
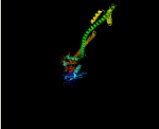
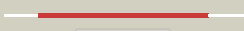






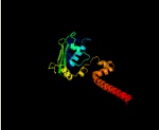



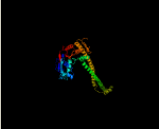
















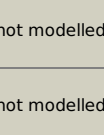


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1278 (-) _1427420_1430047
Date	Wed Jul 31 22:05:37 BST 2019
Unique Job ID	4bca94f8be533df3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xeiA_</a>	 Alignment		100.0	19	<b>PDB header:</b> dna binding protein, cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of the smc head domain with a coiled coil and joint2 derived from pyrococcus yayanosii
2	<a href="#">c4ad8A_</a>	 Alignment		99.9	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dna repair protein recn; <b>PDBTitle:</b> crystal structure of a deletion mutant of deinococcus radiodurans2 recn
3	<a href="#">c3qg5A_</a>	 Alignment		99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> rad50; <b>PDBTitle:</b> the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
4	<a href="#">c6qj1A_</a>	 Alignment		99.9	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> structural maintenance of chromosomes protein,structural <b>PDBTitle:</b> crystal structure of the c. thermophilum condensin smc2 atpase head2 (crystal from i)
5	<a href="#">c1ii8A_</a>	 Alignment		99.8	18	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> rad50 abc-atpase; <b>PDBTitle:</b> crystal structure of the p. furiosus rad50 atpase domain
6	<a href="#">c5dacA_</a>	 Alignment		99.8	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein,putative uncharacterized <b>PDBTitle:</b> atp-gamma-s bound rad50 from chaetomium thermophilum in complex with2 dna
7	<a href="#">c4ux3A_</a>	 Alignment		99.8	12	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> structural maintenance of chromosomes protein 3; <b>PDBTitle:</b> cohesin smc3-hd:scc1-n complex from yeast
8	<a href="#">c6qj2A_</a>	 Alignment		99.8	19	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> smc4; <b>PDBTitle:</b> crystal structure of the c. thermophilum condensin smc4 atpase head in2 complex with the c-terminal domain of brn1
9	<a href="#">c3auyB_</a>	 Alignment		99.8	13	<b>PDB header:</b> recombination <b>Chain:</b> B; <b>PDB Molecule:</b> dna double-strand break repair rad50 atpase; <b>PDBTitle:</b> crystal structure of rad50 bound to adp
10	<a href="#">c5xnsA_</a>	 Alignment		99.8	27	<b>PDB header:</b> dna binding protein/cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of the smc head domain with an extended coiled coil2 bound to the c-terminal domain of scpa derived from pyrococcus3 furiosus
11	<a href="#">c3qkuB_</a>	 Alignment		99.8	15	<b>PDB header:</b> replication <b>Chain:</b> B; <b>PDB Molecule:</b> dna double-strand break repair rad50 atpase; <b>PDBTitle:</b> mre11 rad50 binding domain in complex with rad50 and amp-prp

12	<a href="#">c1ii8B_</a>	Alignment		99.8	17	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> rad50 abc-atpase; <b>PDBTitle:</b> crystal structure of the p. furiosus rad50 atpase domain
13	<a href="#">c1xexA_</a>	Alignment		99.8	17	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> smc protein; <b>PDBTitle:</b> structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
14	<a href="#">c4abyC_</a>	Alignment		99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein recn; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans recn head2 domain
15	<a href="#">c1us8A_</a>	Alignment		99.7	20	<b>PDB header:</b> dna repair <b>Chain:</b> A: <b>PDB Molecule:</b> dna double-strand break repair rad50 atpase; <b>PDBTitle:</b> the rad50 signature motif: essential to atp binding and d2 biological function
16	<a href="#">d1e69a_</a>	Alignment		99.7	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
17	<a href="#">c3zgxA_</a>	Alignment		99.7	30	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of the kleisin-n smc interface in2 prokaryotic condensin
18	<a href="#">c4i99A_</a>	Alignment		99.7	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of the smchead bound to the c-winged helix domain of2 scpa
19	<a href="#">c1f2uD_</a>	Alignment		99.7	20	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> rad50 abc-atpase; <b>PDBTitle:</b> crystal structure of rad50 abc-atpase
20	<a href="#">c2o5vA_</a>	Alignment		99.6	23	<b>PDB header:</b> replication/recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna replication and repair protein recf; <b>PDBTitle:</b> recombination mediator recf
21	<a href="#">c5zwuA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna replication and repair protein recf; <b>PDBTitle:</b> crystal structure of recombination mediator protein recf
22	<a href="#">d1w1wa_</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
23	<a href="#">c1xexB_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> smc protein; <b>PDBTitle:</b> structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
24	<a href="#">c5h68B_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> dna binding protein, cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of an engaged dimer of the geobacillus2 stearothermophilus smc head domain
25	<a href="#">c5z68D_</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna replication and repair protein recf; <b>PDBTitle:</b> structure of the recombination mediator protein recf-atp in recfor2 pathway
26	<a href="#">c4abyD_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dna repair protein recn; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans recn head2 domain
27	<a href="#">d1qhla_</a>	Alignment	not modelled	99.5	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
28	<a href="#">c6qj4C_</a>	Alignment	not modelled	99.4	26	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein,uncharacterized protein; <b>PDBTitle:</b> crystal structure of the c. thermophilum condensin ycs4-brn12 subcomplex bound to the smc4 atpase head in complex with

						the c-3 terminal domain of brn1
29	<a href="#">c1yqtA</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> rnase-I inhibitor
30	<a href="#">c5mkkA</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
31	<a href="#">c3pihA</a>	Alignment	not modelled	98.5	24	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> t. maritima uvra in complex with fluorescein-modified dna
32	<a href="#">c3zqjC</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
33	<a href="#">c2yl4A</a>	Alignment	not modelled	98.5	28	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 10, <b>PDBTitle:</b> structure of the human mitochondrial abc transporter, abcb10
34	<a href="#">c3ozxA</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> hydrolase, translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
35	<a href="#">c3eukC</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> chromosome partition protein mukb, linker; <b>PDBTitle:</b> crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammas complex, asymmetric dimer
36	<a href="#">c2vf7B</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> excinuclease abc, subunit a.; <b>PDBTitle:</b> crystal structure of uvra2 from deinococcus radiodurans
37	<a href="#">c3qf4A</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
38	<a href="#">c3bk7A</a>	Alignment	not modelled	98.5	22	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abce1/rnase-I inhibitor protein from2 pyrococcus abyssi
39	<a href="#">c5ochH</a>	Alignment	not modelled	98.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 8, mitochondrial; <b>PDBTitle:</b> the crystal structure of human abcb8 in an outward-facing state
40	<a href="#">c5ochF</a>	Alignment	not modelled	98.5	31	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 8, mitochondrial; <b>PDBTitle:</b> the crystal structure of human abcb8 in an outward-facing state
41	<a href="#">c3j16B</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> rli1p; <b>PDBTitle:</b> models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
42	<a href="#">c3ux8A</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc, a subunit; <b>PDBTitle:</b> crystal structure of uvra
43	<a href="#">c3qf4B</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized abc transporter atp-binding protein <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
44	<a href="#">c3zqjF</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
45	<a href="#">d1vpla</a>	Alignment	not modelled	98.4	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
46	<a href="#">c5l22B</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter (hlyb subfamily); <b>PDBTitle:</b> prtD t1ss abc transporter
47	<a href="#">c2hydB</a>	Alignment	not modelled	98.4	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter homolog; <b>PDBTitle:</b> multidrug abc transporter sav1866
48	<a href="#">c4pl0B</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> microcin-j25 export atp-binding/permease protein mcjd; <b>PDBTitle:</b> crystal structure of the antibacterial peptide abc transporter mcjd in2 an outward occluded state
49	<a href="#">c6n9lA</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> crystal structure of t. maritima uvra d117-399 with adp
50	<a href="#">c4fwiB</a>	Alignment	not modelled	98.4	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc-type dipeptide/oligopeptide/nickel transport system, <b>PDBTitle:</b> crystal structure of the nucleotide-binding domain of a dipeptide abc2 transporter
51	<a href="#">c4rvcA</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of atp binding subunit of abc transporter
52	<a href="#">c4mrnB</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter related protein; <b>PDBTitle:</b> structure of a bacterial atm1-family abc transporter
						<b>PDB header:</b> membrane protein/hydrolase

