






















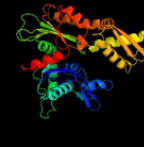

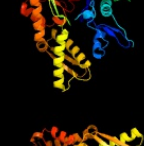
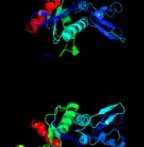


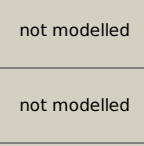


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2264c (-) _2536582_2538360
Date	Mon Aug 5 13:25:40 BST 2019
Unique Job ID	bab2cca28bb46679

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3d2fC_	 Alignment		100.0	20	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
2	c5mb9B_	 Alignment		100.0	24	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
3	c5tkyA_	 Alignment		100.0	24	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
4	c4j8fA_	 Alignment		100.0	23	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
5	c3c7nB_	 Alignment		100.0	23	PDB header: chaperone/chaperone Chain: B: PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
6	c2v7yA_	 Alignment		100.0	23	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
7	c5obuA_	 Alignment		100.0	22	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.
8	c2khoA_	 Alignment		100.0	24	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
9	c5e84B_	 Alignment		100.0	23	PDB header: chaperone Chain: B: PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
10	c4gniA_	 Alignment		100.0	24	PDB header: chaperone Chain: A: PDB Molecule: putative heat shock protein; PDBTitle: structure of the ssz1 atpase bound to atp and magnesium
11	c6gfaA_	 Alignment		100.0	22	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

12	c4kboA_	Alignment		100.0	22	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
13	c1dkgD_	Alignment		100.0	23	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	c2v7zA_	Alignment		100.0	22	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
15	c1hpmA_	Alignment		100.0	22	PDB header: hydrolase (acting on acid anhydrides) Chain: A: PDB Molecule: 44k atpase fragment (n-terminal) of 7o kd heat- PDBTitle: how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
16	c3iucC_	Alignment		100.0	24	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
17	c4rtfD_	Alignment		100.0	26	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
18	c4czeA_	Alignment		100.0	18	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreb; PDBTitle: c. crescentus mreb, double filament, empty
19	c1jcgA_	Alignment		100.0	20	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreb; PDBTitle: mreb from thermotoga maritima, amppnp
20	c3h1qB_	Alignment		100.0	21	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrmus hydrogenoformans
21	c5jygA_	Alignment	not modelled	100.0	14	PDB header: structural protein Chain: A: PDB Molecule: actin-like atpase; PDBTitle: cryo-em structure of the mamk filament at 6.5 a
22	c1e4gT_	Alignment	not modelled	100.0	15	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
23	d1dkgd2	Alignment	not modelled	100.0	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
24	d1bupa2	Alignment	not modelled	100.0	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
25	c1o1f4_	Alignment	not modelled	100.0	15	PDB header: contractile protein Chain: 4: PDB Molecule: skeletal muscle actin; PDBTitle: molecular models of averaged rigor crossbridges from tomograms of2 insect flight muscle
26	d2e8aa2	Alignment	not modelled	100.0	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
27	c2d0oA_	Alignment	not modelled	100.0	13	PDB header: chaperone Chain: A: PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+ 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
28	c6izrK_	Alignment	not modelled	100.0	13	

29	c4xe7A_	Alignment	not modelled	100.0	9	PDB header: structural protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: bacillus thuringiensis parm in apo form
30	c5afuB_	Alignment	not modelled	100.0	15	PDB header: motor protein Chain: B: PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex
31	c3wqtB_	Alignment	not modelled	100.0	14	PDB header: structural genomics Chain: B: PDB Molecule: cell division protein ftsa; PDBTitle: staphylococcus aureus ftsa complexed with amppnp
32	c5eoxB_	Alignment	not modelled	99.9	17	PDB header: peptide binding protein Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilm; PDBTitle: pseudomonas aeruginosa pilm bound to adp
33	c1mwmA_	Alignment	not modelled	99.9	13	PDB header: structural protein Chain: A: PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
34	c4jd2B_	Alignment	not modelled	99.9	18	PDB header: structural protein Chain: B: PDB Molecule: actin-related protein 2; PDBTitle: crystal structure of bos taurus arp2/3 complex binding with mus2 musculus gmf
35	c4pl7B_	Alignment	not modelled	99.9	14	PDB header: structural protein, contractile protein Chain: B: PDB Molecule: actin,thymosin beta-4; PDBTitle: structure of komagataella pastoris actin-thymosin beta4 hybrid
36	c2p9IA_	Alignment	not modelled	99.9	15	PDB header: structural protein Chain: A: PDB Molecule: actin-like protein 3; PDBTitle: crystal structure of bovine arp2/3 complex
37	d1jcea2	Alignment	not modelled	99.9	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
38	c6igmG_	Alignment	not modelled	99.9	14	PDB header: transcription Chain: G: PDB Molecule: actin-related protein 6; PDBTitle: cryo-em structure of human srcap complex
39	c2fsnB_	Alignment	not modelled	99.9	17	PDB header: structural protein Chain: B: PDB Molecule: hypothetical protein ta0583; PDBTitle: crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
40	c3dwIB_	Alignment	not modelled	99.9	15	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
41	c4apwH_	Alignment	not modelled	99.9	12	PDB header: structural protein Chain: H: PDB Molecule: alp12; PDBTitle: alp12 filament structure
42	d2e8aa1	Alignment	not modelled	99.9	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
43	d1bupa1	Alignment	not modelled	99.9	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
44	c2ychA_	Alignment	not modelled	99.9	25	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilm; PDBTitle: pilm-piln type iv pilus biogenesis complex
45	d1e4ft2	Alignment	not modelled	99.9	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
46	d1jcea1	Alignment	not modelled	99.9	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
47	d1dkgd1	Alignment	not modelled	99.8	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
48	c6gejR_	Alignment	not modelled	99.8	15	PDB header: nuclear protein Chain: R: PDB Molecule: actin-like protein arp6; PDBTitle: chromatin remodeller-nucleosome complex at 3.6 a resolution.
49	c3js6A_	Alignment	not modelled	99.8	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized parm protein; PDBTitle: crystal structure of apo psk41 parm protein
50	c4i6mA_	Alignment	not modelled	99.8	16	PDB header: transcription/hydrolase Chain: A: PDB Molecule: actin-related protein 7; PDBTitle: structure of arp7-arp9-snf2(hsa)-rtt102 subcomplex of swi/snf2 chromatin remodeler.
51	c3qb0C_	Alignment	not modelled	99.8	14	PDB header: structural protein Chain: C: PDB Molecule: actin-related protein 4; PDBTitle: crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
52	d2zgya2	Alignment	not modelled	99.7	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
53	c6etxH_	Alignment	not modelled	99.7	14	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
54	d1huxa_	Alignment	not modelled	99.7	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
55	c4fo0A_	Alignment	not modelled	99.6	18	PDB header: gene regulation Chain: A: PDB Molecule: actin-related protein 8; PDBTitle: human actin-related protein arp8 in its atp-bound state
						Fold: Ribonuclease H-like motif

56	d2fsja1	Alignment	not modelled	99.6	18	Superfamily: Actin-like ATPase domain Family: Ta0583-like
57	c5aftj	Alignment	not modelled	99.6	16	PDB header: motor protein Chain: J: PDB Molecule: actin related protein 11; PDBTitle: cryoem structure of dynactin complex at 4.0 angstrom2 resolution
58	c4cj7B	Alignment	not modelled	99.5	13	PDB header: structural protein Chain: B: PDB Molecule: actin/actin family protein; PDBTitle: structure of crenactin, an archeal actin-like protein
59	c3uleB	Alignment	not modelled	99.5	21	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
60	c6fhsj	Alignment	not modelled	99.5	14	PDB header: dna binding protein Chain: J: PDB Molecule: arp5; PDBTitle: cryoem structure of ino80core
61	c4i6mB	Alignment	not modelled	99.5	16	PDB header: transcription/hydrolase Chain: B: PDB Molecule: actin-like protein arp9; PDBTitle: structure of arp7-arp9-snf2(hsa)-rtt102 subcomplex of swi/snf2 chromatin remodeler.
62	c4am6A	Alignment	not modelled	99.4	17	PDB header: nuclear protein Chain: A: PDB Molecule: actin-like protein arp8; PDBTitle: c-terminal domain of actin-related protein arp8 from s. cerevisiae
63	c6fmjl	Alignment	not modelled	99.4	16	PDB header: dna binding protein Chain: J: PDB Molecule: actin related protein 5; PDBTitle: cryoem structure ino80core nucleosome complex
64	d1nm1a2	Alignment	not modelled	99.4	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
65	d2fxua2	Alignment	not modelled	99.3	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
66	d2hf3a2	Alignment	not modelled	99.3	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
67	c4ehtA	Alignment	not modelled	99.2	17	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
68	c3gg4B	Alignment	not modelled	99.2	16	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
69	c2p9kB	Alignment	not modelled	99.1	20	PDB header: structural protein Chain: B: PDB Molecule: actin-like protein 2; PDBTitle: crystal structure of bovine arp2/3 complex co-crystallized with atp2 and crosslinked with glutaraldehyde
70	d1k8kb1	Alignment	not modelled	99.1	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
71	d1yaga2	Alignment	not modelled	99.0	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
72	d1k8ka2	Alignment	not modelled	98.9	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
73	c2e2pA	Alignment	not modelled	98.9	14	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfobolus tokodaii hexokinase in2 complex with adp
74	c4xhpA	Alignment	not modelled	98.4	10	PDB header: structural protein Chain: A: PDB Molecule: parm hybrid fusion protein; PDBTitle: bacillus thuringiensis parm hybrid protein with adp, containing two2 parm mutants
75	c6da0A	Alignment	not modelled	98.3	14	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from naegleria fowleri
76	c6bqwH	Alignment	not modelled	98.2	12	PDB header: cytosolic protein Chain: H: PDB Molecule: bacterial actin alfa; PDBTitle: alfa filament bound to amppnp
77	d2ewsal	Alignment	not modelled	98.2	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
78	c6fpeG	Alignment	not modelled	98.2	17	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
79	c2qm1D	Alignment	not modelled	98.1	17	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
80	c1nbwA	Alignment	not modelled	98.1	24	PDB header: hydrolase Chain: A: PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
81	c1t6dB	Alignment	not modelled	98.1	13	PDB header: hydrolase Chain: B: PDB Molecule: exopolyphosphatase; PDBTitle: miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
82	c2ap1A	Alignment	not modelled	98.1	18	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein

83	c2ch5D	Alignment	not modelled	98.1	15	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
84	c1z6rC	Alignment	not modelled	98.0	18	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
85	c3cetA	Alignment	not modelled	97.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: crystal structure of the pantheonate kinase-like protein q6m145 at the2 resolution 1.8 a. northeast structural genomics consortium target3 mrr63
86	c3vovC	Alignment	not modelled	97.9	19	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
87	c3cerD	Alignment	not modelled	97.9	14	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
88	d2d0oa3	Alignment	not modelled	97.8	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
89	c5vm1A	Alignment	not modelled	97.8	21	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylofucose kinase from brucella ovis
90	c3hz6A	Alignment	not modelled	97.8	22	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
91	c1zc6A	Alignment	not modelled	97.7	14	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.
92	c2nlxA	Alignment	not modelled	97.7	20	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
93	d1nbwa3	Alignment	not modelled	97.7	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
94	c1z05A	Alignment	not modelled	97.7	16	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.
95	c5htxA	Alignment	not modelled	97.6	19	PDB header: transferase Chain: A: PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp
96	c1xupO	Alignment	not modelled	97.6	19	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
97	c2floA	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
98	c4bc2A	Alignment	not modelled	97.6	21	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
99	c2zf5O	Alignment	not modelled	97.5	16	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
100	c3mdqA	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
101	c3i8bA	Alignment	not modelled	97.5	26	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
102	d1r59o2	Alignment	not modelled	97.5	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
103	c3htvA	Alignment	not modelled	97.5	15	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
104	c4htlA	Alignment	not modelled	97.5	15	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
105	c2dnpB	Alignment	not modelled	97.5	22	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
106	c3ifrB	Alignment	not modelled	97.5	22	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
107	c4ijaA	Alignment	not modelled	97.5	13	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mecrc2
108	c4db3A	Alignment	not modelled	97.5	14	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.
109	d2p3ra2	Alignment	not modelled	97.5	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
110	c5f7rA	Alignment	not modelled	97.5	11	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
111	c5hv7A	Alignment	not modelled	97.5	23	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribose
112	c3jvpA	Alignment	not modelled	97.4	17	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
113	c3gbtA	Alignment	not modelled	97.4	20	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
114	c3hi0B	Alignment	not modelled	97.4	17	PDB header: hydrolase Chain: B: PDB Molecule: putative exopolyphosphatase; PDBTitle: crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
115	c5ya2A	Alignment	not modelled	97.4	20	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
116	c3vpzA	Alignment	not modelled	97.3	17	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
117	c3zyyX	Alignment	not modelled	97.3	16	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
118	c1glbG	Alignment	not modelled	97.3	21	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiiglc with2 glycerol kinase
119	c3g25B	Alignment	not modelled	97.3	20	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.
120	c2cgkB	Alignment	not modelled	97.3	16	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.