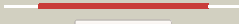
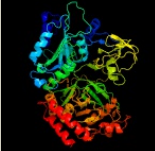


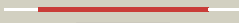
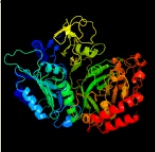



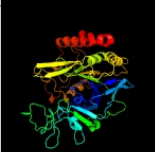


















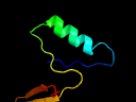
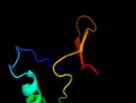



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0211_(pckA)_251782_253602
Date	Tue Jul 23 14:50:26 BST 2019
Unique Job ID	8c2604ba60ec3d62

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4wiuA_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase [gtp]; <b>PDBTitle:</b> crystal structure of pepck (rv0211) from mycobacterium tuberculosis in2 complex with oxalate and mn2+
2	<a href="#">c2qeyA_</a>	 Alignment		100.0	53	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase, cytosolic [gtp]; <b>PDBTitle:</b> rat cytosolic pepck in complex with gtp
3	<a href="#">c2zciD_</a>	 Alignment		100.0	65	<b>PDB header:</b> signaling protein, lyase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase [gtp]; <b>PDBTitle:</b> structure of a gtp-dependent bacterial pep-carboxykinase2 from corynebacterium glutamicum
4	<a href="#">c2fahB_</a>	 Alignment		100.0	52	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase; <b>PDBTitle:</b> the structure of mitochondrial pepck, complex with mn and gdp
5	<a href="#">d1khba1</a>	 Alignment		100.0	54	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> PEP carboxykinase C-terminal domain
6	<a href="#">d1khba2</a>	 Alignment		100.0	50	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
7	<a href="#">c1yvyA_</a>	 Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase [atp]; <b>PDBTitle:</b> crystal strucutre of anaerobiospirillum succiniciproducens2 phosphoenolpyruvate carboxykinase
8	<a href="#">c1ylhA_</a>	 Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase; <b>PDBTitle:</b> crystal structure of phosphoenolpyruvate carboxykinase from2 actinobacillus succinogenes in complex with manganese and3 pyruvate
9	<a href="#">d1j3ba1</a>	 Alignment		100.0	19	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> PEP carboxykinase C-terminal domain
10	<a href="#">c1ii2B_</a>	 Alignment		100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase; <b>PDBTitle:</b> crystal structure of phosphoenolpyruvate carboxykinase2 (pepck) from trypanosoma cruzi
11	<a href="#">c2pc9B_</a>	 Alignment		100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate carboxykinase [atp]; <b>PDBTitle:</b> crystal structure of atp-dependent phosphoenolpyruvate carboxykinase2 from thermus thermophilus hb8

12	<a href="#">d1ii2a1</a>	Alignment		100.0	16	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> PEP carboxykinase C-terminal domain
13	<a href="#">d2olra1</a>	Alignment		100.0	16	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> PEP carboxykinase C-terminal domain
14	<a href="#">d1j3ba2</a>	Alignment		98.6	17	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
15	<a href="#">d2olra2</a>	Alignment		98.4	15	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
16	<a href="#">d1ii2a2</a>	Alignment		98.1	17	<b>Fold:</b> PEP carboxykinase N-terminal domain <b>Superfamily:</b> PEP carboxykinase N-terminal domain <b>Family:</b> PEP carboxykinase N-terminal domain
17	<a href="#">c2qmhK_</a>	Alignment		96.0	19	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> hpr kinase/phosphorylase; <b>PDBTitle:</b> structure of v267f mutant hprk/p
18	<a href="#">c3tqfA_</a>	Alignment		95.7	17	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hpr(ser) kinase; <b>PDBTitle:</b> structure of the hpr(ser) kinase/phosphatase from coxiella burnetii
19	<a href="#">d1ko7a2</a>	Alignment		95.6	21	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> HPr kinase HprK C-terminal domain
20	<a href="#">d1knxa2</a>	Alignment		95.6	21	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> HPr kinase HprK C-terminal domain
21	<a href="#">d1kkma_</a>	Alignment	not modelled	95.4	19	<b>Fold:</b> PEP carboxykinase-like <b>Superfamily:</b> PEP carboxykinase-like <b>Family:</b> HPr kinase HprK C-terminal domain
22	<a href="#">c3tqcB_</a>	Alignment	not modelled	94.1	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> structure of the pantothenate kinase (coaa) from coxiella burnetii
23	<a href="#">d1sq5a_</a>	Alignment	not modelled	93.8	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
24	<a href="#">c5u32A_</a>	Alignment	not modelled	93.7	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna ligase; <b>PDBTitle:</b> crystal structure of fungal rna kinase
25	<a href="#">c3cmvG_</a>	Alignment	not modelled	92.9	29	<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-ssdna/dsdna2 structures
26	<a href="#">c2ak3B_</a>	Alignment	not modelled	92.8	13	<b>PDB header:</b> transferase (phosphotransferase) <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase isoenzyme-3; <b>PDBTitle:</b> the three-dimensional structure of the complex between2 mitochondrial matrix adenylate kinase and its substrate3 amp at 1.85 angstroms resolution
27	<a href="#">c2ygrD_</a>	Alignment	not modelled	92.4	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvrA
28	<a href="#">c3lncB_</a>	Alignment	not modelled	92.2	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 anaplasma phagocytophilum

29	<a href="#">c1ko7B</a>	Alignment	not modelled	92.0	21	<b>PDB header:</b> transferase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hpr kinase/phosphatase; <b>PDBTitle:</b> x-ray structure of the hpr kinase/phosphatase from staphylococcus2 xylosus at 1.95 a resolution
30	<a href="#">c6cckgA</a>	Alignment	not modelled	91.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-glycerate 3-kinase; <b>PDBTitle:</b> d-glycerate 3-kinase from cryptococcus neoformans var. grubii serotype2 a (h99 / atcc 208821 / cbs 10515 / fgsc 9487)
31	<a href="#">d2ak3a1</a>	Alignment	not modelled	91.9	13	<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
32	<a href="#">d1okkd2</a>	Alignment	not modelled	91.5	20	<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
33	<a href="#">c3zqjF</a>	Alignment	not modelled	91.0	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
34	<a href="#">c5b3fB</a>	Alignment	not modelled	90.7	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribulokinase/uridine kinase; <b>PDBTitle:</b> crystal structure of phosphoribulokinase from methanospirillum2 hungatei
35	<a href="#">c3tauB</a>	Alignment	not modelled	90.3	21	<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
36	<a href="#">d1knqa</a>	Alignment	not modelled	90.3	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Gluconate kinase
37	<a href="#">d1rz3a</a>	Alignment	not modelled	90.3	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
38	<a href="#">c2gesA</a>	Alignment	not modelled	90.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
39	<a href="#">c6n9lA</a>	Alignment	not modelled	90.2	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> crystal structure of t. maritima uvra d117-399 with adp
40	<a href="#">c3zqjC</a>	Alignment	not modelled	90.1	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> uvrabc system protein a; <b>PDBTitle:</b> mycobacterium tuberculosis uvra
41	<a href="#">c3c8uA</a>	Alignment	not modelled	89.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
42	<a href="#">c3pihA</a>	Alignment	not modelled	89.6	38	<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
43	<a href="#">c5uivA</a>	Alignment	not modelled	89.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional thymidylate/uridylate kinase; <b>PDBTitle:</b> structure of thymidylate kinase from candida albicans reveals origin2 of broad substrate specificity and a novel structural element.
44	<a href="#">c2r6fA</a>	Alignment	not modelled	89.2	32	<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
45	<a href="#">c2vf7B</a>	Alignment	not modelled	89.1	33	<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
46	<a href="#">c4bzbP</a>	Alignment	not modelled	89.0	41	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional enzyme cysn/cysc; <b>PDBTitle:</b> structure of the mycobacterium tuberculosis aps kinase cysc2 in complex with adp
47	<a href="#">c4huqB</a>	Alignment	not modelled	88.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein ecfa <b>PDBTitle:</b> crystal structure of a transporter
48	<a href="#">c1xnjB</a>	Alignment	not modelled	88.7	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> aps complex of human paps synthetase 1
49	<a href="#">d2qy9a2</a>	Alignment	not modelled	88.7	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
50	<a href="#">c5cb6A</a>	Alignment	not modelled	88.7	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable adenyllyl-sulfate kinase; <b>PDBTitle:</b> structure of adenosine-5'-phosphosulfate kinase
51	<a href="#">c3ux8A</a>	Alignment	not modelled	88.4	35	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excinuclease abc, a subunit; <b>PDBTitle:</b> crystal structure of uvra
52	<a href="#">d1r6bx3</a>	Alignment	not modelled	88.4	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
53	<a href="#">c1knxF</a>	Alignment	not modelled	88.4	21	<b>PDB header:</b> transferase/hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> probable hpr(ser) kinase/phosphatase; <b>PDBTitle:</b> hpr kinase/phosphatase from mycoplasma pneumoniae
54	<a href="#">d1odfa</a>	Alignment	not modelled	88.4	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

55	<a href="#">d1qzxa3</a>	Alignment	not modelled	88.4	20	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
56	<a href="#">d1qhxa_</a>	Alignment	not modelled	88.4	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Chloramphenicol phosphotransferase
57	<a href="#">c3asyB_</a>	Alignment	not modelled	88.3	42	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uridine kinase; <b>PDBTitle:</b> ligand-free structure of uridine kinase from thermus thermophilus hb8
58	<a href="#">c2j41A_</a>	Alignment	not modelled	88.3	21	<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
59	<a href="#">d1m8pa3</a>	Alignment	not modelled	88.0	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ATP sulfurylase C-terminal domain
60	<a href="#">c1xjqA_</a>	Alignment	not modelled	88.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> adp complex of human paps synthetase 1
61	<a href="#">d1zpa1</a>	Alignment	not modelled	87.8	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Atu3015-like
62	<a href="#">d1l8qa2</a>	Alignment	not modelled	87.8	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
63	<a href="#">c3tlxA_</a>	Alignment	not modelled	87.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 2; <b>PDBTitle:</b> crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
64	<a href="#">c3akcA_</a>	Alignment	not modelled	87.8	40	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cytidylate kinase; <b>PDBTitle:</b> crystal structure of cmp kinase in complex with cdp and adp from2 thermus thermophilus hb8
65	<a href="#">d1ye8a1</a>	Alignment	not modelled	87.8	24	<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)
66	<a href="#">d1ofha_</a>	Alignment	not modelled	87.8	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
67	<a href="#">d1qvra3</a>	Alignment	not modelled	87.7	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
68	<a href="#">c2z0hA_</a>	Alignment	not modelled	87.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate kinase; <b>PDBTitle:</b> crystal structure of thymidylate kinase in complex with dtdp2 and adp from thermotoga maritima
69	<a href="#">c2iw3B_</a>	Alignment	not modelled	87.7	27	<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
70	<a href="#">c6b8vA_</a>	Alignment	not modelled	87.6	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylsulfate kinase; <b>PDBTitle:</b> crystal structure of adenylyl-sulfate kinase from cryptococcus2 neoformans
71	<a href="#">d2vp4a1</a>	Alignment	not modelled	87.6	17	<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
72	<a href="#">d1y63a_</a>	Alignment	not modelled	87.6	25	<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
73	<a href="#">c6gveG_</a>	Alignment	not modelled	87.3	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> phosphoribulokinase; <b>PDBTitle:</b> gapdh-cp12-prk complex
74	<a href="#">c5d3mF_</a>	Alignment	not modelled	87.3	23	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> folate ecf transporter: amppnp bound state
75	<a href="#">c3cr8C_</a>	Alignment	not modelled	87.1	27	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenylyltransferase, adenylylsulfate kinase; <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
76	<a href="#">d1ki9a_</a>	Alignment	not modelled	87.1	21	<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
77	<a href="#">c4gp6A_</a>	Alignment	not modelled	87.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> metallophosphoesterase; <b>PDBTitle:</b> polynucleotide kinase
78	<a href="#">c2plrB_</a>	Alignment	not modelled	87.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thymidylate kinase; <b>PDBTitle:</b> crystal structure of dtmp kinase (st1543) from sulfobolus tokodaii2 strain7
79	<a href="#">d1znwa1</a>	Alignment	not modelled	86.8	28	<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
80	<a href="#">c4cw7A_</a>	Alignment	not modelled	86.7	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative adenylate kinase; <b>PDBTitle:</b> structure of the fap7-rps14 complex in complex with atp
81	<a href="#">c2jatA_</a>	Alignment	not modelled	86.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> deoxyguanosine kinase; <b>PDBTitle:</b> structure of deoxyadenosine kinase from m.mycoides with2 products dcmp and a flexible dcdp bound
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

82	<a href="#">d1uf9a_</a>	Alignment	not modelled	86.5	16	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
83	<a href="#">d1ak2a1</a>	Alignment	not modelled	86.5	25	<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
84	<a href="#">c3fvqB_</a>	Alignment	not modelled	86.5	32	<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 fbpc complexed with2 atp
85	<a href="#">d1sxc2</a>	Alignment	not modelled	86.4	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
86	<a href="#">d1iqpa2</a>	Alignment	not modelled	86.4	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
87	<a href="#">c2nq2C_</a>	Alignment	not modelled	86.4	23	<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.
88	<a href="#">c6mdnF_</a>	Alignment	not modelled	86.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> vesicle-fusing atpase; <b>PDBTitle:</b> the 20s supercomplex engaging the snap-25 n-terminus (class 2)
89	<a href="#">c1sxb_</a>	Alignment	not modelled	86.3	14	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> activator 1 37 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
90	<a href="#">c3be4A_</a>	Alignment	not modelled	86.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of cryptosporidium parvum adenylate kinase cgd5_3360
91	<a href="#">c2ccjA_</a>	Alignment	not modelled	86.1	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidylate kinase; <b>PDBTitle:</b> crystal structure of s. aureus thymidylate kinase complexed2 with thymidine monophosphate
92	<a href="#">c3nhaA_</a>	Alignment	not modelled	86.0	16	<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)
93	<a href="#">c4hzuB_</a>	Alignment	not modelled	86.0	21	<b>PDB header:</b> hydrolase, transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein ecfa <b>PDBTitle:</b> structure of a bacterial energy-coupling factor transporter
94	<a href="#">d1vmaa2</a>	Alignment	not modelled	85.9	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
95	<a href="#">c1yqtA_</a>	Alignment	not modelled	85.9	16	<b>PDB header:</b> hydrolyase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> rnase I inhibitor; <b>PDBTitle:</b> rnase-I inhibitor
96	<a href="#">d1qvra2</a>	Alignment	not modelled	85.9	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
97	<a href="#">c6amxA_</a>	Alignment	not modelled	85.8	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter; <b>PDBTitle:</b> crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
98	<a href="#">d1qf9a_</a>	Alignment	not modelled	85.7	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
99	<a href="#">d1gkya_</a>	Alignment	not modelled	85.7	33	<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
100	<a href="#">c2yvua_</a>	Alignment	not modelled	85.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable adenyllyl-sulfate kinase; <b>PDBTitle:</b> crystal structure of ape1195
101	<a href="#">c5l22B_</a>	Alignment	not modelled	85.7	23	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> abc transporter (hlyb subfamily); <b>PDBTitle:</b> prt1 t1ss abc transporter
102	<a href="#">c1iqpF_</a>	Alignment	not modelled	85.6	26	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> rfcs; <b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
103	<a href="#">d1kaga_</a>	Alignment	not modelled	85.6	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
104	<a href="#">c1ueiB_</a>	Alignment	not modelled	85.5	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> uridine-cytidine kinase 2; <b>PDBTitle:</b> crystal structure of human uridine-cytidine kinase 22 complexed with a feedback-inhibitor, utp
105	<a href="#">c4i1vB_</a>	Alignment	not modelled	85.5	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dephospho-coa kinase; <b>PDBTitle:</b> crystal structure of a dephospho-coa kinase from burkholderia2 vietnamiensis bound to adp
106	<a href="#">c2ar7A_</a>	Alignment	not modelled	85.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 4; <b>PDBTitle:</b> crystal structure of human adenylate kinase 4, ak4
107	<a href="#">c5b57D_</a>	Alignment	not modelled	85.5	16	<b>PDB header:</b> metal transport <b>Chain:</b> D: <b>PDB Molecule:</b> hemin import atp-binding protein hmuv; <b>PDBTitle:</b> inward-facing conformation of abc heme importer bhuv

						from2 burkholderia cenocepacia
108	<a href="#">c5d3mA_</a>	Alignment	not modelled	85.5	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> energy-coupling factor transporter atp-binding protein <b>PDBTitle:</b> folate ecf transporter: amppnp bound state
109	<a href="#">d2bdta1</a>	Alignment	not modelled	85.3	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Atu3015-like
110	<a href="#">c3uk6L_</a>	Alignment	not modelled	85.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> crystal structure of the tip48 (tip49b) hexamer
111	<a href="#">d1sxb2</a>	Alignment	not modelled	85.1	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
112	<a href="#">c3crqA_</a>	Alignment	not modelled	85.1	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate <b>PDBTitle:</b> structure of trna dimethylallyltransferase: rna2 modification through a channel
113	<a href="#">c2vp4D_</a>	Alignment	not modelled	85.1	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> deoxynucleoside kinase; <b>PDBTitle:</b> structural studies of nucleoside analog and feedback2 inhibitor binding to drosophila melanogaster3 multisubstrate deoxyribonucleoside kinase
114	<a href="#">d2i3ba1</a>	Alignment	not modelled	85.0	28	<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="#">c3a8tA_</a>	Alignment	not modelled	85.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate isopentenyltransferase; <b>PDBTitle:</b> plant adenylate isopentenyltransferase in complex with atp
116	<a href="#">c2ql6H_</a>	Alignment	not modelled	84.9	32	<b>PDB header:</b> signaling protein,transferase <b>Chain:</b> H: <b>PDB Molecule:</b> nicotinamide riboside kinase 1; <b>PDBTitle:</b> human nicotinamide riboside kinase (nrk1)
117	<a href="#">d1tmka_</a>	Alignment	not modelled	84.9	15	<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
118	<a href="#">c2if2C_</a>	Alignment	not modelled	84.8	28	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> dephosfo-coa kinase; <b>PDBTitle:</b> crystal structure of the putative dephosfo-coa kinase from aquifex2 aeolicus, northeast structural genomics target qr72.
119	<a href="#">c2w0sB_</a>	Alignment	not modelled	84.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidylate kinase; <b>PDBTitle:</b> crystal structure of vaccinia virus thymidylate kinase2 bound to brivudin-5'-monophosphate
120	<a href="#">d1a5ta2</a>	Alignment	not modelled	84.8	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain