Phyre2

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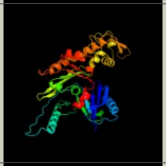
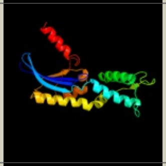
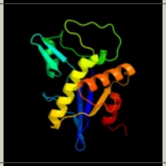
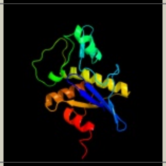
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d2fC_	Alignment		100.0	20	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
2	c2khoA_	Alignment		100.0	32	**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
3	c2v7yA_	Alignment		100.0	35	**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
4	c1dkgD_	Alignment		100.0	37	**PDB header:**complex (hsp24/hsp70) **Chain:** D: **PDB Molecule:**molecular chaperone dnak; **PDBTitle:** crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
5	c3iucC_	Alignment		100.0	39	**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
6	c1hpmA_	Alignment		100.0	38	**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
7	c2v7zA_	Alignment		100.0	38	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock cognate 71 kda protein; **PDBTitle:** crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
8	c1jcgA_	Alignment		100.0	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
9	c3h1qB_	Alignment		100.0	23	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
10	c1e4gT_	Alignment		100.0	13	**PDB header:**bacterial cell division **Chain:** T: **PDB Molecule:**cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
11	c1o1f4_	Alignment		100.0	13	**PDB header:**contractile protein **Chain:** 4: **PDB Molecule:**skeletal muscle actin; **PDBTitle:** molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle

12	d1dkgd2	Alignment		100.0	34	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
13	d1bupa2	Alignment		100.0	35	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
14	d2e8aa1	Alignment		100.0	42	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
15	d2e8aa2	Alignment		100.0	37	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
16	d1dkgd1	Alignment		100.0	42	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
17	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+
18	d1bupa1	Alignment		100.0	40	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
19	c3dwlB_	Alignment		100.0	15	**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	c2p9lA_	Alignment		100.0	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin-like protein 3; **PDBTitle:** crystal structure of bovine arp2/3 complex
21	c3dpqE_	Alignment	not modelled	100.0	22	**PDB header:**chaperone, peptide binding protein **Chain:** E: **PDB Molecule:**chaperone protein dnak; **PDBTitle:** crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrhocoricin-derived3 inhibitor peptide (form b)
22	c1u00A_	Alignment	not modelled	100.0	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hsca; **PDBTitle:** hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
23	c1mwmA_	Alignment	not modelled	100.0	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
24	d1jcea2	Alignment	not modelled	99.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
25	c2fsnB_	Alignment	not modelled	99.9	20	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**hypothetical protein ta0583; **PDBTitle:** crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
26	d1jcea1	Alignment	not modelled	99.9	33	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
27	c3qb0C_	Alignment	not modelled	99.9	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
28	c3js6A_	Alignment	not modelled	99.9	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized parm protein; **PDBTitle:** crystal structure of apo psk41 parm protein

29	c3n8eA_	Alignment	not modelled	99.9	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**stress-70 protein, mitochondrial; **PDBTitle:** substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
30	c2ychA_	Alignment	not modelled	99.8	21	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
31	c1bprA_	Alignment	not modelled	99.8	21	**PDB header:**molecular chaperone **Chain:** A: **PDB Molecule:**dnak; **PDBTitle:** nmr structure of the substrate binding domain of dnak,2 minimized average structure
32	d1e4ft2	Alignment	not modelled	99.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
33	d1yuwa1	Alignment	not modelled	99.8	27	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
34	c2op6A_	Alignment	not modelled	99.8	25	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**heat shock 70 kda protein d; **PDBTitle:** peptide-binding domain of heat shock 70 kda protein d precursor from2 c.elegans
35	d2zgya2	Alignment	not modelled	99.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
36	d1u00a2	Alignment	not modelled	99.7	27	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
37	d1dkza2	Alignment	not modelled	99.7	25	**Fold:**Heat shock protein 70kD (HSP70), peptide-binding domain **Superfamily:**Heat shock protein 70kD (HSP70), peptide-binding domain **Family:**Heat shock protein 70kD (HSP70), peptide-binding domain
38	c3dqgC_	Alignment	not modelled	99.7	25	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock 70 kda protein f; **PDBTitle:** peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.
39	d1huxa_	Alignment	not modelled	99.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
40	d2fsja1	Alignment	not modelled	99.5	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
41	d1nm1a2	Alignment	not modelled	99.3	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
42	d2hf3a2	Alignment	not modelled	99.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
43	d2fxua2	Alignment	not modelled	99.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
44	d1yaga2	Alignment	not modelled	99.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
45	d1k8ka2	Alignment	not modelled	99.1	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
46	c2p9kB_	Alignment	not modelled	99.0	18	**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
47	d1k8kb1	Alignment	not modelled	99.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
48	c2e2pA_	Alignment	not modelled	98.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
49	c3ifrB_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
50	d2fxua1	Alignment	not modelled	98.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
51	c3gg4B_	Alignment	not modelled	98.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
52	d1c0fa1	Alignment	not modelled	98.3	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
53	d2hf3a1	Alignment	not modelled	98.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
54	d2ewsa1	Alignment	not modelled	98.2	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
55	d1yaga1	Alignment	not modelled	98.2	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70

56	d1k8ka1	Alignment	not modelled	98.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
57	c3hz6A_	Alignment	not modelled	98.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
58	c2nlxA_	Alignment	not modelled	97.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
59	c1nbwA_	Alignment	not modelled	97.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
60	c3htvA_	Alignment	not modelled	97.7	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
61	d1r59o2	Alignment	not modelled	97.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
62	d2p3ra2	Alignment	not modelled	97.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
63	c2dpnB_	Alignment	not modelled	97.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
64	c3i8bA_	Alignment	not modelled	97.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
65	c3gbtA_	Alignment	not modelled	97.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
66	c2zf5O_	Alignment	not modelled	97.7	20	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
67	c3jvpA_	Alignment	not modelled	97.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
68	c2cgkB_	Alignment	not modelled	97.7	17	**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.
69	c2ch5D_	Alignment	not modelled	97.6	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
70	c1xupO_	Alignment	not modelled	97.6	18	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
71	c2ap1A_	Alignment	not modelled	97.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
72	c3flcX_	Alignment	not modelled	97.6	19	**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
73	c2qm1D_	Alignment	not modelled	97.6	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
74	c1glbG_	Alignment	not modelled	97.5	16	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
75	c3g25B_	Alignment	not modelled	97.5	20	**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.
76	c2d4wA_	Alignment	not modelled	97.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
77	c3ezwD_	Alignment	not modelled	97.4	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
78	c2floA_	Alignment	not modelled	97.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
79	c2ivoC_	Alignment	not modelled	97.3	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
80	c2w40C_	Alignment	not modelled	97.3	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
81	c3vgkB_	Alignment	not modelled	97.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus

82	d1nbwa3	Alignment	not modelled	97.2	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
83	d1dkza1	Alignment	not modelled	97.2	17	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
84	d1e4ft1	Alignment	not modelled	97.2	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
85	d1u00a1	Alignment	not modelled	97.1	16	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
86	d2d0oa3	Alignment	not modelled	96.9	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
87	c3mdqA_	Alignment	not modelled	96.9	14	**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
88	d1dkyb1	Alignment	not modelled	96.9	18	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
89	c1t6dB_	Alignment	not modelled	96.4	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
90	c1z05A_	Alignment	not modelled	96.3	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.
91	c1z6rC_	Alignment	not modelled	96.1	10	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
92	c2q2rA_	Alignment	not modelled	96.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
93	d2fsja2	Alignment	not modelled	96.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
94	c3hi0B_	Alignment	not modelled	95.6	22	**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
95	c3en9B_	Alignment	not modelled	95.5	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
96	c3lofF_	Alignment	not modelled	95.3	16	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**heat shock 70 kda protein 1; **PDBTitle:** c-terminal domain of human heat shock 70kda protein 1b.
97	c3cqyA_	Alignment	not modelled	95.1	19	**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
98	d1sz2a1	Alignment	not modelled	94.7	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
99	d1ud0a_	Alignment	not modelled	94.6	17	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Heat shock protein 70kD (HSP70), C-terminal subdomain **Family:**Heat shock protein 70kD (HSP70), C-terminal subdomain
100	c3tsuA_	Alignment	not modelled	94.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
101	c3enoB_	Alignment	not modelled	94.3	13	**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
102	c1ud0B_	Alignment	not modelled	94.1	16	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**70 kda heat-shock-like protein; **PDBTitle:** crystal structure of the c-terminal 10-kda subdomain of hsc70
103	c2p32B_	Alignment	not modelled	93.9	18	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock 70 kda protein a; **PDBTitle:** crystal structure of the c-terminal 10 kda subdomain from c. elegans2 hsp70
104	c3h6eB_	Alignment	not modelled	93.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
105	c3cerD_	Alignment	not modelled	93.7	16	**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
106	d2p3ra1	Alignment	not modelled	93.5	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
						PDB header:transferase

107	c2aa4B_	Alignment	not modelled	93.5	14	**Chain:** B: **PDB Molecule:**putative n-acetylmannosamine kinase; **PDBTitle:** crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
108	d2ap1a1	Alignment	not modelled	92.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
109	c1zc6A_	Alignment	not modelled	92.0	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.
110	d2i7na2	Alignment	not modelled	92.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
111	c2hoeA_	Alignment	not modelled	92.0	16	**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
112	c3cetA_	Alignment	not modelled	91.7	15	**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
113	d2i7pa1	Alignment	not modelled	91.5	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
114	d2aa4a2	Alignment	not modelled	91.5	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
115	c3eo3B_	Alignment	not modelled	91.4	16	**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
116	d1z05a2	Alignment	not modelled	91.0	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
117	d2ch5a2	Alignment	not modelled	90.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
118	d1r59o1	Alignment	not modelled	90.0	27	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
119	c3aapA_	Alignment	not modelled	89.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleoside triphosphate diphosphohydrolase i; **PDBTitle:** crystal structure of lp1ntpdase from legionella pneumophila
120	d1u6za3	Alignment	not modelled	89.1	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase