Phyre2

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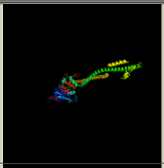
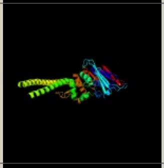
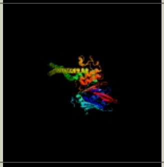
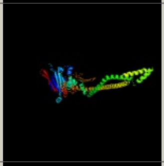
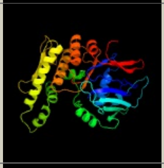
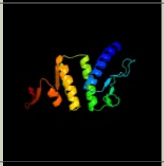
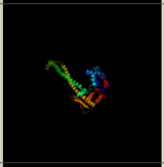
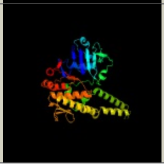
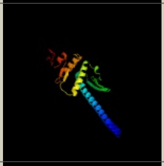
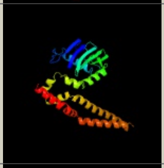
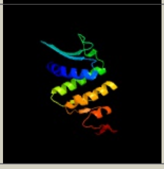
Description	RVBD2922c_(smc)_3234199_3237816
Date	Thu Aug 8 16:20:08 BST 2019
Unique Job ID	b1878329a8248607

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xeiA_	Alignment		100.0	41	**PDB header:**dna binding protein, cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein smc; **PDBTitle:** crystal structure of the smc head domain with a coiled coil and joint2 derived from pyrococcus yayanosii
2	c5xnsA_	Alignment		100.0	40	**PDB header:**dna binding protein/cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein smc; **PDBTitle:** crystal structure of the smc head domain with an extended coiled coil2 bound to the c-terminal domain of scpa derived from pyrococcus3 furiosus
3	c6qj1A_	Alignment		100.0	30	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**structural maintenance of chromosomes protein,structural **PDBTitle:** crystal structure of the c. thermophilum condensin smc2 atpase head2 (crystal from i)
4	c4ad8A_	Alignment		100.0	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein recn; **PDBTitle:** crystal structure of a deletion mutant of deinococcus radiodurans2 recn
5	c5h68B_	Alignment		100.0	82	**PDB header:**dna binding protein, cell cycle **Chain:** B: **PDB Molecule:**chromosome partition protein smc; **PDBTitle:** crystal structure of an engaged dimer of the geobacillus2 stearothermophilus smc head domain
6	c1xexA_	Alignment		100.0	38	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**smc protein; **PDBTitle:** structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
7	c6qj2A_	Alignment		100.0	37	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**smc4; **PDBTitle:** crystal structure of the c. thermophilum condensin smc4 atpase head in2 complex with the c-terminal domain of brn1
8	c1xexB_	Alignment		100.0	42	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**smc protein; **PDBTitle:** structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
9	c4ux3A_	Alignment		100.0	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**structural maintenance of chromosomes protein 3; **PDBTitle:** cohesin smc3-hd:scc1-n complex from yeast
10	c4i99A_	Alignment		100.0	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**chromosome partition protein smc; **PDBTitle:** crystal structure of the smchead bound to the c-winged helix domain of2 scpa
11	c3qg5A_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rad50; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair

12	c6qj4C_	Alignment		99.9	58	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**uncharacterized protein,uncharacterized protein; **PDBTitle:** 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
13	c1ii8B_	Alignment		99.9	20	**PDB header:**replication **Chain:** B: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
14	c1ii8A_	Alignment		99.9	21	**PDB header:**replication **Chain:** A: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
15	d1e69a_	Alignment		99.9	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
16	c4abyC_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dna repair protein recn; **PDBTitle:** crystal structure of deinococcus radiodurans recn head2 domain
17	c3auyB_	Alignment		99.9	17	**PDB header:**recombination **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** crystal structure of rad50 bound to adp
18	c3qkuB_	Alignment		99.9	20	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** mre11 rad50 binding domain in complex with rad50 and amp-pnp
19	d1w1wa_	Alignment		99.8	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
20	c1f2uD_	Alignment		99.8	22	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
21	c1us8A_	Alignment	not modelled	99.8	25	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** the rad50 signature motif: essential to atp binding and2 biological function
22	c5dacA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein,putative uncharacterized **PDBTitle:** atp-gamma-s bound rad50 from chaetomium thermophilum in complex with2 dna
23	c3zgxA_	Alignment	not modelled	99.8	49	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein smc; **PDBTitle:** crystal structure of the kleisin-n smc interface in2 prokaryotic condensin
24	c2o5vA_	Alignment	not modelled	99.7	25	**PDB header:**replication/recombination **Chain:** A: **PDB Molecule:**dna replication and repair protein recf; **PDBTitle:** recombination mediator recf
25	c5zwuA_	Alignment	not modelled	99.7	23	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna replication and repair protein recf; **PDBTitle:** crystal structure of recombination mediator protein recf
26	c5z68D_	Alignment	not modelled	99.7	24	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**dna replication and repair protein recf; **PDBTitle:** structure of the recombination mediator protein recf-atp in recfor2 pathway
27	c4abyD_	Alignment	not modelled	99.7	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**dna repair protein recn; **PDBTitle:** crystal structure of deinococcus radiodurans recn head2 domain
28	d1qhla_	Alignment	not modelled	99.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like

29	c6n9lA_	Alignment	not modelled	99.2	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** crystal structure of t. maritima uvra d117-399 with adp
30	c2vf7B_	Alignment	not modelled	99.2	22	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
31	c3pihA_	Alignment	not modelled	99.2	26	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
32	c5ochH_	Alignment	not modelled	99.1	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
33	c3zqjC_	Alignment	not modelled	99.1	25	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
34	c3ux8A_	Alignment	not modelled	99.1	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc, a subunit; **PDBTitle:** crystal structure of uvra
35	c2yl4A_	Alignment	not modelled	99.1	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
36	c4pl0B_	Alignment	not modelled	99.1	34	**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
37	c2iw3B_	Alignment	not modelled	99.1	25	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 3a; **PDBTitle:** elongation factor 3 in complex with adp
38	c2ygrD_	Alignment	not modelled	99.1	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
39	c5mkkA_	Alignment	not modelled	99.1	30	**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
40	c3qf4A_	Alignment	not modelled	99.1	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, atp-binding protein; **PDBTitle:** crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
41	c2hydB_	Alignment	not modelled	99.1	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
42	c5ochF_	Alignment	not modelled	99.1	25	**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
43	c3qf4B_	Alignment	not modelled	99.1	25	**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
44	c4mrnB_	Alignment	not modelled	99.1	30	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter related protein; **PDBTitle:** structure of a bacterial atm1-family abc transporter
45	c3wmeA_	Alignment	not modelled	99.1	28	**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
46	c3bk7A_	Alignment	not modelled	99.0	26	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein from2 pyrococcus abysii
47	c5mkkB_	Alignment	not modelled	99.0	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance abc transporter atp-binding and **PDBTitle:** crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
48	c3b5xB_	Alignment	not modelled	99.0	35	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
49	c3b5wE_	Alignment	not modelled	99.0	37	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba
50	c6c0vA_	Alignment	not modelled	99.0	29	**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
51	c3zqjF_	Alignment	not modelled	99.0	23	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
52	c1yqtA_	Alignment	not modelled	99.0	27	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
53	c4ry2A_	Alignment	not modelled	99.0	27	**PDB header:**transport protein/hydrolase **Chain:** A: **PDB Molecule:**abc-type bacteriocin transporter;

53	c4ry2A_	Alignment	not modelled	99.0	27	**PDBTitle:** crystal structure of the peptidase-containing abc transporter pcat1
54	c3j16B_	Alignment	not modelled	99.0	18	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rli1p; **PDBTitle:** models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
55	c3ozxA_	Alignment	not modelled	99.0	21	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
56	c5c76D_	Alignment	not modelled	99.0	25	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**wlab protein; **PDBTitle:** atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
57	c5l22B_	Alignment	not modelled	99.0	23	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**abc transporter (hlyb subfamily); **PDBTitle:** prtd t1ss abc transporter
58	c2pcjB_	Alignment	not modelled	99.0	26	**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
59	c5lj7B_	Alignment	not modelled	98.9	23	**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)
60	c5ws4A_	Alignment	not modelled	98.9	23	**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
61	c5zxdB_	Alignment	not modelled	98.9	27	**PDB header:**translation **Chain:** B: **PDB Molecule:**atp-binding cassette sub-family f member 1; **PDBTitle:** crystal structure of atp-bound human abcf1
62	c5u1dA_	Alignment	not modelled	98.9	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
63	d2pmka1	Alignment	not modelled	98.9	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
64	c4mycC_	Alignment	not modelled	98.9	27	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**iron-sulfur clusters transporter atm1, mitochondrial; **PDBTitle:** structure of the mitochondrial abc transporter, atm1
65	c3g5uB_	Alignment	not modelled	98.9	30	**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
66	c5nikK_	Alignment	not modelled	98.9	23	**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
67	c5u1dB_	Alignment	not modelled	98.9	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
68	c5x7kB_	Alignment	not modelled	98.9	21	**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
69	d3b60a1	Alignment	not modelled	98.9	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
70	c4finA_	Alignment	not modelled	98.9	24	**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
71	c6bzrA_	Alignment	not modelled	98.9	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multidrug resistance-associated protein 6; **PDBTitle:** human abcc6 nbd2 in adp-bound state
72	c3dhwC_	Alignment	not modelled	98.9	29	**PDB header:**membrane protein/hydrolase **Chain:** C: **PDB Molecule:**methionine import atp-binding protein metn; **PDBTitle:** crystal structure of methionine importer metni
73	c5uj9A_	Alignment	not modelled	98.9	21	**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)
74	c5tsiA_	Alignment	not modelled	98.9	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
75	c5ujaA_	Alignment	not modelled	98.9	21	**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
76	c3vx4D_	Alignment	not modelled	98.9	25	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**putative abc transporter, atp-binding protein coma; **PDBTitle:** crystal structure of the nucleotide-binding domain of s. mutans coma,2 a bifunctional atp-binding cassette transporter involved in the3 quorum-sensing pathway
						PDB header:transport protein

77	c1vciA_	Alignment	not modelled	98.9	27	**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
78	c4mkiB_	Alignment	not modelled	98.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**energy-coupling factor transporter atp-binding protein **PDBTitle:** cobalt transporter atp-binding subunit
79	c4u02C_	Alignment	not modelled	98.9	26	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**amino acid abc transporter, atp-binding protein; **PDBTitle:** crystal structure of apo-ttha1159
80	c4hluC_	Alignment	not modelled	98.9	28	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**energy-coupling factor transporter atp-binding protein **PDBTitle:** structure of the ecfa-a' heterodimer bound to adp
81	c2olkD_	Alignment	not modelled	98.8	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acid abc transporter; **PDBTitle:** abc protein artp in complex with adp-beta-s
82	c5x40A_	Alignment	not modelled	98.8	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cobalt abc transporter atp-binding protein; **PDBTitle:** structure of a cbio dimer bound with amppcp
83	d2hyda1	Alignment	not modelled	98.8	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
84	c6bhuA_	Alignment	not modelled	98.8	20	**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)
85	c6ic4I_	Alignment	not modelled	98.8	32	**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
86	c5xu1A_	Alignment	not modelled	98.8	24	**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
87	d1jj7a_	Alignment	not modelled	98.8	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
88	c6c3oE_	Alignment	not modelled	98.8	25	**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
89	d1l2ta_	Alignment	not modelled	98.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
90	c4fwiB_	Alignment	not modelled	98.8	25	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc-type dipeptide/oligopeptide/nickel transport system, **PDBTitle:** crystal structure of the nucleotide-binding domain of a dipeptide abc2 transporter
91	c2nq2C_	Alignment	not modelled	98.8	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.
92	c4g1uD_	Alignment	not modelled	98.8	25	**PDB header:**transport protein/hydrolase **Chain:** D: **PDB Molecule:**hemin import atp-binding protein hmuv; **PDBTitle:** x-ray structure of the bacterial heme transporter hmuuv from yersinia2 pestis
93	d1g2912	Alignment	not modelled	98.8	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
94	c4rvcA_	Alignment	not modelled	98.8	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of atp binding subunit of abc transporter
95	c4yerB_	Alignment	not modelled	98.8	18	**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
96	c3nhaA_	Alignment	not modelled	98.8	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)
97	c5idvA_	Alignment	not modelled	98.8	29	**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
98	c4f4cA_	Alignment	not modelled	98.8	30	**PDB header:**hydrolase,protein transport **Chain:** A: **PDB Molecule:**multidrug resistance protein pgp-1; **PDBTitle:** the crystal structure of the multi-drug transporter
99	c2pjzA_	Alignment	not modelled	98.8	17	**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
100	d1vpla_	Alignment	not modelled	98.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
101	c2yz2B_	Alignment	not modelled	98.8	29	**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
102	d1v43a3	Alignment	not modelled	98.8	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
103	c5ykfH_	Alignment	not modelled	98.8	24	**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)
104	c5d3mA_	Alignment	not modelled	98.8	31	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**energy-coupling factor transporter atp-binding protein **PDBTitle:** folate ecf transporter: amppnp bound state
105	d1oxxk2	Alignment	not modelled	98.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
106	c4wbsA_	Alignment	not modelled	98.8	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter related; **PDBTitle:** crystal structure of an abc transporter related protein from2 burkholderia phymatum
107	c4hzuB_	Alignment	not modelled	98.8	27	**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
108	c2r6fA_	Alignment	not modelled	98.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
109	c3fvqB_	Alignment	not modelled	98.8	23	**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
110	c5u71A_	Alignment	not modelled	98.8	24	**PDB header:**membrane protein, hydrolase **Chain:** A: **PDB Molecule:**cystic fibrosis transmembrane conductance regulator; **PDBTitle:** structure of human cystic fibrosis transmembrane conductance regulator2 (cftr)
111	c4p31B_	Alignment	not modelled	98.8	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-magensium
112	d1mv5a_	Alignment	not modelled	98.8	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
113	c5d3mF_	Alignment	not modelled	98.8	25	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**energy-coupling factor transporter atp-binding protein **PDBTitle:** folate ecf transporter: amppnp bound state
114	c5x5yB_	Alignment	not modelled	98.8	26	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable atp-binding component of abc transporter; **PDBTitle:** a membrane protein complex
115	d3d31a2	Alignment	not modelled	98.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
116	c6bzsA_	Alignment	not modelled	98.7	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multidrug resistance-associated protein 6; **PDBTitle:** human abcc6 nbd1 in apo state
117	c2cbzA_	Alignment	not modelled	98.7	22	**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
118	d1b0ua_	Alignment	not modelled	98.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
119	c4tqvO_	Alignment	not modelled	98.7	24	**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
120	d3dhwc1	Alignment	not modelled	98.7	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like