53	<a href="#">c3dhwC_</a>	Alignment	not modelled	98.4	25	<b>Chain:</b> C: <b>PDB Molecule:</b> methionine import atp-binding protein metn; <b>PDBTitle:</b> crystal structure of methionine importer metni
54	<a href="#">c5mkkB_</a>	Alignment	not modelled	98.4	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
55	<a href="#">c2olkD_</a>	Alignment	not modelled	98.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> amino acid abc transporter; <b>PDBTitle:</b> abc protein artp in complex with adp-beta-s
56	<a href="#">c4tqvO_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> transport protein <b>Chain:</b> O: <b>PDB Molecule:</b> algls; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
57	<a href="#">c4p31B_</a>	Alignment	not modelled	98.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide export system atp-binding protein lptb; <b>PDBTitle:</b> crystal structure of a selenomethionine derivative of e. coli lptb in2 complex with adp-magnesium
58	<a href="#">c2d62A_</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multiple sugar-binding transport atp-binding <b>PDBTitle:</b> crystal structure of multiple sugar binding transport atp-2 binding protein
59	<a href="#">c5nikK_</a>	Alignment	not modelled	98.4	20	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of the macab-tolc abc-type tripartite multidrug efflux pump
60	<a href="#">c5u1dA_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> antigen peptide transporter 1; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
61	<a href="#">c1oxtB_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp binding protein; <b>PDBTitle:</b> crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
62	<a href="#">c5ws4A_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
63	<a href="#">c4u02C_</a>	Alignment	not modelled	98.3	27	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> amino acid abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of apo-ttha1159
64	<a href="#">c5xu1A_</a>	Alignment	not modelled	98.3	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
65	<a href="#">c4wbsA_</a>	Alignment	not modelled	98.3	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter related; <b>PDBTitle:</b> crystal structure of an abc transporter related protein from2 burkholderia phymatum
66	<a href="#">c4ry2A_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> transport protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type bacteriocin transporter; <b>PDBTitle:</b> crystal structure of the peptidase-containing abc transporter pcat1
67	<a href="#">c2iw3B_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 3a; <b>PDBTitle:</b> elongation factor 3 in complex with adp
68	<a href="#">c4ymuJ_</a>	Alignment	not modelled	98.3	29	<b>PDB header:</b> protein binding/transport protein <b>Chain:</b> J: <b>PDB Molecule:</b> abc-type polar amino acid transport system, atpase <b>PDBTitle:</b> crystal structure of an amino acid abc transporter complex with2 arginines and atps
69	<a href="#">c3b5wE_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> crystal structure of eschericia coli msba
70	<a href="#">c2yyzA_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of sugar abc transporter, atp-binding protein
71	<a href="#">d3d31a2</a>	Alignment	not modelled	98.3	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
72	<a href="#">c5lj7B_</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb; <b>PDBTitle:</b> structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21)
73	<a href="#">c2nq2C_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> metal transport <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical abc transporter atp-binding protein <b>PDBTitle:</b> an inward-facing conformation of a putative metal-chelate2 type abc transporter.
74	<a href="#">c3wmeA_</a>	Alignment	not modelled	98.3	25	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette, sub-family b, member 1; <b>PDBTitle:</b> crystal structure of an inward-facing eukaryotic abc multidrug2 transporter
75	<a href="#">c1vciA_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar-binding transport atp-binding protein; <b>PDBTitle:</b> crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
76	<a href="#">c4myrC_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> iron-sulfur clusters transporter atm1,

76	<a href="#">c4mytC_</a>	Alignment	not modelled	98.3	18	mitochondrial; <b>PDBTitle:</b> structure of the mitochondrial abc transporter, atm1 <b>PDB header:</b> hydrolase
77	<a href="#">c4mkiB_</a>	Alignment	not modelled	98.3	21	<b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> cobalt transporter atp-binding subunit
78	<a href="#">c6bzaA_</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance-associated protein 6; <b>PDBTitle:</b> human abcc6 nbd2 in adp-bound state
79	<a href="#">d1g2912</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
80	<a href="#">c3gfoA_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> atp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cobalt import atp-binding protein cbio 1; <b>PDBTitle:</b> structure of cbio1 from clostridium perfringens: part of the abc2 transporter complex cbionq.
81	<a href="#">d1b0ua_</a>	Alignment	not modelled	98.3	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
82	<a href="#">c2pcjB_</a>	Alignment	not modelled	98.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoprotein-releasing system atp-binding protein lold; <b>PDBTitle:</b> crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
83	<a href="#">c3fvqB_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fe(3+) ions import atp-binding protein fbpc; <b>PDBTitle:</b> crystal structure of the nucleotide binding domain fbpc complexed with2 atp
84	<a href="#">c2pjzA_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein st1066; <b>PDBTitle:</b> the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066
85	<a href="#">c2ygrD_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
86	<a href="#">c5zxdB_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> atp-binding cassette sub-family f member 1; <b>PDBTitle:</b> crystal structure of atp-bound human abcf1
87	<a href="#">c2it1B_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> 362aa long hypothetical maltose/maltodextrin <b>PDBTitle:</b> structure of ph0203 protein from pyrococcus horikoshii
88	<a href="#">c5c76D_</a>	Alignment	not modelled	98.3	26	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> wlab protein; <b>PDBTitle:</b> atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
89	<a href="#">c2yz2B_</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc transporter atp-binding protein tm_0222; <b>PDBTitle:</b> crystal structure of the abc transporter in the cobalt transport2 system
90	<a href="#">c5d3mF_</a>	Alignment	not modelled	98.2	25	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> folate ecf transporter: amppnp bound state
91	<a href="#">c4g1uD_</a>	Alignment	not modelled	98.2	12	<b>PDB header:</b> transport protein/hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> hemin import atp-binding protein hmuu; <b>PDBTitle:</b> x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
92	<a href="#">d3dhwc1</a>	Alignment	not modelled	98.2	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
93	<a href="#">c6ic4I_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> protein transport <b>Chain:</b> I: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> cryo-em structure of the a. baumannii mia complex at 8.7 a resolution
94	<a href="#">c5x5yB_</a>	Alignment	not modelled	98.2	23	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-binding component of abc transporter; <b>PDBTitle:</b> a membrane protein complex
95	<a href="#">c5x40A_</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cobalt abc transporter atp-binding protein; <b>PDBTitle:</b> structure of a cbio dimer bound with amppcp
96	<a href="#">d1l2ta_</a>	Alignment	not modelled	98.2	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
97	<a href="#">c4hzuB_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein ecfa <b>PDBTitle:</b> structure of a bacterial energy-coupling factor transporter
98	<a href="#">c6c0vA_</a>	Alignment	not modelled	98.2	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein 1; <b>PDBTitle:</b> molecular structure of human p-glycoprotein in the atp-bound, outward-2 facing conformation
99	<a href="#">d2pmka1</a>	Alignment	not modelled	98.2	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
100	<a href="#">c1z47B_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> ligand binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative abc-transporter atp-binding protein; <b>PDBTitle:</b> structure of the atpase subunit cysa of the putative sulfate atp-2 binding cassette (abc) transporter from alicyclobacillus3 acidocaldarius <b>PDB header:</b> atp-binding protein

101	<a href="#">c4finA_</a>	Alignment	not modelled	98.2	18	<b>Chain:</b> A: <b>PDB Molecule:</b> etta (yjjk) abcf family protein; <b>PDBTitle:</b> crystal structure of etta (formerly yjjk) - an e. coli abc-type atpase
102	<a href="#">d3b60a1</a>	Alignment	not modelled	98.2	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
103	<a href="#">c3g5uB_</a>	Alignment	not modelled	98.2	25	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance protein 1a; <b>PDBTitle:</b> structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
104	<a href="#">c3b5xB_</a>	Alignment	not modelled	98.2	24	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> crystal structure of msba from vibrio cholerae
105	<a href="#">c4yerB_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> crystal structure of an abc transporter atp-binding protein (tm_1403)2 from thermotoga maritima msb8 at 2.35 a resolution
106	<a href="#">d1oxxk2</a>	Alignment	not modelled	98.2	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
107	<a href="#">d1v43a3</a>	Alignment	not modelled	98.2	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
108	<a href="#">d1g6ha_</a>	Alignment	not modelled	98.2	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
109	<a href="#">d1ji0a_</a>	Alignment	not modelled	98.2	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
110	<a href="#">c5x7kB_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipase b; <b>PDBTitle:</b> crystal structure of the nucleotide-binding domain (nbd) of lipb, a2 abc transporter subunit of a type i secretion system
111	<a href="#">c4hziA_</a>	Alignment	not modelled	98.2	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> crystal structure of the leptospira interrogans atpase subunit of an2 orphan abc transporter
112	<a href="#">c4hluC_</a>	Alignment	not modelled	98.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> structure of the ecfa-a' heterodimer bound to adp
113	<a href="#">c3d31B_</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, atp-binding protein; <b>PDBTitle:</b> modbc from methanosarcina acetivorans
114	<a href="#">c2r6fA_</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit a; <b>PDBTitle:</b> crystal structure of bacillus stearotherophilus uvra
115	<a href="#">c5u1dB_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> antigen peptide transporter 2; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
116	<a href="#">c5xjyA_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family a member 1; <b>PDBTitle:</b> cryo-em structure of human abca1
117	<a href="#">d2hyda1</a>	Alignment	not modelled	98.1	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ABC transporter ATPase domain-like
118	<a href="#">c6amxA_</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter; <b>PDBTitle:</b> crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
119	<a href="#">c2d2fA_</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sufc protein; <b>PDBTitle:</b> crystal structure of atypical cytoplasmic abc-atpase suf from thermus2 thermophilus hb8
120	<a href="#">c5idvA_</a>	Alignment	not modelled	98.1	24	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> structure of the nucleotide binding domain of an abc transporter msba2 from acinetobacter baumannii