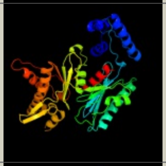
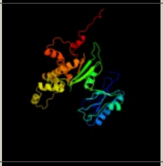
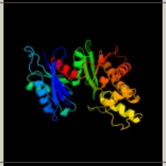
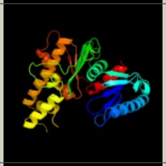
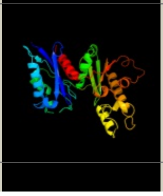
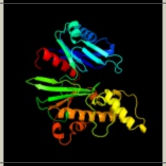
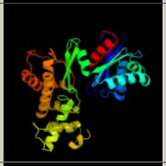
Email	l.a.kelley@imperial.ac.uk
Description	P50456
Date	Thu Jan 5 12:04:43 GMT 2012
Unique Job ID	d92874c542ac9979

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1z05A_	Alignment		100.0	45	**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	98	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
3	c2hoeA_	Alignment		100.0	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
4	c3mcpA_	Alignment		100.0	18	**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
5	c2qm1D_	Alignment		100.0	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
6	c3vgkB_	Alignment		100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
7	c3r8eA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical sugar kinase; **PDBTitle:** crystal structure of a hypothetical sugar kinase (chu_1875) from2 cytophaga hutchinsonii atcc 33406 at 1.65 a resolution
8	c2ap1A_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
9	c2aa4B_	Alignment		100.0	24	**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
10	c3eo3B_	Alignment		100.0	24	**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
11	c3htvA_	Alignment		100.0	15	**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

12	c2gupA_	Alignment		100.0	17	**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
13	c1xc3A_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
14	d1sz2a1	Alignment		100.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
15	d1z6ra3	Alignment		100.0	97	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
16	d1z05a2	Alignment		100.0	42	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
17	c1woqB_	Alignment		100.0	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
18	c2q2rA_	Alignment		100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
19	c2ch5D_	Alignment		100.0	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
20	c3lm2B_	Alignment		100.0	19	**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
21	c2e2pA_	Alignment	not modelled	100.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
22	d2aa4a2	Alignment	not modelled	100.0	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
23	d2ap1a1	Alignment	not modelled	100.0	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
24	c1zc6A_	Alignment	not modelled	100.0	12	**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.
25	d2gupa2	Alignment	not modelled	100.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
26	d2hoea2	Alignment	not modelled	100.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
27	d1q18a2	Alignment	not modelled	99.9	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
28	d1xc3a2	Alignment	not modelled	99.9	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
29	d1z6ra2	Alignment	not modelled	99.9	98	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family:ROK
30	d2hoea3	Alignment	not modelled	99.9	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
31	d1z05a3	Alignment	not modelled	99.9	39	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
32	d1woqa2	Alignment	not modelled	99.8	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
33	d2aa4a1	Alignment	not modelled	99.8	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
34	d2ap1a2	Alignment	not modelled	99.8	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
35	d1woqa1	Alignment	not modelled	99.8	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
36	d2ewsa1	Alignment	not modelled	99.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
37	d2ch5a1	Alignment	not modelled	99.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
38	d2gupa1	Alignment	not modelled	99.7	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
39	d1huxa_	Alignment	not modelled	99.7	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
40	d1xc3a1	Alignment	not modelled	99.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
41	c1bdgA_	Alignment	not modelled	99.7	17	**PDB header:**hexokinase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** hexokinase from schistosoma mansoni complexed with glucose
42	c1v4sA_	Alignment	not modelled	99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase isoform 2; **PDBTitle:** crystal structure of human glucokinase
43	c1ig8A_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase pii; **PDBTitle:** crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
44	c3hm8D_	Alignment	not modelled	99.6	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hexokinase-3; **PDBTitle:** crystal structure of the c-terminal hexokinase domain of human hk3
45	d1z05a1	Alignment	not modelled	99.6	65	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
46	c1qhaA_	Alignment	not modelled	99.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hexokinase); **PDBTitle:** human hexokinase type i complexed with atp analogue amp-pnp
47	d1z6ra1	Alignment	not modelled	99.4	94	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ROK associated domain
48	c1zbsA_	Alignment	not modelled	99.4	10	**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
49	d1q18a1	Alignment	not modelled	99.3	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
50	c1zxoB_	Alignment	not modelled	99.2	10	**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.
51	d1zc6a1	Alignment	not modelled	99.2	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
52	d2ch5a2	Alignment	not modelled	99.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
53	c2dpnB_	Alignment	not modelled	99.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
54	c1sazA_	Alignment	not modelled	99.1	13	**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
55	c3p4iA_	Alignment	not modelled	99.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium

56	c2iirJ_	Alignment	not modelled	98.9	13	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
57	c1tuuA_	Alignment	not modelled	98.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase crystallized with atpgs
58	c2ivoC_	Alignment	not modelled	98.7	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
59	c3h1qB_	Alignment	not modelled	98.7	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
60	c3hz6A_	Alignment	not modelled	98.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
61	c3khyA_	Alignment	not modelled	98.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
62	d1saza2	Alignment	not modelled	98.6	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
63	c3gbtA_	Alignment	not modelled	98.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
64	c3flcX_	Alignment	not modelled	98.5	17	**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
65	d2p3ra1	Alignment	not modelled	98.5	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
66	c2cgkB_	Alignment	not modelled	98.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-rhamnulose kinase; **PDBTitle:** crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
67	c2d4wA_	Alignment	not modelled	98.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
68	c3g25B_	Alignment	not modelled	98.5	12	**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.
69	d2p4wa1	Alignment	not modelled	98.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF1790-like
70	c3ezwD_	Alignment	not modelled	98.4	12	**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
71	c1glbG_	Alignment	not modelled	98.4	12	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
72	c3enoB_	Alignment	not modelled	98.4	13	**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
73	c1x3nA_	Alignment	not modelled	98.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
74	c3gg4B_	Alignment	not modelled	98.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
75	c3ifrB_	Alignment	not modelled	98.4	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
76	c2zf5O_	Alignment	not modelled	98.3	13	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
77	d1ulya_	Alignment	not modelled	98.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein PH1932
78	d1g99a2	Alignment	not modelled	98.2	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
79	d1v4sa1	Alignment	not modelled	98.2	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
80	d1zc6a2	Alignment	not modelled	98.1	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
81	d2e1za2	Alignment	not modelled	98.1	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like

82	d1ub9a_	Alignment	not modelled	98.0	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
83	d1czan2	Alignment	not modelled	98.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
84	d1bdga1	Alignment	not modelled	98.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
85	c1xupO_	Alignment	not modelled	98.0	15	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
86	c2nlxA_	Alignment	not modelled	97.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
87	d1ig8a2	Alignment	not modelled	97.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
88	c3g3zA_	Alignment	not modelled	97.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
89	d1bg3a4	Alignment	not modelled	97.9	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
90	d2etha1	Alignment	not modelled	97.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
91	c3bj6B_	Alignment	not modelled	97.8	13	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
92	d1v4sa2	Alignment	not modelled	97.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
93	d1lnwa_	Alignment	not modelled	97.8	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
94	c2nyxB_	Alignment	not modelled	97.8	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
95	d1jgsa_	Alignment	not modelled	97.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
96	d2fbha1	Alignment	not modelled	97.8	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
97	d1sfxa_	Alignment	not modelled	97.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
98	d1bg3a2	Alignment	not modelled	97.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
99	c3cuoB_	Alignment	not modelled	97.8	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**uncharacterized hth-type transcriptional regulator ygav; **PDBTitle:** crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
100	d2bv6a1	Alignment	not modelled	97.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
101	c2l4aA_	Alignment	not modelled	97.7	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
102	c3nrvC_	Alignment	not modelled	97.7	10	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**putative transcriptional regulator (marr/emrr family); **PDBTitle:** crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
103	c3en9B_	Alignment	not modelled	97.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
104	d1bg3a3	Alignment	not modelled	97.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
105	c2w40C_	Alignment	not modelled	97.7	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
106	d1czan1	Alignment	not modelled	97.7	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
107	d1czan3	Alignment	not modelled	97.7	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
						PDB header:transcription

108	c2fxaB_	Alignment	not modelled	97.7	8	**Chain:** B: **PDB Molecule:**protease production regulatory protein hpr; **PDBTitle:** structure of the protease production regulatory protein hpr from2 bacillus subtilis.
109	c3bpxB_	Alignment	not modelled	97.7	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of marr
110	d1ku9a_	Alignment	not modelled	97.7	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
111	c2qwwB_	Alignment	not modelled	97.7	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
112	d1bg3a1	Alignment	not modelled	97.6	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
113	c3e6mD_	Alignment	not modelled	97.6	11	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**marr family transcriptional regulator; **PDBTitle:** the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
114	c3jvpA_	Alignment	not modelled	97.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
115	c2qufB_	Alignment	not modelled	97.6	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor pf0095; **PDBTitle:** crystal structure of transcription factor axxa-pf0095 from pyrococcus2 furiosus
116	d1bdga2	Alignment	not modelled	97.6	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
117	d1lj9a_	Alignment	not modelled	97.6	3	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
118	d1s3ja_	Alignment	not modelled	97.6	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
119	d1ig8a1	Alignment	not modelled	97.6	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
120	d2fbia1	Alignment	not modelled	97.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators