

























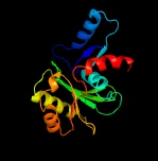






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1887 (-)_2136265_2137407
Date	Fri Aug 2 13:30:50 BST 2019
Unique Job ID	c419a89122c27f16

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h1qB_	 Alignment		99.1	15	PDB header: structural protein Chain: B; PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrnus hydrogenoformans
2	c3c7nB_	 Alignment		98.7	17	PDB header: chaperone/chaperone Chain: B; PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
3	c3d2fC_	 Alignment		98.6	16	PDB header: chaperone Chain: C; PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
4	c2v7yA_	 Alignment		98.5	20	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
5	c2khoA_	 Alignment		98.5	18	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 70; PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate
6	c5obuA_	 Alignment		98.5	17	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein dnak; PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.
7	c5tkyA_	 Alignment		98.5	17	PDB header: chaperone Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation
8	c5mb9B_	 Alignment		98.5	20	PDB header: chaperone Chain: B; PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
9	c5e84B_	 Alignment		98.5	20	PDB header: chaperone Chain: B; PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
10	c6gfaA_	 Alignment		98.4	16	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 105 kda; PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed
11	c4j8fA_	 Alignment		98.4	17	PDB header: chaperone Chain: A; PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein; PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip

12	c1hpmA	Alignment		98.4	18	PDB header: hydrolase (acting on acid anhydrides) Chain: A: PDB Molecule: 44k atpase fragment (n-terminal) of 70 kd heat- PDBTitle: how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
13	c1dkgD	Alignment		98.3	17	PDB header: complex (hsp24/hsp70) Chain: D: PDB Molecule: molecular chaperone dnak; PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
14	c4czeA	Alignment		98.3	17	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreb; PDBTitle: c. crescentus mreb, double filament, empty
15	c2v7zA	Alignment		98.3	19	PDB header: chaperone Chain: A: PDB Molecule: heat shock cognate 71 kda protein; PDBTitle: crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
16	c1jcgA	Alignment		98.3	16	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreb; PDBTitle: mreb from thermotoga maritima, amppnp
17	c4kboA	Alignment		98.3	16	PDB header: signaling protein Chain: A: PDB Molecule: stress-70 protein, mitochondrial; PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form
18	d1jcea2	Alignment		98.0	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
19	c3iucC	Alignment		98.0	18	PDB header: chaperone Chain: C: PDB Molecule: heat shock 70kda protein 5 (glucose-regulated PDBTitle: crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
20	d1dkgd2	Alignment		97.8	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
21	c4gniA	Alignment	not modelled	97.7	21	PDB header: chaperone Chain: A: PDB Molecule: putative heat shock protein; PDBTitle: structure of the ssz1 atpase bound to atp and magnesium
22	c4rtfD	Alignment	not modelled	97.7	20	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
23	c1e4gT	Alignment	not modelled	97.6	16	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
24	c3wqtB	Alignment	not modelled	97.6	11	PDB header: structural genomics Chain: B: PDB Molecule: cell division protein ftsa; PDBTitle: staphylococcus aureus ftsa complexed with amppnp
25	d2e8aa2	Alignment	not modelled	97.3	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
26	d1bupa2	Alignment	not modelled	97.2	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
27	c2d0oA	Alignment	not modelled	97.2	21	PDB header: chaperone Chain: A: PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
28	c1mwmA	Alignment	not modelled	97.2	11	PDB header: structural protein Chain: A: PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
29	c5jygA	Alignment	not modelled	97.1	14	PDB header: structural protein Chain: A: PDB Molecule: actin-like atpase;

					PDBTitle: cryo-em structure of the mamk filament at 6.5 a
30	d2zgya2	Alignment	not modelled	96.8	13 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
31	c6izrK_	Alignment	not modelled	96.8	14 PDB header: protein fibril Chain: K: PDB Molecule: putative plasmid segregation protein parm; PDBTitle: whole structure of a 15-stranded parm filament from clostridium2 botulinum
32	c5vm1A_	Alignment	not modelled	96.3	16 PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylolose kinase from brucella ovis
33	c1o1f4_	Alignment	not modelled	96.1	14 PDB header: contractile protein Chain: 4: PDB Molecule: skeletal muscle actin; PDBTitle: molecular models of averaged rigor crossbridges from tomograms of 2 insect flight muscle
34	c5eoxB_	Alignment	not modelled	95.9	17 PDB header: peptide binding protein Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilm; PDBTitle: pseudomonas aeruginosa pilm bound to adp
35	d1huxa_	Alignment	not modelled	95.9	20 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
36	c2nlxA_	Alignment	not modelled	95.7	18 PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
37	c1xupO_	Alignment	not modelled	95.6	17 PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
38	c3gg4B_	Alignment	not modelled	95.6	9 PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
39	c2ychA_	Alignment	not modelled	95.4	23 PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilm; PDBTitle: pilm-piln type iv pilus biogenesis complex
40	d1e4ft2	Alignment	not modelled	95.2	19 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
41	c3ifrB_	Alignment	not modelled	95.2	15 PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
42	c3gbtA_	Alignment	not modelled	95.0	11 PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
43	c2zf5O_	Alignment	not modelled	94.8	17 PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
44	c2fsnB_	Alignment	not modelled	94.8	18 PDB header: structural protein Chain: B: PDB Molecule: hypothetical protein ta0583; PDBTitle: crystal structure of ta0583, an archaeal actin homolog, complex with 2 adp
45	c2e2pA_	Alignment	not modelled	94.8	15 PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in 2 complex with adp
46	d1r59o2	Alignment	not modelled	94.6	18 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
47	c3hz6A_	Alignment	not modelled	94.6	22 PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
48	c3i8bA_	Alignment	not modelled	94.5	16 PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from 2 bifidobacterium adolescentis
49	c5ya2A_	Alignment	not modelled	94.5	26 PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
50	c4ehtA_	Alignment	not modelled	94.4	16 PDB header: electron transport Chain: A: PDB Molecule: activator of 2-hydroxyisocaproyl-coa dehydratase; PDBTitle: activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
51	c5hv7A_	Alignment	not modelled	94.4	16 PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex 2 with d-ribulose
52	c3dw1B_	Alignment	not modelled	94.3	14 PDB header: structural protein Chain: B: PDB Molecule: actin-related protein 3; PDBTitle: crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
53	d2p3ra2	Alignment	not modelled	94.2	19 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
54	c4bc2A_	Alignment	not modelled	94.2	20 PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of human d-xylulokinase in complex with d-2 xylulose and adenosine diphosphate
55	c5htxA_	Alignment	not modelled	93.9	21 PDB header: transferase Chain: A: PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in

						complex with adp
56	c3flcX_	Alignment	not modelled	93.9	18	PDB header: transferase Chain: X: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
57	c2dnpB_	Alignment	not modelled	93.8	24	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
58	c2d4wA_	Alignment	not modelled	93.4	23	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
59	c3wxib_	Alignment	not modelled	93.1	24	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
60	c4apwH_	Alignment	not modelled	93.1	11	PDB header: structural protein Chain: H: PDB Molecule: alp12; PDBTitle: alp12 filament structure
61	c3g25B_	Alignment	not modelled	92.5	16	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
62	c2cgb_	Alignment	not modelled	92.4	10	PDB header: transferase Chain: B: PDB Molecule: l-rhamnulose kinase; PDBTitle: crystal structure of l-rhamnulose kinase from escherichia coli in an2 open uncomplexed conformation.
63	c1glbG_	Alignment	not modelled	92.2	19	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase
64	c3jvpA_	Alignment	not modelled	91.8	14	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
65	c3ezwD_	Alignment	not modelled	91.8	20	PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
66	c5afuB_	Alignment	not modelled	91.2	15	PDB header: motor protein Chain: B: PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex
67	c4e1jA_	Alignment	not modelled	89.5	19	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
68	c4c23A_	Alignment	not modelled	88.7	13	PDB header: transferase Chain: A: PDB Molecule: l-fucose kinase fuck; PDBTitle: l-fucose kinase
69	c3htvA_	Alignment	not modelled	88.4	18	PDB header: transferase Chain: A: PDB Molecule: d-allose kinase; PDBTitle: crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
70	d2fsja1	Alignment	not modelled	87.5	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
71	c2w40C_	Alignment	not modelled	86.7	11	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
72	c3h6eB_	Alignment	not modelled	84.4	16	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
73	c3vpzA_	Alignment	not modelled	83.7	13	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
74	c3js6A_	Alignment	not modelled	83.2	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized parm protein; PDBTitle: crystal structure of apo psk41 parm protein
75	c6igmG_	Alignment	not modelled	82.6	19	PDB header: transcription Chain: G: PDB Molecule: actin-related protein 6; PDBTitle: cryo-em structure of human srcap complex
76	d2hoea3	Alignment	not modelled	81.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
77	c3eo3B_	Alignment	not modelled	79.2	12	PDB header: isomerase, transferase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
78	c4ix1B_	Alignment	not modelled	79.0	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
79	d2gupa1	Alignment	not modelled	70.2	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
80	c2ap1A_	Alignment	not modelled	64.5	19	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
81	c4fq5B_	Alignment	not modelled	63.2	15	PDB header: isomerase Chain: B: PDB Molecule: maleate cis-trans isomerase; PDBTitle: crystal structure of the maleate isomerase iso(c200a)

						from pseudomonas2 putida s16 with maleate
82	d1zc6a1	Alignment	not modelled	63.0	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
83	d2e8aa1	Alignment	not modelled	62.4	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
84	d1nm1a2	Alignment	not modelled	62.1	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
85	d1jcea1	Alignment	not modelled	60.8	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
86	c1xc3A	Alignment	not modelled	60.7	20	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
87	d1bupa1	Alignment	not modelled	59.7	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
88	d2hf3a2	Alignment	not modelled	59.2	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
89	c4pl7B	Alignment	not modelled	59.2	18	PDB header: structural protein, contractile protein Chain: B: PDB Molecule: actin,thymosin beta-4; PDBTitle: structure of komagataella pastoris actin-thymosin beta4 hybrid
90	c4nl6C	Alignment	not modelled	57.3	10	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
91	c2gupA	Alignment	not modelled	57.3	21	PDB header: transferase Chain: A: PDB Molecule: rok family protein; PDBTitle: structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
92	d2fxua2	Alignment	not modelled	55.9	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
93	d2d0oa3	Alignment	not modelled	54.6	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
94	d1yaga2	Alignment	not modelled	53.9	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
95	c4db3A	Alignment	not modelled	53.6	18	PDB header: transferase Chain: A: PDB Molecule: n-acetyl-d-glucosamine kinase; PDBTitle: 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
96	d1dkgd1	Alignment	not modelled	49.3	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
97	c4htiA	Alignment	not modelled	46.1	17	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
98	c3mcpA	Alignment	not modelled	45.5	14	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (bdi_1628) from parabacteroides2 distansis atcc 8503 at 3.00 a resolution
99	c3fhkF	Alignment	not modelled	44.8	16	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: upf0403 protein yphp; PDBTitle: crystal structure of apc1446, b.subtilis yphp disulfide isomerase
100	c5nckA	Alignment	not modelled	44.7	12	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
101	c2qm1D	Alignment	not modelled	44.3	10	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
102	c3r8eA	Alignment	not modelled	43.6	11	PDB header: transferase Chain: A: PDB Molecule: hypothetical sugar kinase; PDBTitle: crystal structure of a putative sugar kinase (chu_1875) from cytophaga2 hutchinsonii atcc 33406 at 1.65 a resolution
103	d1z6ra2	Alignment	not modelled	43.4	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
104	c3uleB	Alignment	not modelled	39.6	20	PDB header: structural protein Chain: B: PDB Molecule: actin-related protein 2; PDBTitle: structure of bos taurus arp2/3 complex with bound inhibitor ck-869 and2 atp
105	c3vgkB	Alignment	not modelled	36.4	19	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
106	c6etxH	Alignment	not modelled	35.8	21	PDB header: dna binding protein Chain: H: PDB Molecule: actin-related protein 5; PDBTitle: cryo-em structure of the human ino80 complex bound to nucleosome
107	c4xe7A	Alignment	not modelled	34.2	13	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: bacillus thuringiensis parm in apo form
						Fold: Ribonuclease H-like motif

108	d1z05a3	Alignment	not modelled	34.1	24	Superfamily: Actin-like ATPase domain Family: ROK
109	d1r59o1	Alignment	not modelled	31.0	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
110	c2xecD	Alignment	not modelled	28.3	19	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
111	d2aa4a1	Alignment	not modelled	27.9	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
112	c3vovC	Alignment	not modelled	27.6	14	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
113	c2hoeA	Alignment	not modelled	27.4	21	PDB header: transferase Chain: A: PDB Molecule: n-acetylglucosamine kinase; PDBTitle: crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
114	d2ap1a2	Alignment	not modelled	26.7	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
115	d1k8ka2	Alignment	not modelled	26.3	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
116	d2gk3a1	Alignment	not modelled	26.3	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
117	c2aa4B	Alignment	not modelled	25.8	29	PDB header: transferase Chain: B: PDB Molecule: putative n-acetylmannosamine kinase; PDBTitle: crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
118	d1woqa1	Alignment	not modelled	22.2	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK