

Phyre2

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 Description RVBD3102c_(ftsE)_3470677_3471366
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ws4A_	Alignment		100.0	33	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
2	d3dhwc1	Alignment		100.0	40	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
3	c5lj7B_	Alignment		100.0	33	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)
4	c3dhwC_	Alignment		100.0	40	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
5	c2olkD_	Alignment		100.0	35	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
6	d1oxk2	Alignment		100.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
7	c5nikK_	Alignment		100.0	36	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
8	c4rvcA_	Alignment		100.0	23	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
9	c1oxtB_	Alignment		100.0	35	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
10	c2pcjB_	Alignment		100.0	37	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
11	c2yyzA_	Alignment		100.0	34	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein

12	c2it1B_	Alignment		100.0	38	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
13	d1g2912	Alignment		100.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
14	c5x5yB_	Alignment		100.0	26	PDB header: membrane protein Chain: B: PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex
15	c4tqvO_	Alignment		100.0	32	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
16	c4u02C_	Alignment		100.0	35	PDB header: transport protein Chain: C: PDB Molecule: amino acid abc transporter, atp-binding protein; PDBTitle: crystal structure of apo-ttha1159
17	c4p31B_	Alignment		100.0	26	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
18	c3fvqB_	Alignment		100.0	32	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
19	c1z47B_	Alignment		100.0	38	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
20	c3gfoA_	Alignment		100.0	31	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.
21	c4wbsA_	Alignment	not modelled	100.0	24	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from2 burkholderia phymatum
22	c5xu1A_	Alignment	not modelled	100.0	39	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
23	c4ymuj_	Alignment	not modelled	100.0	34	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
24	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
25	c5x40A_	Alignment	not modelled	100.0	30	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
26	c5xjyA_	Alignment	not modelled	100.0	23	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family a member 1; PDBTitle: cryo-em structure of human abca1
27	c6ic4I_	Alignment	not modelled	100.0	28	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
28	c6c0vA_	Alignment	not modelled	100.0	28	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

29	c2d62A	Alignment	not modelled	100.0	35	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
30	d1b0ua	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
31	c5ykhH	Alignment	not modelled	100.0	26	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)
32	c1q1bD	Alignment	not modelled	100.0	36	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
33	c3g5uB	Alignment	not modelled	100.0	29	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
34	c4f4cA	Alignment	not modelled	100.0	27	PDB header: hydrolase,protein transport Chain: A: PDB Molecule: multidrug resistance protein pgp-1; PDBTitle: the crystal structure of the multi-drug transporter
35	d1l2ta	Alignment	not modelled	100.0	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
36	c4fwib	Alignment	not modelled	100.0	29	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
37	c6c3oE	Alignment	not modelled	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 quatrefoil2 form
38	c5d3mF	Alignment	not modelled	100.0	30	PDB header: transport protein Chain: F: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
39	c5ujaA	Alignment	not modelled	100.0	28	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
40	d3d31a2	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
41	c5uj9A	Alignment	not modelled	100.0	28	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)
42	d1g6ha	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
43	c6bhuA	Alignment	not modelled	100.0	27	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)
44	c1vciA	Alignment	not modelled	100.0	35	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
45	d1ji0a	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
46	c5u71A	Alignment	not modelled	100.0	25	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: structure of human cystic fibrosis transmembrane conductance regulator2 (cftr)
47	d1v43a3	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
48	c5wuaF	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: F: PDB Molecule: sur1; PDBTitle: structure of a pancreatic atp-sensitive potassium channel
49	c4mkiB	Alignment	not modelled	100.0	31	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: cobalt transporter atp-binding subunit
50	c4hluC	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp
51	c4hzuB	Alignment	not modelled	100.0	35	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
52	c4vcrB	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: abc transporter atp-binding protein;

52	c4yelB_	Alignment	not modelled	100.0	28	PDBTitle: crystal structure of an abc transporter atp-binding protein (tm_1403)2 from thermotoga maritima msb8 at 2.35 a resolution
53	d2pmka1	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
54	c6bzaA_	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd2 in adp-bound state
55	c3d31B_	Alignment	not modelled	100.0	31	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding protein; PDBTitle: modbc from methanosarcina acetivorans
56	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
57	c2yl4A_	Alignment	not modelled	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
58	c5l22B_	Alignment	not modelled	100.0	27	PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prtD t1ss abc transporter
59	c3qf4A_	Alignment	not modelled	100.0	29	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
60	d3b60a1	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
61	c5tsiA_	Alignment	not modelled	100.0	25	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
62	c2yz2B_	Alignment	not modelled	100.0	33	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
63	c4hziA_	Alignment	not modelled	100.0	24	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
64	c4huqB_	Alignment	not modelled	100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: energy-coupling factor transporter atp-binding protein ecfA PDBTitle: crystal structure of a transporter
65	d1mv5a_	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
66	c3wmeA_	Alignment	not modelled	100.0	30	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
67	c4mycC_	Alignment	not modelled	100.0	30	PDB header: transport protein Chain: C: PDB Molecule: iron-sulfur clusters transporter atm1, mitochondrial; PDBTitle: structure of the mitochondrial abc transporter, atm1
68	c4pl0B_	Alignment	not modelled	100.0	23	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
69	d1lj7a_	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
70	c2hydB_	Alignment	not modelled	100.0	34	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
71	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
72	c5d3mA_	Alignment	not modelled	100.0	35	PDB header: transport protein Chain: A: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
73	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.
74	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
75	c4ry2A_	Alignment	not modelled	100.0	30	PDB header: transport protein/hydrolase Chain: A: PDB Molecule: abc-type bacteriocin transporter; PDBTitle: crystal structure of the peptidase-containing abc transporter pcat1
76	c4mrnB_	Alignment	not modelled	100.0	32	PDB header: transport protein Chain: B: PDB Molecule: abc transporter related protein; PDBTitle: structure of a bacterial atm1-family abc transporter

77	c5ochH	Alignment	not modelled	100.0	30	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
78	c5mkkB	Alignment	not modelled	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
79	c6amxA	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
80	c5u1dA	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: A: PDB Molecule: antigen peptide transporter 1; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
81	c5x7kB	Alignment	not modelled	100.0	27	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
82	c5mkkA	Alignment	not modelled	100.0	29	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
83	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 sufcr from thermus2 thermophilus hb8
84	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
85	d2hyda1	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
86	c5idvA	Alignment	not modelled	100.0	27	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
87	c3qf4B	Alignment	not modelled	100.0	29	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
88	c3nhaA	Alignment	not modelled	100.0	29	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)
89	c5nj3B	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
90	c5ochF	Alignment	not modelled	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
91	c4aa3A	Alignment	not modelled	100.0	31	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)
92	d1pf4a1	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
93	c6bzsa	Alignment	not modelled	100.0	25	PDB header: transport protein Chain: A: PDB Molecule: multidrug resistance-associated protein 6; PDBTitle: human abcc6 nbd1 in apo state
94	c5c76D	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: D: PDB Molecule: wlab protein; PDBTitle: atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
95	c3gd7C	Alignment	not modelled	100.0	20	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)
96	c2cbzA	Alignment	not modelled	100.0	23	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
97	c2d3wB	Alignment	not modelled	100.0	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcr; PDBTitle: crystal structure of escherichia coli sufcr, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
98	c3b5xB	Alignment	not modelled	100.0	30	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
99	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 PDB header: transport protein

100	c5u1dB_	Alignment	not modelled	100.0	30	Chain: B: PDB Molecule: antigen peptide transporter 2; PDBTitle: cryo-em structure of the human tap atp-binding cassette transporter
101	c2ihyB_	Alignment	not modelled	100.0	30	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
102	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
103	c2pzfB_	Alignment	not modelled	100.0	22	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
104	c1yqtA_	Alignment	not modelled	100.0	30	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
105	c5b57D_	Alignment	not modelled	100.0	25	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
106	c3ozxA_	Alignment	not modelled	100.0	23	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
107	d1sgwa_	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
108	c2pjzA_	Alignment	not modelled	100.0	28	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
109	c2ghiD_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance protein 2
110	c5dgxA_	Alignment	not modelled	100.0	27	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
111	d1xmia_	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
112	d1l7vc_	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
113	c5zxdB_	Alignment	not modelled	100.0	28	PDB header: translation Chain: B: PDB Molecule: atp-binding cassette sub-family f member 1; PDBTitle: crystal structure of atp-bound human abcf1
114	c4finA_	Alignment	not modelled	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
115	d1r0wa_	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
116	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
117	d2awna2	Alignment	not modelled	100.0	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
118	c3j16B_	Alignment	not modelled	100.0	20	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
119	c2iw3B_	Alignment	not modelled	100.0	22	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
120	c6n9lA_	Alignment	not modelled	100.0	22	PDB header: dna binding protein Chain: A: PDB Molecule: uvrac system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp