Phyre2

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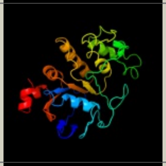
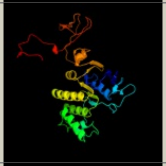
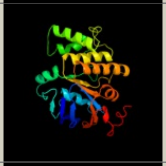
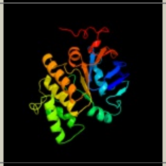
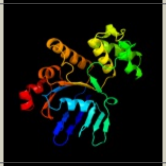
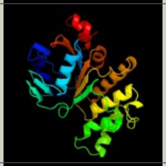
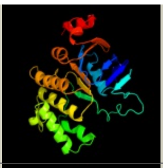
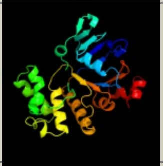
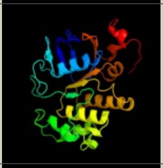
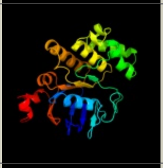
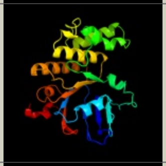
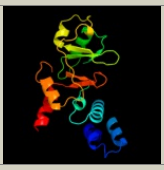
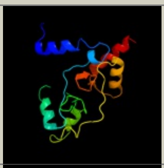
Description	P14175
Date	Thu Jan 5 11:33:55 GMT 2012
Unique Job ID	a4e6f437c4d63661

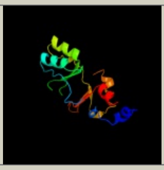
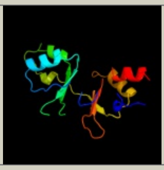
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yyzA_	Alignment		100.0	39	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein; **PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein
2	c1q1bD_	Alignment		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
3	c1oxtB_	Alignment		100.0	30	**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
4	c2it1B_	Alignment		100.0	39	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin **PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii
5	c3fvqB_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fe(3+) ions import atp-binding protein fbpc; **PDBTitle:** crystal structure of the nucleotide binding domain fbpc2 complexed with atp
6	c1z47B_	Alignment		100.0	35	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative abc-transporter atp-binding protein; **PDBTitle:** structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
7	d3dhwc1	Alignment		100.0	39	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
8	c3dhwC_	Alignment		100.0	39	**PDB header:**membrane protein/hydrolase **Chain:** C: **PDB Molecule:**methionine import atp-binding protein metn; **PDBTitle:** crystal structure of methionine importer metni
9	d1g2912	Alignment		100.0	43	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
10	d1oxxk2	Alignment		100.0	34	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
11	c1vciA_	Alignment		100.0	41	**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

12	c2olkD_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acid abc transporter; **PDBTitle:** abc protein artp in complex with adp-beta-s
13	c2d62A_	Alignment		100.0	40	**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
14	c3d31B_	Alignment		100.0	38	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sulfate/molybdate abc transporter, atp-binding **PDBTitle:** modbc from methanosarcina acetivorans
15	d3d31a2	Alignment		100.0	40	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
16	d1b0ua_	Alignment		100.0	37	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
17	d1v43a3	Alignment		100.0	40	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
18	d1vpla_	Alignment		100.0	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
19	c3gfoA_	Alignment		100.0	27	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**cobalt import atp-binding protein cbio 1; **PDBTitle:** structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.
20	c2pcjB_	Alignment		100.0	34	**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
21	c3gd7C_	Alignment	not modelled	100.0	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fusion complex of cystic fibrosis transmembrane **PDBTitle:** crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)
22	d1g6ha_	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
23	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
24	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
25	d2pmka1	Alignment	not modelled	100.0	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
26	c3g5uB_	Alignment	not modelled	100.0	34	**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
27	d1jj7a_	Alignment	not modelled	100.0	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
28	c2yz2B_	Alignment	not modelled	100.0	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
29	c2d2fA_	Alignment	not modelled	100.0	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
30	d1mv5a_	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
31	d3b60a1	Alignment	not modelled	100.0	34	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
32	d2onka1	Alignment	not modelled	100.0	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
33	c2nq2C_	Alignment	not modelled	100.0	24	**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.
34	d2hyda1	Alignment	not modelled	100.0	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
35	c3nhaA_	Alignment	not modelled	100.0	32	**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)
36	c2hydB_	Alignment	not modelled	100.0	33	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
37	c2yl4A_	Alignment	not modelled	100.0	36	**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
38	c2d3wB_	Alignment	not modelled	100.0	23	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**probable atp-dependent transporter sufc; **PDBTitle:** crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
39	d1xmia_	Alignment	not modelled	100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
40	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
41	c3b5xB_	Alignment	not modelled	100.0	34	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
42	c2cbzA_	Alignment	not modelled	100.0	24	**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
43	d1r0wa_	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
44	c1yqtA_	Alignment	not modelled	100.0	28	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
45	c3b5wE_	Alignment	not modelled	100.0	34	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba
46	c2ihyB_	Alignment	not modelled	100.0	26	**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
47	c3ozxA_	Alignment	not modelled	100.0	26	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
48	d1pf4a1	Alignment	not modelled	100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
49	c2pzfB_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cystic fibrosis transmembrane conductance regulator; **PDBTitle:** minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
50	c2pjzA_	Alignment	not modelled	100.0	26	**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
51	d1l7vc_	Alignment	not modelled	100.0	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
52	c2ghiD_	Alignment	not modelled	100.0	27	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport protein; **PDBTitle:** crystal structure of plasmodium yoelii multidrug resistance2 protein 2

53	c3bk7A_	Alignment	not modelled	100.0	25	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
54	d1sgwa_	Alignment	not modelled	100.0	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
55	c2r6fA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
56	c2iw3B_	Alignment	not modelled	100.0	18	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 3a; **PDBTitle:** elongation factor 3 in complex with adp
57	c2ygrD_	Alignment	not modelled	100.0	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
58	c3pihA_	Alignment	not modelled	100.0	29	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
59	c2vf7B_	Alignment	not modelled	100.0	27	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
60	d1cr2a_	Alignment	not modelled	99.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
61	c3tauB_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of a putative guanylate monophosphaste kinase from2 listeria monocytogenes egd-e
62	d1w1wa_	Alignment	not modelled	99.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
63	c2j41A_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
64	c3a4mB_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-seryl-trna(sec) kinase; **PDBTitle:** crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
65	d1ls1a2	Alignment	not modelled	99.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
66	d2qy9a2	Alignment	not modelled	99.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
67	d1vmaa2	Alignment	not modelled	99.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
68	c1f2uD_	Alignment	not modelled	99.7	23	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
69	c3kxrA_	Alignment		99.6	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**magnesium transporter, putative; **PDBTitle:** structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.
70	c1xexB_	Alignment	not modelled	99.6	20	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**smc protein; **PDBTitle:** structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
71	c2yvxD_	Alignment		99.6	19	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
72	c2ouxB_	Alignment		99.6	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium transporter; **PDBTitle:** crystal structure of the soluble part of a magnesium transporter
73	c2o5vA_	Alignment	not modelled	99.6	22	**PDB header:**replication/recombination **Chain:** A: **PDB Molecule:**dna replication and repair protein recf; **PDBTitle:** recombination mediator recf
74	d1okkd2	Alignment	not modelled	99.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
75	c1u9iA_	Alignment	not modelled	99.5	14	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
						PDB header:transferase

76	c3lncB_	Alignment	not modelled	99.5	11	**Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of guanylate kinase from anaplasma2 phagocytophilum
77	c2v8qE_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** E: **PDB Molecule:**5'-amp-activated protein kinase subunit gamma-1; **PDBTitle:** crystal structure of the regulatory fragment of mammalian2 ampk in complexes with amp
78	c2qh1B_	Alignment		99.5	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ta0289; **PDBTitle:** structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
79	c3geiB_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
80	c3ocmA_	Alignment		99.5	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
81	d1np6a_	Alignment	not modelled	99.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
82	c3jtfB_	Alignment		99.5	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**magnesium and cobalt efflux protein; **PDBTitle:** the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp
83	d1vr9a3	Alignment	not modelled	99.5	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
84	d2ouxa2	Alignment	not modelled	99.5	23	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
85	c1zfjA_	Alignment	not modelled	99.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
86	c3lqnA_	Alignment	not modelled	99.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
87	c1vr9B_	Alignment	not modelled	99.5	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**cbs domain protein/act domain protein; **PDBTitle:** crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
88	c1ii8B_	Alignment	not modelled	99.5	30	**PDB header:**replication **Chain:** B: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
89	d3ddja1	Alignment	not modelled	99.5	18	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
90	c3gbyA_	Alignment	not modelled	99.5	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ct1051; **PDBTitle:** crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
91	c2yvzA_	Alignment	not modelled	99.4	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
92	d2d4za3	Alignment	not modelled	99.4	15	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
93	c2qlvF_	Alignment	not modelled	99.4	16	**PDB header:**transferase/protein binding **Chain:** F: **PDB Molecule:**nuclear protein snf4; **PDBTitle:** crystal structure of the heterotrimer core of the s.2 cerevisiae ampk homolog snf1
94	c3lhhA_	Alignment	not modelled	99.4	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**cbs domain protein; **PDBTitle:** the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
95	c2emqA_	Alignment	not modelled	99.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical conserved protein; **PDBTitle:** hypothetical conserved protein (gk1048) from geobacillus kaustophilus
96	d2yzqa1	Alignment	not modelled	99.4	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
97	c3fwrB_	Alignment	not modelled	99.4	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**yqzb protein; **PDBTitle:** crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
98	d1pvma4	Alignment	not modelled	99.4	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
						PDB header:lyase

99	c3pc3A_	Alignment	not modelled	99.4	12	**Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
100	d1yava3	Alignment	not modelled	99.4	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
101	c3i8nB_	Alignment	not modelled	99.4	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp2912; **PDBTitle:** a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633.
102	c2qr1E_	Alignment	not modelled	99.4	13	**PDB header:**transferase **Chain:** E: **PDB Molecule:**protein c1556.08c; **PDBTitle:** crystal structure of the adenylate sensor from amp-activated protein2 kinase in complex with adp
103	c3ocmB_	Alignment	not modelled	99.4	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**putative membrane protein; **PDBTitle:** the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
104	d2yzia1	Alignment	not modelled	99.4	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
105	d1o50a3	Alignment	not modelled	99.4	19	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
106	c2d4zB_	Alignment	not modelled	99.4	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride channel protein; **PDBTitle:** crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
107	d2v8qe1	Alignment	not modelled	99.4	16	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
108	c2p9mD_	Alignment	not modelled	99.4	21	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0922; **PDBTitle:** crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
109	c3lfrB_	Alignment	not modelled	99.4	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative metal ion transporter; **PDBTitle:** the crystal structure of a cbs domain from a putative metal2 ion transporter bound to amp from pseudomonas syringae to3 1.55a
110	d2j9la1	Alignment	not modelled	99.4	17	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
111	c3kpbA_	Alignment	not modelled	99.4	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0100; **PDBTitle:** crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
112	c3ctuB_	Alignment	not modelled	99.4	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cbs domain protein; **PDBTitle:** crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4
113	c3hf7A_	Alignment	not modelled	99.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized cbs-domain protein; **PDBTitle:** the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
114	c3nqrD_	Alignment	not modelled	99.3	13	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**magnesium and cobalt efflux protein corc; **PDBTitle:** a putative cbs domain-containing protein from salmonella typhimurium2 lt2
115	d2ooxe2	Alignment	not modelled	99.3	14	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
116	c1q57G_	Alignment	not modelled	99.3	14	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
117	c3fnaA_	Alignment	not modelled	99.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**possible arabinose 5-phosphate isomerase; **PDBTitle:** crystal structure of the cbs pair of possible d-arabinose 5-phosphate2 isomerase yrbh from escherichia coli cft073
118	c1yavB_	Alignment	not modelled	99.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14130; **PDBTitle:** crystal structure of cbs domain-containing protein ykul2 from bacillus subtilis
119	d2ef7a1	Alignment	not modelled	99.3	21	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
120	c3lv9A_	Alignment	not modelled	99.3	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**putative transporter; **PDBTitle:** crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630