Phyre2

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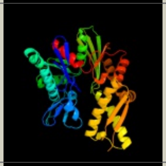
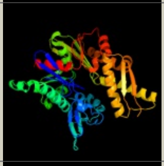
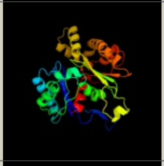
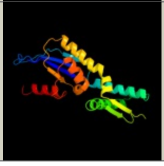
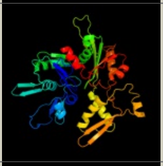
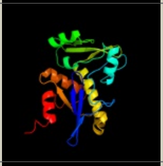
Description	P36928
Date	Thu Jan 5 11:53:57 GMT 2012
Unique Job ID	dd1358dc0b0b1e9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d2fC_	Alignment		100.0	20	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
2	c2v7yA_	Alignment		100.0	26	**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
3	c2khoA_	Alignment		100.0	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 70; **PDBTitle:** nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
4	c1dkgD_	Alignment		100.0	25	**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
5	c1hpmA_	Alignment		100.0	21	**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
6	c3iucC_	Alignment		100.0	23	**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
7	c2v7zA_	Alignment		100.0	21	**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
8	c1jcgA_	Alignment		100.0	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
9	c1e4gT_	Alignment		100.0	15	**PDB header:**bacterial cell division **Chain:** T: **PDB Molecule:**cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
10	c3h1qB_	Alignment		100.0	24	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
11	d1dkgd2	Alignment		100.0	30	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70

12	d1bupa2	Alignment		100.0	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
13	c1o1f4_	Alignment		100.0	18	**PDB header:**contractile protein **Chain:** 4: **PDB Molecule:**skeletal muscle actin; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
14	d2e8aa1	Alignment		100.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
15	d2e8aa2	Alignment		100.0	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
16	d1bupa1	Alignment		100.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
17	c2d0oA_	Alignment		100.0	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**diol dehydratase-reactivating factor large **PDBTitle:** strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
18	c1mwmA_	Alignment		99.9	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
19	d1dkgd1	Alignment		99.9	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
20	d1jcea2	Alignment		99.9	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
21	c2fsnB_	Alignment	not modelled	99.9	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**hypothetical protein ta0583; **PDBTitle:** crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
22	c3dwlB_	Alignment	not modelled	99.9	17	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**actin-related protein 3; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
23	c2p9lA_	Alignment	not modelled	99.9	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin-like protein 3; **PDBTitle:** crystal structure of bovine arp2/3 complex
24	d1jcea1	Alignment	not modelled	99.9	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
25	c2ychA_	Alignment	not modelled	99.9	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
26	c3js6A_	Alignment	not modelled	99.8	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized parm protein; **PDBTitle:** crystal structure of apo psk41 parm protein
27	d1e4ft2	Alignment	not modelled	99.8	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
28	c3qb0C_	Alignment	not modelled	99.7	14	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**actin-related protein 4; **PDBTitle:** crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
						Fold: Ribonuclease H-like motif

29	d2zgya2	Alignment	not modelled	99.7	21	**Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
30	d1huxa_	Alignment	not modelled	99.7	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
31	d2fsja1	Alignment	not modelled	99.6	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
32	d1nm1a2	Alignment	not modelled	99.3	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
33	d2hf3a2	Alignment	not modelled	99.2	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
34	d2fxua2	Alignment	not modelled	99.1	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
35	d1yaga2	Alignment	not modelled	98.8	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
36	d1k8ka2	Alignment	not modelled	98.8	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
37	c3gg4B_	Alignment	not modelled	98.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
38	d1k8kb1	Alignment	not modelled	98.6	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
39	c2e2pA_	Alignment	not modelled	98.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
40	c2p9kB_	Alignment	not modelled	98.5	19	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**actin-like protein 2; **PDBTitle:** crystal structure of bovine arp2/3 complex co-crystallized2 with atp and crosslinked with glutaraldehyde
41	c3i8bA_	Alignment	not modelled	98.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
42	d2p3ra2	Alignment	not modelled	98.3	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
43	c2nlxA_	Alignment	not modelled	98.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
44	d1r59o2	Alignment	not modelled	98.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
45	c2cgkB_	Alignment	not modelled	98.3	12	**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.
46	c2d4wA_	Alignment	not modelled	98.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
47	c2dpnB_	Alignment	not modelled	98.3	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
48	c3flcX_	Alignment	not modelled	98.3	14	**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
49	c3ifrB_	Alignment	not modelled	98.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
50	c1glbG_	Alignment	not modelled	98.3	9	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
51	c3jvpA_	Alignment	not modelled	98.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
52	c3gbtA_	Alignment	not modelled	98.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
53	c3g25B_	Alignment	not modelled	98.2	11	**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.
54	c3hz6A_	Alignment	not modelled	98.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
55	c1xupO_	Alignment	not modelled	98.2	15	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol

56	c1nbwA_	Alignment	not modelled	98.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
57	c3ezwD_	Alignment	not modelled	98.1	10	**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
58	c2zf5O_	Alignment	not modelled	98.1	13	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
59	d2ewsa1	Alignment	not modelled	97.9	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
60	c2w40C_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
61	c1t6dB_	Alignment	not modelled	97.6	20	**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
62	d2d0oa3	Alignment	not modelled	97.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
63	c2ap1A_	Alignment	not modelled	97.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
64	d1nbwa3	Alignment	not modelled	97.4	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
65	c2qm1D_	Alignment	not modelled	97.3	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
66	c3h6eB_	Alignment	not modelled	97.2	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
67	c2floA_	Alignment	not modelled	97.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
68	c3htvA_	Alignment	not modelled	96.7	18	**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
69	c3hi0B_	Alignment	not modelled	96.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
70	d1e4ft1	Alignment	not modelled	96.3	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
71	c3eo3B_	Alignment	not modelled	96.1	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
72	c2ch5D_	Alignment	not modelled	95.8	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
73	d1t6ca2	Alignment	not modelled	95.7	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
74	c3r8eA_	Alignment	not modelled	95.6	17	**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
75	c3cqyA_	Alignment	not modelled	95.5	22	**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
76	d1saza2	Alignment	not modelled	95.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
77	c1z6rC_	Alignment	not modelled	95.2	21	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
78	d1yaga1	Alignment	not modelled	94.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
79	c1z05A_	Alignment	not modelled	94.9	11	**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.
80	c1sazA_	Alignment	not modelled	94.9	15	**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

81	d1z05a2	Alignment	not modelled	94.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
82	c3tsuA_	Alignment	not modelled	94.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
83	c3cerD_	Alignment	not modelled	94.4	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**possible exopolyphosphatase-like protein; **PDBTitle:** crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
84	d2fxua1	Alignment	not modelled	94.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
85	d2ap1a1	Alignment	not modelled	93.9	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
86	c3mdqA_	Alignment	not modelled	93.8	19	**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
87	c2aa4B_	Alignment	not modelled	93.8	12	**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
88	c3qbwA_	Alignment	not modelled	93.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 actetylmuramic acid kinase (anmk) bound to adenosine diphosphate
89	d2p3ra1	Alignment	not modelled	93.5	25	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
90	d2ap1a2	Alignment	not modelled	93.5	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
91	d1c0fa1	Alignment	not modelled	93.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
92	d2aa4a2	Alignment	not modelled	92.8	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
93	d2hf3a1	Alignment	not modelled	92.6	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
94	c3enoB_	Alignment	not modelled	92.5	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
95	d3bexa1	Alignment	not modelled	91.6	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like
96	c3vgkB_	Alignment	not modelled	91.3	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
97	c1zc6A_	Alignment	not modelled	91.3	20	**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	d1r59o1	Alignment	not modelled	90.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
99	c2ivoC_	Alignment	not modelled	90.3	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
100	d1xc3a1	Alignment	not modelled	89.7	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
101	d1u6za3	Alignment	not modelled	89.0	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
102	d1vhxa_	Alignment	not modelled	88.6	30	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
103	c3cetA_	Alignment	not modelled	88.4	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved archaeal protein; **PDBTitle:** crystal structure of the pantheonate kinase-like protein2 q6m145 at the resolution 1.8 a. northeast structural3 genomics consortium target mrr63
104	d2hoea2	Alignment	not modelled	87.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
105	d1z6ra3	Alignment	not modelled	87.4	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
106	d1zc6a1	Alignment	not modelled	87.4	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

							Family: BadF/BadG/BcrA/BcrD-like
107	c2gupA_		Alignment	not modelled	87.2	13	**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
108	d1iv0a_		Alignment	not modelled	86.9	30	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
109	c2q2rA_		Alignment	not modelled	86.5	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
110	d2zgya1		Alignment	not modelled	86.4	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
111	d2ch5a2		Alignment	not modelled	86.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
112	d2ch5a1		Alignment	not modelled	85.4	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
113	d1nu0a_		Alignment	not modelled	85.1	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
114	c2h3gX_		Alignment	not modelled	85.0	24	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**biosynthetic protein; **PDBTitle:** structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
115	d1b74a2		Alignment	not modelled	84.8	25	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
116	d2gupa2		Alignment	not modelled	82.1	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
117	c2hoeA_		Alignment	not modelled	81.1	14	**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
118	c3bf1C_		Alignment	not modelled	80.9	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**type iii pantothenate kinase; **PDBTitle:** type iii pantothenate kinase from thermotoga maritima2 complexed with pantothenate and adp
119	c3djcA_		Alignment	not modelled	80.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type iii pantothenate kinase; **PDBTitle:** crystal structure of pantothenate kinase from legionella pneumophila
120	d1czan3		Alignment	not modelled	80.1	32	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase