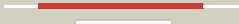



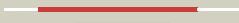












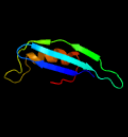



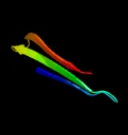
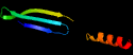


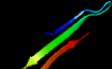



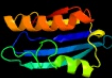



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2594c_(ruvC)_2924827_2925393
 Date Wed Aug 7 12:50:23 BST 2019
 Unique Job ID 1e8736ac2ca8120a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hjra_	 Alignment		100.0	40	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
2	c4ep5A	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endodeoxyribonuclease ruvc; PDBTitle: thermus thermophilus ruvc structure
3	c4ktzB	 Alignment		98.7	15	PDB header: hydrolase Chain: B: PDB Molecule: ruvc endonuclease; PDBTitle: lactococcus phage 67 ruvc
4	d1kcf2	 Alignment		98.5	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Mitochondrial resolvase ydc2 catalytic domain
5	d3bzka5	 Alignment		98.2	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
6	d1vhxa	 Alignment		98.2	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
7	c1kcfB	 Alignment		98.1	15	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical 30.2 kd protein c25g10.02 in PDBTitle: crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
8	d1nu0a	 Alignment		97.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
9	d1iv0a	 Alignment		97.8	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
10	c2oceA	 Alignment		97.3	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
11	c6jooA	 Alignment		97.0	29	PDB header: hydrolase/dna/rna Chain: A: PDB Molecule: crispr-associated protein,crispr-associated endonuclease PDBTitle: crystal structure of corynebacterium diphtheriae cas9 in complex with2 sgrna and target dna

12	c5x2hA	Alignment		96.9	22	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of campylobacter jejuni cas9 in complex with sgrna2 and target dna (agaaaca pam)
13	c5axwA	Alignment		96.6	15	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of staphylococcus aureus cas9 in complex with sgrna2 and target dna (ttgggt pam)
14	d1saza1	Alignment		96.5	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
15	c4ogeA	Alignment		96.3	23	PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease domain protein; PDBTitle: crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii
16	c4cmqB	Alignment		96.1	15	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endonuclease cas9/csn1; PDBTitle: crystal structure of mn-bound s.pyogenes cas9
17	d1okja1	Alignment		95.2	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
18	c6gmhM	Alignment		95.2	20	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor spt6,transcription PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
19	c1okjB	Alignment		95.1	16	PDB header: hydrolase Chain: B: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of the essential e. coli yea2 protein by mad method using the gadolinium complex3 "dotma"
20	c3eo3B	Alignment		95.1	15	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
21	c2aa4B	Alignment	not modelled	95.0	21	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
22	c5br9C	Alignment	not modelled	94.9	18	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein with similarity to2 peptidase yea2 from pseudomonas aeruginosa
23	c6fpeG	Alignment	not modelled	94.8	14	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
24	c3vovC	Alignment	not modelled	94.8	28	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
25	c5e6fA	Alignment	not modelled	94.5	16	PDB header: viral protein Chain: A: PDB Molecule: cnpv261 holliday junction resolvase protein; PDBTitle: canarypox virus resolvase
26	c3psfA	Alignment	not modelled	94.4	12	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
27	c3psiA	Alignment	not modelled	94.4	12	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
28	c3r6mD	Alignment	not modelled	94.3	10	PDB header: hydrolase Chain: D: PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz

29	c3p4iA	Alignment	not modelled	94.2	15	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
30	c5m1oA	Alignment	not modelled	94.0	18	PDB header: viral protein Chain: A: PDB Molecule: phage terminase large subunit; PDBTitle: crystal structure of the large terminase nuclease from thermophilic2 phage g20c with bound cobalt
31	c2ivoC	Alignment	not modelled	93.7	10	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
32	c4ijnB	Alignment	not modelled	93.7	16	PDB header: transferase Chain: B: PDB Molecule: acetate kinase; PDBTitle: crystal structure of an acetate kinase from mycobacterium smegmatis2 bound to amp and sulfate
33	c1sazA	Alignment	not modelled	93.6	14	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
34	c1zc6A	Alignment	not modelled	93.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable n-acetylglucosamine kinase; PDBTitle: crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
35	c2qm1D	Alignment	not modelled	93.5	16	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
36	c3zeuE	Alignment	not modelled	93.5	13	PDB header: hydrolase Chain: E: PDB Molecule: probable trna threonylcarbamoyladenine biosynthesis PDBTitle: structure of a salmonella typhimurium ygd-yeaz heterodimer bound to2 atp gammas
37	c5nckA	Alignment	not modelled	93.3	21	PDB header: transferase Chain: A: PDB Molecule: n-acetylmannosamine kinase; PDBTitle: the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
38	d1zc6a1	Alignment	not modelled	93.3	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
39	d2aa4a1	Alignment	not modelled	92.7	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
40	c2e2pA	Alignment	not modelled	92.6	15	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
41	c4ehtA	Alignment	not modelled	91.0	15	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
42	d1huxa	Alignment	not modelled	90.9	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
43	c5f7rA	Alignment	not modelled	88.9	10	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
44	d2a6aa1	Alignment	not modelled	88.0	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
45	c3enoB	Alignment	not modelled	88.0	9	PDB header: hydrolase/unknown function Chain: B: PDB Molecule: putative o-sialoglycoprotein endopeptidase; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
46	c6gwjK	Alignment	not modelled	87.5	15	PDB header: rna binding protein Chain: K: PDB Molecule: probable trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: protein complex
47	c3i8bA	Alignment	not modelled	87.4	17	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
48	c2ch5D	Alignment	not modelled	86.9	19	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
49	c3htvA	Alignment	not modelled	86.6	22	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
50	c6n9aB	Alignment	not modelled	86.1	15	PDB header: biosynthetic protein Chain: B: PDB Molecule: trna threonylcarbamoyladenine biosynthesis protein tsab; PDBTitle: crystal structure of thermotoga maritima threonylcarbamoyladenine2 biosynthesis complex tsab2d2e2 bound to atp and carboxy-amp
51	c2a6aB	Alignment	not modelled	85.9	15	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein tm0874; PDBTitle: crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution
52	c4htIA	Alignment	not modelled	85.6	11	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
						PDB header: structural genomics, unknown function

53	c1zbsA	Alignment	not modelled	85.4	11	Chain: A: PDB Molecule: hypothetical protein pg1100; PDBTitle: crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
54	c3en9B	Alignment	not modelled	85.0	7	PDB header: hydrolase Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
55	c5olaD	Alignment	not modelled	83.8	10	PDB header: transcription Chain: D: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of mitochondrial transcription elongation complex in complex2 with elongation factor tefm
56	c3gbtA	Alignment	not modelled	83.1	15	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
57	d1g99a1	Alignment	not modelled	82.8	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
58	d1dkgd1	Alignment	not modelled	82.7	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
59	c5hv7A	Alignment	not modelled	82.0	14	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
60	c3vpzA	Alignment	not modelled	81.0	14	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
61	d2e8aa1	Alignment	not modelled	80.7	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
62	d2ch5a2	Alignment	not modelled	80.5	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
63	d2h0ea3	Alignment	not modelled	79.8	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
64	c3r8eA	Alignment	not modelled	79.2	13	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
65	d2ews1	Alignment	not modelled	78.5	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
66	c4bgaB	Alignment	not modelled	78.1	18	PDB header: transferase Chain: B: PDB Molecule: predicted molecular chaperone distantly related to PDBTitle: nucleotide-bound open form of a putative sugar kinase2 mk0840 from methanopyrus kandleri
67	c2gupA	Alignment	not modelled	76.9	20	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
68	c1z05A	Alignment	not modelled	76.1	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
69	c2iirJ	Alignment	not modelled	75.1	16	PDB header: transferase Chain: J: PDB Molecule: acetate kinase; PDBTitle: acetate kinase from a hyperthermophile thermotoga maritima
70	c3cerD	Alignment	not modelled	73.8	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: possible exopolyphosphatase-like protein; PDBTitle: crystal structure of the exopolyphosphatase-like protein q8g5j2.2 northeast structural genomics consortium target blr13
71	c2d0oA	Alignment	not modelled	73.7	17	PDB header: chaperone Chain: A: PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: structure of diol dehydratase-reactivating factor complexed2 with adp and mg2+
72	c4k25A	Alignment	not modelled	73.3	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable trna threonylcarbamoyladenine biosynthesis PDBTitle: crystal structure of yeast qri7 homodimer
73	d1bupa1	Alignment	not modelled	72.9	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
74	c6da0A	Alignment	not modelled	72.5	19	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from naegleria fowleri
75	c1tuuA	Alignment	not modelled	72.5	20	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: acetate kinase crystallized with atpgs
76	c5m45K	Alignment	not modelled	72.4	24	PDB header: ligase Chain: K: PDB Molecule: acetone carboxylase beta subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus
77	c1xc3A	Alignment	not modelled	72.4	17	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
						PDB header: peptide binding protein

78	c5eoxB	Alignment	not modelled	72.0	17	Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilm; PDBTitle: pseudomonas aeruginosa pilm bound to adp
79	d1z6ra2	Alignment	not modelled	71.5	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
80	c2cgkB	Alignment	not modelled	70.9	17	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.
81	c5ya2A	Alignment	not modelled	69.6	12	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
82	c1e4gT	Alignment	not modelled	69.5	18	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
83	c3ezkB	Alignment	not modelled	68.5	18	PDB header: hydrolase Chain: B: PDB Molecule: dna packaging protein gp17; PDBTitle: bacteriophage t4 gp17 motor assembly based on crystal structures and2 cryo-em reconstructions
84	c3ifrb	Alignment	not modelled	68.4	14	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylose kinase from rhodospirillum rubrum
85	c1dkgD	Alignment	not modelled	67.5	20	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
86	c1woqB	Alignment	not modelled	67.1	17	PDB header: transferase Chain: B: PDB Molecule: inorganic polyphosphate/atp-glucomannokinase; PDBTitle: crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
87	c3gg4B	Alignment	not modelled	66.9	14	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
88	c2v7yA	Alignment	not modelled	65.7	29	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
89	d1z05a3	Alignment	not modelled	64.7	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
90	c3vgkB	Alignment	not modelled	63.6	32	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
91	c2w40C	Alignment	not modelled	62.1	3	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
92	c1z6rC	Alignment	not modelled	61.4	9	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
93	d2gupa1	Alignment	not modelled	60.8	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
94	c6idjC	Alignment	not modelled	60.6	26	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of acric2 dimer in complex with partial nme1cas9
95	c4rtfD	Alignment	not modelled	59.6	40	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
96	d2p3ra1	Alignment	not modelled	59.4	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
97	d1t6ca1	Alignment	not modelled	58.8	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
98	c3hlzA	Alignment	not modelled	58.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bt_1490; PDBTitle: crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution
99	c5mb9B	Alignment	not modelled	58.1	16	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
100	d1ig8a1	Alignment	not modelled	57.7	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
101	c4xe7A	Alignment	not modelled	57.6	17	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: bacillus thuringiensis parm in apo form
102	c3c7nB	Alignment	not modelled	56.6	24	PDB header: chaperone/chaperone Chain: B: PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
103	c5e84B	Alignment	not modelled	56.5	32	PDB header: chaperone Chain: B: PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
104	c5obuA	Alignment	not modelled	56.4	27	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak;

104	c3000A	Alignment	not modelled	50.4	97	PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp. PDB header: unknown function
105	c1zxoB	Alignment	not modelled	54.9	10	Chain: B: PDB Molecule: conserved hypothetical protein q8a1p1; PDBTitle: x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
106	c3wxiB	Alignment	not modelled	54.3	14	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
107	c2khoA	Alignment	not modelled	53.8	21	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
108	c4kboA	Alignment	not modelled	53.7	32	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
109	c1hpmA	Alignment	not modelled	53.6	24	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
110	c6gfaA	Alignment	not modelled	53.2	30	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
111	c3mcpA	Alignment	not modelled	51.8	25	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
112	c4j8fA	Alignment	not modelled	49.2	26	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
113	c2v7zA	Alignment	not modelled	49.1	26	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
114	d2d0oa2	Alignment	not modelled	49.1	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
115	c4gniA	Alignment	not modelled	48.8	13	PDB header: chaperone Chain: A: PDB Molecule: putative heat shock protein; PDBTitle: structure of the ssz1 atpase bound to atp and magnesium
116	c3jvpA	Alignment	not modelled	48.1	23	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
117	c1x3nA	Alignment	not modelled	46.9	20	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
118	c3h6eB	Alignment	not modelled	46.5	18	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
119	c5tkyA	Alignment	not modelled	46.2	25	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
120	d1woqa1	Alignment	not modelled	43.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK