





















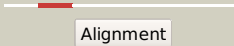

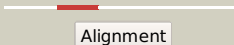

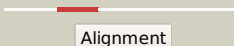



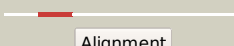

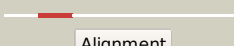

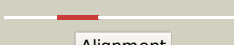





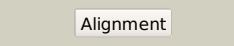
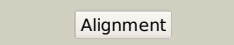
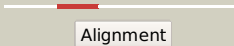
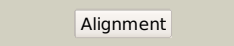
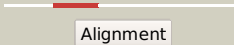
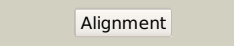
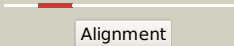
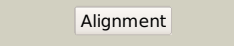


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0266c_(opA)_317525_321154
Date	Tue Jul 23 14:50:33 BST 2019
Unique Job ID	923ba0a346467c9f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5m45K_</a>	 Alignment		100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> K; <b>PDB Molecule:</b> acetone carboxylase beta subunit; <b>PDBTitle:</b> structure of acetone carboxylase purified from xanthobacter2 autotrophicus
2	<a href="#">c5I9wB_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
3	<a href="#">c5I9wb_</a>	 Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> B; <b>PDB Molecule:</b> acetophenone carboxylase gamma subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
4	<a href="#">c5I9wA_</a>	 Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> acetophenone carboxylase delta subunit; <b>PDBTitle:</b> crystal structure of the apc core complex
5	<a href="#">c5svbD_</a>	 Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> acetone carboxylase alpha subunit; <b>PDBTitle:</b> mechanism of atp-dependent acetone carboxylation, acetone carboxylase2 amp bound structure
6	<a href="#">c3cetA_</a>	 Alignment		100.0	13	<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 protein q6m145 at the2 resolution 1.8 a. northeast structural genomics consortium target3 mrr63
7	<a href="#">c3h1qB_</a>	 Alignment		98.7	30	<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 carboxydotherrnus hydrogenoformans
8	<a href="#">d1huxa_</a>	 Alignment		98.4	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
9	<a href="#">d1bupa2</a>	 Alignment		97.7	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
10	<a href="#">c1e4gT_</a>	 Alignment		97.6	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
11	<a href="#">c4ehtA_</a>	 Alignment		97.5	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

12	<a href="#">c5ya2A_</a>	 Alignment		97.4	16	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> autoinducer-2 kinase; <b>PDBTitle:</b> crystal structure of Isrk-hpr complex with adp
13	<a href="#">d1jcea2</a>	 Alignment		97.3	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
14	<a href="#">d2zgya2</a>	 Alignment		97.3	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
15	<a href="#">d2e8aa2</a>	 Alignment		97.2	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
16	<a href="#">d2ch5a2</a>	 Alignment		97.1	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="#">c3hz6A_</a>	 Alignment		97.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from chromobacterium violaceum
18	<a href="#">c3wqtB_</a>	 Alignment		97.0	17	<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
19	<a href="#">c3i8bA_</a>	 Alignment		97.0	13	<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
20	<a href="#">c2ap1A_</a>	 Alignment		97.0	19	<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
21	<a href="#">c1zc6A_</a>	 Alignment	not modelled	96.9	19	<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.
22	<a href="#">c2qm1D_</a>	 Alignment	not modelled	96.9	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase from enterococcus faecalis
23	<a href="#">d1e4ft2</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
24	<a href="#">c2dnpB_</a>	 Alignment	not modelled	96.9	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
25	<a href="#">c1mwmA_</a>	 Alignment	not modelled	96.9	15	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> parm; <b>PDBTitle:</b> parm from plasmid r1 adp form
26	<a href="#">c2ch5D_</a>	 Alignment	not modelled	96.8	17	<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
27	<a href="#">d1zc6a1</a>	 Alignment	not modelled	96.8	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
28	<a href="#">c3vgkB_</a>	 Alignment	not modelled	96.7	26	<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

29	<a href="#">c3gg4B</a>	Alignment	not modelled	96.7	15	<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
30	<a href="#">c2d4wA</a>	Alignment	not modelled	96.7	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 cellulomonas sp.2 nt3060
31	<a href="#">c3g25B</a>	Alignment	not modelled	96.6	11	<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.
32	<a href="#">d1dkgd2</a>	Alignment	not modelled	96.6	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
33	<a href="#">d2p3ra1</a>	Alignment	not modelled	96.5	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
34	<a href="#">c2zf5O</a>	Alignment	not modelled	96.5	13	<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
35	<a href="#">c3flcX</a>	Alignment	not modelled	96.5	12	<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
36	<a href="#">c2d0oA</a>	Alignment	not modelled	96.4	18	<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+
37	<a href="#">c5hv7A</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> transferase <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-ribulose
38	<a href="#">c3ifrB</a>	Alignment	not modelled	96.4	21	<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
39	<a href="#">c5f7rA</a>	Alignment	not modelled	96.4	8	<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
40	<a href="#">c3ezwD</a>	Alignment	not modelled	96.3	16	<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
41	<a href="#">c3c7nB</a>	Alignment	not modelled	96.3	15	<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
42	<a href="#">c4db3A</a>	Alignment	not modelled	96.3	15	<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.
43	<a href="#">c4e1jA</a>	Alignment	not modelled	96.2	16	<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
44	<a href="#">c3iucC</a>	Alignment	not modelled	96.1	15	<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="#">c4htlA</a>	Alignment	not modelled	96.1	23	<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
46	<a href="#">c1zbsA</a>	Alignment	not modelled	96.1	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pg1100; <b>PDBTitle:</b> crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
47	<a href="#">c2e2pA</a>	Alignment	not modelled	96.0	21	<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
48	<a href="#">c2aa4B</a>	Alignment	not modelled	96.0	21	<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
49	<a href="#">d1q18a1</a>	Alignment	not modelled	96.0	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
50	<a href="#">c1hpmA</a>	Alignment	not modelled	95.9	16	<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
51	<a href="#">c3r8eA</a>	Alignment	not modelled	95.9	19	<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
52	<a href="#">c4apwH</a>	Alignment	not modelled	95.9	12	<b>PDB header:</b> structural protein <b>Chain:</b> H: <b>PDB Molecule:</b> alp12; <b>PDBTitle:</b> alp12 filament structure
53	<a href="#">d2ewsal</a>	Alignment	not modelled	95.7	25	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain

						<b>Family:</b> Fumble-like
54	<a href="#">c1glbG</a>	Alignment	not modelled	95.7	16	<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 iiglc with2 glycerol kinase
55	<a href="#">c3eo3B</a>	Alignment	not modelled	95.7	21	<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
56	<a href="#">c1zxoB</a>	Alignment	not modelled	95.7	18	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein q8a1p1; <b>PDBTitle:</b> x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
57	<a href="#">c5nckA</a>	Alignment	not modelled	95.7	15	<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
58	<a href="#">c5f7pA</a>	Alignment	not modelled	95.6	6	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0178 protein; <b>PDBTitle:</b> rok repressor lmo0178 from listeria monocytogenes
59	<a href="#">d1z6ra2</a>	Alignment	not modelled	95.6	9	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
60	<a href="#">c2nlxA</a>	Alignment	not modelled	95.5	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
61	<a href="#">d2aa4a1</a>	Alignment	not modelled	95.5	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
62	<a href="#">d1z05a3</a>	Alignment	not modelled	95.5	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
63	<a href="#">d2ap1a2</a>	Alignment	not modelled	95.5	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
64	<a href="#">c6izrK</a>	Alignment	not modelled	95.5	11	<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
65	<a href="#">c4kboA</a>	Alignment	not modelled	95.4	17	<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
66	<a href="#">c2gupA</a>	Alignment	not modelled	95.4	28	<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
67	<a href="#">c6gfaA</a>	Alignment	not modelled	95.2	15	<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
68	<a href="#">d1sz2a1</a>	Alignment	not modelled	95.2	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
69	<a href="#">c1z05A</a>	Alignment	not modelled	95.2	10	<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.
70	<a href="#">c3h6eB</a>	Alignment	not modelled	95.1	19	<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
71	<a href="#">c1dkgD</a>	Alignment	not modelled	95.1	16	<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
72	<a href="#">c3htvA</a>	Alignment	not modelled	95.0	17	<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
73	<a href="#">c5eoxB</a>	Alignment	not modelled	95.0	20	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> type 4 fimbrial biogenesis protein pilm; <b>PDBTitle:</b> pseudomonas aeruginosa pilm bound to adp
74	<a href="#">c4czeA</a>	Alignment	not modelled	95.0	15	<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
75	<a href="#">c1z6rC</a>	Alignment	not modelled	94.7	10	<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
76	<a href="#">c6da0A</a>	Alignment	not modelled	94.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase (nfhk) from naegleria fowleri
77	<a href="#">c3vovC</a>	Alignment	not modelled	94.7	13	<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
78	<a href="#">c3gbtA</a>	Alignment	not modelled	94.6	18	<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

79	<a href="#">d2hoea3</a>	Alignment	not modelled	94.6	6	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
80	<a href="#">c3wxiB</a>	Alignment	not modelled	94.6	17	<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)
81	<a href="#">c3jvpA</a>	Alignment	not modelled	94.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulokinase; <b>PDBTitle:</b> crystal structure of ribulokinase from bacillus halodurans
82	<a href="#">c3mcpA</a>	Alignment	not modelled	94.2	15	<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
83	<a href="#">d2gupa1</a>	Alignment	not modelled	94.1	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
84	<a href="#">c1xupO</a>	Alignment	not modelled	94.1	13	<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
85	<a href="#">c4ijaA</a>	Alignment	not modelled	94.0	13	<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
86	<a href="#">c5vm1A</a>	Alignment	not modelled	94.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of a xylolyse kinase from brucella ovis
87	<a href="#">c1xc3A</a>	Alignment	not modelled	93.9	14	<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
88	<a href="#">c5tkyA</a>	Alignment	not modelled	93.9	17	<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
89	<a href="#">c5htxA</a>	Alignment	not modelled	93.9	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
90	<a href="#">c2q2rA</a>	Alignment	not modelled	93.8	19	<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
91	<a href="#">d1xc3a1</a>	Alignment	not modelled	93.7	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
92	<a href="#">c3vpzA</a>	Alignment	not modelled	93.6	11	<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
93	<a href="#">d2fsja1</a>	Alignment	not modelled	93.5	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ta0583-like
94	<a href="#">c4bc2A</a>	Alignment	not modelled	93.3	13	<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
95	<a href="#">c2v7zA</a>	Alignment	not modelled	93.1	16	<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
96	<a href="#">c4c23A</a>	Alignment	not modelled	92.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-fuculose kinase fuck; <b>PDBTitle:</b> l-fuculose kinase
97	<a href="#">c3lm2B</a>	Alignment	not modelled	92.7	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
98	<a href="#">c5ey2A</a>	Alignment	not modelled	92.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from bacillus cereus
99	<a href="#">c6ediA</a>	Alignment	not modelled	92.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of leishmania braziliensis glucokinase
100	<a href="#">c1woqB</a>	Alignment	not modelled	92.3	15	<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
101	<a href="#">c2v7yA</a>	Alignment	not modelled	92.1	18	<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
102	<a href="#">d1woqa1</a>	Alignment	not modelled	92.0	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
103	<a href="#">c4j8fA</a>	Alignment	not modelled	91.9	24	<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
104	<a href="#">c2w40C</a>	Alignment	not modelled	91.4	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

105	<a href="#">c5e84B_</a>	Alignment	not modelled	91.2	16	<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
106	<a href="#">c5ey0A_</a>	Alignment	not modelled	91.0	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from staphylococcus aureus with gtp and ile
107	<a href="#">d1r59o1</a>	Alignment	not modelled	90.9	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
108	<a href="#">d2d0oa2</a>	Alignment	not modelled	90.3	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ATPase domain of dehydratase reactivase alpha subunit
109	<a href="#">c2cgb_</a>	Alignment	not modelled	90.2	23	<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.
110	<a href="#">c5mb9B_</a>	Alignment	not modelled	89.8	18	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
111	<a href="#">c5obuA_</a>	Alignment	not modelled	89.8	13	<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 sbdalalpha in complex2 with amppnp.
112	<a href="#">c2hoeA_</a>	Alignment	not modelled	89.1	6	<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
113	<a href="#">c3d2fC_</a>	Alignment	not modelled	89.1	18	<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
114	<a href="#">d3bexa1</a>	Alignment	not modelled	88.5	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> CoaX-like
115	<a href="#">c3hi0B_</a>	Alignment	not modelled	88.5	17	<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
116	<a href="#">c2gx5B_</a>	Alignment	not modelled	87.1	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> n-terminal gaf domain of transcriptional pleiotropic repressor cody
117	<a href="#">c3js6A_</a>	Alignment	not modelled	86.9	11	<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
118	<a href="#">c3smpA_</a>	Alignment	not modelled	86.7	33	<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
119	<a href="#">c2fsnB_</a>	Alignment	not modelled	86.4	18	<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
120	<a href="#">c1o1f4_</a>	Alignment	not modelled	85.9	21	<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 from tomograms of2 insect flight muscle