

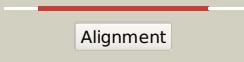

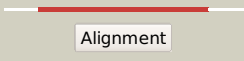
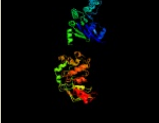
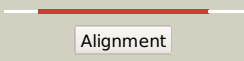

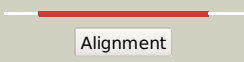

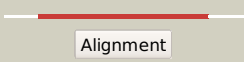

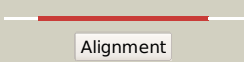

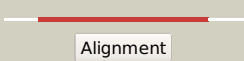

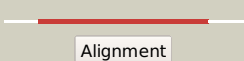

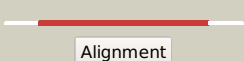

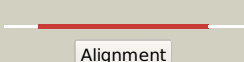












Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3663c_(dppD)_4102210_4103856
 Date Fri Aug 9 18:20:35 BST 2019
 Unique Job ID 1e8eae2cbb0d236e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yqtA_	 Alignment		100.0	24	PDB header: hydrolyase/translation Chain: A; PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
2	c5zxdB_	 Alignment		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
3	c4finA_	 Alignment		100.0	26	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
4	c5xjyA_	 Alignment		100.0	27	PDB header: transport protein Chain: A; PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
5	c2iw3B_	 Alignment		100.0	19	PDB header: translation Chain: B; PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
6	c3ozxA_	 Alignment		100.0	19	PDB header: hydrolase, translation Chain: A; PDB Molecule: rnase I inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
7	c4f4cA_	 Alignment		100.0	31	PDB header: hydrolase,protein transport Chain: A; PDB Molecule: multidrug resistance protein pgp-1; PDBTitle: the crystal structure of the multi-drug transporter
8	c3bk7A_	 Alignment		100.0	25	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
9	c3g5uB_	 Alignment		100.0	35	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
10	c6c0vA_	 Alignment		100.0	35	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
11	c3j16B_	 Alignment		100.0	19	PDB header: ribosome Chain: B; PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners

12	c6c3oE_	Alignment		100.0	26	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
13	c6n9lA_	Alignment		100.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp
14	c5uj9A_	Alignment		100.0	25	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)
15	c5ujaA_	Alignment		100.0	26	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
16	c6bhuA_	Alignment		100.0	26	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)
17	c5ykh_	Alignment		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)
18	c3ux8A_	Alignment		100.0	28	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc, a subunit; PDBTitle: crystal structure of uvra
19	c5wuaF_	Alignment		100.0	25	PDB header: transport protein Chain: F: PDB Molecule: sur1; PDBTitle: structure of a pancreatic atp-sensitive potassium channel
20	c5u7lA_	Alignment		100.0	21	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: structure of human cystic fibrosis transmembrane conductance regulator2 (cftr)
21	c5tsia_	Alignment	not modelled	100.0	23	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
22	c3zqjC_	Alignment	not modelled	100.0	30	PDB header: dna binding protein Chain: C: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
23	c3pihA_	Alignment	not modelled	100.0	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
24	c2ygrD_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
25	c3zqjF_	Alignment	not modelled	100.0	33	PDB header: dna binding protein Chain: F: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
26	c2vf7B_	Alignment	not modelled	100.0	25	PDB header: dna binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
27	c2r6fA_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearohermophilus uvra
28	c4tqvO_	Alignment	not modelled	100.0	23	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 PDB header: transport protein Chain: B: PDB Molecule: abc-type dipeptide/oligopeptide/nickel

29	c4fwIB_	Alignment	not modelled	100.0	37	transport system, PDBTitle: crystal structure of the nucleotide-binding domain of a dipeptide abc2 transporter PDB header: transport protein
30	c2yyzA_	Alignment	not modelled	100.0	26	Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
31	c2it1B_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
32	c1oxtB_	Alignment	not modelled	100.0	22	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
33	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
34	c2olkD_	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
35	d1g2912	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
36	c3fvqB_	Alignment	not modelled	100.0	26	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
37	c5ws4A_	Alignment	not modelled	100.0	30	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
38	c2d62A_	Alignment	not modelled	100.0	22	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
39	d3dhwc1	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
40	c1z47B_	Alignment	not modelled	100.0	32	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
41	c5lj7B_	Alignment	not modelled	100.0	28	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	c1vciA_	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: A: PDB Molecule: sugar-binding transport atp-binding protein; PDBTitle: crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
43	c4u02C_	Alignment	not modelled	100.0	35	PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein; PDBTitle: crystal structure of apo-ttha1159
44	c1q1bD_	Alignment	not modelled	100.0	22	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
45	c3gfoA_	Alignment	not modelled	100.0	28	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.
46	d1loxk2	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
47	d1b0ua_	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
48	c5x40A_	Alignment	not modelled	100.0	34	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
49	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 with2 arginines and atps
50	c5nikK_	Alignment	not modelled	100.0	33	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
51	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
52	c2pcjB_	Alignment	not modelled	100.0	33	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
53	c4wbsA	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from2 burkholderia phymatum
54	c5x5yB	Alignment	not modelled	100.0	26	PDB header: membrane protein Chain: B: PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex
55	c4p31B	Alignment	not modelled	100.0	27	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
56	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
57	c4rvcA	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
58	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
59	d1g6ha	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
60	c4yerB	Alignment	not modelled	100.0	25	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
61	d3d31a2	Alignment	not modelled	100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
62	d1ji0a	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
63	c5d3mF	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: F: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
64	d1l2ta	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
65	c5xu1A	Alignment	not modelled	100.0	33	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
66	c4hzuB	Alignment	not modelled	100.0	29	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
67	d1vpla	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
68	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
69	c6ic4I	Alignment	not modelled	100.0	27	PDB header: protein transport Chain: I: PDB Molecule: abc transporter atp-binding protein; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
70	c4huqB	Alignment	not modelled	100.0	33	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfA PDBTitle: crystal structure of a transporter
71	c3gd7C	Alignment	not modelled	100.0	17	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)
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	c2yz2B	Alignment	not modelled	100.0	30	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
74	d2pmka1	Alignment	not modelled	100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
75	c2d2fA	Alignment	not modelled	100.0	23	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufC from thermus2 thermophilus hb8
76	c4g1uD	Alignment	not modelled	100.0	30	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
77	c4mycC	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: C: PDB Molecule: iron-sulfur clusters transporter atm1, mitochondrial;

						PDBTitle: structure of the mitochondrial abc transporter, atm1
78	d1jj7a_	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
79	d3b60a1	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
80	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
81	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
82	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
83	c2nq2C_	Alignment	not modelled	100.0	28	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.
84	c4ry2A_	Alignment	not modelled	100.0	27	PDB header: transport protein/hydrolase Chain: A: PDB Molecule: abc-type bacteriocin transporter; PDBTitle: crystal structure of the peptidase-containing abc transporter pcat1
85	c5d3mA_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: A: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
86	c3wmeA_	Alignment	not modelled	100.0	31	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
87	c3vx4D_	Alignment	not modelled	100.0	27	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
88	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
89	d1mv5a_	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
90	c5mkkB_	Alignment	not modelled	100.0	29	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
91	c2yl4A_	Alignment	not modelled	100.0	29	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
92	c2hydB_	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
93	c2d3wB_	Alignment	not modelled	100.0	28	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
94	c3qf4A_	Alignment	not modelled	100.0	32	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
95	c5u1dA_	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: A: PDB Molecule: antigen peptide transporter 1; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
96	c5l22B_	Alignment	not modelled	100.0	27	PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prtd t1ss abc transporter
97	c3qf4B_	Alignment	not modelled	100.0	26	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
98	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
99	c5ochH_	Alignment	not modelled	100.0	28	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
100	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 PDB header: transport protein

101	c3nhaA	Alignment	not modelled	100.0	28	Chain: A; PDB Molecule: atp-binding cassette sub-family b member 6, mitochondrial; PDBTitle: nucleotide binding domain of human abcb6 (adp mg bound structure)
102	d2hyda1	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
103	c5ochF	Alignment	not modelled	100.0	29	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
104	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
105	c5do7B	Alignment	not modelled	100.0	27	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
106	c6amxA	Alignment	not modelled	100.0	19	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	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
108	c6bzsa	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: A; PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbdl in apo state
109	c5do7A	Alignment	not modelled	100.0	25	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
110	c2cbzA	Alignment	not modelled	100.0	25	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
111	c3b5wE	Alignment	not modelled	100.0	31	PDB header: membrane protein Chain: E; PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
112	c3b5xB	Alignment	not modelled	100.0	29	PDB header: membrane protein Chain: B; PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
113	c4aa3A	Alignment	not modelled	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)
114	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
115	c5b57D	Alignment	not modelled	100.0	31	PDB header: metal transport Chain: D; PDB Molecule: hemin import atp-binding protein hmuV; PDBTitle: inward-facing conformation of abc heme importer bhuv from2 burkholderia cenocepacia
116	c5nj3B	Alignment	not modelled	100.0	22	PDB header: transport protein Chain: B; PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
117	c5c76D	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: D; PDB Molecule: wlab protein; PDBTitle: atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
118	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
119	c5u1dB	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: B; PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
120	d1pf4a1	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