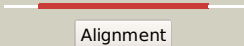

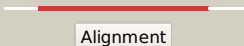

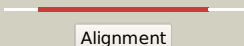







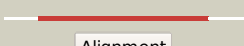











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1687c_(-)_1912160_1912927
Date	Fri Aug 2 13:30:28 BST 2019
Unique Job ID	8a324af4cc4ab306

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yyzA_	 Alignment		100.0	28	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
2	c1q1bD_	 Alignment		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
3	c2o1kD_	 Alignment		100.0	28	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
4	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
5	c3fvqB_	 Alignment		100.0	31	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
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	c4u02C_	 Alignment		100.0	30	PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein; PDBTitle: crystal structure of apo-ttha1159
8	c4rvcA_	 Alignment		100.0	27	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
9	c6c0vA_	 Alignment		100.0	23	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
10	c2it1B_	 Alignment		100.0	29	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
11	d1vpla_	 Alignment		100.0	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like

12	c4f4cA_	Alignment		100.0	24	PDB header: hydrolase,protein transport Chain: A: PDB Molecule: multidrug resistance protein pgp-1; PDBTitle: the crystal structure of the multi-drug transporter
13	c1z47B_	Alignment		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
14	d1g2912	Alignment		100.0	29	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	28	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	c1oxtB_	Alignment		100.0	29	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
17	c6c3oE_	Alignment		100.0	23	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 quaterfoil2 form
18	c5xjvA_	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
19	c6bhuA_	Alignment		100.0	25	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)
20	c4wbsA_	Alignment		100.0	30	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from2 burkholderia phymatum
21	c4ymuj_	Alignment	not modelled	100.0	28	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
22	d1b0ua_	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
23	c5x5yB_	Alignment	not modelled	100.0	30	PDB header: membrane protein Chain: B: PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex
24	d1oxxk2	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
25	c5ujaA_	Alignment	not modelled	100.0	24	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
26	c5uj9A_	Alignment	not modelled	100.0	24	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	c4p31B_	Alignment	not modelled	100.0	31	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 PDB header: membrane protein

28	c5ykfH_	Alignment	not modelled	100.0	23	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)
29	c5nikK_	Alignment	not modelled	100.0	26	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
30	d3dhwc1	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
31	c4hluC_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp
32	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
33	c1vciA_	Alignment	not modelled	100.0	26	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
34	d3d31a2	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
35	d1jj0a_	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
36	c3gfoA_	Alignment	not modelled	100.0	26	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.
37	c2d62A_	Alignment	not modelled	100.0	30	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
38	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
39	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)
40	d1g6ha_	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
41	c5lj7B_	Alignment	not modelled	100.0	26	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)
42	c5x40A_	Alignment	not modelled	100.0	33	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
43	c3d31B_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding protein; PDBTitle: modbc from methanosarcina acetivorans
44	c5wuaF_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: F: PDB Molecule: sur1; PDBTitle: structure of a pancreatic atp-sensitive potassium channel
45	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
46	d1v43a3	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
47	c5mkkB_	Alignment	not modelled	100.0	26	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
48	c5tsiA_	Alignment	not modelled	100.0	24	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
49	c4mrnB_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: B: PDB Molecule: abc transporter related protein; PDBTitle: structure of a bacterial atm1-family abc transporter
50	c4mycC_	Alignment	not modelled	100.0	20	PDB header: transport protein Chain: C: PDB Molecule: iron-sulfur clusters transporter atm1, mitochondrial; PDBTitle: structure of the mitochondrial abc transporter, atm1
51	c2pcjB_	Alignment	not modelled	100.0	23	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
52	d2pmka1	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
53	c4ry2A	Alignment	not modelled	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
54	c4huqB	Alignment	not modelled	100.0	27 PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfa PDBTitle: crystal structure of a transporter
55	c4yerB	Alignment	not modelled	100.0	29 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
56	c3qf4A	Alignment	not modelled	100.0	24 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
57	c3wmeA	Alignment	not modelled	100.0	22 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
58	c2hydB	Alignment	not modelled	100.0	22 PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
59	c5l22B	Alignment	not modelled	100.0	28 PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prt1 t1ss abc transporter
60	c5u1dA	Alignment	not modelled	100.0	24 PDB header: transport protein Chain: A: PDB Molecule: antigen peptide transporter 1; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
61	c4pl0B	Alignment	not modelled	100.0	25 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
62	c5mkkA	Alignment	not modelled	100.0	25 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
63	c5ochH	Alignment	not modelled	100.0	24 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
64	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
65	c5x7kB	Alignment	not modelled	100.0	28 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
66	c5xu1A	Alignment	not modelled	100.0	26 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
67	c3nhaA	Alignment	not modelled	100.0	26 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)
68	c2yz2B	Alignment	not modelled	100.0	24 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
69	c2yl4A	Alignment	not modelled	100.0	27 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
70	c4g1uD	Alignment	not modelled	100.0	29 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
71	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
72	c5idvA	Alignment	not modelled	100.0	24 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	c4hziA	Alignment	not modelled	100.0	21 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
74	c3qf4B	Alignment	not modelled	100.0	20 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
75	c5d3mE	Alignment	not modelled	100.0	20 PDB header: transport protein Chain: F: PDB Molecule: energy-coupling factor transporter atp-

75	c3g9m1	Alignment	not modelled	100.0	30	binding protein PDBTitle: folate ecf transporter: amppnp bound state
76	c6bzaA	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd2 in adp-bound state
77	c5do7B	Alignment	not modelled	100.0	26	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
78	c4mkiB	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: cobalt transporter atp-binding subunit
79	c5ochF	Alignment	not modelled	100.0	24	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
80	d3b60a1	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
81	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
82	d2hyda1	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
83	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
84	c2d2fA	Alignment	not modelled	100.0	20	PDB header: protein binding Chain: A: PDB Molecule: suflc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase suflc from thermus2 thermophilus hb8
85	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
86	c3b5wE	Alignment	not modelled	100.0	25	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
87	c3b5xB	Alignment	not modelled	100.0	25	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
88	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.
89	c4hzuB	Alignment	not modelled	100.0	31	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
90	c6bzsa	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd1 in apo state
91	c6amxA	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
92	c3gd7C	Alignment	not modelled	100.0	21	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)
93	d1l2ta	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
94	c2cbzA	Alignment	not modelled	100.0	21	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
95	c4aa3A	Alignment	not modelled	100.0	27	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)
96	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
97	d1pf4a1	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
98	c2pzfB	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cfr first nucleotide binding domain as a head-to-tail2 dimer with delta f508 PDB header: transport protein

99	c5c76D_	Alignment	not modelled	100.0	23	Chain: D: PDB Molecule: wlab protein; PDBTitle: atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
100	d2onka1	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
101	c2d3wB_	Alignment	not modelled	100.0	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcc; PDBTitle: crystal structure of escherichia coli sufcc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
102	c5nj3B_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
103	c5u1dB_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: B: PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
104	d2awna2	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
105	c1yqtA_	Alignment	not modelled	100.0	22	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
106	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
107	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
108	d1r0wa_	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
109	c2pjzA_	Alignment	not modelled	100.0	25	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
110	c2ghID_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance protein 2
111	c5b57D_	Alignment	not modelled	100.0	26	PDB header: metal transport Chain: D: PDB Molecule: hemin import atp-binding protein hmuu; PDBTitle: inward-facing conformation of abc heme importer bhuvv from2 burkholderia cenocepacia
112	c3ozxA_	Alignment	not modelled	100.0	24	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
113	d1l7vc_	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
114	c4finA_	Alignment	not modelled	100.0	25	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
115	d1sgwa_	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
116	c2r6fA_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra
117	c5zxdB_	Alignment	not modelled	100.0	20	PDB header: translation Chain: B: PDB Molecule: atp-binding cassette sub-family f member 1; PDBTitle: crystal structure of atp-bound human abcf1
118	c3bk7A_	Alignment	not modelled	100.0	23	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
119	c6n9lA_	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	c3j16B_	Alignment	not modelled	100.0	21	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners