



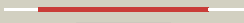




























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1r6bX_	 Alignment		100.0	100	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
2	c1qvrB_	 Alignment		100.0	44	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
3	c3pxiB_	 Alignment		100.0	42	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/meclb; PDBTitle: structure of meca108:clpc
4	c3pxgA_	 Alignment		100.0	35	PDB header: protein binding Chain: A: PDB Molecule: negative regulator of genetic competence clpc/meclb; PDBTitle: structure of meca121 and clpc1-485 complex
5	c3cf1C_	 Alignment		100.0	21	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
6	d1r6bx3	 Alignment		100.0	100	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
7	d1qvra2	 Alignment		100.0	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
8	d1qvra3	 Alignment		100.0	45	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
9	d1um8a_	 Alignment		100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
10	d1r6bx2	 Alignment		100.0	99	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
11	d1e94e_	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

12	c2p65A	Alignment		100.0	53	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pf08_0063; PDBTitle: crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
13	d1g41a	Alignment		100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
14	d1jbka	Alignment		100.0	51	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
15	d1ofha	Alignment		100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
16	c3hteC	Alignment		100.0	23	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
17	c3hu2C	Alignment		100.0	24	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
18	c2ce7B	Alignment		99.9	18	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
19	c2dhrC	Alignment		99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
20	c1s3sA	Alignment		99.9	21	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
21	c1xwiA	Alignment	not modelled	99.9	22	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
22	c3b9pA	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
23	d1k6ka	Alignment	not modelled	99.9	100	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
24	d2ce7a2	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
25	d1ny5a2	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
26	c3eihB	Alignment	not modelled	99.9	24	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: crystal structure of s.cerevisiae vps4 in the presence of atpgammas
27	c3pvsA	Alignment	not modelled	99.9	21	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
28	c1ny5A	Alignment	not modelled	99.9	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the

						inactive2 state
29	dlixza_	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
30	c2c99A_	Alignment	not modelled	99.9	19	PDB header: transcription regulation Chain: A: PDB Molecule: psp operon transcriptional activator; PDBTitle: structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
31	c2zamA_	Alignment	not modelled	99.9	20	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
32	cliy2A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
33	c3pfiB_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
34	c3d8bB_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
35	c2r65A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
36	c3dzdA_	Alignment	not modelled	99.9	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
37	c1ojlF_	Alignment	not modelled	99.9	20	PDB header: response regulator Chain: F: PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
38	c3m6aC_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon c-terminal domain
39	c2r44A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
40	c3h4mC_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
41	d1e32a2	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c2qz4A_	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
43	d1w5sa2	Alignment	not modelled	99.8	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
44	c3fh2A_	Alignment	not modelled	99.8	24	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent protease (heat shock protein); PDBTitle: the crystal structure of the probable atp-dependent protease (heat2 shock protein) from corynebacterium glutamicum
45	c2k77A_	Alignment	not modelled	99.8	21	PDB header: chaperone, protein binding Chain: A: PDB Molecule: negative regulator of genetic competence PDBTitle: nmr solution structure of the bacillus subtilis clpc n-2 domain
46	clin8A_	Alignment	not modelled	99.8	21	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
47	d1khya_	Alignment	not modelled	99.8	21	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
48	c1nsfA_	Alignment	not modelled	99.8	17	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
49	c2x8aA_	Alignment	not modelled	99.8	15	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
50	c3fesB_	Alignment	not modelled	99.8	20	PDB header: atp binding protein Chain: B: PDB Molecule: atp-dependent clp endopeptidase; PDBTitle: crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile
51	d1d2na_	Alignment	not modelled	99.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
52	d1lv7a_	Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
53	d1in4a2	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate

53	d1m4a2	Alignment	not modelled	99.8	21	hydrolases Family: Extended AAA-ATPase domain
54	d1iqa2	Alignment	not modelled	99.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
55	c3nbxX	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
56	c3zriA	Alignment	not modelled	99.8	19	PDB header: chaperone Chain: A: PDB Molecule: clpb protein; PDBTitle: n-domain of clpv from vibrio cholerae
57	d1sxb2	Alignment	not modelled	99.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
58	c2chgB	Alignment	not modelled	99.8	19	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
59	d1fnna2	Alignment	not modelled	99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
60	d1r7ra3	Alignment	not modelled	99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
61	c3u5zM	Alignment	not modelled	99.8	18	PDB header: dna binding protein/dna Chain: M: PDB Molecule: dna polymerase accessory protein 44; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
62	d1g8pa	Alignment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
63	d1ixsb2	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
64	c1sxC	Alignment	not modelled	99.7	16	PDB header: replication Chain: C: PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
65	c3qmA	Alignment	not modelled	99.7	16	PDB header: motor protein Chain: A: PDB Molecule: cytoplasmic dynein heavy chain; PDBTitle: crystal structure of the cytoplasmic dynein heavy chain motor domain
66	d1sxc2	Alignment	not modelled	99.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
67	d1qva1	Alignment	not modelled	99.7	17	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
68	c1hqCB	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
69	c1sxB	Alignment	not modelled	99.7	15	PDB header: replication Chain: B: PDB Molecule: activator 1 37 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
70	c3kljA	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
71	d1sxd2	Alignment	not modelled	99.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
72	c2c9oC	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
73	d1njfa	Alignment	not modelled	99.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
74	c1fnnB	Alignment	not modelled	99.7	14	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
75	c2hbcC	Alignment	not modelled	99.7	10	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
76	c2chvE	Alignment	not modelled	99.7	18	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
77	c1iqpF	Alignment	not modelled	99.7	18	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
78	c1sxE	Alignment	not modelled	99.7	12	PDB header: replication Chain: E: PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)

79	c2qbyA	Alignment	not modelled	99.7	18	PDB header: replication/dna Chain: A: PDB Molecule: cell division control protein 6 homolog 1; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
80	c3te6A	Alignment	not modelled	99.7	10	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
81	c1sxjD	Alignment	not modelled	99.7	14	PDB header: replication Chain: D: PDB Molecule: activator 1 41 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
82	c2z4rB	Alignment	not modelled	99.7	17	PDB header: dna binding protein Chain: B: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
83	c1w5sB	Alignment	not modelled	99.7	12	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
84	c1sxjA	Alignment	not modelled	99.6	14	PDB header: replication Chain: A: PDB Molecule: activator 1 95 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
85	d1sxja2	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
86	d1l8qa2	Alignment	not modelled	99.6	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
87	d1a5ta2	Alignment	not modelled	99.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
88	d1oz4a3	Alignment	not modelled	99.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
89	c2qbyB	Alignment	not modelled	99.6	17	PDB header: replication/dna Chain: B: PDB Molecule: cell division control protein 6 homolog 3; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
90	c1xxhB	Alignment	not modelled	99.6	18	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
91	c3bosA	Alignment	not modelled	99.6	11	PDB header: hydrolase regulator,dna binding protein Chain: A: PDB Molecule: putative dna replication factor; PDBTitle: crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
92	d1sxje2	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
93	d1gvnb	Alignment	not modelled	99.6	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Plasmid maintenance system epsilon/zeta, toxin zeta subunit
94	c2v1uA	Alignment	not modelled	99.6	20	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
95	c1jr3E	Alignment	not modelled	99.5	14	PDB header: transferase Chain: E: PDB Molecule: dna polymerase iii, delta' subunit; PDBTitle: crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
96	c3f8tA	Alignment	not modelled	99.5	19	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase involved in replication control, PDBTitle: crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
97	c3cmvG	Alignment	not modelled	99.3	17	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
98	c3ec2A	Alignment	not modelled	99.3	23	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnac; PDBTitle: crystal structure of the dnac helicase loader
99	c2fnaA	Alignment	not modelled	99.2	19	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal dnaa+ atpase (sso1545) from sulfolobus2 solfataricus p2 at 2.00 a resolution
100	c2p5tD	Alignment	not modelled	99.2	15	PDB header: transcription regulator Chain: D: PDB Molecule: pez2; PDBTitle: molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
101	d2gnoa2	Alignment	not modelled	99.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
102	d2fnaa2	Alignment	not modelled	99.2	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain PDB header: hydrolase

103	c3f9vA_	Alignment	not modelled	99.1	14	Chain: A: PDB Molecule: minichromosome maintenance protein mcm; PDBTitle: crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
104	c2w58B_	Alignment	not modelled	99.1	18	PDB header: hydrolase Chain: B: PDB Molecule: primosome component (helicase loader); PDBTitle: crystal structure of the dnaI
105	c2qenA_	Alignment	not modelled	99.0	17	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
106	c2kjqA_	Alignment	not modelled	99.0	18	PDB header: replication Chain: A: PDB Molecule: dnaa-related protein; PDBTitle: solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
107	c3co5B_	Alignment	not modelled	98.8	11	PDB header: transcription regulator Chain: B: PDB Molecule: putative two-component system transcriptional response PDBTitle: crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
108	c2qgzA_	Alignment	not modelled	98.8	23	PDB header: hydrolase Chain: A: PDB Molecule: putative primosome component; PDBTitle: crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
109	d1ye8a1	Alignment	not modelled	98.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
110	d1svma_	Alignment	not modelled	98.5	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
111	d1kaga_	Alignment	not modelled	98.4	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
112	c3iytG_	Alignment	not modelled	98.4	14	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
113	c1ii0A_	Alignment	not modelled	98.3	19	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
114	d1tuea_	Alignment	not modelled	98.3	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
115	c2gxaA_	Alignment	not modelled	98.2	20	PDB header: replication/dna Chain: A: PDB Molecule: replication protein e1; PDBTitle: crystal structure of papillomavirus e1 hexameric helicase2 with ssdna and mgadp
116	c1mkvA_	Alignment	not modelled	98.2	17	PDB header: ligand binding protein Chain: A: PDB Molecule: probable gtp-binding protein enga; PDBTitle: structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains
117	c2qy9A_	Alignment	not modelled	98.2	19	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
118	c3b9qA_	Alignment	not modelled	98.2	15	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts from arabidopsis thaliana
119	c2yhsA_	Alignment	not modelled	98.1	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
120	c2og2A_	Alignment	not modelled	98.1	16	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana