Phyre2

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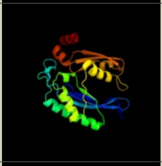
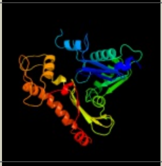
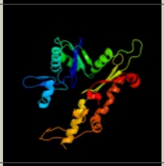
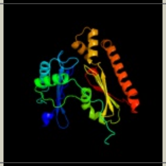
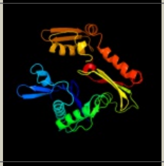
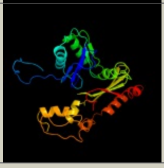
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h1qB_	Alignment		99.9	19	**PDB header:** structural protein **Chain:** B: **PDB Molecule:** ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
2	c2floA_	Alignment		99.9	14	**PDB header:** hydrolase **Chain:** A: **PDB Molecule:** exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
3	c3hi0B_	Alignment		99.9	16	**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
4	c1t6dB_	Alignment		99.9	18	**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
5	c3cerD_	Alignment		99.9	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
6	c3mdqA_	Alignment		99.9	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
7	c2d0oA_	Alignment		99.9	14	**PDB header:** chaperone **Chain:** A: **PDB Molecule:** diol dehydratase-reactivating factor large **PDBTitle:** strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
8	c1e4gT_	Alignment		99.9	14	**PDB header:** bacterial cell division **Chain:** T: **PDB Molecule:** cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
9	c1jcgA_	Alignment		99.8	17	**PDB header:** structural protein **Chain:** A: **PDB Molecule:** rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
10	c2v7yA_	Alignment		99.8	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
11	c3iucC_	Alignment		99.8	18	**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	c1dkgD_	Alignment		99.8	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
13	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
14	c2ychA_	Alignment		99.8	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
15	c2v7zA_	Alignment		99.7	20	**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
16	c2khoA_	Alignment		99.7	17	**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
17	c3dwlB_	Alignment		99.7	12	**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
18	c1hpmA_	Alignment		99.7	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
19	d1jcea2	Alignment		99.7	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
20	c1o1f4_	Alignment		99.7	11	**PDB header:**contractile protein **Chain:** 4: **PDB Molecule:**skeletal muscle actin; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
21	d1e4ft2	Alignment	not modelled	99.6	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
22	c2p9lA_	Alignment	not modelled	99.6	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin-like protein 3; **PDBTitle:** crystal structure of bovine arp2/3 complex
23	c2fsnB_	Alignment	not modelled	99.6	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**hypothetical protein ta0583; **PDBTitle:** crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
24	c1mwmA_	Alignment	not modelled	99.6	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
25	c3qb0C_	Alignment	not modelled	99.5	16	**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
26	d1u6za2	Alignment	not modelled	99.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
27	d1t6ca1	Alignment	not modelled	99.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
28	c3aapA_	Alignment	not modelled	99.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleoside triphosphate diphosphohydrolase i; **PDBTitle:** crystal structure of lp1ntpdase from legionella pneumophila
						PDB header:hydrolase

29	c3zx2A_	Alignment	not modelled	99.3	13	**Chain:** A: **PDB Molecule:**ectonucleoside triphosphate diphosphohydrolase 1; **PDBTitle:** ntpdase1 in complex with decavanadate
30	c3js6A_	Alignment	not modelled	99.2	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized parm protein; **PDBTitle:** crystal structure of apo psk41 parm protein
31	d2e8aa2	Alignment	not modelled	99.1	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
32	d1dkgd2	Alignment	not modelled	99.0	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
33	d1bupa2	Alignment	not modelled	98.9	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
34	c3cj9A_	Alignment	not modelled	98.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleoside triphosphate diphosphohydrolase 2; **PDBTitle:** structure of rattus norvegicus ntpdase2 in complex with2 calcium, amp and phosphate
35	d2zgya2	Alignment	not modelled	98.8	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
36	d2fsja1	Alignment	not modelled	98.8	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
37	d1huxa_	Alignment	not modelled	98.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
38	d1jcea1	Alignment	not modelled	98.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
39	d1u6za3	Alignment	not modelled	98.3	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
40	d1t6ca2	Alignment	not modelled	98.3	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
41	d2fxua2	Alignment	not modelled	98.2	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
42	d1k8kb1	Alignment	not modelled	98.2	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
43	d1nm1a2	Alignment	not modelled	98.1	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
44	c3cetA_	Alignment	not modelled	98.1	13	**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
45	d1k8ka2	Alignment	not modelled	98.0	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
46	c1nbwA_	Alignment	not modelled	98.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
47	d2hf3a2	Alignment	not modelled	97.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
48	c2p9kB_	Alignment	not modelled	97.9	20	**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
49	c3agrB_	Alignment	not modelled	97.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphate hydrolase; **PDBTitle:** crystal structure of nucleoside triphosphate hydrolases from neospora2 caninum
50	d1yaga2	Alignment	not modelled	97.8	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
51	c4a5bA_	Alignment	not modelled	97.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside-triphosphatase 2; **PDBTitle:** crystal structure of the c258s/c268s variant of toxoplasma gondii2 nucleoside triphosphate diphosphohydrolase 1 (ntpdase1)
52	d1e4ft1	Alignment	not modelled	97.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
53	d1bupa1	Alignment	not modelled	97.5	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
54	d2e8aa1	Alignment	not modelled	97.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
55	d2d0oa3	Alignment	not modelled	97.2	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family:ATPase domain of dehydratase reactivase alpha subunit
56	d1nbwa3	Alignment	not modelled	97.1	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
57	d2ewsa1	Alignment	not modelled	97.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
58	c1z6rC_	Alignment	not modelled	96.6	15	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
59	d1zc6a1	Alignment	not modelled	96.5	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
60	d1dkgd1	Alignment	not modelled	96.4	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
61	d1c0fa1	Alignment	not modelled	96.4	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
62	d2fxua1	Alignment	not modelled	96.3	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
63	d2ch5a2	Alignment	not modelled	95.7	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
64	c3vgkB_	Alignment	not modelled	95.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
65	d2p3ra1	Alignment	not modelled	95.3	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
66	d2d0oa2	Alignment	not modelled	95.1	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
67	c1woqB_	Alignment	not modelled	94.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inorganic polyphosphate/atp-glucomannokinase; **PDBTitle:** crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
68	c2ch5D_	Alignment	not modelled	94.8	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
69	c1z05A_	Alignment	not modelled	94.6	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.
70	c2cgkB_	Alignment	not modelled	94.5	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.
71	c3flcX_	Alignment	not modelled	94.4	18	**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
72	c3htvA_	Alignment	not modelled	94.4	17	**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
73	d1nbwa2	Alignment	not modelled	94.2	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
74	c3g25B_	Alignment	not modelled	94.1	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.
75	c2ap1A_	Alignment	not modelled	94.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
76	c2aa4B_	Alignment	not modelled	94.0	17	**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
77	d1yaga1	Alignment	not modelled	93.7	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
78	c2zf5O_	Alignment	not modelled	93.7	17	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
79	c3ezwD_	Alignment	not modelled	93.7	18	**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
80	c3i8bA_	Alignment	not modelled	93.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
						PDB header:transferase

81	c2d4wA_	Alignment	not modelled	93.4	14	**Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
82	c1glbG_	Alignment	not modelled	93.4	19	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
83	c3hz6A_	Alignment	not modelled	93.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
84	c2dpnB_	Alignment	not modelled	93.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
85	c3r8eA_	Alignment	not modelled	93.2	16	**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
86	c2w40C_	Alignment	not modelled	92.7	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
87	c3ifrB_	Alignment	not modelled	92.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
88	c1zc6A_	Alignment	not modelled	92.4	13	**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.
89	c3gg4B_	Alignment	not modelled	92.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
90	c2e2pA_	Alignment	not modelled	91.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
91	c2qm1D_	Alignment	not modelled	91.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
92	c3h6eB_	Alignment	not modelled	91.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
93	c3jvpA_	Alignment	not modelled	91.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
94	c3gbtA_	Alignment	not modelled	91.2	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
95	d2hf3a1	Alignment	not modelled	91.1	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
96	c1xupO_	Alignment	not modelled	89.4	19	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
97	c2hoeA_	Alignment	not modelled	89.2	12	**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
98	d1r59o1	Alignment	not modelled	88.4	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
99	d1z6ra2	Alignment	not modelled	88.2	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
100	c1zbsA_	Alignment	not modelled	87.8	12	**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
101	d1k8ka1	Alignment	not modelled	87.2	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
102	c3eo3B_	Alignment	not modelled	85.9	12	**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
103	c2iirJ_	Alignment	not modelled	85.0	23	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
104	c2nlxA_	Alignment	not modelled	84.5	39	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
105	d1woqa1	Alignment	not modelled	84.4	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
106	d1g99a2	Alignment	not modelled	83.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain

						Family: Acetokinase-like
107	c3khyA_	Alignment	not modelled	83.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
108	c3p4iA_	Alignment	not modelled	82.1	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium
109	d2hoea3	Alignment	not modelled	80.1	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
110	c3enoB_	Alignment	not modelled	79.9	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
111	d1saza1	Alignment	not modelled	79.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
112	d2e1za2	Alignment	not modelled	78.2	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
113	c2i7pA_	Alignment	not modelled	78.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
114	d1z05a3	Alignment	not modelled	77.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
115	c3djcA_	Alignment	not modelled	75.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type iii pantothenate kinase; **PDBTitle:** crystal structure of pantothenate kinase from legionella pneumophila
116	d2aa4a1	Alignment	not modelled	75.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
117	c1tuuA_	Alignment	not modelled	75.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase crystallized with atpgs
118	c2ivoC_	Alignment	not modelled	74.9	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
119	c3mixA_	Alignment		72.9	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** crystal structure of the cytosolic domain of b. subtilis flha
120	c2h3gX_	Alignment	not modelled	71.9	11	**PDB header:**biosynthetic protein **Chain:** X: **PDB Molecule:**biosynthetic protein; **PDBTitle:** structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis