



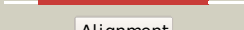

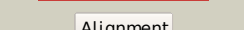

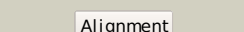

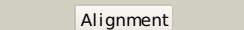





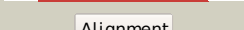

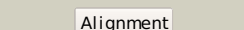

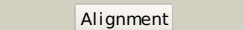












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1q1bD_</a>	 Alignment		100.0	100	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> maltose/maltodextrin transport atp-binding protein malk; <b>PDBTitle:</b> crystal structure of e. coli malk in the nucleotide-free form
2	<a href="#">c3gd7C_</a>	 Alignment		100.0	54	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> fusion complex of cystic fibrosis transmembrane <b>PDBTitle:</b> crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)
3	<a href="#">c2yyzA_</a>	 Alignment		100.0	40	<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
4	<a href="#">c2it1B_</a>	 Alignment		100.0	40	<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
5	<a href="#">c1vcia_</a>	 Alignment		100.0	44	<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
6	<a href="#">c1oxtb_</a>	 Alignment		100.0	37	<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
7	<a href="#">c1z47B_</a>	 Alignment		100.0	36	<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 putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
8	<a href="#">c3fvqB_</a>	 Alignment		100.0	31	<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 fbpc2 complexed with atp
9	<a href="#">c3d31B_</a>	 Alignment		100.0	32	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate/molybdate abc transporter, atp-binding <b>PDBTitle:</b> modbc from methanosarcina acetivorans
10	<a href="#">c2d62A_</a>	 Alignment		100.0	45	<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
11	<a href="#">d1g2912</a>	 Alignment		100.0	57	<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

12	<a href="#">d1oxxk2</a>	Alignment		100.0	44	<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
13	<a href="#">c2olkD_</a>	Alignment		100.0	34	<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
14	<a href="#">d1v43a3</a>	Alignment		100.0	54	<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
15	<a href="#">d3dhwc1</a>	Alignment		100.0	30	<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="#">c3dhwC_</a>	Alignment		100.0	30	<b>PDB header:</b> membrane protein/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> methionine import atp-binding protein metn; <b>PDBTitle:</b> crystal structure of methionine importer metni
17	<a href="#">d3d31a2</a>	Alignment		100.0	39	<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
18	<a href="#">d1b0ua_</a>	Alignment		100.0	30	<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
19	<a href="#">d1vp1a_</a>	Alignment		100.0	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
20	<a href="#">c3gfoA_</a>	Alignment		100.0	30	<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 of2 the abc transporter complex cbionq.
21	<a href="#">d1g6ha_</a>	Alignment	not modelled	100.0	29	<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
22	<a href="#">d1ji0a_</a>	Alignment	not modelled	100.0	26	<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="#">c2pcjB_</a>	Alignment	not modelled	100.0	33	<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
24	<a href="#">d2pmka1</a>	Alignment	not modelled	100.0	30	<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
25	<a href="#">c3g5uB_</a>	Alignment	not modelled	100.0	30	<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
26	<a href="#">c2d2fA_</a>	Alignment	not modelled	100.0	26	<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 sufc from thermus2 thermophilus hb8
27	<a href="#">c2yz2B_</a>	Alignment	not modelled	100.0	31	<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
28	<a href="#">d3onka1</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate

28	<a href="#">d2vha1</a>	Alignment	not modelled	100.0	38	hydrolases <b>Family:</b> ABC transporter ATPase domain-like
29	<a href="#">d1jj7a</a>	Alignment	not modelled	100.0	30	<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
30	<a href="#">d1l2ta</a>	Alignment	not modelled	100.0	38	<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
31	<a href="#">d1mv5a</a>	Alignment	not modelled	100.0	26	<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="#">c2nq2C</a>	Alignment	not modelled	100.0	27	<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.
33	<a href="#">d3b60a1</a>	Alignment	not modelled	100.0	29	<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
34	<a href="#">c3nhaA</a>	Alignment	not modelled	100.0	27	<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)
35	<a href="#">d2hya1</a>	Alignment	not modelled	100.0	31	<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
36	<a href="#">d2awna2</a>	Alignment	not modelled	100.0	96	<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
37	<a href="#">c2d3wB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable atp-dependent transporter sufC; <b>PDBTitle:</b> crystal structure of escherichia coli sufC, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
38	<a href="#">c2hydB</a>	Alignment	not modelled	100.0	34	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter homolog; <b>PDBTitle:</b> multidrug abc transporter sav1866
39	<a href="#">c2yl4A</a>	Alignment	not modelled	100.0	34	<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
40	<a href="#">c2cbzA</a>	Alignment	not modelled	100.0	29	<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
41	<a href="#">c2ihyB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter
42	<a href="#">c3b5wE</a>	Alignment	not modelled	100.0	30	<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
43	<a href="#">c3b5xB</a>	Alignment	not modelled	100.0	29	<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
44	<a href="#">d1pf4a1</a>	Alignment	not modelled	100.0	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
45	<a href="#">d1xmia</a>	Alignment	not modelled	100.0	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
46	<a href="#">c1yqtA</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase l inhibitor; <b>PDBTitle:</b> rnase-l inhibitor
47	<a href="#">c2pzfB</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cystic fibrosis transmembrane conductance regulator; <b>PDBTitle:</b> minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
48	<a href="#">c2pjzA</a>	Alignment	not modelled	100.0	29	<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
49	<a href="#">c3ozxA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase, translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase l inhibitor; <b>PDBTitle:</b> crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
50	<a href="#">d1r0wa</a>	Alignment	not modelled	100.0	28	<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
51	<a href="#">c2ghiD</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> transport protein; <b>PDBTitle:</b> crystal structure of plasmodium yoelii multidrug resistance2 protein 2
52	<a href="#">d1sgwa</a>	Alignment	not modelled	100.0	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

53	<a href="#">d1l7vc_</a>	Alignment	not modelled	100.0	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
54	<a href="#">c3bk7A_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> hydrolase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi
55	<a href="#">c2r6fA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc subunit a; <b>PDBTitle:</b> crystal structure of bacillus stearothermophilus uvra
56	<a href="#">c2iw3B_</a>	Alignment	not modelled	100.0	22	<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
57	<a href="#">c2ygrD_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
58	<a href="#">c3pihA_</a>	Alignment	not modelled	100.0	28	<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
59	<a href="#">c2vf7B_</a>	Alignment	not modelled	100.0	28	<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
60	<a href="#">d1cr2a_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
61	<a href="#">c3tauB_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e
62	<a href="#">d1w1wa_</a>	Alignment	not modelled	99.9	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
63	<a href="#">c2j41A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
64	<a href="#">c3a4mB_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l-seryl-trna(sec) kinase; <b>PDBTitle:</b> crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
65	<a href="#">d1ls1a2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
66	<a href="#">d2awna1</a>	Alignment	not modelled	99.8	100	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
67	<a href="#">d2qy9a2</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
68	<a href="#">d1vmaa2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
69	<a href="#">c2o5vA_</a>	Alignment	not modelled	99.7	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
70	<a href="#">c1f2uD_</a>	Alignment	not modelled	99.7	29	<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
71	<a href="#">c1xexB_</a>	Alignment	not modelled	99.7	24	<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.
72	<a href="#">c1u9iA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> circadian clock protein <b>Chain:</b> A: <b>PDB Molecule:</b> kaic; <b>PDBTitle:</b> crystal structure of circadian clock protein kaic with phosphorylation2 sites
73	<a href="#">c3lncB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> crystal structure of guanylate kinase from anaplasma2 phagocytophilum
74	<a href="#">d1okkd2</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
75	<a href="#">c1ii8B_</a>	Alignment	not modelled	99.6	33	<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
76	<a href="#">c3geiB_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from chlorobium tepidum in complex2 with gcp
77	<a href="#">d1np6a_</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
78	<a href="#">d1ye8a1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
						<b>PDB header:</b> transferase

79	<a href="#">c1q57G_</a>	Alignment	not modelled	99.4	12	<b>Chain:</b> G: <b>PDB Molecule:</b> dna primase/helicase; <b>PDBTitle:</b> the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
80	<a href="#">d1qzxa3</a>	Alignment	not modelled	99.3	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
81	<a href="#">d2i3ba1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
82	<a href="#">d1e69a_</a>	Alignment	not modelled	99.3	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
83	<a href="#">d1oxk1</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
84	<a href="#">c2dr3A_</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0273 protein ph0284; <b>PDBTitle:</b> crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
85	<a href="#">c2w0mA_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfolobus solfataricus2 p2
86	<a href="#">c1pznG_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
87	<a href="#">d3d31a1</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
88	<a href="#">d1n1fa_</a>	Alignment	not modelled	98.8	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
89	<a href="#">c3auyB_</a>	Alignment	not modelled	98.8	22	<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
90	<a href="#">c3thxB_</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein msh3; <b>PDBTitle:</b> human mutsbeta complexed with an idl of 3 bases (loop3) and adp
91	<a href="#">d1ewqa2</a>	Alignment	not modelled	98.6	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
92	<a href="#">c2o8bA_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein msh2; <b>PDBTitle:</b> human mutsalph (msh2/msh6) bound to adp and a g t mispair
93	<a href="#">d1tf7a1</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
94	<a href="#">d1wb9a2</a>	Alignment	not modelled	98.5	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="#">c1wxqA_</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
96	<a href="#">c3cmvG_</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
97	<a href="#">c2o8dB_</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna mismatch repair protein msh6; <b>PDBTitle:</b> human mutsalph (msh2/msh6) bound to adp and a g du mispair
98	<a href="#">c1ewqA_</a>	Alignment	not modelled	98.4	26	<b>PDB header:</b> replication/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution
99	<a href="#">c1wbdA_</a>	Alignment	not modelled	98.4	23	<b>PDB header:</b> dna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g.t mismatch
100	<a href="#">c1ewrA_</a>	Alignment	not modelled	98.3	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of taq muts
101	<a href="#">d1yrba1</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> Nitrogenase iron protein-like
102	<a href="#">d1g2914</a>	Alignment	not modelled	98.2	19	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
103	<a href="#">d2i1qa2</a>	Alignment	not modelled	98.2	8	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
104	<a href="#">d1tf7a2</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> RecA protein-like (ATPase-domain)
						<b>Fold:</b> OB-fold



105	<a href="#">d1v43a2</a>	Alignment	not modelled	98.2	21	<b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
106	<a href="#">c3bh0A</a>	Alignment	not modelled	98.2	12	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p
107	<a href="#">c3qg5A</a>	Alignment	not modelled	98.1	28	<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
108	<a href="#">d1znwa1</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
109	<a href="#">c3qkuB</a>	Alignment	not modelled	98.1	33	<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
110	<a href="#">c2vyeA</a>	Alignment	not modelled	98.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnac-ssdna complex
111	<a href="#">d1mo6a1</a>	Alignment	not modelled	98.1	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
112	<a href="#">d1n0wa</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
113	<a href="#">c2recB</a>	Alignment	not modelled	98.0	19	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
114	<a href="#">d1szpa2</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
115	<a href="#">d1xp8a1</a>	Alignment	not modelled	98.0	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
116	<a href="#">d1v5wa</a>	Alignment	not modelled	98.0	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
117	<a href="#">c1h9mB</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdenum-binding-protein; <b>PDBTitle:</b> two crystal structures of the cytoplasmic molybdate-binding2 protein modg suggest a novel cooperative binding mechanism3 and provide insights into ligand-binding specificity.4 peg-grown form with molybdate bound
118	<a href="#">c1h9sA</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum transport protein mode; <b>PDBTitle:</b> molybdate bound complex of dimop domain of mode from e.coli
119	<a href="#">c1szpC</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> a crystal structure of the rad51 filament
120	<a href="#">c2q6tB</a>	Alignment	not modelled	97.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dnab replication fork helicase; <b>PDBTitle:</b> crystal structure of the thermus aquaticus dnab monomer