

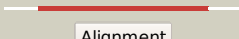

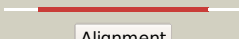




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0350_(dnaK)_419835_421712
Date	Tue Jul 23 14:50:42 BST 2019
Unique Job ID	4207ac6bc4c30aaf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2khoA_	 Alignment		100.0	59	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
2	c5e84B_	 Alignment		100.0	52	PDB header: chaperone Chain: B: PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
3	c3d2fC_	 Alignment		100.0	26	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
4	c5tkyA_	 Alignment		100.0	45	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
5	c3c7nB_	 Alignment		100.0	55	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	67	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	58	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnaK; PDBTitle: mycoplasma genitalium dnaK deletion mutant lacking sbdalpha in complex2 with amppnp.
8	c5mb9B_	 Alignment		100.0	28	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	c4j8fA_	 Alignment		100.0	51	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
10	c4kboA_	 Alignment		100.0	58	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
11	c4gniA_	 Alignment		100.0	31	PDB header: chaperone Chain: A: PDB Molecule: putative heat shock protein; PDBTitle: structure of the sss21 atpase bound to atp and magnesium

12	c1dkgD_	Alignment		100.0	58	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
13	c3iucC_	Alignment		100.0	55	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
14	c6gfaA_	Alignment		100.0	34	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
15	c1hpmA_	Alignment		100.0	51	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	c2v7zA_	Alignment		100.0	50	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
17	c4rtfD_	Alignment		100.0	99	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
18	c1jcgA_	Alignment		100.0	23	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreb; PDBTitle: mreb from thermotoga maritima, amppnp
19	c4czeA_	Alignment		100.0	19	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreb; PDBTitle: c. crescentus mreb, double filament, empty
20	c1u00A_	Alignment		100.0	35	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein hsca; PDBTitle: hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
21	c3h1qB_	Alignment	not modelled	100.0	30	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrnus hydrogenoformans
22	c5jygA_	Alignment	not modelled	100.0	19	PDB header: structural protein Chain: A: PDB Molecule: actin-like atpase; PDBTitle: cryo-em structure of the mamk filament at 6.5 a
23	c5e85A_	Alignment	not modelled	100.0	47	PDB header: chaperone Chain: A: PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: isolated sbd of bip
24	d1dkgd2	Alignment	not modelled	100.0	56	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
25	c4po2A_	Alignment	not modelled	100.0	50	PDB header: chaperone Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b; PDBTitle: crystal structure of the stress-inducible human heat shock protein2 hsp70 substrate-binding domain in complex with peptide substrate
26	d1bupa2	Alignment	not modelled	100.0	44	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
27	d2e8aa2	Alignment	not modelled	100.0	44	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
28	c3dpqE_	Alignment	not modelled	100.0	59	PDB header: chaperone, peptide binding protein Chain: E: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrolicorcin-derived3 inhibitor peptide (form b)

29	c1e4gT_	Alignment	not modelled	100.0	16	PDB header: bacterial cell division Chain: T; PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
30	d2e8aa1	Alignment	not modelled	100.0	59	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
31	d1dkgd1	Alignment	not modelled	100.0	63	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
32	c4xe7A_	Alignment	not modelled	100.0	15	PDB header: structural protein Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: bacillus thuringiensis parm in apo form
33	c1o1f4_	Alignment	not modelled	100.0	16	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	c5gjjA_	Alignment	not modelled	100.0	43	PDB header: chaperone Chain: A; PDB Molecule: heat shock 70 kda protein 1a; PDBTitle: glutathionylated hsp70 sbd
35	c5afuB_	Alignment	not modelled	100.0	14	PDB header: motor protein Chain: B; PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex
36	d1bupa1	Alignment	not modelled	100.0	57	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
37	c2d0oA_	Alignment	not modelled	100.0	15	PDB header: chaperone Chain: A; PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: structure of diol dehydratase-reactivating factor complexed 2 with adp and mg2+
38	c6izrK_	Alignment	not modelled	100.0	17	PDB header: protein fibril Chain: K; PDB Molecule: putative plasmid segregation protein parm; PDBTitle: whole structure of a 15-stranded parm filament from clostridium 2 botulinum
39	c3wqtB_	Alignment	not modelled	100.0	15	PDB header: structural genomics Chain: B; PDB Molecule: cell division protein ftsa; PDBTitle: staphylococcus aureus ftsa complexed with amppnp
40	c4jd2B_	Alignment	not modelled	99.9	14	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
41	c3n8eA_	Alignment	not modelled	99.9	65	PDB header: chaperone Chain: A; PDB Molecule: stress-70 protein, mitochondrial; PDBTitle: substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
42	c1bprA_	Alignment	not modelled	99.9	63	PDB header: molecular chaperone Chain: A; PDB Molecule: dnak; PDBTitle: nmr structure of the substrate binding domain of dnak, 2 minimized average structure
43	c5eoxB_	Alignment	not modelled	99.9	20	PDB header: peptide binding protein Chain: B; PDB Molecule: type 4 fimbrial biogenesis protein pilm; PDBTitle: pseudomonas aeruginosa pilm bound to adp
44	c3dwlB_	Alignment	not modelled	99.9	17	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
45	d1jcea1	Alignment	not modelled	99.9	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
46	c2p9lA_	Alignment	not modelled	99.9	17	PDB header: structural protein Chain: A; PDB Molecule: actin-like protein 3; PDBTitle: crystal structure of bovine arp2/3 complex
47	c4pl7B_	Alignment	not modelled	99.9	18	PDB header: structural protein, contractile protein Chain: B; PDB Molecule: actin, thymosin beta-4; PDBTitle: structure of komagataella pastoris actin-thymosin beta4 hybrid
48	c1mwmA_	Alignment	not modelled	99.9	21	PDB header: structural protein Chain: A; PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
49	d1jcea2	Alignment	not modelled	99.9	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
50	c2fsnB_	Alignment	not modelled	99.9	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
51	d1yuwa1	Alignment	not modelled	99.9	66	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
52	c2op6A_	Alignment	not modelled	99.9	58	PDB header: peptide binding protein Chain: A; PDB Molecule: heat shock 70 kda protein d; PDBTitle: peptide-binding domain of heat shock 70 kda protein d precursor from 2 c.elegans
53	c6gejR_	Alignment	not modelled	99.9	13	PDB header: nuclear protein Chain: R; PDB Molecule: actin-like protein arp6; PDBTitle: chromatin remodeler-nucleosome complex at 3.6 a resolution.
54	c4apwH_	Alignment	not modelled	99.9	15	PDB header: structural protein Chain: H; PDB Molecule: alp12; PDBTitle: alp12 filament structure
55	c4f6mA_	Alignment	not modelled	99.9	20	PDB header: transcription/hydrolase Chain: A; PDB Molecule: actin-related protein 7;

55	c4umA	Alignment	not modelled	99.9	20	PDBTitle: structure of arp7-arp9-snf2(hsa)-rtt102 subcomplex of swi/snf2 chromatin remodeler.
56	c2ychA	Alignment	not modelled	99.8	21	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilm; PDBTitle: pilm-piln type iv pilus biogenesis complex
57	c3js6A	Alignment	not modelled	99.8	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized parm protein; PDBTitle: crystal structure of apo psk41 parm protein
58	c3qb0C	Alignment	not modelled	99.8	16	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
59	d1u00a2	Alignment	not modelled	99.8	48	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
60	c3dggC	Alignment	not modelled	99.8	70	PDB header: chaperone Chain: C: PDB Molecule: heat shock 70 kda protein f; PDBTitle: peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.
61	d1dkza2	Alignment	not modelled	99.8	71	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
62	c4fo0A	Alignment	not modelled	99.8	17	PDB header: gene regulation Chain: A: PDB Molecule: actin-related protein 8; PDBTitle: human actin-related protein arp8 in its atp-bound state
63	c6etxH	Alignment	not modelled	99.7	15	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
64	d1e4ft2	Alignment	not modelled	99.7	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
65	c5aftJ	Alignment	not modelled	99.7	14	PDB header: motor protein Chain: J: PDB Molecule: actin related protein 11; PDBTitle: cryoem structure of dynactin complex at 4.0 angstrom2 resolution
66	c4i6mB	Alignment	not modelled	99.7	12	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.
67	c4cj7B	Alignment	not modelled	99.7	15	PDB header: structural protein Chain: B: PDB Molecule: actin/actin family protein; PDBTitle: structure of crenactin, an archeal actin-like protein
68	c6fhsJ	Alignment	not modelled	99.6	16	PDB header: dna binding protein Chain: J: PDB Molecule: arp5; PDBTitle: cryoem structure of ino80core
69	d1huxa	Alignment	not modelled	99.6	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
70	d2zgya2	Alignment	not modelled	99.6	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
71	c4am6A	Alignment	not modelled	99.6	18	PDB header: nuclear protein Chain: A: PDB Molecule: actin-like protein arp8; PDBTitle: c-terminal domain of actin-related protein arp8 from s. cerevisiae
72	d1u00a1	Alignment	not modelled	99.5	21	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
73	c6fmJ	Alignment	not modelled	99.5	14	PDB header: dna binding protein Chain: J: PDB Molecule: actin related protein 5; PDBTitle: cryoem structure ino80core nucleosome complex
74	d1dkza1	Alignment	not modelled	99.4	42	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
75	d2fsja1	Alignment	not modelled	99.4	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
76	c5z8qA	Alignment	not modelled	99.3	25	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein ssa1; PDBTitle: solution structure of the sbdalpha domain of yeast ssa1
77	d1dkyb1	Alignment	not modelled	99.2	42	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
78	c3uleB	Alignment	not modelled	99.2	17	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
79	d1nm1a2	Alignment	not modelled	99.1	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
80	c3gg4B	Alignment	not modelled	99.1	17	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
81	d2hf3a2	Alignment	not modelled	99.0	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
						Fold: Ribonuclease H-like motif

82	d2fxua2	Alignment	not modelled	99.0	18	Superfamily: Actin-like ATPase domain Family: Actin/HSP70
83	c4ehtA	Alignment	not modelled	99.0	20	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
84	c2e2pA	Alignment	not modelled	99.0	15	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
85	d1ud0a	Alignment	not modelled	98.9	11	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
86	c4xhpA	Alignment	not modelled	98.9	15	PDB header: structural protein Chain: A: PDB Molecule: parm hybrid fusion protein; PDBTitle: bacillus thuringiensis parm hybrid protein with adp, containing two2 parm mutants
87	c3lofF	Alignment	not modelled	98.9	18	PDB header: chaperone Chain: F: PDB Molecule: heat shock 70 kda protein 1; PDBTitle: c-terminal domain of human heat shock 70kda protein 1b.
88	c6fpeG	Alignment	not modelled	98.9	20	PDB header: rna binding protein Chain: G: PDB Molecule: trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: bacterial protein complex
89	c2p32B	Alignment	not modelled	98.8	10	PDB header: chaperone Chain: B: PDB Molecule: heat shock 70 kda protein a; PDBTitle: crystal structure of the c-terminal 10 kda subdomain from c. elegans2 hsp70
90	d1yaga2	Alignment	not modelled	98.8	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
91	c1ud0B	Alignment	not modelled	98.7	11	PDB header: chaperone Chain: B: PDB Molecule: 70 kda heat-shock-like protein; PDBTitle: crystal structure of the c-terminal 10-kda subdomain of hsc70
92	c2p9kB	Alignment	not modelled	98.7	16	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
93	d1k8kb1	Alignment	not modelled	98.6	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
94	d1k8ka2	Alignment	not modelled	98.6	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
95	c6bqwH	Alignment	not modelled	98.4	21	PDB header: cytosolic protein Chain: H: PDB Molecule: bacterial actin alfa; PDBTitle: alfa filament bound to amppnp
96	c3vovC	Alignment	not modelled	98.1	20	PDB header: transferase Chain: C: PDB Molecule: glucokinase; PDBTitle: crystal structure of rok hexokinase from thermus thermophilus
97	c6da0A	Alignment	not modelled	98.0	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (nfhk) from naegleria fowleri
98	d2ewsa1	Alignment	not modelled	98.0	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
99	c3hz6A	Alignment	not modelled	97.9	15	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
100	d2hf3a1	Alignment	not modelled	97.9	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
101	d2fxua1	Alignment	not modelled	97.9	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
102	d1sz2a1	Alignment	not modelled	97.8	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
103	d1c0fa1	Alignment	not modelled	97.8	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
104	d1r59o2	Alignment	not modelled	97.8	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
105	c5f7rA	Alignment	not modelled	97.8	13	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes bound to inducer
106	d1yaga1	Alignment	not modelled	97.8	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
107	c2nlxA	Alignment	not modelled	97.8	17	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
108	c5vm1A	Alignment	not modelled	97.7	17	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylolyose kinase from brucella ovis

109	d2p3ra2	Alignment	not modelled	97.7	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
110	c5ya2A	Alignment	not modelled	97.6	19	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
111	c2aa4B	Alignment	not modelled	97.6	18	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
112	c2zf5O	Alignment	not modelled	97.6	18	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
113	c4bc2A	Alignment	not modelled	97.6	12	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
114	c3ifrB	Alignment	not modelled	97.6	19	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
115	c1xupO	Alignment	not modelled	97.6	22	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
116	c4c23A	Alignment	not modelled	97.5	21	PDB header: transferase Chain: A: PDB Molecule: l-fuculose kinase fuck; PDBTitle: l-fuculose kinase
117	c3vpzA	Alignment	not modelled	97.5	12	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from antarctic psychrotroph at 1.69a
118	c2dpnB	Alignment	not modelled	97.5	20	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
119	c3gbtA	Alignment	not modelled	97.5	10	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
120	c5htxA	Alignment	not modelled	97.5	21	PDB header: transferase Chain: A: PDB Molecule: putative xylulose kinase; PDBTitle: putative sugar kinases from arabidopsis thaliana in complex with adp