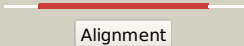

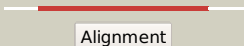

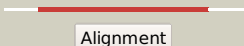







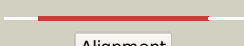




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0729 (xylB)_821510_822856
Date	Fri Jul 26 01:50:30 BST 2019
Unique Job ID	9ad5659b9460499d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3flcX_	 Alignment		100.0	19	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
2	c3gbtA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
3	c2zf5O_	 Alignment		100.0	21	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
4	c2d4wA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
5	c5vm1A_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xyloflose kinase from brucella ovis
6	c3hz6A_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
7	c3g25B_	 Alignment		100.0	21	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.
8	c3wxiB_	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
9	c1gIbG_	 Alignment		100.0	20	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
10	c2w40C_	 Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
11	c2nlxA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase

12	c3ifrB_	Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
13	c2dnpB_	Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermophilus hb8
14	c3jvpA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
15	c3ezwD_	Alignment		100.0	19	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
16	c4e1jA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
17	c3gg4B_	Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
18	c1xupO_	Alignment		100.0	20	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
19	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
20	c4bc2A_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of human d-xylulokinase in complex with d-2 xylulose and adenosine diphosphate
21	c3i8bA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
22	c4c23A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: l-fuculose kinase fuck; PDBTitle: l-fuculose kinase
23	c2cgkB_	Alignment	not modelled	100.0	16	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.
24	c5hv7A_	Alignment	not modelled	100.0	21	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 xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp
26	c3h6eB_	Alignment	not modelled	100.0	17	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	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
28	d1r59o1	Alignment	not modelled	100.0	18	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	22	Superfamily: Actin-like ATPase domain Family: Glycerol kinase
30	d1r59o2	Alignment	not modelled	100.0	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
31	d1huxa_	Alignment	not modelled	99.5	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
32	c3h1qB_	Alignment	not modelled	99.4	18	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrmus hydrogenoformans
33	c4ehtA_	Alignment	not modelled	99.4	23	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	d2ewsal	Alignment	not modelled	98.8	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
35	d1zc6a1	Alignment	not modelled	98.6	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
36	c1dkgD_	Alignment	not modelled	98.2	21	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
37	c2v7zA_	Alignment	not modelled	98.0	23	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 rattus norvegicus in post-atp hydrolysis state
38	c4kboA_	Alignment	not modelled	98.0	19	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
39	c1zc6A_	Alignment	not modelled	98.0	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.
40	c3d2fC_	Alignment	not modelled	98.0	24	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
41	d1z6ra2	Alignment	not modelled	98.0	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
42	c2ap1A_	Alignment	not modelled	98.0	15	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
43	c4gniA_	Alignment	not modelled	97.9	22	PDB header: chaperone Chain: A: PDB Molecule: putative heat shock protein; PDBTitle: structure of the ssz1 atpase bound to atp and magnesium
44	c2v7yA_	Alignment	not modelled	97.9	28	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
45	c4yh5B_	Alignment	not modelled	97.9	11	PDB header: transferase Chain: B: PDB Molecule: levoglucosan kinase; PDBTitle: lipomyces starkeyi levoglucosan kinase bound to adp and manganese
46	d1dkgd2	Alignment	not modelled	97.9	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
47	c2ch5D_	Alignment	not modelled	97.9	14	PDB header: transferase Chain: D: PDB Molecule: nanagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
48	d1jcea2	Alignment	not modelled	97.9	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
49	c2e2pA_	Alignment	not modelled	97.9	21	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
50	c6gfaA_	Alignment	not modelled	97.9	24	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
51	c3en9B_	Alignment	not modelled	97.9	19	PDB header: hydrolase Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
52	d1z05a3	Alignment	not modelled	97.9	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
53	c5nckA_	Alignment	not modelled	97.8	15	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
54	c1hpmA_	Alignment	not modelled	97.8	22	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
55	d2ch5a2	Alignment	not modelled	97.8	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
56	c3wqtB	Alignment	not modelled	97.8	14	PDB header: structural genomics Chain: B: PDB Molecule: cell division protein ftsa; PDBTitle: staphylococcus aureus ftsa complexed with amppnp
57	c4db3A	Alignment	not modelled	97.8	12	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.
58	c1xc3A	Alignment	not modelled	97.8	13	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
59	d2hoea3	Alignment	not modelled	97.8	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
60	c3iucC	Alignment	not modelled	97.8	24	PDB header: chaperone 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
61	c3vgkB	Alignment	not modelled	97.7	29	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
62	c5e84B	Alignment	not modelled	97.7	23	PDB header: chaperone Chain: B: PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
63	c5tkyA	Alignment	not modelled	97.7	28	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
64	c5f7rA	Alignment	not modelled	97.7	11	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
65	d2e8aa2	Alignment	not modelled	97.7	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
66	c3c7nB	Alignment	not modelled	97.7	22	PDB header: chaperone/chaperone Chain: B: PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
67	d2gupa1	Alignment	not modelled	97.7	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
68	c5mb9B	Alignment	not modelled	97.7	21	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
69	c4bgaB	Alignment	not modelled	97.7	19	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
70	c3htvA	Alignment	not modelled	97.6	19	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
71	c2qm1D	Alignment	not modelled	97.6	14	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
72	c1z6rC	Alignment	not modelled	97.6	11	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
73	c5obuA	Alignment	not modelled	97.6	21	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.
74	c4htIA	Alignment	not modelled	97.6	20	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
75	c4rtfD	Alignment	not modelled	97.6	19	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
76	d1bupa2	Alignment	not modelled	97.6	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
77	c4czeA	Alignment	not modelled	97.6	24	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: c. crescentus mreB, double filament, empty
78	c2gupA	Alignment	not modelled	97.6	25	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
79	c3cqyA	Alignment	not modelled	97.6	16	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
						Fold: Ribonuclease H-like motif

80	d1sz2a1	Alignment	not modelled	97.5	13	Superfamily: Actin-like ATPase domain Family: Glucokinase
81	c4j8fA	Alignment	not modelled	97.5	25	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
82	d1woqa1	Alignment	not modelled	97.5	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
83	c2aa4B	Alignment	not modelled	97.5	17	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
84	c2khoA	Alignment	not modelled	97.5	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
85	d2aa4a1	Alignment	not modelled	97.5	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
86	c1jcgA	Alignment	not modelled	97.4	23	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
87	c5f7pA	Alignment	not modelled	97.4	9	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes
88	c3eo3B	Alignment	not modelled	97.4	12	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
89	d1q18a1	Alignment	not modelled	97.4	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
90	c6da0A	Alignment	not modelled	97.3	14	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from naegleria fowleri
91	c1z05A	Alignment	not modelled	97.3	12	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.
92	c3r8eA	Alignment	not modelled	97.3	18	PDB header: transferase Chain: A: PDB Molecule: hypothetical sugar kinase; PDBTitle: crystal structure of a putative sugar kinase (chu_1875) from cytophaga2 hutchinsonii atcc 33406 at 1.65 a resolution
93	d1xc3a1	Alignment	not modelled	97.3	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
94	c6ediA	Alignment	not modelled	97.3	13	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of leishmania braziliensis glucokinase
95	c2ivoC	Alignment	not modelled	97.3	15	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
96	c3lm2B	Alignment	not modelled	97.2	16	PDB header: transferase Chain: B: PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
97	c4ijaA	Alignment	not modelled	97.2	9	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecR2
98	c3mcpA	Alignment	not modelled	97.2	16	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
99	d2ap1a2	Alignment	not modelled	97.1	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
100	c3vthA	Alignment	not modelled	97.1	15	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
101	c3vewA	Alignment	not modelled	97.1	17	PDB header: transferase Chain: A: PDB Molecule: o-carbamoyltransferase tobz; PDBTitle: crystal structure of the o-carbamoyltransferase tobz in complex with2 adp
102	c3vthB	Alignment	not modelled	97.1	16	PDB header: transferase Chain: B: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
103	c2hoeA	Alignment	not modelled	97.1	23	PDB header: transferase Chain: A: PDB Molecule: n-acetylglucosamine kinase; PDBTitle: crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
104	c1e4gT	Alignment	not modelled	97.0	19	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsA; PDBTitle: ftsA (atp-bound form) from thermotoga maritima
105	c3zeuE	Alignment	not modelled	97.0	22	PDB header: hydrolase Chain: E: PDB Molecule: probable trna threonylcarbamoyladenose biosynthesis PDBTitle: structure of a salmonella typhimurium ygdj-yeaz heterodimer bound to2 atpgammas

106	c3qbwA_	Alignment	not modelled	96.9	24	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 acetilmuramic acid kinase (anmk) bound to adenosine diphosphate
107	c2q2rA_	Alignment	not modelled	96.9	10	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
108	c3tsuA_	Alignment	not modelled	96.9	13	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
109	c3vpzA_	Alignment	not modelled	96.9	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
110	c3zyyX_	Alignment	not modelled	96.8	29	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
111	c6gwjK_	Alignment	not modelled	96.8	15	PDB header: rna binding protein Chain: K: PDB Molecule: probable trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: protein complex
112	c5eoxB_	Alignment	not modelled	96.8	31	PDB header: peptide binding protein Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilm; PDBTitle: pseudomonas aeruginosa pilm bound to adp
113	c6fpeG_	Alignment	not modelled	96.7	11	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
114	c1woqB_	Alignment	not modelled	96.7	16	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
115	c3vovC_	Alignment	not modelled	96.7	22	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
116	c3zyyY_	Alignment	not modelled	96.7	24	PDB header: iron-sulfur-binding protein Chain: Y: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
117	c3enoB_	Alignment	not modelled	96.6	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
118	c2ychA_	Alignment	not modelled	96.5	21	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilm; PDBTitle: pilm-piln type iv pilus biogenesis complex
119	d1e4ft2	Alignment	not modelled	96.5	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
120	c5jygA_	Alignment	not modelled	96.3	20	PDB header: structural protein Chain: A: PDB Molecule: actin-like atpase; PDBTitle: cryo-em structure of the mamk filament at 6.5 a