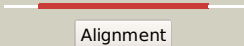

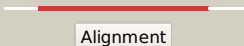

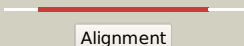


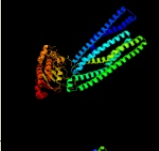




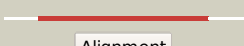
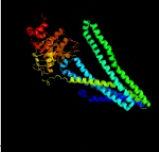



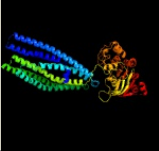






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1273c_(-)_1422308_1424056
Date	Wed Jul 31 22:05:36 BST 2019
Unique Job ID	51671a5c1f433625

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qf4A_	 Alignment		100.0	38	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
2	c5mkkB_	 Alignment		100.0	27	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
3	c5mkkA_	 Alignment		100.0	30	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
4	c5ochF_	 Alignment		100.0	28	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
5	c4ry2A_	 Alignment		100.0	23	PDB header: transport protein/hydrolase Chain: A: PDB Molecule: abc-type bacteriocin transporter; PDBTitle: crystal structure of the peptidase-containing abc transporter pcat1
6	c2hydB_	 Alignment		100.0	27	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
7	c3qf4B_	 Alignment		100.0	28	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
8	c2yl4A_	 Alignment		100.0	28	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
9	c5u1dA_	 Alignment		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
10	c3wmeA_	 Alignment		100.0	27	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
11	c4mycC_	 Alignment		100.0	23	PDB header: transport protein Chain: C: PDB Molecule: iron-sulfur clusters transporter atm1, mitochondrial; PDBTitle: structure of the mitochondrial abc transporter, atm1

12	c4aa3A_	Alignment		100.0	28	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)
13	c3b5wE_	Alignment		100.0	27	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
14	c4mrnB_	Alignment		100.0	24	PDB header: transport protein Chain: B: PDB Molecule: abc transporter related protein; PDBTitle: structure of a bacterial atm1-family abc transporter
15	c4f4cA_	Alignment		100.0	26	PDB header: hydrolase,protein transport Chain: A: PDB Molecule: multidrug resistance protein pgp-1; PDBTitle: the crystal structure of the multi-drug transporter
16	c4pl0B_	Alignment		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
17	c5ochH_	Alignment		100.0	29	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
18	c5u1dB_	Alignment		100.0	26	PDB header: transport protein Chain: B: PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
19	c3g5uB_	Alignment		100.0	25	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
20	c6bhuA_	Alignment		100.0	21	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)
21	c5l22B_	Alignment	not modelled	100.0	20	PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prtd t1ss abc transporter
22	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
23	c5ykhH_	Alignment	not modelled	100.0	22	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)
24	c6c0vA_	Alignment	not modelled	100.0	25	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
25	c3b5xB_	Alignment	not modelled	100.0	26	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
26	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)
27	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
28	c5wuaF_	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: F: PDB Molecule: sur1;

						PDBTitle: structure of a pancreatic atp-sensitive potassium channel
29	c5c76D_	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: D: PDB Molecule: wlab protein; PDBTitle: atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
30	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
31	c5u71A_	Alignment	not modelled	100.0	18	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: structure of human cystic fibrosis transmembrane conductance regulator2 (cftr)
32	c3nhaA_	Alignment	not modelled	100.0	36	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)
33	c5idvA_	Alignment	not modelled	100.0	32	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
34	d3b60a1	Alignment	not modelled	100.0	42	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
35	d2pmka1	Alignment	not modelled	100.0	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
36	d2hyda1	Alignment	not modelled	100.0	40	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
37	c3vx4D_	Alignment	not modelled	100.0	36	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
38	c6bzaA_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd2 in adp-bound state
39	d1jj7a_	Alignment	not modelled	100.0	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
40	d1mv5a_	Alignment	not modelled	100.0	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
41	c2cbzA_	Alignment	not modelled	100.0	33	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
42	c6bzsa_	Alignment	not modelled	100.0	33	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd1 in apo state
43	c5xjyA_	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
44	c2iw3B_	Alignment	not modelled	100.0	13	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
45	c2r6fA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra
46	c5dgaA_	Alignment	not modelled	100.0	38	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
47	d1pf4a1	Alignment	not modelled	100.0	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
48	c2olkD_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
49	c2ghiD_	Alignment	not modelled	100.0	36	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance protein 2
50	c5x5yB_	Alignment	not modelled	100.0	22	PDB header: membrane protein Chain: B: PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex
51	c5x7kB_	Alignment	not modelled	100.0	31	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
52	c4huqB_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfa PDBTitle: crystal structure of a transporter

53	c5ws4A	Alignment	not modelled	100.0	29	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from <i>2 acinetobacter baumannii</i>
54	c4p31B	Alignment	not modelled	100.0	20	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 in 2 complex with adp-magnesium
55	c2pzfB	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cfr first nucleotide binding domain as a head-to-tail 2 dimer with delta f508
56	c4ymuj	Alignment	not modelled	100.0	32	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 with 2 arginines and atps
57	c5do7A	Alignment	not modelled	100.0	23	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
58	c3gd7C	Alignment	not modelled	100.0	27	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)
59	c4u02C	Alignment	not modelled	100.0	31	PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein; PDBTitle: crystal structure of apo-ttha1159
60	c1z47B	Alignment	not modelled	100.0	30	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 <i>alicyclobacillus3 acidocaldarius</i>
61	c5nikK	Alignment	not modelled	100.0	34	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
62	d3d31a2	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
63	c4hluC	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp
64	c3gfoA	Alignment	not modelled	100.0	23	PDB header: atp binding protein Chain: A: PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from <i>clostridium perfringens</i> : part of the abc2 transporter complex cbionq.
65	c4wbsA	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from <i>2 burkholderia phymatum</i>
66	c5lj7B	Alignment	not modelled	100.0	32	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)
67	c4tqvO	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: O: PDB Molecule: algs; PDBTitle: crystal structure of a bacterial abc transporter involved in the 2 import of the acidic polysaccharide alginate
68	d1ji0a	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
69	c2yyzA	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
70	d3dhwc1	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
71	c3fvqB	Alignment	not modelled	100.0	27	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 with 2 atp
72	c1oxtB	Alignment	not modelled	100.0	25	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 <i>sulfolobus solfataricus</i>
73	d1vpla	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
74	c2it1B	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from <i>pyrococcus horikoshii</i>
75	c4fwib	Alignment	not modelled	100.0	28	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

76	d1b0ua_	Alignment	not modelled	100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
77	c5d3mF_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: F; PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
78	c5d3mA_	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: A; PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
79	c3dhwC_	Alignment	not modelled	100.0	29	PDB header: membrane protein/hydrolase Chain: C; PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
80	d1oxxk2	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
81	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 sufcd from thermus2 thermophilus hb8
82	c4mkiB_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: cobalt transporter atp-binding subunit
83	c5x40A_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: A; PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
84	c4rvca_	Alignment	not modelled	100.0	21	PDB header: transport protein Chain: A; PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
85	d1g6ha_	Alignment	not modelled	100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
86	d1g2912	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
87	c6ic4l_	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
88	d1xmia_	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
89	c5do7B_	Alignment	not modelled	100.0	23	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
90	c1vcia_	Alignment	not modelled	100.0	24	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
91	d1r0wa_	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
92	c4hzuB_	Alignment	not modelled	100.0	26	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
93	c1q1bD_	Alignment	not modelled	100.0	27	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
94	c2d62A_	Alignment	not modelled	100.0	27	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
95	d1v43a3	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
96	c2yz2B_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: B; PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
97	d1l2ta_	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
98	c4g1uD_	Alignment	not modelled	100.0	24	PDB header: transport protein/hydrolase Chain: D; PDB Molecule: hemin import atp-binding protein hmuu; PDBTitle: x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
99	c3d31B_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: B; PDB Molecule: sulfate/molybdate abc transporter, atp-binding protein; PDBTitle: modbc from methanosarcina acetivorans
100	c2pcjB_	Alignment	not modelled	100.0	27	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
101	c4hziA_	Alignment	not modelled	100.0	18	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
102	c5xu1A_	Alignment	not modelled	100.0	32	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
103	c5nj3B_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
104	c4yerB_	Alignment	not modelled	100.0	27	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
105	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.
106	c6amxA_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
107	d2onka1	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
108	c2d3wB_	Alignment	not modelled	100.0	23	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
109	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
110	c2ihyB_	Alignment	not modelled	100.0	23	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
111	c2ygrD_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
112	d1l7vc_	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
113	c2pjzA_	Alignment	not modelled	100.0	21	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
114	c5b57D_	Alignment	not modelled	100.0	23	PDB header: metal transport Chain: D: PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
115	d1sgwa_	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
116	c3ozxA_	Alignment	not modelled	100.0	19	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
117	c4finA_	Alignment	not modelled	100.0	19	PDB header: atp-binding protein Chain: A: PDB Molecule: etta (yjjk) abcf family protein; PDBTitle: crystal structure of etta (formerly yjjk) - an e. coli abc-type atpase
118	c1yqtA_	Alignment	not modelled	100.0	23	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
119	c6n9IA_	Alignment	not modelled	100.0	22	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp
120	d2awna2	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