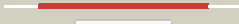



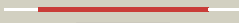






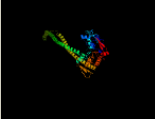

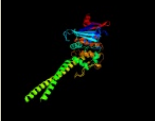










# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1696_(recN)_1919690_1921453
Date	Fri Aug 2 13:30:29 BST 2019
Unique Job ID	b09d6895d8110066

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ad8A_</a>	Alignment 		100.0	40	<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
2	<a href="#">c5xeiA_</a>	Alignment 		100.0	16	<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
3	<a href="#">c4abyC_</a>	Alignment 		100.0	51	<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
4	<a href="#">c4abyD_</a>	Alignment 		100.0	49	<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
5	<a href="#">c6qj1A_</a>	Alignment 		100.0	21	<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)
6	<a href="#">c4ux3A_</a>	Alignment 		100.0	14	<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
7	<a href="#">c5xnsA_</a>	Alignment 		100.0	18	<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
8	<a href="#">c6qj2A_</a>	Alignment 		100.0	18	<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="#">c5dacA_</a>	Alignment 		100.0	20	<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
10	<a href="#">c6qj4C_</a>	Alignment 		100.0	24	<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
11	<a href="#">c5h68B_</a>	Alignment 		100.0	20	<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 steaerotherophilus smc head domain

12	<a href="#">c3auyB_</a>	Alignment		100.0	19	<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
13	<a href="#">c4i99A_</a>	Alignment		100.0	20	<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
14	<a href="#">c5z68D_</a>	Alignment		99.9	21	<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
15	<a href="#">dlw1wa_</a>	Alignment		99.9	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
16	<a href="#">c3zgxA_</a>	Alignment		99.9	18	<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
17	<a href="#">c2o5vA_</a>	Alignment		99.9	20	<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
18	<a href="#">c5zwuA_</a>	Alignment		99.9	18	<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
19	<a href="#">dl1e69a_</a>	Alignment		99.9	22	<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
20	<a href="#">c3qg5A_</a>	Alignment		99.9	14	<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
21	<a href="#">c1xexB_</a>	Alignment	not modelled	99.9	20	<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.
22	<a href="#">c1ii8B_</a>	Alignment	not modelled	99.9	16	<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
23	<a href="#">c1xexA_</a>	Alignment	not modelled	99.8	24	<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.
24	<a href="#">c1ii8A_</a>	Alignment	not modelled	99.8	12	<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
25	<a href="#">c3qkuB_</a>	Alignment	not modelled	99.8	16	<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-pnp
26	<a href="#">c1f2uD_</a>	Alignment	not modelled	99.8	17	<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
27	<a href="#">c5u71A_</a>	Alignment	not modelled	99.7	30	<b>PDB header:</b> membrane protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cystic fibrosis transmembrane conductance regulator; <b>PDBTitle:</b> structure of human cystic fibrosis transmembrane conductance regulator2 (cftr)
28	<a href="#">c6c3oE_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> atp-binding cassette sub-family c member 8;

						<b>PDBTitle:</b> cryo-em structure of human katp bound to atp and adp in quatrefoil2 form
29	<a href="#">c5uj9A_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> bovine multidrug resistance protein 1 (mrp1),multidrug <b>PDBTitle:</b> cryo-em structure of bovine multidrug resistance protein 1 (mrp1)
30	<a href="#">c1us8A_</a>	Alignment	not modelled	99.6	16	<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 and2 biological function
31	<a href="#">d1qghA_</a>	Alignment	not modelled	99.6	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
32	<a href="#">c2vf7B_</a>	Alignment	not modelled	99.5	32	<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
33	<a href="#">c3pihA_</a>	Alignment	not modelled	99.5	27	<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
34	<a href="#">c3zqiC_</a>	Alignment	not modelled	99.5	24	<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
35	<a href="#">c5ochF_</a>	Alignment	not modelled	99.5	18	<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
36	<a href="#">c5mkkA_</a>	Alignment	not modelled	99.5	19	<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
37	<a href="#">c5ochH_</a>	Alignment	not modelled	99.5	18	<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
38	<a href="#">c6n9IA_</a>	Alignment	not modelled	99.5	26	<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
39	<a href="#">c2hydB_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter homolog; <b>PDBTitle:</b> multidrug abc transporter sav1866
40	<a href="#">c4mrnB_</a>	Alignment	not modelled	99.5	24	<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
41	<a href="#">c2ygrD_</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
42	<a href="#">c3qf4A_</a>	Alignment	not modelled	99.5	21	<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
43	<a href="#">c2yl4A_</a>	Alignment	not modelled	99.5	19	<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
44	<a href="#">c3qf4B_</a>	Alignment	not modelled	99.5	18	<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
45	<a href="#">c4ry2A_</a>	Alignment	not modelled	99.5	16	<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
46	<a href="#">c5mkkB_</a>	Alignment	not modelled	99.5	20	<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
47	<a href="#">c4pl0B_</a>	Alignment	not modelled	99.5	14	<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
48	<a href="#">c3ux8A_</a>	Alignment	not modelled	99.4	28	<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
49	<a href="#">c3zqiF_</a>	Alignment	not modelled	99.4	25	<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
50	<a href="#">c5c76D_</a>	Alignment	not modelled	99.4	13	<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)
51	<a href="#">c6c0vA_</a>	Alignment	not modelled	99.4	18	<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
52	<a href="#">c3g5uB_</a>	Alignment	not modelled	99.4	19	<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



77	<a href="#">c6bhuA</a>	Alignment	not modelled	99.3	16	<b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance-associated protein 1; <b>PDBTitle:</b> cryo-em structure of atp-bound, outward-facing bovine multidrug2 resistance protein 1 (mrp1)
78	<a href="#">c2iw3B</a>	Alignment	not modelled	99.3	17	<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
79	<a href="#">c5nj3B</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 2; <b>PDBTitle:</b> structure of an abc transporter: complete structure
80	<a href="#">c5do7A</a>	Alignment	not modelled	99.3	30	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 5; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
81	<a href="#">c3vx4D</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative abc transporter, atp-binding protein coma; <b>PDBTitle:</b> crystal structure of the nucleotide-binding domain of s. mutans coma,2 a bifunctional atp-binding cassette transporter involved in the3 quorum-sensing pathway
82	<a href="#">c5ykfH</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> atp-binding cassette sub-family c member 8 isoform x2; <b>PDBTitle:</b> structure of pancreatic atp-sensitive potassium channel bound with2 glibenclamide and atpgammas (3d class1 at 4.33a)
83	<a href="#">c5zxdB</a>	Alignment	not modelled	99.3	17	<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
84	<a href="#">d2hyda1</a>	Alignment	not modelled	99.3	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
85	<a href="#">c4fwiB</a>	Alignment	not modelled	99.3	24	<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
86	<a href="#">c5u1dB</a>	Alignment	not modelled	99.3	18	<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
87	<a href="#">c4finA</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> etta (yijk) abcf family protein; <b>PDBTitle:</b> crystal structure of etta (formerly yijk) - an e. coli abc-type atpase
88	<a href="#">c4hluC</a>	Alignment	not modelled	99.3	19	<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
89	<a href="#">c2olkD</a>	Alignment	not modelled	99.3	24	<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
90	<a href="#">c2r6fA</a>	Alignment	not modelled	99.3	25	<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
91	<a href="#">c5x7kB</a>	Alignment	not modelled	99.3	18	<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
92	<a href="#">c3eukC</a>	Alignment	not modelled	99.2	14	<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
93	<a href="#">c5d3mA</a>	Alignment	not modelled	99.2	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> folate ecf transporter: amppnp bound state
94	<a href="#">d1g2912</a>	Alignment	not modelled	99.2	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
95	<a href="#">c1vciA</a>	Alignment	not modelled	99.2	20	<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
96	<a href="#">c4p31B</a>	Alignment	not modelled	99.2	26	<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
97	<a href="#">c5wuaF</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> sur1; <b>PDBTitle:</b> structure of a pancreatic atp-sensitive potassium channel
98	<a href="#">d1vpla</a>	Alignment	not modelled	99.2	14	<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
99	<a href="#">c3fvqB</a>	Alignment	not modelled	99.2	20	<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
100	<a href="#">c3nhaA</a>	Alignment	not modelled	99.2	28	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 6, mitochondrial; <b>PDBTitle:</b> nucleotide binding domain of human abcb6 (adp mg

						bound structure)
101	<a href="#">c5xjvA_</a>	Alignment	not modelled	99.2	23	<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
102	<a href="#">c4u02C_</a>	Alignment	not modelled	99.2	22	<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
103	<a href="#">d1oxxk2</a>	Alignment	not modelled	99.2	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
104	<a href="#">c6ic4I_</a>	Alignment	not modelled	99.2	25	<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 mla complex at 8.7 a resolution
105	<a href="#">d3dhwc1</a>	Alignment	not modelled	99.2	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
106	<a href="#">c3gfoA_</a>	Alignment	not modelled	99.2	22	<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.
107	<a href="#">c2nq2C_</a>	Alignment	not modelled	99.2	18	<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.
108	<a href="#">c5idvA_</a>	Alignment	not modelled	99.2	16	<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
109	<a href="#">d1mv5a_</a>	Alignment	not modelled	99.2	19	<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="#">c2cbzA_</a>	Alignment	not modelled	99.2	24	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance-associated protein 1; <b>PDBTitle:</b> structure of the human multidrug resistance protein 12 nucleotide binding domain 1
111	<a href="#">c4tqvO_</a>	Alignment	not modelled	99.2	24	<b>PDB header:</b> transport protein <b>Chain:</b> O: <b>PDB Molecule:</b> algs; <b>PDBTitle:</b> crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
112	<a href="#">c4rvcA_</a>	Alignment	not modelled	99.2	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
113	<a href="#">d1b0ua_</a>	Alignment	not modelled	99.2	22	<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
114	<a href="#">c4mkiB_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> cobalt transporter atp-binding subunit
115	<a href="#">c5do7B_</a>	Alignment	not modelled	99.2	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 8; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
116	<a href="#">d1v43a3</a>	Alignment	not modelled	99.2	19	<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
117	<a href="#">c4wbsA_</a>	Alignment	not modelled	99.2	27	<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
118	<a href="#">c1oxtB_</a>	Alignment	not modelled	99.2	20	<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
119	<a href="#">c2pjzA_</a>	Alignment	not modelled	99.2	21	<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
120	<a href="#">c2yz2B_</a>	Alignment	not modelled	99.2	20	<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