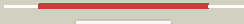



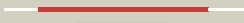



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3600c_(-)_4043220_4044038
Date	Fri Aug 9 18:20:28 BST 2019
Unique Job ID	e9bd87675c8f3cda

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3djcA_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of pantothenate kinase from legionella pneumophila
2	c2h3gX_	 Alignment		100.0	36	PDB header: biosynthetic protein Chain: X: PDB Molecule: biosynthetic protein; PDBTitle: structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
3	c3bf1C_	 Alignment		100.0	31	PDB header: transferase Chain: C: PDB Molecule: type iii pantothenate kinase; PDBTitle: type iii pantothenate kinase from thermotoga maritima2 complexed with pantothenate and adp
4	c4o8kB_	 Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of type iii pantothenate kinase from burkholderia2 thailandensis, apo structure
5	c2f9tB_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: pantothenate kinase; PDBTitle: structure of the type iii coaa from pseudomonas aeruginosa
6	c2nrhA_	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: transcriptional activator, putative, baf family; PDBTitle: crystal structure of conserved putative baf family transcriptional2 activator from campylobacter jejuni
7	d3bexa2	 Alignment		100.0	33	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
8	d2f9wa1	 Alignment		100.0	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
9	d2nrha2	 Alignment		100.0	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
10	d3bexa1	 Alignment		100.0	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
11	d2f9wa2	 Alignment		99.9	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like

12	c2fsnB_	Alignment		98.3	17	PDB header: structural protein Chain: B; PDB Molecule: hypothetical protein ta0583; PDBTitle: crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
13	d2nrha1	Alignment		98.3	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
14	c4ehtA_	Alignment		97.6	15	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
15	c1zxoB_	Alignment		97.5	13	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.
16	c1zbsA_	Alignment		96.8	16	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
17	c1mwmA_	Alignment		96.8	10	PDB header: structural protein Chain: A; PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
18	c3lm2B_	Alignment		96.8	15	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
19	c6izrK_	Alignment		96.7	10	PDB header: protein fibril Chain: K; PDB Molecule: putative plasmid segregation protein parm; PDBTitle: whole structure of a 15-stranded parm filament from clostridium2 botulinum
20	c3h1qB_	Alignment		96.7	14	PDB header: structural protein Chain: B; PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrnus hydrogenoformans
21	c2ap1A_	Alignment	not modelled	96.6	17	PDB header: transferase Chain: A; PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
22	d2aa4a1	Alignment	not modelled	96.5	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
23	c2aa4B_	Alignment	not modelled	96.2	16	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
24	d1huxa_	Alignment	not modelled	96.2	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
25	c5eoxB_	Alignment	not modelled	95.9	17	PDB header: peptide binding protein Chain: B; PDB Molecule: type 4 fimbrial biogenesis protein pilm; PDBTitle: pseudomonas aeruginosa pilm bound to adp
26	c4db3A_	Alignment	not modelled	95.7	19	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.
27	c3cetA_	Alignment	not modelled	95.6	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved archaeal protein; PDBTitle: crystal structure of the pantheonate kinase-like protein q6m145 at the2 resolution 1.8 a. northeast structural genomics consortium target3 mrr63
28	c4czeA_	Alignment	not modelled	95.5	18	PDB header: structural protein Chain: A; PDB Molecule: rod shape-determining protein mreB; PDBTitle: c. crescentus mreB, double filament, empty

29	c3eo3B	Alignment	not modelled	95.1	17	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
30	c2nlxA	Alignment	not modelled	95.0	16	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
31	c3zyyX	Alignment	not modelled	94.8	20	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
32	c2dnpB	Alignment	not modelled	94.7	16	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
33	c1xc3A	Alignment	not modelled	94.6	12	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
34	c3hz6A	Alignment	not modelled	94.5	16	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
35	c6da0A	Alignment	not modelled	94.4	12	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from naegleria fowleri
36	c2gupA	Alignment	not modelled	94.2	16	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
37	c1e4gT	Alignment	not modelled	94.0	11	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
38	d1sz2a1	Alignment	not modelled	93.8	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
39	c2q2rA	Alignment	not modelled	93.6	13	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
40	c5jygA	Alignment	not modelled	93.5	17	PDB header: structural protein Chain: A: PDB Molecule: actin-like atpase; PDBTitle: cryo-em structure of the mamk filament at 6.5 a
41	d1q18a1	Alignment	not modelled	93.4	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
42	c5hv7A	Alignment	not modelled	93.0	12	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
43	c3js6A	Alignment	not modelled	93.0	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized parm protein; PDBTitle: crystal structure of apo psk41 parm protein
44	d1xc3a1	Alignment	not modelled	93.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
45	d2ap1a2	Alignment	not modelled	92.8	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
46	d1zc6a1	Alignment	not modelled	92.8	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
47	c3i8bA	Alignment	not modelled	92.4	8	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
48	c3h6eB	Alignment	not modelled	92.3	15	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
49	d2gupa1	Alignment	not modelled	92.3	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
50	c3vpzA	Alignment	not modelled	92.0	10	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
51	c2ch5D	Alignment	not modelled	92.0	16	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
52	c3vovC	Alignment	not modelled	91.9	21	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
53	c3zyyY	Alignment	not modelled	91.6	20	PDB header: iron-sulfur-binding protein Chain: Y: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
54	c2qm1D	Alignment	not modelled	91.4	20	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
						PDB header: transferase

55	c5nckA	Alignment	not modelled	91.4	27	Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
56	c3vgkB	Alignment	not modelled	91.4	15	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
57	c2e2pA	Alignment	not modelled	91.2	11	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
58	c1jcgA	Alignment	not modelled	91.1	17	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
59	c3jvpA	Alignment	not modelled	91.0	13	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
60	c3gbtA	Alignment	not modelled	91.0	21	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
61	c3flcX	Alignment	not modelled	90.6	20	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
62	c5ya2A	Alignment	not modelled	90.4	12	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
63	c1xupO	Alignment	not modelled	90.0	20	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
64	d2ch5a2	Alignment	not modelled	89.9	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
65	c4e1jA	Alignment	not modelled	89.4	15	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
66	c3ifrB	Alignment	not modelled	89.4	18	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
67	c1glbG	Alignment	not modelled	89.1	13	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase
68	c5vm1A	Alignment	not modelled	88.9	13	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylolyose kinase from brucella ovis
69	c6ediA	Alignment	not modelled	88.3	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of leishmania braziliensis glucokinase
70	d2h0ea3	Alignment	not modelled	88.3	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
71	c4htlA	Alignment	not modelled	87.9	14	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
72	c2d4wA	Alignment	not modelled	87.9	11	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
73	c3mcpA	Alignment	not modelled	87.7	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
74	c5htxA	Alignment	not modelled	87.5	8	PDB header: transferase Chain: A: PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp
75	c2ychA	Alignment	not modelled	87.3	13	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilM; PDBTitle: pilM-pilN type iv pilus biogenesis complex
76	d2fsja1	Alignment	not modelled	87.3	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
77	c3gg4B	Alignment	not modelled	87.2	11	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
78	d2p3ra1	Alignment	not modelled	87.2	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
79	c2w40C	Alignment	not modelled	86.8	18	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
80	c2zf5O	Alignment	not modelled	85.8	10	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
81	c3g25B	Alignment	not modelled	85.8	15	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. 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
82	c2hoeA_	Alignment	not modelled	85.5	14	
83	d1jcea2	Alignment	not modelled	85.0	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
84	d1z05a3	Alignment	not modelled	84.1	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
85	c3ezwD_	Alignment	not modelled	84.1	15	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
86	d2ewsal	Alignment	not modelled	83.5	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
87	c5f7rA_	Alignment	not modelled	81.9	20	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
88	c1woqB_	Alignment	not modelled	81.7	19	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
89	c3wxib_	Alignment	not modelled	81.1	12	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
90	c2floA_	Alignment	not modelled	80.3	11	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
91	c6bqwH_	Alignment	not modelled	79.6	16	PDB header: cytosolic protein Chain: H: PDB Molecule: bacterial actin alfa; PDBTitle: alfa filament bound to amppnp
92	c5f7pA_	Alignment	not modelled	79.5	17	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes
93	c3mdqA_	Alignment	not modelled	79.1	12	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
94	d1woqa1	Alignment	not modelled	78.3	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
95	d2e1za1	Alignment	not modelled	78.2	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
96	c4bc2A_	Alignment	not modelled	77.8	11	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
97	c1zc6A_	Alignment	not modelled	77.3	10	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.
98	c4apwH_	Alignment	not modelled	76.4	15	PDB header: structural protein Chain: H: PDB Molecule: alp12; PDBTitle: alp12 filament structure
99	c3r8eA_	Alignment	not modelled	75.3	19	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
100	c1t6dB_	Alignment	not modelled	75.2	17	PDB header: hydrolase Chain: B: PDB Molecule: exopolyphosphatase; PDBTitle: miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
101	c6etxH_	Alignment	not modelled	73.9	10	PDB header: dna binding protein Chain: H: PDB Molecule: actin-related protein 5; PDBTitle: cryo-em structure of the human ino80 complex bound to nucleosome
102	c3htvA_	Alignment	not modelled	73.4	14	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
103	c3p4iA_	Alignment	not modelled	72.1	15	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
104	d1r59o1	Alignment	not modelled	70.5	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
105	d1g99a1	Alignment	not modelled	69.4	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
106	d1z6ra2	Alignment	not modelled	68.7	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
						PDB header: transferase

107	c1x3nA_	Alignment	not modelled	68.1	17	Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
108	d1zbsa2	Alignment	not modelled	67.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
109	c3slcA_	Alignment	not modelled	65.3	3	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of apo form of acetate kinase (acka) from salmonella2 typhimurium
110	c4ijaA_	Alignment	not modelled	65.2	15	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecR2
111	c3khyA_	Alignment	not modelled	63.8	7	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of a propionate kinase from francisella tularensis2 subsp. tularensis schu s4
112	c1z05A_	Alignment	not modelled	63.7	14	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.
113	d2zgya1	Alignment	not modelled	63.4	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
114	d2fsja2	Alignment	not modelled	63.3	33	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
115	c1sazA_	Alignment	not modelled	63.2	17	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
116	d1hjra_	Alignment	not modelled	63.1	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
117	c1z6rC_	Alignment	not modelled	60.6	21	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
118	d1u6za3	Alignment	not modelled	60.1	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
119	c4xe7A_	Alignment	not modelled	59.8	16	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: bacillus thuringiensis parm in apo form
120	d2zgya2	Alignment	not modelled	59.6	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70