
































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2khoA_</a>	 Alignment		100.0	43	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 70; <b>PDBTitle:</b> nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
2	<a href="#">c3d2fC_</a>	 Alignment		100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein homolog sse1; <b>PDBTitle:</b> crystal structure of a complex of sse1p and hsp70
3	<a href="#">c2v7yA_</a>	 Alignment		100.0	48	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
4	<a href="#">c1dkgD_</a>	 Alignment		100.0	45	<b>PDB header:</b> complex (hsp24/hsp70) <b>Chain:</b> D: <b>PDB Molecule:</b> molecular chaperone dnak; <b>PDBTitle:</b> crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
5	<a href="#">c1hpmA_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase (acting on acid anhydrides) <b>Chain:</b> A: <b>PDB Molecule:</b> 44k atpase fragment (n-terminal) of 7o kd heat- <b>PDBTitle:</b> how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
6	<a href="#">c3iucC_</a>	 Alignment		100.0	40	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock 70kda protein 5 (glucose-regulated <b>PDBTitle:</b> crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
7	<a href="#">c2v7zA_</a>	 Alignment		100.0	39	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock cognate 71 kda protein; <b>PDBTitle:</b> crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
8	<a href="#">c1jcgA_</a>	 Alignment		100.0	24	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> rod shape-determining protein mreB; <b>PDBTitle:</b> mreB from thermotoga maritima, amppnp
9	<a href="#">c3h1qB_</a>	 Alignment		100.0	25	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> ethanolamine utilization protein eutJ; <b>PDBTitle:</b> crystal structure of ethanolamine utilization protein eutJ from2 carboxydotherrus hydrogenoformans
10	<a href="#">c1u00A_</a>	 Alignment		100.0	100	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein hsca; <b>PDBTitle:</b> hsca substrate binding domain complexed with the iscu2 recognition peptide elppkvhc
11	<a href="#">c1e4gT_</a>	 Alignment		100.0	15	<b>PDB header:</b> bacterial cell division <b>Chain:</b> T: <b>PDB Molecule:</b> cell division protein ftsa; <b>PDBTitle:</b> ftsa (atp-bound form) from thermotoga maritima

12	<a href="#">d2e8aa1</a>	Alignment		100.0	41	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
13	<a href="#">d1dkgd2</a>	Alignment		100.0	46	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
14	<a href="#">d1dkgd1</a>	Alignment		100.0	44	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
15	<a href="#">d1bupa2</a>	Alignment		100.0	39	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
16	<a href="#">d1bupa1</a>	Alignment		100.0	39	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
17	<a href="#">c2d0oA_</a>	Alignment		100.0	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> diol dehydratase-reactivating factor large <b>PDBTitle:</b> strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
18	<a href="#">c1o1f4_</a>	Alignment		100.0	17	<b>PDB header:</b> contractile protein <b>Chain:</b> 4: <b>PDB Molecule:</b> skeletal muscle actin; <b>PDBTitle:</b> molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
19	<a href="#">d2e8aa2</a>	Alignment		100.0	41	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
20	<a href="#">c3dpgE_</a>	Alignment		100.0	40	<b>PDB header:</b> chaperone, peptide binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrococricin-derived3 inhibitor peptide (form b)
21	<a href="#">c3n8eA_</a>	Alignment	not modelled	99.9	43	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> stress-70 protein, mitochondrial; <b>PDBTitle:</b> substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
22	<a href="#">c1mwmA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> parM; <b>PDBTitle:</b> parM from plasmid r1 adp form
23	<a href="#">c3dwlB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin-related protein 3; <b>PDBTitle:</b> crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
24	<a href="#">c2p9lA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> actin-like protein 3; <b>PDBTitle:</b> crystal structure of bovine arp2/3 complex
25	<a href="#">c2fsnB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ta0583; <b>PDBTitle:</b> crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
26	<a href="#">d1jcea2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
27	<a href="#">c1bprA_</a>	Alignment	not modelled	99.9	42	<b>PDB header:</b> molecular chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> dnak; <b>PDBTitle:</b> nmr structure of the substrate binding domain of dnak,2 minimized average structure
28	<a href="#">d1jcea1</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
						<b>PDB header:</b> peptide binding protein

29	<a href="#">c2op6A</a>	Alignment	not modelled	99.9	39	<b>Chain:</b> A: <b>PDB Molecule:</b> heat shock 70 kda protein d; <b>PDBTitle:</b> peptide-binding domain of heat shock 70 kda protein d precursor from <i>C. elegans</i>
30	<a href="#">d1yuwa1</a>	Alignment	not modelled	99.9	42	<b>Fold:</b> Heat shock protein 70kD (HSP70), peptide-binding domain <b>Superfamily:</b> Heat shock protein 70kD (HSP70), peptide-binding domain <b>Family:</b> Heat shock protein 70kD (HSP70), peptide-binding domain
31	<a href="#">c2ychA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> competence protein pilM; <b>PDBTitle:</b> pilM-pilN type IV pilus biogenesis complex
32	<a href="#">c3js6A</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized <i>parM</i> protein; <b>PDBTitle:</b> crystal structure of apo <i>psk41</i> <i>parM</i> protein
33	<a href="#">d1e4ft2</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
34	<a href="#">c3qb0C</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> actin-related protein 4; <b>PDBTitle:</b> crystal structure of actin-related protein arp4 from <i>S. cerevisiae</i> 2 complexed with <i>atp</i>
35	<a href="#">d1u00a2</a>	Alignment	not modelled	99.7	99	<b>Fold:</b> Heat shock protein 70kD (HSP70), peptide-binding domain <b>Superfamily:</b> Heat shock protein 70kD (HSP70), peptide-binding domain <b>Family:</b> Heat shock protein 70kD (HSP70), peptide-binding domain
36	<a href="#">c3dggC</a>	Alignment	not modelled	99.7	46	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock 70 kda protein f; <b>PDBTitle:</b> peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from <i>Caenorhabditis elegans</i> .
37	<a href="#">d1dkza2</a>	Alignment	not modelled	99.7	53	<b>Fold:</b> Heat shock protein 70kD (HSP70), peptide-binding domain <b>Superfamily:</b> Heat shock protein 70kD (HSP70), peptide-binding domain <b>Family:</b> Heat shock protein 70kD (HSP70), peptide-binding domain
38	<a href="#">d2zgya2</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
39	<a href="#">d1u00a1</a>	Alignment	not modelled	99.6	100	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain <b>Family:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain
40	<a href="#">d1huxa</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
41	<a href="#">d2fsja1</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ta0583-like
42	<a href="#">d1nmla2</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
43	<a href="#">d1dkza1</a>	Alignment	not modelled	99.2	24	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain <b>Family:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain
44	<a href="#">d2hf3a2</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
45	<a href="#">d2fxua2</a>	Alignment	not modelled	99.1	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
46	<a href="#">d1dkyb1</a>	Alignment	not modelled	98.9	26	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain <b>Family:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain
47	<a href="#">d1yaga2</a>	Alignment	not modelled	98.8	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
48	<a href="#">c2e2pA</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase; <b>PDBTitle:</b> crystal structure of <i>Sulfolobus tokodaii</i> hexokinase in2 complex with <i>adp</i>
49	<a href="#">d1k8kb1</a>	Alignment	not modelled	98.7	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
50	<a href="#">c2p9kB</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin-like protein 2; <b>PDBTitle:</b> crystal structure of bovine arp2/3 complex co-crystallized2 with <i>atp</i> and crosslinked with glutaraldehyde
51	<a href="#">d1k8ka2</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
52	<a href="#">c3hz6A</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from <i>Chromobacterium violaceum</i>
53	<a href="#">c2p32B</a>	Alignment	not modelled	98.4	10	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock 70 kda protein a; <b>PDBTitle:</b> crystal structure of the c-terminal 10 kda subdomain from <i>C. elegans</i> 2 hsp70
54	<a href="#">c3loff</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> heat shock 70 kda protein 1; <b>PDBTitle:</b> c-terminal domain of human heat shock 70kda protein 1b.
55	<a href="#">c3gg4B</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> the crystal structure of glycerol kinase from <i>Yersinia</i> 2 pseudotuberculosis

56	<a href="#">d1ud0a_</a>	Alignment	not modelled	98.3	10	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain <b>Family:</b> Heat shock protein 70kD (HSP70), C-terminal subdomain
57	<a href="#">c1ud0B_</a>	Alignment	not modelled	98.0	10	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> 70 kda heat-shock-like protein; <b>PDBTitle:</b> crystal structure of the c-terminal 10-kda subdomain of hsc70
58	<a href="#">c2nlxA_</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> crystal structure of the apo e. coli xylulose kinase
59	<a href="#">c2qm1D_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase from enterococcus faecalis
60	<a href="#">d1e4ft1_</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
61	<a href="#">c1nbwA_</a>	Alignment	not modelled	97.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydratase reactivase alpha subunit; <b>PDBTitle:</b> glycerol dehydratase reactivase
62	<a href="#">d2p3ra2_</a>	Alignment	not modelled	97.8	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
63	<a href="#">c3ifrB_</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase, fggy; <b>PDBTitle:</b> the crystal structure of xylulose kinase from rhodospirillum rubrum
64	<a href="#">d1r59o2_</a>	Alignment	not modelled	97.7	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
65	<a href="#">d2hf3a1_</a>	Alignment	not modelled	97.7	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
66	<a href="#">c3gbtA_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gluconate kinase; <b>PDBTitle:</b> crystal structure of gluconate kinase from lactobacillus acidophilus
67	<a href="#">d2fxua1_</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
68	<a href="#">c2dnpB_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of the glycerol kinase from thermus2 thermophilus hb8
69	<a href="#">d1c0fa1_</a>	Alignment	not modelled	97.6	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
70	<a href="#">c3flcX_</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
71	<a href="#">c2cgkB_</a>	Alignment	not modelled	97.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l-rhamnulose kinase; <b>PDBTitle:</b> crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
72	<a href="#">c3jvpA_</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulokinase; <b>PDBTitle:</b> crystal structure of ribulokinase from bacillus halodurans
73	<a href="#">c2d4wA_</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
74	<a href="#">c3g25B_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
75	<a href="#">c1glbG_</a>	Alignment	not modelled	97.5	13	<b>PDB header:</b> phosphotransferase <b>Chain:</b> G: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
76	<a href="#">c2zf5O_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transferase <b>Chain:</b> O: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
77	<a href="#">d2ewsA1_</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
78	<a href="#">c3i8bA_</a>	Alignment	not modelled	97.5	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
79	<a href="#">c3ezwD_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
80	<a href="#">c1xupO_</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> transferase <b>Chain:</b> O: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> enterococcus casseliflavus glycerol kinase complexed with glycerol
81	<a href="#">c2w40C_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerol kinase, putative; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol

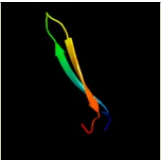
82	<a href="#">dlyaga1</a>	Alignment	not modelled	97.4	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
83	<a href="#">c3htvA</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-allose kinase; <b>PDBTitle:</b> crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
84	<a href="#">c2floA</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
85	<a href="#">c2ivoC</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> up1; <b>PDBTitle:</b> structure of up1 protein
86	<a href="#">c1z6rC</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mlc protein; <b>PDBTitle:</b> crystal structure of mlc from escherichia coli
87	<a href="#">d1nbwa3</a>	Alignment	not modelled	97.2	27	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ATPase domain of dehydratase reactivase alpha subunit
88	<a href="#">d2d0oa3</a>	Alignment	not modelled	97.1	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ATPase domain of dehydratase reactivase alpha subunit
89	<a href="#">c1t6dB</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
90	<a href="#">c1z05A</a>	Alignment	not modelled	97.0	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rok family; <b>PDBTitle:</b> crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
91	<a href="#">d1k8ka1</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
92	<a href="#">c3cerD</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> possible exopolyphosphatase-like protein; <b>PDBTitle:</b> crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
93	<a href="#">c2ch5D</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nagk protein; <b>PDBTitle:</b> crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
94	<a href="#">c3hi0B</a>	Alignment	not modelled	96.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative exopolyphosphatase; <b>PDBTitle:</b> crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
95	<a href="#">c3mdqA</a>	Alignment	not modelled	96.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
96	<a href="#">c2ap1A</a>	Alignment	not modelled	96.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative regulator protein; <b>PDBTitle:</b> crystal structure of the putative regulatory protein
97	<a href="#">c3cetA</a>	Alignment	not modelled	96.3	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved archaeal protein; <b>PDBTitle:</b> crystal structure of the pantheonate kinase-like protein2 q6m145 at the resolution 1.8 a. northeast structural3 genomics consortium target mrr63
98	<a href="#">c1zc6A</a>	Alignment	not modelled	96.3	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable n-acetylglucosamine kinase; <b>PDBTitle:</b> crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
99	<a href="#">c3vgkB</a>	Alignment	not modelled	96.2	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of a rok family glucokinase from streptomyces2 griseus
100	<a href="#">c3r8eA</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical sugar kinase; <b>PDBTitle:</b> crystal structure of a hypothetical sugar kinase (chu_1875) from2 cytophaga hutchinsonii atcc 33406 at 1.65 a resolution
101	<a href="#">c2hoeA</a>	Alignment	not modelled	95.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine kinase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
102	<a href="#">d1sz2a1</a>	Alignment	not modelled	95.5	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
103	<a href="#">c1woqB</a>	Alignment	not modelled	95.4	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> inorganic polyphosphate/atp-glucomannokinase; <b>PDBTitle:</b> crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
104	<a href="#">c2q2rA</a>	Alignment	not modelled	94.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase 1, putative; <b>PDBTitle:</b> trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
105	<a href="#">d2p3ra1</a>	Alignment	not modelled	94.6	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
106	<a href="#">d1t6ca2</a>	Alignment	not modelled	94.5	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase



107	<a href="#">c3enoB_</a>	Alignment	not modelled	94.3	20	<b>PDB header:</b> hydrolase/unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-sialoglycoprotein endopeptidase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
108	<a href="#">c3h6eB_</a>	Alignment	not modelled	94.2	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase, fggy; <b>PDBTitle:</b> the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
109	<a href="#">c1xc3A_</a>	Alignment	not modelled	93.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fructokinase; <b>PDBTitle:</b> structure of a putative fructokinase from bacillus subtilis
110	<a href="#">c2gupA_</a>	Alignment	not modelled	93.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rok family protein; <b>PDBTitle:</b> structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
111	<a href="#">c3cqyA_</a>	Alignment	not modelled	93.8	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anhydro-n-acetylmuramic acid kinase; <b>PDBTitle:</b> crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
112	<a href="#">dlu6za3</a>	Alignment	not modelled	93.5	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase
113	<a href="#">c3en9B_</a>	Alignment	not modelled	92.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> o-sialoglycoprotein endopeptidase/protein kinase; <b>PDBTitle:</b> structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
114	<a href="#">c3eo3B_</a>	Alignment	not modelled	92.4	18	<b>PDB header:</b> isomerase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional udp-n-acetylglucosamine 2-epimerase/n- <b>PDBTitle:</b> crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
115	<a href="#">c3tsuA_</a>	Alignment	not modelled	92.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
116	<a href="#">c3hm8D_</a>	Alignment	not modelled	91.9	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hexokinase-3; <b>PDBTitle:</b> crystal structure of the c-terminal hexokinase domain of human hk3
117	<a href="#">c3aapA_</a>	Alignment	not modelled	91.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleoside triphosphate diphosphohydrolase i; <b>PDBTitle:</b> crystal structure of lp1ntpdase from legionella pneumophila
118	<a href="#">d2ap1a1</a>	Alignment	not modelled	91.6	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
119	<a href="#">dlczan1</a>	Alignment	not modelled	91.1	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase

120 [dlzc6a1](#)

Alignment



90.5

24

**Fold:**Ribonuclease H-like motif  
**Superfamily:**Actin-like ATPase domain  
**Family:**BadF/BadG/BcrA/BcrD-like