Phyre2

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Description	P39383
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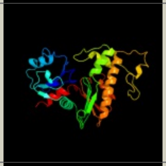
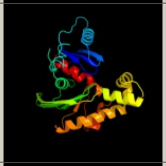
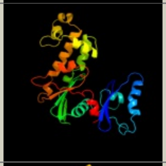
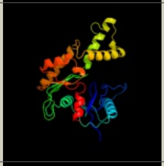
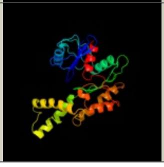
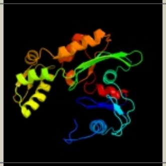
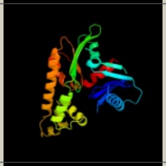
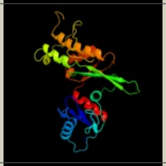
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1huxa_	Alignment		100.0	42	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
2	d2ewsa1	Alignment		100.0	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
3	c3h1qB_	Alignment		100.0	18	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
4	c2ivoC_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
5	c3enoB_	Alignment		99.9	17	**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
6	c3en9B_	Alignment		99.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
7	c2i7pA_	Alignment		99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
8	c3smpA_	Alignment		99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 1; **PDBTitle:** monoclinic crystal structure of human pantothenate kinase 1 alpha
9	c2e2pA_	Alignment		99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
10	c2v7yA_	Alignment		99.8	22	**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
11	c3d2fC_	Alignment		99.8	16	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70

12	c1jcgA_	Alignment		99.7	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
13	c3gbtA_	Alignment		99.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
14	c2khoA_	Alignment		99.7	20	**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
15	c1mwmA_	Alignment		99.7	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
16	c2v7zA_	Alignment		99.7	19	**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
17	c3hz6A_	Alignment		99.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
18	c1dkgD_	Alignment		99.7	21	**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
19	c3iucC_	Alignment		99.7	19	**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
20	c1hpmA_	Alignment		99.7	18	**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
21	c1e4gT_	Alignment	not modelled	99.7	17	**PDB header:**bacterial cell division **Chain:** T: **PDB Molecule:**cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
22	c3ifrB_	Alignment	not modelled	99.6	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
23	c3eo3B_	Alignment	not modelled	99.6	13	**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
24	c2zf5O_	Alignment	not modelled	99.6	19	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
25	c3g25B_	Alignment	not modelled	99.6	16	**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.
26	c1glbG_	Alignment	not modelled	99.6	13	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
27	c2nlxA_	Alignment	not modelled	99.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
28	c3i8bA_	Alignment	not modelled	99.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis

29	c2cgkB_	Alignment	not modelled	99.6	16	**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.
30	c3flcX_	Alignment	not modelled	99.6	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
31	c2dpnB_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
32	c2w40C_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
33	c2ap1A_	Alignment	not modelled	99.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
34	c2d4wA_	Alignment	not modelled	99.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
35	c3gg4B_	Alignment	not modelled	99.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
36	c2ch5D_	Alignment	not modelled	99.5	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
37	c2d0oA_	Alignment	not modelled	99.5	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+
38	c2aa4B_	Alignment	not modelled	99.5	19	**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
39	d1jcea2	Alignment	not modelled	99.5	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
40	c3ezwD_	Alignment	not modelled	99.5	13	**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
41	d2i7na2	Alignment	not modelled	99.5	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
42	c1zc6A_	Alignment	not modelled	99.5	18	**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.
43	c3jvpA_	Alignment	not modelled	99.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
44	d2i7pa1	Alignment	not modelled	99.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
45	d1dkgd2	Alignment	not modelled	99.4	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
46	c3vgkB_	Alignment	not modelled	99.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
47	d1bupa2	Alignment	not modelled	99.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
48	c2qm1D_	Alignment	not modelled	99.4	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
49	d2e8aa2	Alignment	not modelled	99.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
50	c2ychA_	Alignment	not modelled	99.4	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
51	c2gupA_	Alignment	not modelled	99.4	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
52	d1e4ft2	Alignment	not modelled	99.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
53	c1zbsA_	Alignment	not modelled	99.3	18	**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

54	c2fsnB_	Alignment	not modelled	99.3	17	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**hypothetical protein ta0583; **PDBTitle:** crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
55	c3htvA_	Alignment	not modelled	99.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-allose kinase; **PDBTitle:** crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
56	c3r8eA_	Alignment	not modelled	99.3	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
57	c3js6A_	Alignment	not modelled	99.2	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized parm protein; **PDBTitle:** crystal structure of apo psk41 parm protein
58	c1o1f4_	Alignment	not modelled	99.2	17	**PDB header:**contractile protein **Chain:** 4: **PDB Molecule:**skeletal muscle actin; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
59	c1z05A_	Alignment	not modelled	99.2	15	**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.
60	c1xc3A_	Alignment	not modelled	99.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
61	d2zgya2	Alignment	not modelled	99.2	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
62	c1z6rC_	Alignment	not modelled	99.1	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
63	c1sazA_	Alignment	not modelled	99.1	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
64	c3dwlB_	Alignment	not modelled	99.0	14	**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
65	c1zxoB_	Alignment	not modelled	99.0	18	**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.
66	c3tsuA_	Alignment	not modelled	98.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
67	d2p3ra2	Alignment	not modelled	98.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
68	d2fsja1	Alignment	not modelled	98.8	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
69	d1r59o2	Alignment	not modelled	98.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
70	c3cqyA_	Alignment	not modelled	98.7	17	**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
71	c1xupO_	Alignment	not modelled	98.7	18	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
72	d1sz2a1	Alignment	not modelled	98.7	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
73	c2p9lA_	Alignment	not modelled	98.6	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin-like protein 3; **PDBTitle:** crystal structure of bovine arp2/3 complex
74	c3cetA_	Alignment	not modelled	98.6	11	**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
75	c2hoeA_	Alignment	not modelled	98.6	17	**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
76	d2hf3a2	Alignment	not modelled	98.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
77	d1nm1a2	Alignment	not modelled	98.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
78	d2fxua2	Alignment	not modelled	98.3	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
79	c3mcpA_	Alignment	not modelled	98.3	17	**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
80	d1zc6a1	Alignment	not modelled	98.3	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
81	d2p3ra1	Alignment	not modelled	98.3	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
82	c3p4iA_	Alignment	not modelled	98.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium
83	c3qbwA_	Alignment	not modelled	98.2	17	**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
84	c1woqB_	Alignment	not modelled	98.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inorganic polyphosphate/atp-glucomannokinase; **PDBTitle:** crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
85	d2ch5a1	Alignment	not modelled	98.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
86	d1yaga2	Alignment	not modelled	98.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
87	c2q2rA_	Alignment	not modelled	98.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
88	c1x3nA_	Alignment	not modelled	97.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
89	d2ch5a2	Alignment	not modelled	97.8	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
90	d1saza2	Alignment	not modelled	97.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
91	d1zc6a2	Alignment	not modelled	97.8	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
92	d1k8ka2	Alignment	not modelled	97.8	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
93	d1r59o1	Alignment	not modelled	97.7	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
94	c3lm2B_	Alignment	not modelled	97.6	13	**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
95	c3djcA_	Alignment	not modelled	97.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type iii pantothenate kinase; **PDBTitle:** crystal structure of pantothenate kinase from legionella pneumophila
96	d2gupa1	Alignment	not modelled	97.6	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
97	c3h6eB_	Alignment	not modelled	97.6	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
98	c1t6dB_	Alignment	not modelled	97.5	15	**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
99	c3khyA_	Alignment	not modelled	97.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
100	c1tuuA_	Alignment	not modelled	97.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase crystallized with atpgs
101	c3qb0C_	Alignment	not modelled	97.5	18	**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
102	c2iirJ_	Alignment	not modelled	97.4	22	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
103	d2i7pa2	Alignment	not modelled	97.4	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
104	c2p9kB_	Alignment	not modelled	97.3	22	**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
105	d1q18a1	Alignment	not modelled	97.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family: Glucokinase
106	d2ap1a2	Alignment	not modelled	97.2	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
107	d1z6ra2	Alignment	not modelled	97.1	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
108	d1g99a2	Alignment	not modelled	97.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
109	d2aa4a1	Alignment	not modelled	97.0	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
110	d2ap1a1	Alignment	not modelled	96.9	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
111	d2i7na1	Alignment	not modelled	96.9	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
112	c2h3gX_	Alignment	not modelled	96.9	17	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**biosynthetic protein; **PDBTitle:** structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
113	d2aa4a2	Alignment	not modelled	96.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
114	d2e1za2	Alignment	not modelled	96.8	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
115	d1z05a3	Alignment	not modelled	96.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
116	c1nbwA_	Alignment	not modelled	96.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
117	d1zbsa1	Alignment	not modelled	96.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
118	c3cerD_	Alignment	not modelled	96.6	19	**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
119	d1k8kb1	Alignment	not modelled	96.6	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
120	d1xc3a1	Alignment	not modelled	96.6	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK