



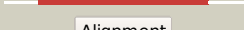

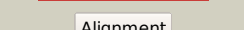

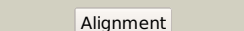





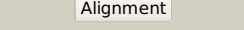

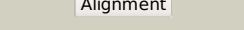

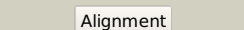














Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3696c_glpK_4138380_4139933
Date	Fri Aug 9 18:20:39 BST 2019
Unique Job ID	cf6dd80e4360ad36

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d4wA_	 Alignment		100.0	62	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
2	c3flcX_	 Alignment		100.0	49	PDB header: transferase Chain: X: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
3	c3g25B_	 Alignment		100.0	49	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
4	c1glbG_	 Alignment		100.0	51	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase
5	c2zf5O_	 Alignment		100.0	50	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
6	c3ezwD_	 Alignment		100.0	52	PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
7	c2dnpB_	 Alignment		100.0	52	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
8	c3wxiB_	 Alignment		100.0	46	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
9	c2w40C_	 Alignment		100.0	41	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
10	c4e1jA_	 Alignment		100.0	47	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
11	c3gbtA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus

12	c1xupO_	Alignment		100.0	50	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
13	c5vm1A_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: xyloxykinase; PDBTitle: crystal structure of a xyloxylose kinase from brucella ovis
14	c3ifrB_	Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xyloxylose kinase from rhodospirillum rubrum
15	c3hz6A_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: xyloxykinase; PDBTitle: crystal structure of xyloxykinase from chromobacterium violaceum
16	c2nlxA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: xyloxylose kinase; PDBTitle: crystal structure of the apo e. coli xyloxylose kinase
17	c3jvpA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
18	c3gg4B_	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
19	c4bc2A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: xyloxylose kinase; PDBTitle: crystal structure of human d-xyloxykinase in complex with d-2 xyloxylose and adenosine diphosphate
20	c5ya2A_	Alignment		100.0	24	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
21	c2cgb_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: l-rhamnulose kinase; PDBTitle: crystal structure of l-rhamnulose kinase from escherichia coli in an2 open uncomplexed conformation.
22	c4c23A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: l-fuculose kinase fuck; PDBTitle: l-fuculose kinase
23	c3i8bA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: xyloxylose kinase; PDBTitle: the crystal structure of xyloxylose kinase from2 bifidobacterium adolescentis
24	c5hv7A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
25	c5htxA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: putative xyloxylose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp
26	c3h6eB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
27	d2p3ra1	Alignment	not modelled	100.0	51	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
28	d1r59o1	Alignment	not modelled	100.0	48	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
						Fold: Ribonuclease H-like motif

29	d2p3ra2	Alignment	not modelled	100.0	51	Superfamily: Actin-like ATPase domain Family: Glycerol kinase
30	d1r59o2	Alignment	not modelled	100.0	53	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
31	c3h1qB	Alignment	not modelled	99.4	17	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrnus hydrogenoformans
32	d1huxa	Alignment	not modelled	99.3	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
33	c4ehtA	Alignment	not modelled	99.3	19	PDB header: electron transport Chain: A: PDB Molecule: activator of 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
34	c2ap1A	Alignment	not modelled	99.0	17	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
35	d1zc6a1	Alignment	not modelled	98.9	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
36	c2e2pA	Alignment	not modelled	98.9	15	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
37	d2ewsa1	Alignment	not modelled	98.9	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
38	c2ivoC	Alignment	not modelled	98.7	12	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
39	c3enoB	Alignment	not modelled	98.7	15	PDB header: hydrolase/unknown function Chain: B: PDB Molecule: putative o-sialoglycoprotein endopeptidase; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
40	d1z05a3	Alignment	not modelled	98.6	8	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
41	d2h0ea3	Alignment	not modelled	98.5	7	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
42	c3eo3B	Alignment	not modelled	98.5	21	PDB header: isomerase, transferase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
43	c1zc6A	Alignment	not modelled	98.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable n-acetylglucosamine kinase; PDBTitle: crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
44	c2qm1D	Alignment	not modelled	98.4	17	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
45	d2ch5a2	Alignment	not modelled	98.4	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
46	c1z05A	Alignment	not modelled	98.4	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
47	d1z6ra2	Alignment	not modelled	98.4	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
48	c2ch5D	Alignment	not modelled	98.3	12	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
49	c1z6rC	Alignment	not modelled	98.3	9	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
50	c4ht1A	Alignment	not modelled	98.2	20	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
51	c4db3A	Alignment	not modelled	98.2	15	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-d-glucosamine kinase; PDBTitle: 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
52	c3zyyX	Alignment	not modelled	98.2	18	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
53	c5f7rA	Alignment	not modelled	98.2	10	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
54	c3htvA	Alignment	not modelled	98.2	13	PDB header: transferase Chain: A: PDB Molecule: d-allose kinase; PDBTitle: crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution

55	c3zyyY	Alignment	not modelled	98.2	20	PDB header: iron-sulfur-binding protein Chain: Y; PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
56	c2hoeA	Alignment	not modelled	98.1	7	PDB header: transferase Chain: A; PDB Molecule: n-acetylglucosamine kinase; PDBTitle: crystal structure of n-acetylglucosamine kinase (tm1224) from <i>thermotoga maritima</i> at 2.46 a resolution
57	d1woqa1	Alignment	not modelled	98.0	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
58	c1dkgD	Alignment	not modelled	97.9	16	PDB header: complex (hsp24/hsp70) Chain: D; PDB Molecule: molecular chaperone dnak; PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
59	d2ap1a2	Alignment	not modelled	97.9	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
60	c5nckA	Alignment	not modelled	97.9	14	PDB header: transferase Chain: A; PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in <i>fusobacterium2 nucleatum</i>
61	c4yh5B	Alignment	not modelled	97.8	13	PDB header: transferase Chain: B; PDB Molecule: levoglucosan kinase; PDBTitle: lipomyces starkeyi levoglucosan kinase bound to adp and manganese
62	d1q18a1	Alignment	not modelled	97.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
63	c3r8eA	Alignment	not modelled	97.8	17	PDB header: transferase Chain: A; PDB Molecule: hypothetical sugar kinase; PDBTitle: crystal structure of a putative sugar kinase (chu_1875) from <i>cytophaga2 hutchinsonii</i> atcc 33406 at 1.65 a resolution
64	d1sz2a1	Alignment	not modelled	97.8	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
65	c3vgkB	Alignment	not modelled	97.8	17	PDB header: transferase Chain: B; PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from <i>streptomyces2 griseus</i>
66	d1dkgd2	Alignment	not modelled	97.7	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
67	c4kboA	Alignment	not modelled	97.7	17	PDB header: signaling protein Chain: A; PDB Molecule: stress-70 protein, mitochondrial; PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form
68	c5f7pA	Alignment	not modelled	97.7	13	PDB header: transcription Chain: A; PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from <i>listeria monocytogenes</i>
69	c3mcpA	Alignment	not modelled	97.7	9	PDB header: transferase Chain: A; PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (bdi_1628) from <i>parabacteroides2 distasonis</i> atcc 8503 at 3.00 a resolution
70	d2aa4a1	Alignment	not modelled	97.7	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
71	c1e4gT	Alignment	not modelled	97.6	9	PDB header: bacterial cell division Chain: T; PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from <i>thermotoga maritima</i>
72	c2v7zA	Alignment	not modelled	97.6	14	PDB header: chaperone Chain: A; PDB Molecule: heat shock cognate 71 kda protein; PDBTitle: crystal structure of the 70-kda heat shock cognate protein2 from <i>rattus norvegicus</i> in post-atp hydrolysis state
73	d2gupa1	Alignment	not modelled	97.6	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
74	c3d2fC	Alignment	not modelled	97.6	13	PDB header: chaperone Chain: C; PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
75	c2aa4B	Alignment	not modelled	97.6	19	PDB header: transferase Chain: B; PDB Molecule: putative n-acetylmannosamine kinase; PDBTitle: crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
76	c2v7yA	Alignment	not modelled	97.6	18	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the molecular chaperone dnak from <i>geobacillus kaustophilus</i> hta426 in post-atp hydrolysis3 state
77	c6gfaA	Alignment	not modelled	97.6	18	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 105 kda; PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed
78	c4gniA	Alignment	not modelled	97.6	16	PDB header: chaperone Chain: A; PDB Molecule: putative heat shock protein; PDBTitle: structure of the sss1 atpase bound to atp and magnesium
79	d1e4ft1	Alignment	not modelled	97.6	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
80	c6da0A	Alignment	not modelled	97.6	13	PDB header: transferase Chain: A; PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from <i>naegleria fowleri</i>
81	c1xc3A	Alignment	not modelled	97.5	20	PDB header: transferase Chain: A; PDB Molecule: putative fructokinase;

						PDBTitle: structure of a putative fructokinase from bacillus subtilis
82	c1hpmA_	Alignment	not modelled	97.5	13	PDB header: hydrolase (acting on acid anhydrides) Chain: A: PDB Molecule: 44k atpase fragment (n-terminal) of 7o kd heat- PDBTitle: how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
83	c4ijaA_	Alignment	not modelled	97.5	7	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecr2
84	c3wqtB_	Alignment	not modelled	97.5	16	PDB header: structural genomics Chain: B: PDB Molecule: cell division protein ftsa; PDBTitle: staphylococcus aureus ftsa complexed with amppnp
85	d1jcea2	Alignment	not modelled	97.5	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
86	d2e8aa2	Alignment	not modelled	97.4	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
87	c3vewA_	Alignment	not modelled	97.4	25	PDB header: transferase Chain: A: PDB Molecule: o-carbamoyltransferase tobz; PDBTitle: crystal structure of the o-carbamoyltransferase tobz in complex with2 adp
88	d1bupa2	Alignment	not modelled	97.4	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
89	c5mb9B_	Alignment	not modelled	97.4	19	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
90	c3zeuE_	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: E: PDB Molecule: probable trna threonylcarbamoyladenosine biosynthesis PDBTitle: structure of a salmonella typhimurium yggd-yeaz heterodimer bound to2 atpgammas
91	c3vovC_	Alignment	not modelled	97.4	15	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
92	c5e84B_	Alignment	not modelled	97.4	18	PDB header: chaperone Chain: B: PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
93	c4bgaB_	Alignment	not modelled	97.4	16	PDB header: transferase Chain: B: PDB Molecule: predicted molecular chaperone distantly related to PDBTitle: nucleotide-bound open form of a putative sugar kinase2 mk0840 from methanopyrus kandleri
94	d1xc3a1	Alignment	not modelled	97.3	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
95	c5tkyA_	Alignment	not modelled	97.3	16	PDB header: chaperone Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation
96	c2q2rA_	Alignment	not modelled	97.3	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
97	c4czeA_	Alignment	not modelled	97.3	16	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: c. crescentus mreB, double filament, empty
98	c3vthA_	Alignment	not modelled	97.3	18	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
99	c6ediA_	Alignment	not modelled	97.3	14	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of leishmania braziliensis glucokinase
100	c3c7nB_	Alignment	not modelled	97.3	15	PDB header: chaperone/chaperone Chain: B: PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
101	c2gupA_	Alignment	not modelled	97.2	22	PDB header: transferase Chain: A: PDB Molecule: rok family protein; PDBTitle: structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
102	c6gwiK_	Alignment	not modelled	97.2	17	PDB header: rna binding protein Chain: K: PDB Molecule: probable trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: protein complex
103	c3cqyA_	Alignment	not modelled	97.2	18	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
104	c1woqB_	Alignment	not modelled	97.2	20	PDB header: transferase Chain: B: PDB Molecule: inorganic polyphosphate/atp-glucomannokinase; PDBTitle: crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
105	c3vthB_	Alignment	not modelled	97.2	14	PDB header: transferase Chain: B: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
						PDB header: chaperone

106	c3iucC	Alignment	not modelled	97.2	18	Chain: C: PDB Molecule: heat shock 70kda protein 5 (glucose-regulated PDBTitle: crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
107	c1jcgA	Alignment	not modelled	97.2	14	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
108	c4rtfD	Alignment	not modelled	97.1	17	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein dnaK; PDBTitle: crystal structure of molecular chaperone dnaK from mycobacterium2 tuberculosis h37rv
109	c5obuA	Alignment	not modelled	97.1	18	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnaK; PDBTitle: mycoplasma genitalium dnaK deletion mutant lacking sbdalpha in complex2 with amppnp.
110	c3vpzA	Alignment	not modelled	97.1	18	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
111	d1bg3a3	Alignment	not modelled	97.0	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
112	c2khoA	Alignment	not modelled	97.0	21	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 70; PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnaK) chaperone (1-605)2 complexed with adp and substrate
113	c6fpeG	Alignment	not modelled	96.9	12	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
114	d1bdga1	Alignment	not modelled	96.9	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
115	c4j8fA	Alignment	not modelled	96.8	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein; PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip
116	c5eoxB	Alignment	not modelled	96.8	17	PDB header: peptide binding protein Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilM; PDBTitle: pseudomonas aeruginosa pilM bound to adp
117	c1bdgA	Alignment	not modelled	96.6	17	PDB header: hexokinase Chain: A: PDB Molecule: hexokinase; PDBTitle: hexokinase from schistosoma mansoni complexed with glucose
118	d1v4sa1	Alignment	not modelled	96.6	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
119	d1e4ft2	Alignment	not modelled	96.5	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
120	c3qbwA	Alignment	not modelled	96.5	19	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 acetylmuramic acid kinase (anmk) bound to adenosine diphosphate