Phyre^{2}

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Description	P0ABH0
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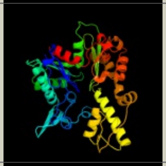
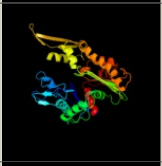
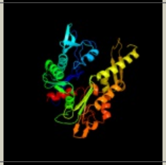
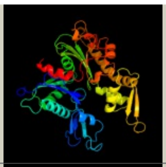
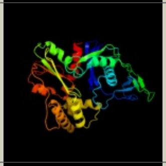
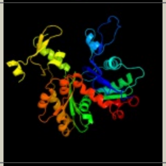
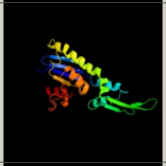
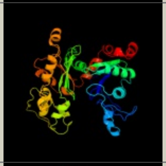
Unique Job ID	b6395351a9ad6cc0

Detailed template information

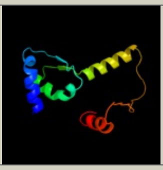
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1e4gT_	Alignment		100.0	20	**PDB header:**bacterial cell division **Chain:** T: **PDB Molecule:**cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
2	c2d0oA_	Alignment		100.0	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**diol dehydratase-reactivating factor large **PDBTitle:** strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
3	c3d2fC_	Alignment		100.0	19	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
4	c2ychA_	Alignment		100.0	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
5	c2v7yA_	Alignment		100.0	19	**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
6	c3h1qB_	Alignment		100.0	26	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
7	c2khoA_	Alignment		100.0	18	**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
8	c1dkgD_	Alignment		100.0	18	**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
9	c1hpmA_	Alignment		100.0	19	**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
10	c2v7zA_	Alignment		100.0	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock cognate 71 kda protein; **PDBTitle:** crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
11	c3iucC_	Alignment		100.0	20	**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

12	c1jcgA_	Alignment		100.0	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
13	d1e4ft1	Alignment		100.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
14	d1e4ft2	Alignment		100.0	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
15	c1mwmA_	Alignment		100.0	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
16	d1jcea2	Alignment		99.9	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
17	c1o1f4_	Alignment		99.9	16	**PDB header:**contractile protein **Chain:** 4: **PDB Molecule:**skeletal muscle actin; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
18	d1dkgd2	Alignment		99.9	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
19	c3dwlB_	Alignment		99.9	16	**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
20	d1bupa2	Alignment		99.9	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
21	c2p9lA_	Alignment	not modelled	99.9	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin-like protein 3; **PDBTitle:** crystal structure of bovine arp2/3 complex
22	d2e8aa2	Alignment	not modelled	99.9	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
23	c2fsnB_	Alignment	not modelled	99.9	16	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**hypothetical protein ta0583; **PDBTitle:** crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
24	c3qb0C_	Alignment	not modelled	99.8	17	**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
25	d1huxa_	Alignment	not modelled	99.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
26	d2zgya2	Alignment	not modelled	99.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
27	d2e8aa1	Alignment	not modelled	99.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
28	c3js6A_	Alignment	not modelled	99.6	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized parm protein; **PDBTitle:** crystal structure of apo psk41 parm protein
29	d1nm1a2	Alignment	not modelled	99.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family: Actin/HSP70
30	d2fsja1	Alignment	not modelled	99.5	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
31	d2fxua2	Alignment	not modelled	99.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
32	d2hf3a2	Alignment	not modelled	99.5	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
33	d1bupa1	Alignment	not modelled	99.5	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
34	c3gg4B_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
35	c1nbwA_	Alignment	not modelled	99.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
36	d1yaga2	Alignment	not modelled	99.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
37	d2d0oa3	Alignment	not modelled	99.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
38	d1k8ka2	Alignment	not modelled	99.4	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
39	d1dkgd1	Alignment	not modelled	99.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
40	d1jcea1	Alignment	not modelled	99.3	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
41	c3hz6A_	Alignment	not modelled	99.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
42	d1nbwa3	Alignment	not modelled	99.3	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
43	c3gbtA_	Alignment	not modelled	99.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
44	c2nlxA_	Alignment	not modelled	99.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
45	c2p9kB_	Alignment	not modelled	99.3	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
46	c3i8bA_	Alignment	not modelled	99.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
47	c2dpnB_	Alignment	not modelled	99.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
48	c3ifrB_	Alignment	not modelled	99.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
49	c3ezwD_	Alignment	not modelled	99.2	16	**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
50	c3flcX_	Alignment	not modelled	99.1	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
51	c3jvpA_	Alignment	not modelled	99.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
52	d1k8kb1	Alignment	not modelled	99.1	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
53	c2zf5O_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
54	c3g25B_	Alignment	not modelled	99.1	13	**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.
55	c2d4wA_	Alignment	not modelled	99.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060

56	c2w40C_	Alignment	not modelled	98.9	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
57	c2floA_	Alignment	not modelled	98.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
58	c1t6dB_	Alignment	not modelled	98.7	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
59	c3mdqA_	Alignment	not modelled	98.7	15	**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
60	c3htvA_	Alignment	not modelled	98.6	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
61	c3cerD_	Alignment	not modelled	98.6	17	**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
62	c3hi0B_	Alignment	not modelled	98.5	18	**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
63	c1glbG_	Alignment	not modelled	98.5	13	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
64	d2ewsa1	Alignment	not modelled	98.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
65	d2p3ra1	Alignment	not modelled	98.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
66	c2e2pA_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
67	c2cgkB_	Alignment	not modelled	97.9	19	**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.
68	d2p3ra2	Alignment	not modelled	97.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
69	c3cetA_	Alignment	not modelled	97.7	18	**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
70	c1xupO_	Alignment	not modelled	97.7	16	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
71	d1r59o2	Alignment	not modelled	97.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
72	c2ap1A_	Alignment	not modelled	97.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
73	c2qm1D_	Alignment	not modelled	97.6	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
74	d1u6za3	Alignment	not modelled	97.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
75	c2ch5D_	Alignment	not modelled	97.5	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
76	d2d0oa2	Alignment	not modelled	97.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
77	c1z6rC_	Alignment	not modelled	97.2	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
78	c1woqB_	Alignment	not modelled	97.2	13	**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
79	c3cqyA_	Alignment	not modelled	97.1	14	**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
80	c3r8eA_	Alignment	not modelled	97.1	13	**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
81	c2aa4B_	Alignment	not modelled	97.1	14	**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
82	d1t6ca2	Alignment	not modelled	97.0	31	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
83	c2hoeA_	Alignment	not modelled	96.8	18	**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
84	c2gupA_	Alignment	not modelled	96.8	14	**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
85	c3h6eB_	Alignment	not modelled	96.7	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
86	c1z05A_	Alignment	not modelled	96.7	12	**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.
87	d1r59o1	Alignment	not modelled	96.5	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
88	d1nbwa2	Alignment	not modelled	96.5	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
89	c1xc3A_	Alignment	not modelled	95.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
90	d1zc6a1	Alignment	not modelled	95.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
91	d2ch5a2	Alignment	not modelled	95.6	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
92	c1zc6A_	Alignment	not modelled	95.4	8	**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.
93	d1woqa1	Alignment	not modelled	95.0	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
94	d2i7na2	Alignment	not modelled	94.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
95	c2ivoC_	Alignment	not modelled	94.8	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
96	c3mcpA_	Alignment	not modelled	94.8	14	**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
97	d2bh1a2	Alignment	not modelled	94.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Cyto-EpsL domain
98	c3aapA_	Alignment	not modelled	94.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleoside triphosphate diphosphohydrolase i; **PDBTitle:** crystal structure of lp1ntpdase from legionella pneumophila
99	c2q2rA_	Alignment	not modelled	94.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
100	c3vgkB_	Alignment	not modelled	94.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
101	c2i7pA_	Alignment	not modelled	94.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
102	c3smpA_	Alignment	not modelled	94.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 1; **PDBTitle:** monoclinic crystal structure of human pantothenate kinase 1 alpha
103	d1q18a1	Alignment	not modelled	94.2	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
104	d2i7pa1	Alignment	not modelled	93.2	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
105	d2gupa2	Alignment	not modelled	92.1	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
						PDB header:isomerase, transferase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-

106	c3eo3B_	Alignment	not modelled	91.6	13	epimerase/n- **PDBTitle:** crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
107	d1t6ca1	Alignment	not modelled	91.5	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
108	c3qbwA_	Alignment	not modelled	91.2	12	**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
109	c3en9B_	Alignment	not modelled	90.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
110	d2ap1a2	Alignment	not modelled	90.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
111	d2aa4a2	Alignment	not modelled	90.3	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
112	d1z6ra2	Alignment	not modelled	90.3	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
113	c2h3gX_	Alignment	not modelled	90.1	14	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**biosynthetic protein; **PDBTitle:** structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
114	d2hoea3	Alignment	not modelled	90.0	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
115	c2gzmB_	Alignment		89.2	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
116	d1iv0a_	Alignment	not modelled	87.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
117	d2gupa1	Alignment	not modelled	87.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
118	c3enoB_	Alignment	not modelled	86.9	11	**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
119	c1zuwA_	Alignment	not modelled	86.8	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
120	c3zx2A_	Alignment	not modelled	86.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleoside triphosphate diphosphohydrolase 1; **PDBTitle:** ntpdase1 in complex with decavanadate