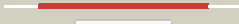



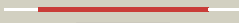

















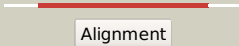
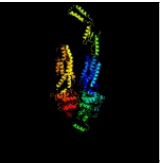





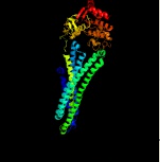



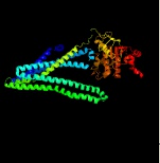
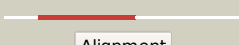
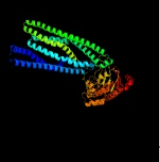

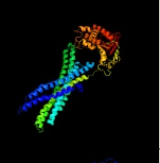





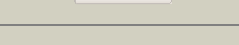

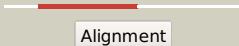




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0194 (-) _226876_230460
Date	Tue Jul 23 14:50:25 BST 2019
Unique Job ID	4815e95e7e663133

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4f4cA_	 Alignment		100.0	25	PDB header: hydrolase,protein transport Chain: A: PDB Molecule: multidrug resistance protein pgp-1; PDBTitle: the crystal structure of the multi-drug transporter
2	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)
3	c3g5uB_	 Alignment		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
4	c5ykhH_	 Alignment		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)
5	c6c0vA_	 Alignment		100.0	27	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
6	c5ujaA_	 Alignment		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
7	c5uj9A_	 Alignment		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)
8	c6c3oE_	 Alignment		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
9	c5wuaF_	 Alignment		100.0	21	PDB header: transport protein Chain: F: PDB Molecule: sur1; PDBTitle: structure of a pancreatic atp-sensitive potassium channel
10	c5tsiA_	 Alignment		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
11	c5u71A_	 Alignment		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)

12	c5xyjA_	 Alignment		100.0	16	PDB header: transport protein Chain: A; PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
13	c3qf4A_	 Alignment		100.0	27	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
14	c4ry2A_	 Alignment		100.0	25	PDB header: transport protein/hydrolase Chain: A; PDB Molecule: abc-type bacteriocin transporter; PDBTitle: crystal structure of the peptidase-containing abc transporter pcat1
15	c5mkkA_	 Alignment		100.0	31	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
16	c5mkkB_	 Alignment		100.0	33	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
17	c3qf4B_	 Alignment		100.0	30	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
18	c5ochF_	 Alignment		100.0	30	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
19	c2hydB_	 Alignment		100.0	32	PDB header: transport protein Chain: B; PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
20	c2yl4A_	 Alignment		100.0	31	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
21	c3wmeA_	 Alignment	not modelled	100.0	29	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
22	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
23	c4mrnB_	 Alignment	not modelled	100.0	28	PDB header: transport protein Chain: B; PDB Molecule: abc transporter related protein; PDBTitle: structure of a bacterial atm1-family abc transporter
24	c4aa3A_	 Alignment	not modelled	100.0	30	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)
25	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
26	c3b5wE_	 Alignment	not modelled	100.0	28	PDB header: membrane protein Chain: E; PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
27	c4pl0B_	 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
		 Alignment				PDB header: transport protein Chain: B; PDB Molecule: uncharacterized abc transporter atp-binding protein

28	c5u1dB_	Alignment	not modelled	100.0	27	Chain: B: PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
29	c5ochH_	Alignment	not modelled	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
30	c5l22B_	Alignment	not modelled	100.0	22	PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prtd t1ss abc transporter
31	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
32	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)
33	c2iw3B_	Alignment	not modelled	100.0	16	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
34	c2r6fA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra
35	c4finA_	Alignment	not modelled	100.0	26	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
36	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
37	c1yqtA_	Alignment	not modelled	100.0	28	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
38	c3ozxA_	Alignment	not modelled	100.0	22	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
39	c3bk7A_	Alignment	not modelled	100.0	29	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
40	c6n9lA_	Alignment	not modelled	100.0	26	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp
41	c3j16B_	Alignment	not modelled	100.0	30	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
42	c3nhaA_	Alignment	not modelled	100.0	38	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)
43	c2ygrD_	Alignment	not modelled	100.0	40	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
44	c5ykeB_	Alignment	not modelled	100.0	19	PDB header: membrane protein Chain: B: 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 (focused refinement on tm at 4.11a)
45	c3ux8A_	Alignment	not modelled	100.0	27	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc, a subunit; PDBTitle: crystal structure of uvra
46	c3pihA_	Alignment	not modelled	100.0	36	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
47	c5idvA_	Alignment	not modelled	100.0	38	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
48	d2pmka1	Alignment	not modelled	100.0	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
49	c3zqjC_	Alignment	not modelled	100.0	39	PDB header: dna binding protein Chain: C: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
50	d2hyda1	Alignment	not modelled	100.0	45	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
51	d3b60a1	Alignment	not modelled	100.0	44	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
52	c2vf7B_	Alignment	not modelled	100.0	26	PDB header: dna binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
53	c3vx4D_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: D: PDB Molecule: putative abc transporter, atp-binding protein coma;

53	c3vx4D_	Alignment	not modelled	100.0	30	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
54	c6bzxA_	Alignment	not modelled	100.0	33	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd2 in adp-bound state
55	d1jj7a_	Alignment	not modelled	100.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
56	d1mv5a_	Alignment	not modelled	100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
57	c3zqjF_	Alignment	not modelled	100.0	33	PDB header: dna binding protein Chain: F: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvrA
58	c6bzsa_	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd1 in apo state
59	c2cbzA_	Alignment	not modelled	100.0	26	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
60	c5dgxA_	Alignment	not modelled	100.0	36	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
61	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
62	c5do7A_	Alignment	not modelled	100.0	19	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
63	c5x7kB_	Alignment	not modelled	100.0	30	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
64	d1pf4a1	Alignment	not modelled	100.0	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
65	c2olkD_	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
66	c2pzfB_	Alignment	not modelled	100.0	28	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
67	c3gd7C_	Alignment	not modelled	100.0	29	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)
68	c5x5yB_	Alignment	not modelled	100.0	24	PDB header: membrane protein Chain: B: PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex
69	c5ws4A_	Alignment	not modelled	100.0	27	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
70	c5do7B_	Alignment	not modelled	100.0	19	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
71	c2vyzA_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
72	c4hluC_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp
73	c4p31B_	Alignment	not modelled	100.0	21	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
74	c3gfoA_	Alignment	not modelled	100.0	25	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.
75	c1z47B_	Alignment	not modelled	100.0	29	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
76	c4wbsA_	Alignment	not modelled	100.0	21	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein

						from2 burkholderia phymatum
77	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
78	d3dhwc1	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
79	d1loxk2	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
80	c4ymuJ_	Alignment	not modelled	100.0	29	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
81	c1oxtB_	Alignment	not modelled	100.0	28	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
82	c2it1B_	Alignment	not modelled	100.0	31	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
83	d1ji0a_	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
84	c3fvqB_	Alignment	not modelled	100.0	29	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
85	c4tqvO_	Alignment	not modelled	100.0	29	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
86	c5lj7B_	Alignment	not modelled	100.0	25	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)
87	c5nj3B_	Alignment	not modelled	100.0	17	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
88	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
89	d1vpla_	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
90	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
91	c5d3mF_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: F: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
92	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
93	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
94	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
95	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
96	c5nikK_	Alignment	not modelled	100.0	29	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
97	d1r0wa_	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	c3dhwC_	Alignment	not modelled	100.0	30	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
99	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
100	c1vciA_	Alignment	not modelled	100.0	27	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
101	c5x40A_	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp

102	d1g2912	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
103	c2d2fA	Alignment	not modelled	100.0	21	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufC from thermus2 thermophilus hb8
104	c4fwiB	Alignment	not modelled	100.0	27	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
105	c6ic4I	Alignment	not modelled	100.0	29	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
106	c4mkiB	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: cobalt transporter atp-binding subunit
107	c1q1bD	Alignment	not modelled	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
108	c2d62A	Alignment	not modelled	100.0	26	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
109	c2yz2B	Alignment	not modelled	100.0	32	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
110	c4g1uD	Alignment	not modelled	100.0	27	PDB header: transport protein/hydrolase Chain: D: PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: x-ray structure of the bacterial heme transporter hmuV from yersinia2 pestis
111	c5d3mA	Alignment	not modelled	100.0	30	PDB header: transport protein Chain: A: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
112	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
113	c4hziA	Alignment	not modelled	100.0	22	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
114	c4hzuB	Alignment	not modelled	100.0	27	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
115	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
116	c3d31B	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding protein; PDBTitle: modbc from methanosarcina acetivorans
117	c5xu1A	Alignment	not modelled	100.0	29	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
118	c4yerB	Alignment	not modelled	100.0	26	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
119	d2onka1	Alignment	not modelled	100.0	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
120	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.