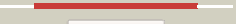



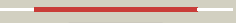


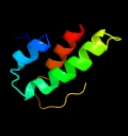







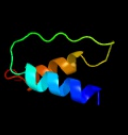



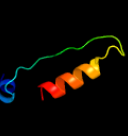

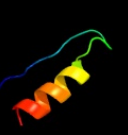


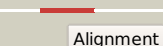

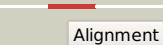

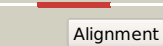
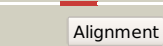







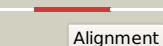
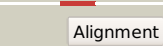





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3422c_(-)_3839871_3840377
Date	Fri Aug 9 18:20:09 BST 2019
Unique Job ID	f93bec103c90ee86

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1htwa_	 Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: YjeE-like
2	c6fpeE_	 Alignment		100.0	36	PDB header: rna binding protein Chain: E; PDB Molecule: atpase yjee, predicted to have essential role in cell wall PDBTitle: bacterial protein complex
3	c5mvrA_	 Alignment		100.0	31	PDB header: transferase Chain: A; PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsae; PDBTitle: crystal structure of bacillus subtilus ydib
4	d1ixsb2	 Alignment		97.4	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
5	c1ojfE_	 Alignment		97.4	16	PDB header: response regulator Chain: F; PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
6	d1ny5a2	 Alignment		97.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
7	c3tlxA_	 Alignment		97.4	13	PDB header: transferase Chain: A; PDB Molecule: adenylate kinase 2; PDBTitle: crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
8	c5ep4A_	 Alignment		97.3	20	PDB header: transcription Chain: A; PDB Molecule: putative repressor protein luxo; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
9	d1d2na_	 Alignment		97.3	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
10	c3uiEB_	 Alignment		97.3	25	PDB header: transferase/transferase inhibitor Chain: B; PDB Molecule: adenylyl-sulfate kinase 1, chloroplastic; PDBTitle: crystal structure of adenosine 5'-phosphosulfate kinase from2 arabidopsis thaliana in complex with amppnp and aps
11	c5cb6A_	 Alignment		97.2	31	PDB header: transferase Chain: A; PDB Molecule: probable adenylyl-sulfate kinase; PDBTitle: structure of adenosine-5'-phosphosulfate kinase

12	d1knqa_	 Alignment		97.2	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Gluconate kinase
13	c3c8uA_	 Alignment		97.2	33	PDB header: transferase Chain: A; PDB Molecule: fructokinase; PDBTitle: crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
14	c3uk6L_	 Alignment		97.2	31	PDB header: hydrolase Chain: L; PDB Molecule: ruvb-like 2; PDBTitle: crystal structure of the tip48 (tip49b) hexamer
15	d1a5ta2	 Alignment		97.2	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
16	d1qhxa_	 Alignment		97.2	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Chloramphenicol phosphotransferase
17	c6b8vA_	 Alignment		97.2	25	PDB header: transferase Chain: A; PDB Molecule: adenyllylsulfate kinase; PDBTitle: crystal structure of adenylyl-sulfate kinase from cryptococcus2 neoformans
18	c2yvuA_	 Alignment		97.1	35	PDB header: transferase Chain: A; PDB Molecule: probable adenylyl-sulfate kinase; PDBTitle: crystal structure of ape1195
19	c5exsA_	 Alignment		97.1	15	PDB header: transcription Chain: A; PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
20	c3fdiA_	 Alignment		97.1	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
21	c3umfA_	 Alignment	not modelled	97.1	19	PDB header: transferase Chain: A; PDB Molecule: adenylate kinase; PDBTitle: schistosoma mansoni adenylylate kinase
22	c1sxjC_	 Alignment	not modelled	97.1	25	PDB header: replication Chain: C; PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
23	c4cw7A_	 Alignment	not modelled	97.1	33	PDB header: transferase Chain: A; PDB Molecule: putative adenylylate kinase; PDBTitle: structure of the fap7-rps14 complex in complex with atp
24	c4gp6A_	 Alignment	not modelled	97.1	33	PDB header: transferase Chain: A; PDB Molecule: metallophosphoesterase; PDBTitle: polynucleotide kinase
25	c2c99A_	 Alignment	not modelled	97.1	16	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
26	d1m8pa3	 Alignment	not modelled	97.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain
27	c4xgcA_	 Alignment	not modelled	97.0	20	PDB header: dna binding protein Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
28	c2vliB_	 Alignment	not modelled	97.0	25	PDB header: transferase Chain: B; PDB Molecule: antibiotic resistance protein; PDBTitle: structure of deinococcus radiodurans tunicamycin resistance protein

29	d1vmaa2	Alignment	not modelled	97.0	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
30	c4xguB	Alignment	not modelled	97.0	27	PDB header: atp-binding protein Chain: B; PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
31	d1m7ga	Alignment	not modelled	97.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'phosphosulfate kinase (APS kinase)
32	c5b3fB	Alignment	not modelled	97.0	22	PDB header: transferase Chain: B; PDB Molecule: phosphoribulokinase/uridine kinase; PDBTitle: crystal structure of phosphoribulokinase from methanospirillum2 hungatei
33	c2ak2A	Alignment	not modelled	97.0	41	PDB header: phosphotransferase Chain: A; PDB Molecule: adenylate kinase isoenzyme-2; PDBTitle: adenylate kinase isoenzyme-2
34	c2gksB	Alignment	not modelled	97.0	26	PDB header: transferase Chain: B; PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
35	c5oafB	Alignment	not modelled	97.0	26	PDB header: gene regulation Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexameric ino80 complex
36	c5lnkk	Alignment	not modelled	97.0	24	PDB header: oxidoreductase Chain: K; PDB Molecule: mitochondrial complex i, nd4l subunit; PDBTitle: entire ovine respiratory complex i
37	d1lw7a2	Alignment	not modelled	97.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
38	d1p6xa	Alignment	not modelled	96.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
39	c6i26A	Alignment	not modelled	96.9	19	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin,midasin,midasin; PDBTitle: rea1 wild type amppnp state
40	c3t61A	Alignment	not modelled	96.9	27	PDB header: transferase Chain: A; PDB Molecule: gluconokinase; PDBTitle: crystal structure of a gluconokinase from sinorhizobium melloti 1021
41	d1m7gb	Alignment	not modelled	96.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'phosphosulfate kinase (APS kinase)
42	c3zw6B	Alignment	not modelled	96.9	20	PDB header: photosynthesis Chain: B; PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
43	d1zp6a1	Alignment	not modelled	96.9	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like
44	c2dhrC	Alignment	not modelled	96.9	24	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
45	d1tmka	Alignment	not modelled	96.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
46	d3adka	Alignment	not modelled	96.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
47	c2rhmD	Alignment	not modelled	96.9	20	PDB header: unknown function Chain: D; PDB Molecule: putative kinase; PDBTitle: crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution
48	c3hteC	Alignment	not modelled	96.9	35	PDB header: motor protein Chain: C; PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
49	c4bzpB	Alignment	not modelled	96.9	25	PDB header: transferase Chain: B; PDB Molecule: bifunctional enzyme cysn/cysc; PDBTitle: structure of the mycobacterium tuberculosis aps kinase cysc2 in complex with adp
50	c5vq9D	Alignment	not modelled	96.9	27	PDB header: protein binding Chain: D; PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
51	c4b4tL	Alignment	not modelled	96.9	39	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
52	c2z4rB	Alignment	not modelled	96.9	18	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
53	c5kneA	Alignment	not modelled	96.9	24	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
54	c2c9oC	Alignment	not modelled	96.8	31	PDB header: hydrolase Chain: C; PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
55	d1nija1	Alignment	not modelled	96.8	48	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: Nitrogenase iron protein-like
56	c6az0A_	Alignment	not modelled	96.8	30	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
57	d1rz3a_	Alignment	not modelled	96.8	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
58	c4eunA_	Alignment	not modelled	96.8	36	PDB header: transferase Chain: A; PDB Molecule: thermoresistant glucokinase; PDBTitle: crystal structure of a sugar kinase (target efi-502144 from janibacter2 sp. htcc2649), unliganded structure
59	d1iqpa2	Alignment	not modelled	96.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
60	d1x6va3	Alignment	not modelled	96.8	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'phosphosulfate kinase (APS kinase)
61	c5x7jA_	Alignment	not modelled	96.8	33	PDB header: transferase Chain: A; PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of thymidylate kinase from thermus thermophilus hb8
62	c2grjH_	Alignment	not modelled	96.8	20	PDB header: transferase Chain: H; PDB Molecule: dephospho-coa kinase; PDBTitle: crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution
63	c4ww4B_	Alignment	not modelled	96.8	26	PDB header: hydrolase Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
64	c1in8A_	Alignment	not modelled	96.8	36	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
65	c1nsfA_	Alignment	not modelled	96.8	30	PDB header: protein transport Chain: A; PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
66	d1ki9a_	Alignment	not modelled	96.8	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
67	d1lv7a_	Alignment	not modelled	96.8	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
68	d1sxje2	Alignment	not modelled	96.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
69	c6genX_	Alignment	not modelled	96.8	18	PDB header: nuclear protein Chain: X; PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
70	d1ak2a1	Alignment	not modelled	96.8	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
71	c3nwbB_	Alignment	not modelled	96.8	32	PDB header: transferase Chain: B; PDB Molecule: atsk2; PDBTitle: crystal structure of shikimate kinase from arabidopsis thaliana2 (atsk2)
72	c4ciuA_	Alignment	not modelled	96.8	22	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
73	c2pt5D_	Alignment	not modelled	96.8	16	PDB header: transferase Chain: D; PDB Molecule: shikimate kinase; PDBTitle: crystal structure of shikimate kinase (aq_2177) from aquifex aeolicus2 vf5
74	c3akcA_	Alignment	not modelled	96.8	35	PDB header: transferase Chain: A; PDB Molecule: cytidylate kinase; PDBTitle: crystal structure of cmp kinase in complex with cdp and adp from2 thermus thermophilus hb8
75	c2c9oA_	Alignment	not modelled	96.7	31	PDB header: hydrolase Chain: A; PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
76	c2bwjC_	Alignment	not modelled	96.7	19	PDB header: transferase Chain: C; PDB Molecule: adenylate kinase 5; PDBTitle: structure of adenylate kinase 5
77	c2qz4A_	Alignment	not modelled	96.7	31	PDB header: hydrolase Chain: A; PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
78	d1ls1a2	Alignment	not modelled	96.7	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
79	c5j1sA_	Alignment	not modelled	96.7	17	PDB header: hydrolase Chain: A; PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
80	c4b4tM_	Alignment	not modelled	96.7	32	PDB header: hydrolase Chain: M; PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
81	d1in4a2	Alignment	not modelled	96.7	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
						PDB header: hydrolase

82	c5ubvB_	Alignment	not modelled	96.7	39	Chain: B; PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
83	c5x06G_	Alignment	not modelled	96.7	21	PDB header: replication Chain: G; PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
84	c5l3sF_	Alignment	not modelled	96.7	15	PDB header: protein transport Chain: F; PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
85	c6h7gB_	Alignment	not modelled	96.7	17	PDB header: photosynthesis Chain: B; PDB Molecule: phosphoribulokinase, chloroplastic; PDBTitle: crystal structure of redox-sensitive phosphoribulokinase (prk) from2 the green algae chlamydomonas reinhardtii
86	c3pfiB_	Alignment	not modelled	96.7	24	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
87	d1sxjc2	Alignment	not modelled	96.7	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
88	c2cnwF_	Alignment	not modelled	96.7	21	PDB header: signal recognition Chain: F; PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases fff and ftsy
89	d2bda1	Alignment	not modelled	96.7	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like
90	c6i27A_	Alignment	not modelled	96.7	19	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin,midasin,midasin,midasin,midasin; PDBTitle: rea1 aaa2l-h2alpha deletion mutant in amppnp state
91	c1ojlD_	Alignment	not modelled	96.7	17	PDB header: response regulator Chain: D; PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
92	c3asyB_	Alignment	not modelled	96.7	31	PDB header: transferase Chain: B; PDB Molecule: uridine kinase; PDBTitle: ligand-free structure of uridine kinase from thermus thermophilus hb8
93	c5c3cB_	Alignment	not modelled	96.7	22	PDB header: protein binding Chain: B; PDB Molecule: cbbq/nirq/norq domain protein; PDBTitle: structural characterization of a newly identified component of alpha-2 carboxysomes: the aaa+ domain protein cso-cbbq
94	d1ofha_	Alignment	not modelled	96.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
95	c5udbA_	Alignment	not modelled	96.7	11	PDB header: replication Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
96	d1njfa_	Alignment	not modelled	96.6	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	c2plrB_	Alignment	not modelled	96.6	21	PDB header: transferase Chain: B; PDB Molecule: probable thymidylate kinase; PDBTitle: crystal structure of dtmp kinase (st1543) from sulfobolus tokodaii2 strain7
98	c2qbyB_	Alignment	not modelled	96.6	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)
99	d1okkd2	Alignment	not modelled	96.6	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
100	c3u5zM_	Alignment	not modelled	96.6	23	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
101	d1g41a_	Alignment	not modelled	96.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
102	d1kaga_	Alignment	not modelled	96.6	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Shikimate kinase (AroK)
103	c3cm0A_	Alignment	not modelled	96.6	37	PDB header: transferase Chain: A; PDB Molecule: adenylate kinase; PDBTitle: crystal structure of adenylate kinase from thermus2 thermophilus hb8
104	c6qi8E_	Alignment	not modelled	96.6	31	PDB header: chaperone Chain: E; PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
105	d1lukza_	Alignment	not modelled	96.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
106	c6azyA_	Alignment	not modelled	96.6	24	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
107	c5he8J_	Alignment	not modelled	96.6	20	PDB header: protein binding Chain: J; PDB Molecule: helicase loader; PDBTitle: bacterial initiation protein
						PDB header: hydrolase

108	c4ypnA_	Alignment	not modelled	96.6	39	Chain: A; PDB Molecule: lon protease; PDBTitle: crystal structure of a lon fragment containing the 3-helix bundle and 2 the aaa-alpha/beta domain
109	c6djvE_	Alignment	not modelled	96.6	23	PDB header: chaperone Chain: E; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 2
110	c5uivA_	Alignment	not modelled	96.6	18	PDB header: transferase Chain: A; PDB Molecule: bifunctional thymidylate/uridylate kinase; PDBTitle: structure of thymidylate kinase from candida albicans reveals origin 2 of broad substrate specificity and a novel structural element.
111	c1zuiA_	Alignment	not modelled	96.6	38	PDB header: transferase Chain: A; PDB Molecule: shikimate kinase; PDBTitle: structural basis for shikimate-binding specificity of helicobacter 2 pylori shikimate kinase
112	c4b4tH_	Alignment	not modelled	96.6	32	PDB header: hydrolase Chain: H; PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
113	d1ckeA_	Alignment	not modelled	96.6	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
114	c2wwiC_	Alignment	not modelled	96.6	20	PDB header: transferase Chain: C; PDB Molecule: thymidilate kinase, putative; PDBTitle: plasmodium falciparum thymidilate kinase in complex with 2 aztmp and adp
115	c3be4A_	Alignment	not modelled	96.6	22	PDB header: transferase Chain: A; PDB Molecule: adenylate kinase; PDBTitle: crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360
116	d1e32a2	Alignment	not modelled	96.6	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
117	c1znyA_	Alignment	not modelled	96.6	34	PDB header: transferase Chain: A; PDB Molecule: guanylate kinase; PDBTitle: crystal structure of mycobacterium tuberculosis guanylate kinase in 2 complex with gdp
118	c3r8cB_	Alignment	not modelled	96.6	38	PDB header: transferase Chain: B; PDB Molecule: cytidylate kinase; PDBTitle: crystal structure of cytidylate kinase (cmk) from mycobacterium 2 abscessus
119	d1q3ta_	Alignment	not modelled	96.6	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
120	c3hdtB_	Alignment	not modelled	96.6	15	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase from clostridium symbiosum atcc 2 14940