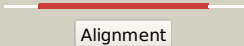

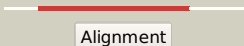

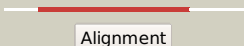







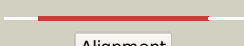




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0254c_cobU_305825_306349
Date	Tue Jul 23 14:50:31 BST 2019
Unique Job ID	febea3320bf9475c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1c9ka_</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> RecA protein-like (ATPase-domain)
2	<a href="#">c1t4gA_</a>	 Alignment		97.5	21	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rada; <b>PDBTitle:</b> atpase in complex with amp-pnp
3	<a href="#">c2dfIA_</a>	 Alignment		97.5	21	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rada; <b>PDBTitle:</b> crystal structure of left-handed rada filament
4	<a href="#">c3hr8A_</a>	 Alignment		97.5	12	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
5	<a href="#">c1pznA_</a>	 Alignment		97.5	26	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair and recombination protein rad51; <b>PDBTitle:</b> rad51 (rada)
6	<a href="#">c2zroA_</a>	 Alignment		97.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
7	<a href="#">d1mo6a1</a>	 Alignment		97.3	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)
8	<a href="#">c1xp8A_</a>	 Alignment		97.3	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> reca protein; <b>PDBTitle:</b> deinococcus radiodurans reca in complex with atp-gamma-s
9	<a href="#">c5jzcG_</a>	 Alignment		97.2	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> dna repair protein rad51 homolog 1; <b>PDBTitle:</b> helical filament
10	<a href="#">c3ldaA_</a>	 Alignment		97.2	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rad51; <b>PDBTitle:</b> yeast rad51 h352y filament interface mutant
11	<a href="#">d1xp8a1</a>	 Alignment		97.1	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)

12	<a href="#">c1szpC</a>	Alignment		97.1	25	<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
13	<a href="#">c4wiaA</a>	Alignment		97.0	19	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flagella-related protein h; <b>PDBTitle:</b> crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
14	<a href="#">d1tf7a2</a>	Alignment		97.0	19	<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)
15	<a href="#">d2i1qa2</a>	Alignment		97.0	22	<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)
16	<a href="#">d1n0wa</a>	Alignment		96.9	21	<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)
17	<a href="#">d1ubea1</a>	Alignment		96.9	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)
18	<a href="#">c2recB</a>	Alignment		96.9	17	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
19	<a href="#">d1v5wa</a>	Alignment		96.8	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)
20	<a href="#">d1szpa2</a>	Alignment		96.8	23	<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)
21	<a href="#">d1pzna2</a>	Alignment	not modelled	96.8	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)
22	<a href="#">d1u94a1</a>	Alignment	not modelled	96.6	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)
23	<a href="#">d1p3ja1</a>	Alignment	not modelled	96.6	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
24	<a href="#">c2zjbB</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> meiotic recombination protein dmc1/lim15 homolog; <b>PDBTitle:</b> crystal structure of the human dmc1-m200v polymorphic2 variant
25	<a href="#">d1zina1</a>	Alignment	not modelled	96.6	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
26	<a href="#">c4ydsA</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagella-related protein h; <b>PDBTitle:</b> flah from sulfobolbus acidocaldarius with atp and mg-ion
27	<a href="#">d1akya1</a>	Alignment	not modelled	96.4	24	<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
28	<a href="#">d2cdna1</a>	Alignment	not modelled	96.4	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
						<b>PDB header:</b> transferase

29	<a href="#">c2ar7A</a>	Alignment	not modelled	96.4	24	<b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase 4; <b>PDBTitle:</b> crystal structure of human adenylate kinase 4, ak4
30	<a href="#">c3vaaC</a>	Alignment	not modelled	96.4	29	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of shikimate kinase from 2 bacteroides thetaiotaomicron
31	<a href="#">d1s3ga1</a>	Alignment	not modelled	96.4	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
32	<a href="#">d1e4va1</a>	Alignment	not modelled	96.4	24	<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
33	<a href="#">c2rh5B</a>	Alignment	not modelled	96.3	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> structure of apo adenylate kinase from aquifex aeolicus
34	<a href="#">d1ak2a1</a>	Alignment	not modelled	96.3	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
35	<a href="#">c1ankA</a>	Alignment	not modelled	96.3	28	<b>PDB header:</b> transferase(phosphotransferase) <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> the closed conformation of a highly flexible protein: the structure of 2 e. coli adenylate kinase with bound amp and amppnp
36	<a href="#">c2jatA</a>	Alignment	not modelled	96.3	24	<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 with 2 products dcmp and a flexible dcdp bound
37	<a href="#">c1u9iA</a>	Alignment	not modelled	96.3	19	<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 phosphorylation 2 sites
38	<a href="#">c4nu0B</a>	Alignment	not modelled	96.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase from streptococcus pneumoniae 2 with ap5a
39	<a href="#">d2ak3a1</a>	Alignment	not modelled	96.2	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
40	<a href="#">c5g3yA</a>	Alignment	not modelled	96.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase ancestor 1 with zn and adp bound
41	<a href="#">c1s3gA</a>	Alignment	not modelled	96.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase from bacillus 2 globisporus
42	<a href="#">c2eu8B</a>	Alignment	not modelled	96.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of a thermostable mutant of bacillus 2 subtilis adenylate kinase (q199r)
43	<a href="#">d2bdta1</a>	Alignment	not modelled	96.2	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Atu3015-like
44	<a href="#">d1y63a</a>	Alignment	not modelled	96.0	27	<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
45	<a href="#">c2ztsB</a>	Alignment	not modelled	96.0	19	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ph0186; <b>PDBTitle:</b> crystal structure of kaic-like protein ph0186 from hyperthermophilic 2 archaea pyrococcus horikoshii ot3
46	<a href="#">c5jwqA</a>	Alignment	not modelled	95.9	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> circadian clock protein kinase kaic; <b>PDBTitle:</b> crystal structure of kaic s431e in complex with foldswitch-stabilized 2 kaib from thermosynechococcus elongatus
47	<a href="#">c3r8cB</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cytidylate kinase; <b>PDBTitle:</b> crystal structure of cytidylate kinase (cmk) from mycobacterium 2 abscessus
48	<a href="#">d1zaka1</a>	Alignment	not modelled	95.8	24	<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
49	<a href="#">c2ak3B</a>	Alignment	not modelled	95.8	21	<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 between 2 mitochondrial matrix adenylate kinase and its substrate 3 amp at 1.85 angstroms resolution
50	<a href="#">c3akyA</a>	Alignment	not modelled	95.7	26	<b>PDB header:</b> adenylate kinase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> stability, activity and structure of adenylate kinase 2 mutants
51	<a href="#">c2xb4A</a>	Alignment	not modelled	95.7	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structures of zinc containing adenylate kinase from 2 desulfovibrio gigas
52	<a href="#">c2ak2A</a>	Alignment	not modelled	95.6	28	<b>PDB header:</b> phosphotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase isoenzyme-2; <b>PDBTitle:</b> adenylate kinase isoenzyme-2
53	<a href="#">c2z0hA</a>	Alignment	not modelled	95.6	20	<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
54	<a href="#">c2pbrB</a>	Alignment	not modelled	95.5	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thymidylate kinase; <b>PDBTitle:</b> crystal structure of thymidylate kinase (aq_969) from aquifex aeolicus 2 vf5
55	<a href="#">d1teva</a>	Alignment	not modelled	95.5	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
56	<a href="#">c4y0aA_</a>	Alignment	not modelled	95.5	21	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> shikimate kinase from acinetobacter baumannii in complex with2 shikimate
57	<a href="#">c1ly1A_</a>	Alignment	not modelled	95.4	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide kinase; <b>PDBTitle:</b> structure and mechanism of t4 polynucleotide kinase
58	<a href="#">d1ly1a_</a>	Alignment	not modelled	95.4	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
59	<a href="#">c2h92C_</a>	Alignment	not modelled	95.3	24	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> cytidylate kinase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus cytidine2 monophosphate kinase in complex with cytidine-5'-3 monophosphate
60	<a href="#">c3fozB_</a>	Alignment	not modelled	95.2	21	<b>PDB header:</b> transferase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate transferase; <b>PDBTitle:</b> structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
61	<a href="#">c1zakB_</a>	Alignment	not modelled	95.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> adenylate kinase from maize in complex with the inhibitor2 p1,p5-bis(adenosine-5'-)pentaphosphate (ap5a)
62	<a href="#">c5bq5A_</a>	Alignment	not modelled	95.2	15	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> insertion sequence is5376 putative atp-binding protein; <b>PDBTitle:</b> crystal structure of the istb aaa+ domain bound to adp-bef3
63	<a href="#">c4eunA_</a>	Alignment	not modelled	95.1	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thermoreistant glucokinase; <b>PDBTitle:</b> crystal structure of a sugar kinase (target efi-502144 from janibacter2 sp. htcc2649), unliganded structure
64	<a href="#">c2ja1A_</a>	Alignment	not modelled	95.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine kinase; <b>PDBTitle:</b> thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
65	<a href="#">c3exaD_</a>	Alignment	not modelled	95.1	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate transferase; <b>PDBTitle:</b> crystal structure of the full-length trna isopentenylpyrophosphate2 transferase (bh2366) from bacillus halodurans, northeast structural3 genomics consortium target bhr41.
66	<a href="#">d1tmka_</a>	Alignment	not modelled	95.0	16	<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
67	<a href="#">c3ch4B_</a>	Alignment	not modelled	95.0	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphomevalonate kinase; <b>PDBTitle:</b> the crystal structure of human phosphomavelonate kinase at2 1.8 a resolution
68	<a href="#">c2ql6H_</a>	Alignment	not modelled	95.0	27	<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)
69	<a href="#">c3gmtB_</a>	Alignment	not modelled	94.9	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase from burkholderia pseudomallei
70	<a href="#">c2w0mA_</a>	Alignment	not modelled	94.9	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfolobus solfataricus p2
71	<a href="#">c2ia5C_</a>	Alignment	not modelled	94.9	30	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> polynucleotide kinase; <b>PDBTitle:</b> t4 polynucleotide kinase/phosphatase with bound sulfate and magnesium.
72	<a href="#">c4i1vB_</a>	Alignment	not modelled	94.8	32	<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
73	<a href="#">d1q3ta_</a>	Alignment	not modelled	94.8	31	<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
74	<a href="#">d1deka_</a>	Alignment	not modelled	94.7	34	<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
75	<a href="#">d1kaga_</a>	Alignment	not modelled	94.6	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
76	<a href="#">c5he8J_</a>	Alignment	not modelled	94.6	13	<b>PDB header:</b> protein binding <b>Chain:</b> J: <b>PDB Molecule:</b> helicase loader; <b>PDBTitle:</b> bacterial initiation protein
77	<a href="#">c6matE_</a>	Alignment	not modelled	94.5	16	<b>PDB header:</b> ribosomal protein <b>Chain:</b> E: <b>PDB Molecule:</b> rix7 mutant; <b>PDBTitle:</b> cryo-em structure of the essential ribosome assembly aaa-atpase rix7
78	<a href="#">c3crqA_</a>	Alignment	not modelled	94.5	24	<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
79	<a href="#">d1sq5a_</a>	Alignment	not modelled	94.5	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
80	<a href="#">c4nmnA_</a>	Alignment	not modelled	94.4	16	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> aquifex aeolicus replicative helicase (dnab) complexed

						with adp, at2 3.3 resolution
81	<a href="#">c3c8uA</a>	Alignment	not modelled	94.4	33	<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
82	<a href="#">c3hdtB</a>	Alignment	not modelled	94.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> crystal structure of putative kinase from clostridium symbiosum atcc2 14940
83	<a href="#">c4pzlC</a>	Alignment	not modelled	94.3	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> the crystal structure of adenylate kinase from francisella tularensis2 subsp. tularensis schu s4
84	<a href="#">c3asyB</a>	Alignment	not modelled	94.3	35	<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
85	<a href="#">c2cvhB</a>	Alignment	not modelled	94.3	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair and recombination protein radb; <b>PDBTitle:</b> crystal structure of the radb recombinase
86	<a href="#">d1uj2a</a>	Alignment	not modelled	94.3	32	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
87	<a href="#">c3akcA</a>	Alignment	not modelled	94.2	24	<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
88	<a href="#">c4zo4A</a>	Alignment	not modelled	94.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dephospho-coa kinase; <b>PDBTitle:</b> dephospho-coa kinase from campylobacter jejuni.
89	<a href="#">c5uivA</a>	Alignment	not modelled	94.2	22	<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.
90	<a href="#">c4xrpA</a>	Alignment	not modelled	94.2	32	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pnkp1; <b>PDBTitle:</b> structure of the pnkp1/rnl/hen1 rna repair complex
91	<a href="#">c3cm0A</a>	Alignment	not modelled	94.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> crystal structure of adenylate kinase from thermus2 thermophilus hb8
92	<a href="#">d1nfa</a>	Alignment	not modelled	94.2	22	<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)
93	<a href="#">c2pt5D</a>	Alignment	not modelled	94.2	34	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> crystal structure of shikimate kinase (aq_2177) from aquifex aeolicus2 vf5
94	<a href="#">d1uf9a</a>	Alignment	not modelled	94.1	48	<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
95	<a href="#">c2vp4D</a>	Alignment	not modelled	94.1	23	<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
96	<a href="#">d1e6ca</a>	Alignment	not modelled	94.0	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
97	<a href="#">d1vh7a</a>	Alignment	not modelled	93.9	48	<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
98	<a href="#">c3a8tA</a>	Alignment	not modelled	93.9	15	<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
99	<a href="#">c3umfA</a>	Alignment	not modelled	93.9	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> schistosoma mansoni adenylate kinase
100	<a href="#">c3d3qB</a>	Alignment	not modelled	93.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna delta(2)-isopentenylpyrophosphate transferase; <b>PDBTitle:</b> crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis. northeast3 structural genomics consortium target ser100
101	<a href="#">c1zuiA</a>	Alignment	not modelled	93.9	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
102	<a href="#">c6h7gB</a>	Alignment	not modelled	93.9	24	<b>PDB header:</b> photosynthesis <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribulokinase, chloroplastic; <b>PDBTitle:</b> crystal structure of redox-sensitive phosphoribulokinase (prk) from2 the green algae chlamydomonas reinhardtii
103	<a href="#">c3io5B</a>	Alignment	not modelled	93.8	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> recombination and repair protein; <b>PDBTitle:</b> crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
104	<a href="#">c5u1dA</a>	Alignment	not modelled	93.8	22	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> antigen peptide transporter 1; <b>PDBTitle:</b> cryo-em structure of the human tap atp-binding cassette transporter
105	<a href="#">c3tgcB</a>	Alignment	not modelled	93.8	24	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate kinase;

105	<a href="#">c3qcb_</a>	Alignment	not modelled	93.8	24	<b>PDBTitle:</b> structure of the pantothenate kinase (coaa) from coxiella burnetii <b>PDB header:</b> transferase
106	<a href="#">c2grjH_</a>	Alignment	not modelled	93.8	39	<b>Chain:</b> H: <b>PDB Molecule:</b> dephospho-coa kinase; <b>PDBTitle:</b> crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution
107	<a href="#">d1rkba_</a>	Alignment	not modelled	93.7	22	<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
108	<a href="#">c4cw7A_</a>	Alignment	not modelled	93.7	28	<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
109	<a href="#">c2plrB_</a>	Alignment	not modelled	93.7	21	<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 sulfolobus tokodaii2 strain7
110	<a href="#">d1gsia_</a>	Alignment	not modelled	93.6	27	<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
111	<a href="#">d1znwa1</a>	Alignment	not modelled	93.6	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
112	<a href="#">c1znyA_</a>	Alignment	not modelled	93.5	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> guanylate kinase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp
113	<a href="#">d2iyva1</a>	Alignment	not modelled	93.3	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Shikimate kinase (AroK)
114	<a href="#">c2ccjA_</a>	Alignment	not modelled	93.3	17	<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
115	<a href="#">d1qf9a_</a>	Alignment	not modelled	93.3	32	<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
116	<a href="#">c3cf2B_</a>	Alignment	not modelled	93.3	15	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/amp-pnp
117	<a href="#">d1zp6a1</a>	Alignment	not modelled	93.3	41	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Atu3015-like
118	<a href="#">d1jjva_</a>	Alignment	not modelled	93.2	38	<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
119	<a href="#">d1nksa_</a>	Alignment	not modelled	93.2	32	<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
120	<a href="#">c2w58B_</a>	Alignment	not modelled	93.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> primosome component (helicase loader); <b>PDBTitle:</b> crystal structure of the dnaI