





















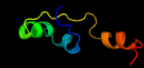

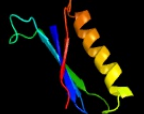


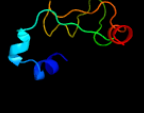





# Phyre2

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Description	RVBD0538 (-) _630043_631689
Date	Fri Jul 26 01:50:09 BST 2019
Unique Job ID	8289ce0578b5cd85

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3h1qB_</a>	 Alignment		96.3	16	<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 from <i>2 carboxydotherrnus hydrogenoformans</i>
2	<a href="#">c4czeA_</a>	 Alignment		93.4	21	<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
3	<a href="#">d1dkgd2</a>	 Alignment		90.5	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
4	<a href="#">c3htvA_</a>	 Alignment		89.6	22	<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 <i>escherichia2 coli k12</i> at 1.95 a resolution
5	<a href="#">d2e8aa2</a>	 Alignment		89.5	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
6	<a href="#">c1dkgD_</a>	 Alignment		88.3	21	<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
7	<a href="#">c4kboA_</a>	 Alignment		87.9	22	<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 the apo form
8	<a href="#">d1bupa2</a>	 Alignment		87.9	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
9	<a href="#">c2e2pA_</a>	 Alignment		87.2	14	<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 adp
10	<a href="#">c5hv7A_</a>	 Alignment		85.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable sugar kinase; <b>PDBTitle:</b> putative sugar kinases from <i>synechococcus elongatus</i> pcc7942 in complex2 with d-ribulose
11	<a href="#">c2ap1A_</a>	 Alignment		84.1	12	<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

12	<a href="#">d1jcea2</a>	Alignment		83.9	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
13	<a href="#">c1jcgA_</a>	Alignment		82.6	19	<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
14	<a href="#">d2hoea3</a>	Alignment		81.7	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
15	<a href="#">c1hpmA_</a>	Alignment		81.2	23	<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
16	<a href="#">d2zgya2</a>	Alignment		76.4	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
17	<a href="#">c6izrK_</a>	Alignment		76.1	22	<b>PDB header:</b> protein fibril <b>Chain:</b> K: <b>PDB Molecule:</b> putative plasmid segregation protein parm; <b>PDBTitle:</b> whole structure of a 15-stranded parm filament from clostridium2 botulinum
18	<a href="#">c2khoA_</a>	Alignment		76.0	21	<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
19	<a href="#">d2ap1a2</a>	Alignment		75.0	7	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
20	<a href="#">c3wqtB_</a>	Alignment		74.3	19	<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
21	<a href="#">c4rtfD_</a>	Alignment	not modelled	72.5	22	<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
22	<a href="#">c6gfaA_</a>	Alignment	not modelled	71.9	16	<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
23	<a href="#">c5jygA_</a>	Alignment	not modelled	71.8	26	<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
24	<a href="#">c3d2fC_</a>	Alignment	not modelled	71.0	21	<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
25	<a href="#">c2v7zA_</a>	Alignment	not modelled	70.6	22	<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
26	<a href="#">c2v7yA_</a>	Alignment	not modelled	67.8	22	<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
27	<a href="#">c2w40C_</a>	Alignment	not modelled	67.0	11	<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
28	<a href="#">c4htIA_</a>	Alignment	not modelled	65.6	10	<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 <b>PDB header:</b> chaperone/chaperone

29	<a href="#">c3c7nB_</a>	Alignment	not modelled	64.6	23	<b>Chain:</b> B: <b>PDB Molecule:</b> heat shock cognate; <b>PDBTitle:</b> structure of the hsp110:hsc70 nucleotide exchange complex
30	<a href="#">d1z6ra2</a>	Alignment	not modelled	64.6	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
31	<a href="#">c4ijaA_</a>	Alignment	not modelled	62.9	11	<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 mecrc2
32	<a href="#">c5vm1A_</a>	Alignment	not modelled	61.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of a xylolylose kinase from brucella ovis
33	<a href="#">c5e84B_</a>	Alignment	not modelled	60.5	21	<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
34	<a href="#">c3gbtA_</a>	Alignment	not modelled	60.3	15	<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
35	<a href="#">c4db3A_</a>	Alignment	not modelled	58.1	16	<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.
36	<a href="#">c1e4gT_</a>	Alignment	not modelled	57.4	20	<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
37	<a href="#">c3eo3B_</a>	Alignment	not modelled	57.1	22	<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
38	<a href="#">c2d0oA_</a>	Alignment	not modelled	56.4	20	<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+
39	<a href="#">c1mwmA_</a>	Alignment	not modelled	55.0	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> parm; <b>PDBTitle:</b> parm from plasmid r1 adp form
40	<a href="#">c3vpzA_</a>	Alignment	not modelled	52.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase from antarctic psychrotroph at 1.69a
41	<a href="#">c5nckA_</a>	Alignment	not modelled	52.1	13	<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
42	<a href="#">c3vovC_</a>	Alignment	not modelled	51.2	16	<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
43	<a href="#">d2gupa1</a>	Alignment	not modelled	51.0	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
44	<a href="#">c3iucC_</a>	Alignment	not modelled	49.0	17	<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
45	<a href="#">c2cgbB_</a>	Alignment	not modelled	48.7	9	<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.
46	<a href="#">c1xc3A_</a>	Alignment	not modelled	48.3	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
47	<a href="#">c3mcpA_</a>	Alignment	not modelled	47.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
48	<a href="#">c5obuA_</a>	Alignment	not modelled	44.8	19	<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.
49	<a href="#">d1z05a3</a>	Alignment	not modelled	44.2	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
50	<a href="#">d3bzka5</a>	Alignment	not modelled	43.3	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
51	<a href="#">d1woqa1</a>	Alignment	not modelled	40.8	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
52	<a href="#">d1pv8a_</a>	Alignment	not modelled	38.9	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
53	<a href="#">d2aa4a1</a>	Alignment	not modelled	35.3	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
54	<a href="#">d1jcea1</a>	Alignment	not modelled	35.2	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
55	<a href="#">c2hcaA_</a>	Alignment	not modelled	33.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine kinase;

55	<a href="#">c2106A_</a>	Alignment	not modelled	33.7	18	<b>PDBTitle:</b> crystal structure of n-acetylglucosamine kinase (tm1224) from <i>Thermotoga maritima</i> at 2.46 Å resolution
56	<a href="#">d2fsja1</a>	Alignment	not modelled	32.3	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ta0583-like
57	<a href="#">c3imoC_</a>	Alignment	not modelled	31.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> integron cassette protein; <b>PDBTitle:</b> structure from the mobile metagenome of <i>Vibrio cholerae</i> . integron2 cassette protein vch_cass14
58	<a href="#">d1dkgd1</a>	Alignment	not modelled	31.1	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
59	<a href="#">d1bdga1</a>	Alignment	not modelled	30.9	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
60	<a href="#">d1e4ft2</a>	Alignment	not modelled	29.3	25	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
61	<a href="#">c1z05A_</a>	Alignment	not modelled	28.0	13	<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 <i>E. coli</i> mlc protein.
62	<a href="#">d1r59o1</a>	Alignment	not modelled	27.4	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
63	<a href="#">c3hz6A_</a>	Alignment	not modelled	26.2	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>
64	<a href="#">c3r8eA_</a>	Alignment	not modelled	26.0	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 <i>Cytophaga hutchinsonii</i> atcc 33406 at 1.65 Å resolution
65	<a href="#">c5f7pA_</a>	Alignment	not modelled	25.4	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0178 protein; <b>PDBTitle:</b> rok repressor lmo0178 from <i>Listeria monocytogenes</i>
66	<a href="#">d1zc6a1</a>	Alignment	not modelled	25.3	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
67	<a href="#">d2i4ra1</a>	Alignment	not modelled	25.0	10	<b>Fold:</b> AtpF-like <b>Superfamily:</b> AtpF-like <b>Family:</b> AtpF-like
68	<a href="#">d2p3ra1</a>	Alignment	not modelled	24.6	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
69	<a href="#">d1bupa1</a>	Alignment	not modelled	24.3	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
70	<a href="#">c1ig8A_</a>	Alignment	not modelled	23.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase pii; <b>PDBTitle:</b> crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
71	<a href="#">c3wxiB_</a>	Alignment	not modelled	21.9	9	<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)
72	<a href="#">d2e8aa1</a>	Alignment	not modelled	20.3	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
73	<a href="#">c4apwH_</a>	Alignment	not modelled	19.9	11	<b>PDB header:</b> structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> alp12; <b>PDBTitle:</b> alp12 filament structure
74	<a href="#">d1ig8a1</a>	Alignment	not modelled	18.6	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
75	<a href="#">c2nlxA_</a>	Alignment	not modelled	18.3	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> crystal structure of the apo <i>E. coli</i> xylulose kinase
76	<a href="#">c2d4wA_</a>	Alignment	not modelled	18.1	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of glycerol kinase from <i>Cellulomonas</i> sp.2 nt3060
77	<a href="#">c2gupA_</a>	Alignment	not modelled	17.1	9	<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 <i>Streptococcus pneumoniae</i> tigr4 in complex with sucrose
78	<a href="#">c2i4rA_</a>	Alignment	not modelled	17.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> v-type atp synthase subunit f; <b>PDBTitle:</b> crystal structure of the v-type atp synthase subunit f from <i>Archaeoglobus fulgidus</i> . nesg target gr52a.
79	<a href="#">c1e1cA_</a>	Alignment	not modelled	16.1	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant
80	<a href="#">c4c23A_</a>	Alignment	not modelled	15.5	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose kinase fuck; <b>PDBTitle:</b> l-fucose kinase
81	<a href="#">c1xupO_</a>	Alignment	not modelled	15.3	22	<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 <b>PDB header:</b> structural genomics, unknown function

82	<a href="#">c1v8dC_</a>	Alignment	not modelled	15.0	32	<b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein (tt1679); <b>PDBTitle:</b> crystal structure of the conserved hypothetical protein2 tt1679 from thermus thermophilus
83	<a href="#">c2fsnB_</a>	Alignment	not modelled	14.6	19	<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
84	<a href="#">c1nm3B_</a>	Alignment	not modelled	14.4	18	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein hi0572; <b>PDBTitle:</b> crystal structure of heamophilus influenza hybrid-prx5
85	<a href="#">c3hm8D_</a>	Alignment	not modelled	12.5	12	<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
86	<a href="#">c3ifrB_</a>	Alignment	not modelled	12.2	24	<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
87	<a href="#">d2hiya1</a>	Alignment	not modelled	11.7	31	<b>Fold:</b> SP0830-like <b>Superfamily:</b> SP0830-like <b>Family:</b> SP0830-like
88	<a href="#">d1v8da_</a>	Alignment	not modelled	11.7	29	<b>Fold:</b> TTHA0583/YokD-like <b>Superfamily:</b> TTHA0583/YokD-like <b>Family:</b> Hypothetical protein TT1679
89	<a href="#">c2w7nA_</a>	Alignment	not modelled	11.7	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
90	<a href="#">d1huxa_</a>	Alignment	not modelled	11.6	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
91	<a href="#">c1v4sA_</a>	Alignment	not modelled	11.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase isoform 2; <b>PDBTitle:</b> crystal structure of human glucokinase
92	<a href="#">c5htxA_</a>	Alignment	not modelled	11.3	16	<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
93	<a href="#">c3js6A_</a>	Alignment	not modelled	11.3	24	<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
94	<a href="#">c2eq5D_</a>	Alignment	not modelled	10.6	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 228aa long hypothetical hydantoin racemase; <b>PDBTitle:</b> crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
95	<a href="#">c4ldnA_</a>	Alignment	not modelled	10.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> purine nucleoside phosphorylase deod-type; <b>PDBTitle:</b> crystal structure of a putative purine nucleoside phosphorylase from2 vibrio fischeri es114 (target nysgrc-029521)
96	<a href="#">c3g85A_</a>	Alignment	not modelled	10.1	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (laci family); <b>PDBTitle:</b> crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
97	<a href="#">d1efpb_</a>	Alignment	not modelled	10.1	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
98	<a href="#">c2yx5A_</a>	Alignment	not modelled	10.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0062 protein mj1593; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
99	<a href="#">c4j8fA_</a>	Alignment	not modelled	10.0	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock 70 kda protein 1a/1b, hsc70-interacting protein; <b>PDBTitle:</b> crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip