Phyre^2

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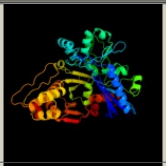
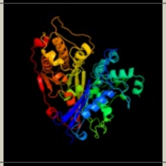
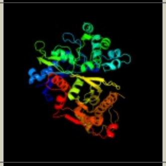
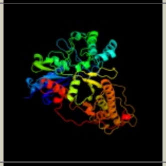
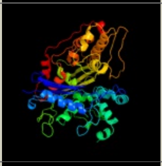
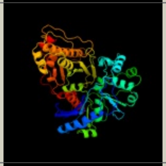
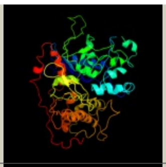
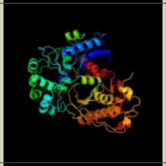
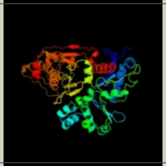
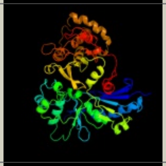
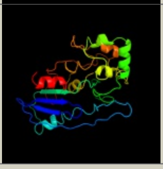
Description	P11553
Date	Thu Jan 5 11:32:45 GMT 2012
Unique Job ID	bdf088c1455a2960

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gbtA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
2	c3ifrB_	Alignment		100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
3	c3flcX_	Alignment		100.0	22	**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
4	c2nlxA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
5	c2zf5O_	Alignment		100.0	25	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
6	c2d4wA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
7	c3hz6A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
8	c3g25B_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
9	c2w40C_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
10	c3jvpA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
11	c1glbG_	Alignment		100.0	20	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase

12	c1xupO_	Alignment		100.0	22	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
13	c3gg4B_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
14	c2dpnB_	Alignment		100.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
15	c3ezwD_	Alignment		100.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
16	c2cgkB_	Alignment		100.0	21	**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.
17	c3i8bA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
18	c3h6eB_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
19	d2p3ra1	Alignment		100.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
20	d1r59o1	Alignment		100.0	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
21	d2p3ra2	Alignment	not modelled	100.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
22	d1r59o2	Alignment	not modelled	100.0	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
23	d1huxa_	Alignment	not modelled	99.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
24	c3h1qB_	Alignment	not modelled	99.4	19	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
25	c2e2pA_	Alignment	not modelled	99.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
26	d2ewsa1	Alignment	not modelled	99.1	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
27	c2ivoC_	Alignment	not modelled	99.0	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
28	c2qm1D_	Alignment	not modelled	99.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
						PDB header:hydrolase/unknown function **Chain:** B: **PDB Molecule:**putative o-sialoglycoprotein

29	c3enoB_	Alignment	not modelled	98.9	18	endopeptidase; **PDBTitle:** crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
30	c2ap1A_	Alignment	not modelled	98.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
31	c3eo3B_	Alignment	not modelled	98.8	23	**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
32	c3r8eA_	Alignment	not modelled	98.8	18	**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
33	d1zc6a1	Alignment	not modelled	98.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
34	c1zc6A_	Alignment	not modelled	98.4	15	**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.
35	d1z05a3	Alignment	not modelled	98.3	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
36	c2ch5D_	Alignment	not modelled	98.2	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
37	d1z6ra2	Alignment	not modelled	98.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
38	c1dkgD_	Alignment	not modelled	98.1	19	**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
39	d2ch5a2	Alignment	not modelled	98.1	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
40	c2gupA_	Alignment	not modelled	98.0	22	**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
41	c3en9B_	Alignment	not modelled	98.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
42	d1woqa1	Alignment	not modelled	98.0	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
43	c2aa4B_	Alignment	not modelled	98.0	20	**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
44	d2ap1a2	Alignment	not modelled	97.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
45	c1z6rC_	Alignment	not modelled	97.9	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
46	d2hoea3	Alignment	not modelled	97.9	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
47	d1dkgd2	Alignment	not modelled	97.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
48	c3htvA_	Alignment	not modelled	97.9	13	**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
49	c2v7zA_	Alignment	not modelled	97.9	14	**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
50	c1z05A_	Alignment	not modelled	97.8	16	**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.
51	c3mcpA_	Alignment	not modelled	97.8	23	**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
52	c3d2fC_	Alignment	not modelled	97.8	17	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
53	d2aa4a1	Alignment	not modelled	97.7	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
						PDB header:chaperone

54	c2v7yA_	Alignment	not modelled	97.7	20	**Chain:** A: **PDB Molecule:**chaperone protein dnak; **PDBTitle:** crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
55	c1hpmA_	Alignment	not modelled	97.7	13	**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
56	c2hoeA_	Alignment	not modelled	97.7	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
57	c3vgkB_	Alignment	not modelled	97.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
58	c1xc3A_	Alignment	not modelled	97.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
59	d1sz2a1	Alignment	not modelled	97.6	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
60	d1jcea2	Alignment	not modelled	97.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
61	d2gupa1	Alignment	not modelled	97.6	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
62	d2e8aa2	Alignment	not modelled	97.6	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
63	d1q18a1	Alignment	not modelled	97.6	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
64	d1bupa2	Alignment	not modelled	97.6	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
65	c3iucC_	Alignment	not modelled	97.5	16	**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
66	c1jcgA_	Alignment	not modelled	97.5	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
67	c3cqyA_	Alignment	not modelled	97.4	18	**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
68	c1woqB_	Alignment	not modelled	97.3	11	**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
69	d1xc3a1	Alignment	not modelled	97.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
70	c2q2rA_	Alignment	not modelled	97.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
71	c2khoA_	Alignment	not modelled	97.2	21	**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
72	c3lm2B_	Alignment	not modelled	97.2	14	**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
73	c1ig8A_	Alignment	not modelled	97.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase pii; **PDBTitle:** crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
74	c1e4gT_	Alignment	not modelled	97.1	19	**PDB header:**bacterial cell division **Chain:** T: **PDB Molecule:**cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
75	c1tuuA_	Alignment	not modelled	97.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase crystallized with atpgs
76	d1e4ft1	Alignment	not modelled	97.0	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
77	d1bg3a3	Alignment	not modelled	96.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
78	c3qbwA_	Alignment	not modelled	96.8	19	**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
79	d1e4ft2	Alignment	not modelled	96.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family: Actin/HSP70
80	c3tsuA_	Alignment	not modelled	96.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
81	d1bdga1	Alignment	not modelled	96.7	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
82	d2i7na2	Alignment	not modelled	96.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
83	d2i7pa1	Alignment	not modelled	96.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
84	c2ychA_	Alignment	not modelled	96.5	24	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
85	c3khyA_	Alignment	not modelled	96.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
86	d1t6ca1	Alignment	not modelled	96.4	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
87	c2d0oA_	Alignment	not modelled	96.3	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**diol dehydratase-reactivating factor large **PDBTitle:** strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
88	d2e1za1	Alignment	not modelled	96.3	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
89	c1zbsA_	Alignment	not modelled	96.2	14	**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
90	d1u6za2	Alignment	not modelled	96.1	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
91	d1ig8a1	Alignment	not modelled	95.9	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
92	c3hi0B_	Alignment	not modelled	95.9	7	**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
93	d3bzka5	Alignment	not modelled	95.8	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
94	d1v4sa1	Alignment	not modelled	95.8	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
95	d1czan3	Alignment	not modelled	95.8	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
96	c1t6dB_	Alignment	not modelled	95.7	12	**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
97	c1bdgA_	Alignment	not modelled	95.6	19	**PDB header:**hexokinase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** hexokinase from schistosoma mansoni complexed with glucose
98	c3t69A_	Alignment	not modelled	95.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 2-dehydro-3-deoxygalactonokinase; **PDBTitle:** crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from sinorhizobium meliloti
99	d1bg3a1	Alignment	not modelled	95.6	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
100	d1czan1	Alignment	not modelled	95.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
101	c2floA_	Alignment	not modelled	95.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
102	c1x3nA_	Alignment	not modelled	95.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
103	d3bexa1	Alignment	not modelled	95.3	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like
104	d2zgya2	Alignment	not modelled	95.1	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
105	c3mdqA_	Alignment	not modelled	95.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase;

105	c3mdqA_	Alignment	not modelled	95.1	14	**PDBTitle:** crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
106	c3cerD_	Alignment	not modelled	95.1	11	**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
107	d1g99a1	Alignment	not modelled	94.8	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
108	c2h3gX_	Alignment	not modelled	94.8	20	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**biosynthetic protein; **PDBTitle:** structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
109	c3hm8D_	Alignment	not modelled	94.4	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hexokinase-3; **PDBTitle:** crystal structure of the c-terminal hexokinase domain of human hk3
110	c3bf1C_	Alignment	not modelled	94.3	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**type iii pantothenate kinase; **PDBTitle:** type iii pantothenate kinase from thermotoga maritima2 complexed with pantothenate and adp
111	c1v4sA_	Alignment	not modelled	94.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase isoform 2; **PDBTitle:** crystal structure of human glucokinase
112	c2i7pA_	Alignment	not modelled	94.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
113	c1mwmA_	Alignment	not modelled	94.1	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
114	c1qhaA_	Alignment	not modelled	94.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (hexokinase); **PDBTitle:** human hexokinase type i complexed with atp analogue amp-pnp
115	d1saza1	Alignment	not modelled	94.1	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
116	d2e8aa1	Alignment	not modelled	94.1	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
117	c1zxoB_	Alignment	not modelled	94.0	19	**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.
118	d2ch5a1	Alignment	not modelled	93.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
119	d1ig8a2	Alignment	not modelled	93.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
120	d2aa4a2	Alignment	not modelled	92.9	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK