding protein hmuV; <b>PDBTitle:</b> x-ray structure of the bacterial heme transporter hmuV from yersinia2 pestis
59	<a href="#">c4mkiB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> cobalt transporter atp-binding subunit
60	<a href="#">c4hziA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> crystal structure of the leptospira interrogans atpase subunit of an2 orphan abc transporter
61	<a href="#">d1l2ta_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
62	<a href="#">c5xu1A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
63	<a href="#">c4hluC_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> structure of the ecfa-a' heterodimer bound to adp
64	<a href="#">d1jj7a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
65	<a href="#">c5x7kB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipase b; <b>PDBTitle:</b> crystal structure of the nucleotide-binding domain (nbd) of lipb, a2 abc transporter subunit of a type i secretion system
66	<a href="#">c3gd7C_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> fusion complex of cystic fibrosis transmembrane conductance <b>PDBTitle:</b> crystal structure of human nbd2 complexed with n6-phenylethyl-atp (p-2 atp)
67	<a href="#">c3ux8A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc, a subunit; <b>PDBTitle:</b> crystal structure of uvra
68	<a href="#">c4hzuB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein ecfa <b>PDBTitle:</b> structure of a bacterial energy-coupling factor transporter
69	<a href="#">c5mkkB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
70	<a href="#">c5d3mF_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> folate ecf transporter: amppnp bound state
71	<a href="#">d2pmka1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
72	<a href="#">c2yz2B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc transporter atp-binding protein tm_0222; <b>PDBTitle:</b> crystal structure of the abc transporter in the cobalt transport2 system
73	<a href="#">c4huqB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein ecfa <b>PDBTitle:</b> crystal structure of a transporter
74	<a href="#">c4mycC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> iron-sulfur clusters transporter atm1, mitochondrial; <b>PDBTitle:</b> structure of the mitochondrial abc transporter, atm1
75	<a href="#">c2yl4A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 10, <b>PDBTitle:</b> structure of the human mitochondrial abc transporter, abcb10
76	<a href="#">d3b60a1</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like

77	<a href="#">c4mrnB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter related protein; <b>PDBTitle:</b> structure of a bacterial atm1-family abc transporter
78	<a href="#">c5u1dA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> antigen peptide transporter 1; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
79	<a href="#">c6bzaA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance-associated protein 6; <b>PDBTitle:</b> human abcc6 nbd2 in adp-bound state
80	<a href="#">c5ochH_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 8, mitochondrial; <b>PDBTitle:</b> the crystal structure of human abcb8 in an outward-facing state
81	<a href="#">c3qf4A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
82	<a href="#">c4ry2A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transport protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type bacteriocin transporter; <b>PDBTitle:</b> crystal structure of the peptidase-containing abc transporter pcat1
83	<a href="#">c4pl0B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> microcin-j25 export atp-binding/permease protein mcjd; <b>PDBTitle:</b> crystal structure of the antibacterial peptide abc transporter mcjd in2 an outward occluded state
84	<a href="#">c6bzaA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance-associated protein 6; <b>PDBTitle:</b> human abcc6 nbd1 in apo state
85	<a href="#">c5mkkA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
86	<a href="#">c3wmeA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette, sub-family b, member 1; <b>PDBTitle:</b> crystal structure of an inward-facing eukaryotic abc multidrug2 transporter
87	<a href="#">c5l22B_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter (hlyb subfamily); <b>PDBTitle:</b> prtD t1ss abc transporter
88	<a href="#">d1mv5a_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
89	<a href="#">c2hydB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter homolog; <b>PDBTitle:</b> multidrug abc transporter sav1866
90	<a href="#">c6amxA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter; <b>PDBTitle:</b> crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
91	<a href="#">c5d3mA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> folate ecf transporter: amppnp bound state
92	<a href="#">c3qf4B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized abc transporter atp-binding protein <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
93	<a href="#">c3nhaA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 6, mitochondrial; <b>PDBTitle:</b> nucleotide binding domain of human abcb6 (adp mg bound structure)
94	<a href="#">c2d2fA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sufc protein; <b>PDBTitle:</b> crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
95	<a href="#">c3vx4D_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative abc transporter, atp-binding protein coma; <b>PDBTitle:</b> crystal structure of the nucleotide-binding domain of s. mutans coma,2 a bifunctional atp-binding cassette transporter involved in the3 quorum-sensing pathway
96	<a href="#">c5idvA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> structure of the nucleotide binding domain of an abc transporter msba2 from acinetobacter baumannii
97	<a href="#">c5ochF_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 8, mitochondrial; <b>PDBTitle:</b> the crystal structure of human abcb8 in an outward-facing state
98	<a href="#">c2ihyB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter
99	<a href="#">c2cbzA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance-associated protein 1; <b>PDBTitle:</b> structure of the human multidrug resistance protein 12 nucleotide binding domain 1 <b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> ato-bindino cassette sub-family a member

100	<a href="#">c5do7B_</a>	Alignment	not modelled	100.0	29	8; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
101	<a href="#">d2hyda1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
102	<a href="#">c2pzfB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cystic fibrosis transmembrane conductance regulator; <b>PDBTitle:</b> minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
103	<a href="#">d2onka1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
104	<a href="#">c5do7A_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 5; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
105	<a href="#">c2pjzA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein st1066; <b>PDBTitle:</b> the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066
106	<a href="#">c2d3wB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent transporter sufc; <b>PDBTitle:</b> crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
107	<a href="#">c3b5wE_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> crystal structure of eschericia coli msba
108	<a href="#">c5c76D_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> wlab protein; <b>PDBTitle:</b> atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
109	<a href="#">c4aa3A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 10, <b>PDBTitle:</b> structure of the human mitochondrial abc transporter,2 abcb10 (plate form)
110	<a href="#">c5u1dB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> antigen peptide transporter 2; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
111	<a href="#">c3b5xB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> crystal structure of msba from vibrio cholerae
112	<a href="#">d1xmia_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
113	<a href="#">c5nj3B_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 2; <b>PDBTitle:</b> structure of an abc transporter: complete structure
114	<a href="#">c5b57D_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> metal transport <b>Chain:</b> D: <b>PDB Molecule:</b> hemin import atp-binding protein hmuV; <b>PDBTitle:</b> inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
115	<a href="#">d2awna2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
116	<a href="#">d1pf4a1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
117	<a href="#">d1r0wa_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
118	<a href="#">d1sgwa_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
119	<a href="#">c5d9xA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> 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
120	<a href="#">c2ghiD_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> transport protein; <b>PDBTitle:</b> crystal structure of plasmodium yoelii multidrug resistance protein 2