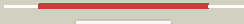



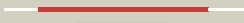



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0650 (-) _747040_747948
Date	Fri Jul 26 01:50:21 BST 2019
Unique Job ID	5b8c96d9284697bc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z05A_	 Alignment		100.0	24	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.
2	c1z6rC_	 Alignment		100.0	24	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
3	c5f7pA_	 Alignment		100.0	22	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes
4	c5f7rA_	 Alignment		100.0	22	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
5	c3r8eA_	 Alignment		100.0	24	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
6	c3vgkB_	 Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
7	c2qm1D_	 Alignment		100.0	30	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
8	c3mcpA_	 Alignment		100.0	21	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
9	c2ap1A_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
10	c3vovC_	 Alignment		100.0	39	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
11	c5nckA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum

12	c2aa4B_	Alignment		100.0	33	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
13	c4htlA_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
14	c2hoeA_	Alignment		100.0	22	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
15	c4db3A_	Alignment		100.0	27	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.
16	c4ijaA_	Alignment		100.0	16	PDB header: protein binding Chain: A: PDB Molecule: xylyl protein; PDBTitle: structure of s. aureus methicillin resistance factor mec2
17	c6ediA_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of leishmania braziliensis glucokinase
18	c3eo3B_	Alignment		100.0	27	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
19	c2gupA_	Alignment		100.0	19	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
20	c6da0A_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from naegleria fowleri
21	c1xc3A_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
22	d1sz2a1	Alignment	not modelled	100.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
23	c3htvA_	Alignment	not modelled	100.0	23	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
24	c3vpzA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
25	c2q2rA_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
26	c1woqB_	Alignment	not modelled	100.0	28	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
27	c2ch5D_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: D: PDB Molecule: magk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
28	c2e2pA_	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp

29	d1z05a2	Alignment	not modelled	100.0	28	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
30	c1zc6A	Alignment	not modelled	100.0	21	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.
31	c3lm2B	Alignment	not modelled	100.0	26	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
32	d1z6ra3	Alignment	not modelled	100.0	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
33	d2aa4a2	Alignment	not modelled	100.0	39	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
34	d2ap1a1	Alignment	not modelled	100.0	33	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
35	d2gupa2	Alignment	not modelled	100.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
36	d2h0ea2	Alignment	not modelled	99.9	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
37	d1q18a2	Alignment	not modelled	99.9	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
38	d1xc3a2	Alignment	not modelled	99.9	27	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
39	d2ews1	Alignment	not modelled	99.9	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
40	c1zbsA	Alignment	not modelled	99.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg1100; PDBTitle: crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
41	d1huxa	Alignment	not modelled	99.8	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
42	d2h0ea3	Alignment	not modelled	99.8	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
43	d2aa4a1	Alignment	not modelled	99.8	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
44	d2ap1a2	Alignment	not modelled	99.8	35	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
45	d1z05a3	Alignment	not modelled	99.8	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
46	c4ehtA	Alignment	not modelled	99.8	14	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
47	d2ch5a1	Alignment	not modelled	99.8	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
48	d1woqa2	Alignment	not modelled	99.8	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
49	d1z6ra2	Alignment	not modelled	99.8	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
50	d1woqa1	Alignment	not modelled	99.8	28	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
51	c1zxoB	Alignment	not modelled	99.7	15	PDB header: unknown function Chain: B: PDB Molecule: conserved hypothetical protein q8a1p1; PDBTitle: x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
52	d2gupa1	Alignment	not modelled	99.7	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
53	c5zqtA	Alignment	not modelled	99.7	20	PDB header: transferase Chain: A: PDB Molecule: hexokinase-6; PDBTitle: crystal structure of oryza sativa hexokinase 6
54	d1xc3a1	Alignment	not modelled	99.7	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
						PDB header: transferase

55	c1v4sA_	Alignment	not modelled	99.7	19	Chain: A: PDB Molecule: glucokinase isoform 2; PDBTitle: crystal structure of human glucokinase
56	c3hm8D_	Alignment	not modelled	99.7	20	PDB header: transferase Chain: D: PDB Molecule: hexokinase-3; PDBTitle: crystal structure of the c-terminal hexokinase domain of human hk3
57	c1bdgA_	Alignment	not modelled	99.6	22	PDB header: hexokinase Chain: A: PDB Molecule: hexokinase; PDBTitle: hexokinase from schistosoma mansoni complexed with glucose
58	c1ig8A_	Alignment	not modelled	99.6	17	PDB header: transferase Chain: A: PDB Molecule: hexokinase pii; PDBTitle: crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
59	c5hg1A_	Alignment	not modelled	99.6	18	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: hexokinase-2; PDBTitle: crystal structure of human hexokinase 2 with compd 1, a c-2-substituted2 glucosamine
60	c4qs9A_	Alignment	not modelled	99.6	21	PDB header: transferase Chain: A: PDB Molecule: hexokinase-1; PDBTitle: arabidopsis hexokinase 1 (athxk1) mutant s177a structure in glucose-2 bound form
61	d1q18a1	Alignment	not modelled	99.6	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
62	c1qhaA_	Alignment	not modelled	99.6	18	PDB header: transferase Chain: A: PDB Molecule: protein (hexokinase); PDBTitle: human hexokinase type i complexed with atp analogue amp-pnp
63	d1zc6a1	Alignment	not modelled	99.5	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
64	c1sazA_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
65	d2ch5a2	Alignment	not modelled	99.5	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
66	c3h1qB_	Alignment	not modelled	99.3	20	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrmus hydrogenoformans
67	c2dpnB_	Alignment	not modelled	99.3	25	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
68	c2iirJ_	Alignment	not modelled	99.3	17	PDB header: transferase Chain: J: PDB Molecule: acetate kinase; PDBTitle: acetate kinase from a hypothermophile thermotoga maritima
69	c3g25B_	Alignment	not modelled	99.3	18	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.
70	c3hz6A_	Alignment	not modelled	99.2	25	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
71	c1x3nA_	Alignment	not modelled	99.2	20	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
72	c2ivoC_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
73	c3wxiB_	Alignment	not modelled	99.2	22	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
74	c3p4iA_	Alignment	not modelled	99.2	14	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
75	c1glbG_	Alignment	not modelled	99.2	21	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
76	c2zf5O_	Alignment	not modelled	99.2	21	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
77	c3ifrB_	Alignment	not modelled	99.2	27	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
78	c3flcX_	Alignment	not modelled	99.2	25	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
79	c1tuuA_	Alignment	not modelled	99.2	16	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: acetate kinase crystallized with atpgs
80	c4ijnB_	Alignment	not modelled	99.2	17	PDB header: transferase Chain: B: PDB Molecule: acetate kinase; PDBTitle: crystal structure of an acetate kinase from mycobacterium smegmatis2 bound to amp and sulfate PDB header: hydrolase/unknown function

81	c3enoB	Alignment	not modelled	99.1	17	Chain: B: PDB Molecule: putative o-sialoglycoprotein endopeptidase; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
82	c3gbtA	Alignment	not modelled	99.1	23	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
83	c3ezwD	Alignment	not modelled	99.1	22	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
84	c1xupO	Alignment	not modelled	99.1	26	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
85	c2d4wA	Alignment	not modelled	99.1	26	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
86	c3khyA	Alignment	not modelled	99.1	14	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of a propionate kinase from francisella tularensis2 subsp. tularensis schu s4
87	d1zc6a2	Alignment	not modelled	99.0	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
88	c6fpeG	Alignment	not modelled	99.0	17	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
89	c2nlxA	Alignment	not modelled	99.0	23	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
90	d1saza2	Alignment	not modelled	99.0	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
91	c1hkgA	Alignment	not modelled	99.0	11	PDB header: transferase Chain: A: PDB Molecule: hexokinase a; PDBTitle: structural dynamics of yeast hexokinase during catalysis
92	c6ioyD	Alignment	not modelled	99.0	13	PDB header: transferase Chain: D: PDB Molecule: acetate kinase; PDBTitle: crystal structure of porphyromonas gingivalis acetate kinase
93	c4h0oB	Alignment	not modelled	98.9	14	PDB header: transferase Chain: B: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from entamoeba histolytica
94	c2w40C	Alignment	not modelled	98.8	16	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
95	c3slcA	Alignment	not modelled	98.8	18	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of apo form of acetate kinase (acka) from salmonella2 typhimurium
96	c3en9B	Alignment	not modelled	98.7	14	PDB header: hydrolase Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
97	c4h0pB	Alignment	not modelled	98.7	13	PDB header: transferase Chain: B: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from cryptococcus neoformans
98	c5hv7A	Alignment	not modelled	98.7	13	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
99	c3zeuE	Alignment	not modelled	98.7	17	PDB header: hydrolase Chain: E: PDB Molecule: probable trna threonylcarbamoyladenine biosynthesis PDBTitle: structure of a salmonella typhimurium ygdj-yeaz heterodimer bound to2 atpgammas
100	c5ya2A	Alignment	not modelled	98.6	24	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
101	d1g99a2	Alignment	not modelled	98.5	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
102	c4c23A	Alignment	not modelled	98.5	18	PDB header: transferase Chain: A: PDB Molecule: l-fucose kinase fuck; PDBTitle: l-fucose kinase
103	d2e1za2	Alignment	not modelled	98.5	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
104	c3gg4B	Alignment	not modelled	98.4	28	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
105	d2p3ra1	Alignment	not modelled	98.4	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
106	c4e1jA	Alignment	not modelled	98.4	21	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with

					glycerol from2 sinorhizobium melliotti 1021
107	c3vewA_	Alignment	not modelled	98.4	20 PDB header: transferase Chain: A: PDB Molecule: o-carbamoyltransferase tobz; PDBTitle: crystal structure of the o-carbamoyltransferase tobz in complex with2 adp
108	c3jvpA_	Alignment	not modelled	98.4	18 PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
109	d1czan2	Alignment	not modelled	98.3	17 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
110	c5vm1A_	Alignment	not modelled	98.2	24 PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylolose kinase from brucella ovis
111	c5htxA_	Alignment	not modelled	98.2	19 PDB header: transferase Chain: A: PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp
112	d1bg3a4	Alignment	not modelled	98.2	19 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
113	d1bg3a2	Alignment	not modelled	98.1	16 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
114	c1hpmA_	Alignment	not modelled	98.1	18 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
115	c4bc2A_	Alignment	not modelled	98.0	13 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
116	c2v7zA_	Alignment	not modelled	98.0	18 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
117	c3c7nB_	Alignment	not modelled	98.0	17 PDB header: chaperone/chaperone Chain: B: PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
118	c3h6eB_	Alignment	not modelled	98.0	18 PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
119	c2cgkB_	Alignment	not modelled	98.0	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.
120	d1v4sa1	Alignment	not modelled	97.9	21 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase