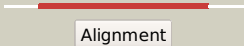

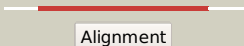

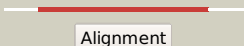







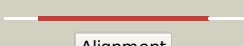











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3419c_gcp_3837735_3838769
Date	Fri Aug 9 18:20:09 BST 2019
Unique Job ID	4406d3a0783c2ef2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3zeuE_</a>	 Alignment		100.0	44	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> probable trna threonylcarbamoyladenine biosynthesis <b>PDBTitle:</b> structure of a salmonella typhimurium ygd-yeaz heterodimer bound to2 atpgammas
2	<a href="#">c3en9B_</a>	 Alignment		100.0	30	<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
3	<a href="#">c6gwk_</a>	 Alignment		100.0	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> K; <b>PDB Molecule:</b> probable trna n6-adenosine threonylcarbamoyltransferase; <b>PDBTitle:</b> protein complex
4	<a href="#">c4k25A_</a>	 Alignment		100.0	29	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> probable trna threonylcarbamoyladenine biosynthesis <b>PDBTitle:</b> crystal structure of yeast qri7 homodimer
5	<a href="#">c2ivoC_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> up1; <b>PDBTitle:</b> structure of up1 protein
6	<a href="#">c3enoB_</a>	 Alignment		100.0	32	<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
7	<a href="#">c6fpeG_</a>	 Alignment		100.0	46	<b>PDB header:</b> rna binding protein <b>Chain:</b> G; <b>PDB Molecule:</b> trna n6-adenosine threonylcarbamoyltransferase; <b>PDBTitle:</b> bacterial protein complex
8	<a href="#">c3vewA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> o-carbamoyltransferase tobz; <b>PDBTitle:</b> crystal structure of the o-carbamoyltransferase tobz in complex with2 adp
9	<a href="#">c3vthB_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
10	<a href="#">c3vthA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
11	<a href="#">c3tsuA_</a>	 Alignment		100.0	27	<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

12	<a href="#">c4g9iA_</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation protein hypf; <b>PDBTitle:</b> crystal structure of t.kodakarensis hypf
13	<a href="#">c5br9C_</a>	Alignment		99.8	23	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein with similarity to2 peptidase yeaz from pseudomonas aeruginosa
14	<a href="#">c3r6mD_</a>	Alignment		99.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> yeaz, resuscitation promoting factor; <b>PDBTitle:</b> crystal structure of vibrio parahaemolyticus yeaz
15	<a href="#">c1okjB_</a>	Alignment		99.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trna threonylcarbamoyladenosine biosynthesis protein tsab; <b>PDBTitle:</b> crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
16	<a href="#">d1huxa_</a>	Alignment		99.7	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
17	<a href="#">c2a6aB_</a>	Alignment		99.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein tm0874; <b>PDBTitle:</b> crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution
18	<a href="#">d1okja1</a>	Alignment		99.7	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> YeaZ-like
19	<a href="#">c6n9aB_</a>	Alignment		99.7	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna threonylcarbamoyladenosine biosynthesis protein tsab; <b>PDBTitle:</b> crystal structure of thermotoga maritima threonylcarbamoyladenosine2 biosynthesis complex tsab2d2e2 bound to atp and carboxy-amp
20	<a href="#">d2a6aa1</a>	Alignment		99.6	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> YeaZ-like
21	<a href="#">c4ehtA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> activator of 2-hydroxyisocaproyl-coa dehydratase; <b>PDBTitle:</b> activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
22	<a href="#">d2ewsal</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
23	<a href="#">c2i7pA_</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase 3; <b>PDBTitle:</b> crystal structure of human pank3 in complex with accoa
24	<a href="#">c2e2pA_</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase; <b>PDBTitle:</b> crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
25	<a href="#">c3smpA_</a>	Alignment	not modelled	98.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase 1; <b>PDBTitle:</b> monoclinic crystal structure of human pantothenate kinase 1 alpha
26	<a href="#">d2i7pa1</a>	Alignment	not modelled	98.1	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
27	<a href="#">d2i7na2</a>	Alignment	not modelled	98.1	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
28	<a href="#">c3h1qB_</a>	Alignment	not modelled	98.0	14	<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 carboxydotherrmus hydrogenoformans

29	<a href="#">c3gbtA</a>	Alignment	not modelled	98.0	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
30	<a href="#">c3vovC</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of rok hexokinase from thermus thermophilus
31	<a href="#">d2p3ra2</a>	Alignment	not modelled	97.6	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
32	<a href="#">c3ifrB</a>	Alignment	not modelled	97.5	20	<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
33	<a href="#">c2aa4B</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine kinase; <b>PDBTitle:</b> crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
34	<a href="#">c4db3A</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-d-glucosamine kinase; <b>PDBTitle:</b> 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
35	<a href="#">c3hz6A</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from chromobacterium violaceum
36	<a href="#">c4yh5B</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> levoglucosan kinase; <b>PDBTitle:</b> lipomyces starkeyi levoglucosan kinase bound to adp and manganese
37	<a href="#">c1zc6A</a>	Alignment	not modelled	97.4	17	<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.
38	<a href="#">c2cgkB</a>	Alignment	not modelled	97.4	20	<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 escherichia coli in an2 open uncomplexed conformation.
39	<a href="#">c3g25B</a>	Alignment	not modelled	97.4	13	<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.
40	<a href="#">c2qm1D</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase from enterococcus faecalis
41	<a href="#">c2zf5O</a>	Alignment	not modelled	97.3	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
42	<a href="#">c2v7yA</a>	Alignment	not modelled	97.3	16	<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
43	<a href="#">c2dpnB</a>	Alignment	not modelled	97.3	22	<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
44	<a href="#">c1glbG</a>	Alignment	not modelled	97.3	17	<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
45	<a href="#">c5nckA</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmannosamine kinase; <b>PDBTitle:</b> the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
46	<a href="#">c3wxib</a>	Alignment	not modelled	97.2	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
47	<a href="#">c2nlxA</a>	Alignment	not modelled	97.1	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
48	<a href="#">c4e1jA</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
49	<a href="#">c2d4wA</a>	Alignment	not modelled	97.1	20	<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
50	<a href="#">c3i8bA</a>	Alignment	not modelled	97.1	18	<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
51	<a href="#">c5ya2A</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> autoinducer-2 kinase; <b>PDBTitle:</b> crystal structure of lsrk-hpr complex with adp
52	<a href="#">d1r59o2</a>	Alignment	not modelled	97.0	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
53	<a href="#">c3flcX</a>	Alignment	not modelled	97.0	17	<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
54	<a href="#">c3cqvA</a>	Alignment	not modelled	96.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anhydro-n-acetylmuramic acid kinase;

54	<a href="#">c3c4yA</a>	Alignment	not modelled	96.9	10	<b>PDBTitle:</b> crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1 <b>PDB header:</b> transferase
55	<a href="#">c5hv7A</a>	Alignment	not modelled	96.9	22	<b>Chain:</b> A: <b>PDB Molecule:</b> probable sugar kinase; <b>PDBTitle:</b> putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribose
56	<a href="#">c2ap1A</a>	Alignment	not modelled	96.8	18	<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
57	<a href="#">c2w40C</a>	Alignment	not modelled	96.7	13	<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
58	<a href="#">c3eo3B</a>	Alignment	not modelled	96.7	15	<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
59	<a href="#">c5htxA</a>	Alignment	not modelled	96.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative xylulose kinase; <b>PDBTitle:</b> putative sugar kinases from arabidopsis thaliana in complex with adp
60	<a href="#">c1xupO</a>	Alignment	not modelled	96.6	16	<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
61	<a href="#">c5vm1A</a>	Alignment	not modelled	96.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of a xylolose kinase from brucella ovis
62	<a href="#">c4bgaB</a>	Alignment	not modelled	96.5	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted molecular chaperone distantly related to <b>PDBTitle:</b> nucleotide-bound open form of a putative sugar kinase2 mk0840 from methanopyrus kandleri
63	<a href="#">c3ezwD</a>	Alignment	not modelled	96.2	19	<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
64	<a href="#">c2ch5D</a>	Alignment	not modelled	96.0	14	<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
65	<a href="#">c2hoeA</a>	Alignment	not modelled	96.0	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
66	<a href="#">c3jvpA</a>	Alignment	not modelled	95.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulokinase; <b>PDBTitle:</b> crystal structure of ribulokinase from bacillus halodurans
67	<a href="#">c5f7rA</a>	Alignment	not modelled	95.8	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0178 protein; <b>PDBTitle:</b> rok repressor lmo0178 from listeria monocytogenes bound to inducer
68	<a href="#">c4bc2A</a>	Alignment	not modelled	95.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> crystal structure of human d-xylulokinase in complex with d-2 xylulose and adenosine diphosphate
69	<a href="#">c4c23A</a>	Alignment	not modelled	95.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose kinase fuck; <b>PDBTitle:</b> l-fucose kinase
70	<a href="#">c4ht1A</a>	Alignment	not modelled	95.4	6	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-glucoside kinase; <b>PDBTitle:</b> lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
71	<a href="#">c3gg4B</a>	Alignment	not modelled	95.1	17	<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 yersinia2 pseudotuberculosis
72	<a href="#">d2e8aa2</a>	Alignment	not modelled	95.1	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
73	<a href="#">c1z05A</a>	Alignment	not modelled	95.0	19	<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.
74	<a href="#">d2gupa2</a>	Alignment	not modelled	94.7	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
75	<a href="#">c5obuA</a>	Alignment	not modelled	94.7	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.
76	<a href="#">c1hpmA</a>	Alignment	not modelled	94.5	9	<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
77	<a href="#">c1mwmA</a>	Alignment	not modelled	94.4	10	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> parm; <b>PDBTitle:</b> parm from plasmid r1 adp form
78	<a href="#">c2v7zA</a>	Alignment	not modelled	94.2	10	<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
79	<a href="#">d1bupa2</a>	Alignment	not modelled	94.2	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain

				Family:Actin/HSP70		
80	<a href="#">c4czeA_</a>	Alignment	not modelled	94.1	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> rod shape-determining protein mreB; <b>PDBTitle:</b> c. crescentus mreB, double filament, empty
81	<a href="#">c3iucC_</a>	Alignment	not modelled	94.0	10	<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
82	<a href="#">d2ch5a1</a>	Alignment	not modelled	93.8	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
83	<a href="#">c5e84B_</a>	Alignment	not modelled	93.6	15	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> 78 kda glucose-regulated protein; <b>PDBTitle:</b> atp-bound state of bip
84	<a href="#">d1jcea2</a>	Alignment	not modelled	93.6	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
85	<a href="#">d1dkgd2</a>	Alignment	not modelled	93.6	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
86	<a href="#">c2gupA_</a>	Alignment	not modelled	93.4	13	<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
87	<a href="#">c3vgkB_</a>	Alignment	not modelled	92.5	12	<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
88	<a href="#">c1z6rC_</a>	Alignment	not modelled	92.4	16	<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
89	<a href="#">c6gfaA_</a>	Alignment	not modelled	92.0	12	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 105 kda; <b>PDBTitle:</b> structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed
90	<a href="#">d2ap1a1</a>	Alignment	not modelled	91.5	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
91	<a href="#">d1zc6a1</a>	Alignment	not modelled	91.3	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
92	<a href="#">c3r8eA_</a>	Alignment	not modelled	91.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical sugar kinase; <b>PDBTitle:</b> crystal structure of a putative sugar kinase (chu_1875) from cytophaga2 hutchinsonii atcc 33406 at 1.65 a resolution
93	<a href="#">c3qbwA_</a>	Alignment	not modelled	90.3	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anhydro-n-acetylmuramic acid kinase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 acetilmuramic acid kinase (anmk) bound to adenosine diphosphate
94	<a href="#">c5tkyA_</a>	Alignment	not modelled	90.3	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation
95	<a href="#">c4rtfD_</a>	Alignment	not modelled	89.0	17	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> chaperone protein dnaK; <b>PDBTitle:</b> crystal structure of molecular chaperone dnaK from mycobacterium2 tuberculosis h37rv
96	<a href="#">c2khoA_</a>	Alignment	not modelled	88.9	17	<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) chaperone (1-605)2 complexed with adp and substrate
97	<a href="#">c3c7nB_</a>	Alignment	not modelled	88.7	12	<b>PDB header:</b> chaperone/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock cognate; <b>PDBTitle:</b> structure of the hsp110:hsc70 nucleotide exchange complex
98	<a href="#">d2hoea2</a>	Alignment	not modelled	88.3	9	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
99	<a href="#">c1jcgA_</a>	Alignment	not modelled	88.2	15	<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
100	<a href="#">d2aa4a2</a>	Alignment	not modelled	87.9	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
101	<a href="#">d2zgya2</a>	Alignment	not modelled	87.0	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
102	<a href="#">c1xc3A_</a>	Alignment	not modelled	86.9	18	<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
103	<a href="#">d1xc3a2</a>	Alignment	not modelled	86.5	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
104	<a href="#">c4apwH_</a>	Alignment	not modelled	86.0	12	<b>PDB header:</b> structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> alp12; <b>PDBTitle:</b> alp12 filament structure
105	<a href="#">c4kboA_</a>	Alignment	not modelled	85.7	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> stress-70 protein, mitochondrial; <b>PDBTitle:</b> crystal structure of the human mortalin (grp75) atpase

						domain in the2 apo form
106	<a href="#">c4gniA_</a>	Alignment	not modelled	85.7	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> structure of the ssz1 atpase bound to atp and magnesium
107	<a href="#">c5jygA_</a>	Alignment	not modelled	85.6	14	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> actin-like atpase; <b>PDBTitle:</b> cryo-em structure of the mamk filament at 6.5 a
108	<a href="#">d1gnla_</a>	Alignment	not modelled	85.4	12	<b>Fold:</b> Prismane protein-like <b>Superfamily:</b> Prismane protein-like <b>Family:</b> Hybrid cluster protein (prismane protein)
109	<a href="#">c3wqtB_</a>	Alignment	not modelled	85.1	16	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsa; <b>PDBTitle:</b> staphylococcus aureus ftsa complexed with amppnp
110	<a href="#">c1dkgD_</a>	Alignment	not modelled	84.1	10	<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
111	<a href="#">d1gnla_</a>	Alignment	not modelled	84.1	14	<b>Fold:</b> Prismane protein-like <b>Superfamily:</b> Prismane protein-like <b>Family:</b> Hybrid cluster protein (prismane protein)
112	<a href="#">c6b6xA_</a>	Alignment	not modelled	83.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide dehydrogenase; <b>PDBTitle:</b> crystal structure of desulfovibrio vulgaris carbon monoxide2 dehydrogenase, dithionite-reduced (protein batch 2), canonical c-3 cluster
113	<a href="#">c3htvA_</a>	Alignment	not modelled	83.0	14	<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
114	<a href="#">c4h0oB_</a>	Alignment	not modelled	82.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of acetate kinase from entamoeba histolytica
115	<a href="#">d2p3ra1</a>	Alignment	not modelled	81.1	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
116	<a href="#">d1woqa2</a>	Alignment	not modelled	80.5	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
117	<a href="#">d1saza2</a>	Alignment	not modelled	80.2	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
118	<a href="#">c5f7pA_</a>	Alignment	not modelled	80.2	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0178 protein; <b>PDBTitle:</b> rok repressor lmo0178 from listeria monocytogenes
119	<a href="#">c3js6A_</a>	Alignment	not modelled	79.8	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized parm protein; <b>PDBTitle:</b> crystal structure of apo psk41 parm protein
120	<a href="#">c4ijaA_</a>	Alignment	not modelled	79.5	8	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> xylr protein; <b>PDBTitle:</b> structure of s. aureus methicillin resistance factor mecR2