
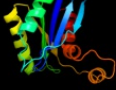

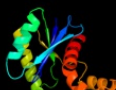
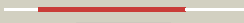


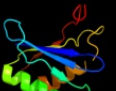
























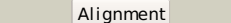
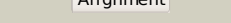
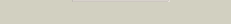





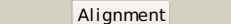
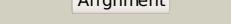
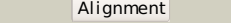
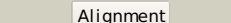

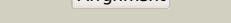
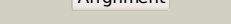
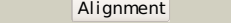
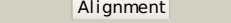
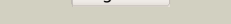




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nu0a_	 Alignment		100.0	97	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
2	d1vhxa_	 Alignment		100.0	32	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
3	d1iv0a_	 Alignment		100.0	28	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
4	d3bzka5	 Alignment		99.2	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
5	c2oceA_	 Alignment		98.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from pseudomonas aeruginosa
6	d1hjra_	 Alignment		98.3	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: RuvC resolvase
7	c3psfA_	 Alignment		98.1	16	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)
8	c3psiA_	 Alignment		98.0	16	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)
9	c1xc3A_	 Alignment		97.4	13	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
10	d2gupa1	 Alignment		97.3	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
11	d1xc3a1	 Alignment		97.1	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK

12	d2aa4a1	Alignment		96.9	10	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
13	d2hoea3	Alignment		96.9	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
14	d2ap1a2	Alignment		96.8	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
15	c3htvA_	Alignment		96.5	12	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
16	dlz6ra2	Alignment		96.4	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
17	dlz05a3	Alignment		96.3	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
18	c1woqB_	Alignment		96.0	12	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
19	dlokja1	Alignment		95.9	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
20	dljcea1	Alignment		95.8	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
21	d1woqa1	Alignment	not modelled	95.8	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
22	c2e2pA_	Alignment	not modelled	95.7	9	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
23	c1z6rC_	Alignment	not modelled	95.7	13	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
24	c1okjB_	Alignment	not modelled	95.5	14	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protease yeaz; PDBTitle: crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
25	d1sz2a1	Alignment	not modelled	95.5	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
26	c3eo3B_	Alignment	not modelled	95.2	17	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
27	c3r6mD_	Alignment	not modelled	95.2	16	PDB header: hydrolase Chain: D: PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz
28	c2ch5D_	Alignment	not modelled	95.1	7	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine

29	c2hoeA	 Alignment	not modelled	95.0	12	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
30	c2gupA	 Alignment	not modelled	94.7	15	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
31	c2qm1D	 Alignment	not modelled	94.7	14	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
32	c1z05A	 Alignment	not modelled	94.6	12	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.
33	c3vgkB	 Alignment	not modelled	94.6	13	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
34	d1q18a1	 Alignment	not modelled	94.5	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
35	c2ap1A	 Alignment	not modelled	94.5	14	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
36	c3mcpA	 Alignment	not modelled	94.5	17	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
37	c3r8eA	 Alignment	not modelled	93.5	10	PDB header: transferase Chain: A: PDB Molecule: hypothetical sugar kinase; PDBTitle: crystal structure of a hypothetical sugar kinase (chu_1875) from2 cytophaga hutchinsonii atcc 33406 at 1.65 a resolution
38	d1bupa1	 Alignment	not modelled	93.3	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
39	d2a6aa1	 Alignment	not modelled	91.2	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
40	c3h1qB	 Alignment	not modelled	91.0	17	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrmus hydrogenoformans
41	c3lm2B	 Alignment	not modelled	90.5	18	PDB header: transferase Chain: B: PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
42	d2ewsal	 Alignment	not modelled	90.4	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
43	d1dkgd1	 Alignment	not modelled	90.4	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
44	d2e8aa1	 Alignment	not modelled	89.9	33	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
45	c1hpmA	 Alignment	not modelled	89.8	33	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
46	d2ch5a2	 Alignment	not modelled	89.5	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
47	c2a6aB	 Alignment	not modelled	89.1	14	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
48	c2v7zA	 Alignment	not modelled	88.8	32	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
49	c3iucC	 Alignment	not modelled	88.4	36	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
50	c2aa4B	 Alignment	not modelled	88.2	12	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
51	d2nu7b1	 Alignment	not modelled	87.3	16	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
52	d3bexa1	 Alignment	not modelled	86.6	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
53	c1dkgD	 Alignment	not modelled	86.0	29	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

54	c2v7yA	Alignment	not modelled	85.7	35	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
55	d1t6ca1	Alignment	not modelled	82.1	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
56	d1huxa	Alignment	not modelled	81.5	10	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
57	c3bf1C	Alignment	not modelled	81.1	14	PDB header: transferase Chain: C: PDB Molecule: type iii pantothenate kinase; PDBTitle: type iii pantothenate kinase from thermotoga maritima2 complexed with pantothenate and adp
58	c3djca	Alignment	not modelled	80.6	16	PDB header: transferase Chain: A: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of pantothenate kinase from legionella pneumophila
59	c1zc6A	Alignment	not modelled	80.5	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.
60	c1jcgA	Alignment	not modelled	80.3	21	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
61	c2nu9E	Alignment	not modelled	77.8	16	PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
62	c3gg4B	Alignment	not modelled	76.9	18	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
63	c2khoA	Alignment	not modelled	74.9	30	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 70; PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
64	c1x7fA	Alignment	not modelled	73.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
65	d1yoba1	Alignment	not modelled	72.6	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
66	c2q2rA	Alignment	not modelled	72.4	12	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
67	c2w40C	Alignment	not modelled	70.6	20	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
68	c2ychA	Alignment	not modelled	70.6	14	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilM; PDBTitle: pilM-pilN type iv pilus biogenesis complex
69	d2p3ra1	Alignment	not modelled	70.5	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
70	d1zc6a1	Alignment	not modelled	70.1	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
71	d2fcra	Alignment	not modelled	68.2	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
72	c3d2fC	Alignment	not modelled	66.7	24	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
73	d1mo6a1	Alignment	not modelled	64.2	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
74	c3fg9B	Alignment	not modelled	64.0	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
75	c3dl0C	Alignment	not modelled	63.3	11	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
76	d1loboa	Alignment	not modelled	62.6	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
77	c3ifrB	Alignment	not modelled	60.2	17	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
78	c2zf5O	Alignment	not modelled	59.8	22	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
79	d2f9wa2	Alignment	not modelled	59.2	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
						PDB header: transferase

80	c1xupO_	Alignment	not modelled	58.6	19	Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
81	d1eucb1	Alignment	not modelled	58.5	14	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
82	d1tq8a_	Alignment	not modelled	58.4	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
83	d1czna_	Alignment	not modelled	58.4	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
84	c3fh0A_	Alignment	not modelled	57.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative universal stress protein kpn_01444; PDBTitle: crystal structure of putative universal stress protein kpn_01444 -2 atpase
85	c3cerD_	Alignment	not modelled	57.5	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: possible exopolyphosphatase-like protein; PDBTitle: crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
86	c3g25B_	Alignment	not modelled	56.9	19	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.
87	c2floA_	Alignment	not modelled	56.9	16	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
88	d1u6za2	Alignment	not modelled	56.2	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
89	c1t6dB_	Alignment	not modelled	55.5	17	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
90	c3mdqA_	Alignment	not modelled	55.4	17	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
91	c2wc1A_	Alignment	not modelled	55.2	15	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
92	c3flcX_	Alignment	not modelled	55.0	19	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
93	c3gbtA_	Alignment	not modelled	55.0	8	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
94	c2cgkB_	Alignment	not modelled	53.2	24	PDB header: transferase Chain: B: PDB Molecule: l-rhamnulose kinase; PDBTitle: crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
95	d2z3va1	Alignment	not modelled	51.9	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
96	c2pfsA_	Alignment	not modelled	51.8	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
97	d1qd1a1	Alignment	not modelled	51.6	29	Fold: Ferredoxin-like Superfamily: Formiminotransferase domain of formiminotransferase-cyclodeaminase. Family: Formiminotransferase domain of formiminotransferase-cyclodeaminase.
98	c1mwmA_	Alignment	not modelled	50.7	18	PDB header: structural protein Chain: A: PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
99	c2dpnB_	Alignment	not modelled	50.1	28	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
100	c3hi0B_	Alignment	not modelled	49.3	20	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
101	c3hgmD_	Alignment	not modelled	49.2	20	PDB header: signaling protein Chain: D: PDB Molecule: universal stress protein tead; PDBTitle: universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
102	c3ezwD_	Alignment	not modelled	48.7	26	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
103	c2h3gX_	Alignment	not modelled	48.3	12	PDB header: biosynthetic protein Chain: X: PDB Molecule: biosynthetic protein; PDBTitle: structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
104	d2i7pa2	Alignment	not modelled	48.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
						PDB header: hydrolase

105	c3en9B_	Alignment	not modelled	47.5	13	Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
106	c1e4gT_	Alignment	not modelled	47.1	15	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
107	c3agiB_	Alignment	not modelled	46.7	14	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
108	c3agiD_	Alignment	not modelled	46.7	14	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
109	c3hz6A_	Alignment	not modelled	45.9	22	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
110	c1qd1A_	Alignment	not modelled	45.9	29	PDB header: transferase Chain: A: PDB Molecule: formiminotransferase-cyclodeaminase; PDBTitle: the crystal structure of the formiminotransferase domain of2 formiminotransferase-cyclodeaminase.
111	c3i8bA_	Alignment	not modelled	45.4	20	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
112	c1glbG_	Alignment	not modelled	43.5	26	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
113	d1b74a1	Alignment	not modelled	42.7	23	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
114	c2d4wA_	Alignment	not modelled	42.4	21	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
115	d1nmpa_	Alignment	not modelled	39.5	15	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
116	d2qi2a2	Alignment	not modelled	39.4	16	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: ERF1/Dom34 middle domain-like
117	c3n2qA_	Alignment	not modelled	36.7	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sex pheromone staph-cam373; PDBTitle: crystal structure of sex pheromone staph-cam373 precursor
118	c3mcaB_	Alignment	not modelled	36.0	8	PDB header: translation regulation/hydrolase Chain: B: PDB Molecule: protein dom34; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
119	c2nlxA_	Alignment	not modelled	35.9	30	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
120	c3obyB_	Alignment	not modelled	35.7	10	PDB header: hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity