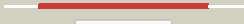



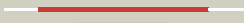

















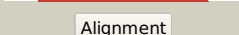





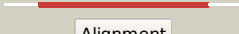














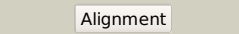
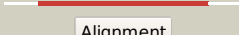





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2436_(rbsK)_2733240_2734154
Date	Wed Aug 7 12:50:06 BST 2019
Unique Job ID	3770c2768f323a02

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3go6B_	 Alignment		100.0	100	PDB header: transferase Chain: B: PDB Molecule: ribokinase rbsk; PDBTitle: crystal structure of m. tuberculosis ribokinase (rv2436) in complex2 with ribose and amp-pnp
2	c4x8fD_	 Alignment		100.0	35	PDB header: transferase Chain: D: PDB Molecule: ribokinase; PDBTitle: vibrio cholerae o395 ribokinase in apo form
3	c2c49A_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: sugar kinase mj0406; PDBTitle: crystal structure of methanocaldococcus jannaschii nucleoside kinase -2 an archaeal member of the ribokinase family
4	c6ilsB_	 Alignment		100.0	29	PDB header: transferase Chain: B: PDB Molecule: ribokinase; PDBTitle: structure of arabidopsis thaliana ribokinase complexed with ribose and2 atp
5	d1rkda_	 Alignment		100.0	36	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
6	c3i3yB_	 Alignment		100.0	27	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase; PDBTitle: crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
7	c2rbcA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: sugar kinase; PDBTitle: crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
8	d1v19a_	 Alignment		100.0	26	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
9	c2nwhA_	 Alignment		100.0	20	PDB header: signaling protein,transferase Chain: A: PDB Molecule: carbohydrate kinase; PDBTitle: carbohydrate kinase from agrobacterium tumefaciens
10	c3iq0B_	 Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: putative ribokinase ii; PDBTitle: crystal structure of a putative ribokinase ii in complex2 with atp and mg+2 from e.coli
11	c5zwyB_	 Alignment		100.0	31	PDB header: transferase Chain: B: PDB Molecule: ribokinase; PDBTitle: ribokinase from leishmania donovani

12	c2pkkA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluoro adenosine
13	c3ry7A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: ribokinase; PDBTitle: crystal structure of sa239
14	d1vm7a_	 Alignment		100.0	32	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
15	c6cw5A_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: ribokinase; PDBTitle: crystal structure of ribokinase from cryptococcus neoformans var.2 grubii serotype a
16	c3pl2D_	 Alignment		100.0	21	PDB header: transferase Chain: D: PDB Molecule: sugar kinase, ribokinase family; PDBTitle: crystal structure of a 5-keto-2-deoxygluconokinase (ncgl0155, cgl0158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution
17	c3kzhA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: crystal structure of a putative sugar kinase from2 clostridium perfringens
18	d2fv7a1	 Alignment		100.0	32	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
19	c3b1qD_	 Alignment		100.0	22	PDB header: transferase Chain: D: PDB Molecule: ribokinase, putative; PDBTitle: structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
20	c5eynA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase from vibrio cholerae o395 in2 fructose, adp, beryllium trifluoride and calcium ion bound form
21	c3in1A_	 Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: uncharacterized sugar kinase ydjh; PDBTitle: crystal structure of a putative ribokinase in complex with2 adp from e.coli
22	c3cqdB_	 Alignment	not modelled	100.0	23	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase isozyme 2; PDBTitle: structure of the tetrameric inhibited form of phosphofructokinase-22 from escherichia coli
23	d1bx4a_	 Alignment	not modelled	100.0	21	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
24	c2xtbA_	 Alignment	not modelled	100.0	24	PDB header: transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator
25	c2qcva_	 Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: putative 5-dehydro-2-deoxygluconokinase; PDBTitle: crystal structure of a putative 5-dehydro-2-deoxygluconokinase (iolc)2 from bacillus halodurans c-125 at 1.90 a resolution
26	c2jg1C_	 Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: tagatose-6-phosphate kinase; PDBTitle: structure of staphylococcus aureus d-tagatose-6-phosphate2 kinase with cofactor and substrate
27	c3ktnA_	 Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: carbohydrate kinase, pfbk family; PDBTitle: crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
28	d2afba1	 Alignment	not modelled	100.0	20	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like

29	c3looC	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C: PDB Molecule: anopheles gambiae adenosine kinase; PDBTitle: crystal structure of anopheles gambiae adenosine kinase in complex2 with p1,p4-di(adenosine-5) tetraphosphate
30	d1tyya	Alignment	not modelled	100.0	30	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
31	d2dcna1	Alignment	not modelled	100.0	21	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
32	c4gm6C	Alignment	not modelled	100.0	16	PDB header: transferase Chain: C: PDB Molecule: pfkb family carbohydrate kinase; PDBTitle: crystal structure of pfkb family carbohydrate kinase(target efi-5021462 from listeria grayi dsm 20601
33	c3bf5A	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: ribokinase related protein; PDBTitle: crystal structure of putative ribokinase (10640157) from thermoplasma2 acidophilum at 1.91 a resolution
34	d2abqa1	Alignment	not modelled	100.0	22	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
35	c4e3aB	Alignment	not modelled	100.0	23	PDB header: transferase Chain: B: PDB Molecule: sugar kinase protein; PDBTitle: crystal structure of probable sugar kinase protein from rhizobium etli2 cfn 42
36	c4u7xA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: ribokinase:carbohydrate kinase, pfkb; PDBTitle: crystal structure of fructokinase from brucella abortus 2308
37	c2varB	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: fructokinase; PDBTitle: crystal structure of sulfolobus solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate
38	d2absa1	Alignment	not modelled	100.0	24	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
39	c2absA	Alignment	not modelled	100.0	24	PDB header: signaling protein,transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of t. gondii adenosine kinase complexed with amp-pcp
40	d2f02a1	Alignment	not modelled	100.0	19	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
41	c2jg5B	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: fructose 1-phosphate kinase; PDBTitle: crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
42	c3uq6B	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: adenosine kinase, putative; PDBTitle: adenosine kinase from schistosoma mansoni in complex with adenosine2 and amp
43	c3gbuD	Alignment	not modelled	100.0	22	PDB header: transferase Chain: D: PDB Molecule: uncharacterized sugar kinase ph1459; PDBTitle: crystal structure of an uncharacterized sugar kinase ph1459 from2 pyrococcus horikoshii in complex with atp
44	c1tz6B	Alignment	not modelled	100.0	29	PDB header: transferase Chain: B: PDB Molecule: putative sugar kinase; PDBTitle: crystal structure of aminoimidazole riboside kinase from2 salmonella enterica complexed with aminoimidazole riboside3 and atp analog
45	c4e8wA	Alignment	not modelled	100.0	20	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: d-beta-d-heptose 7-phosphate kinase; PDBTitle: crystal structure of burkholderia cenocepacia hlda in complex with an2 atp-competitive inhibitor
46	c3b3lC	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C: PDB Molecule: ketohehexokinase; PDBTitle: crystal structures of alternatively-spliced isoforms of human2 ketohehexokinase
47	c3lkiA	Alignment	not modelled	100.0	23	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase with bound atp from2 xylella fastidiosa
48	c4ebuA	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxygluconokinase; PDBTitle: crystal structure of a sugar kinase (target efi-502312) from2 oceanicola granulosis, with bound amp/adp crystal form i
49	c3kd6B	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, pfkb family; PDBTitle: crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
50	c3juIA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: lin2199 protein; PDBTitle: crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
51	c2qhpA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
52	c4du5B	Alignment	not modelled	100.0	24	PDB header: transferase Chain: B: PDB Molecule: pfkb; PDBTitle: crystal structure of pfkb protein from polaromonas sp. js666
53	c3lhxA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: ketodeoxygluconokinase; PDBTitle: crystal structure of a ketodeoxygluconokinase (kdgk) from shigella2 flexneri
54	d2ajra1	Alignment	not modelled	100.0	17	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like

55	c3hj6B_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: B: PDB Molecule: fructokinase; PDBTitle: structure of halothermothrix orenii fructokinase (frk)
56	d1vk4a_	Alignment	not modelled	100.0	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
57	c3w4sB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: carbohydrate/pyrimidine kinase, pfb family; PDBTitle: myo-inositol kinase from thermococcus kodakarensis
58	c2ddmA_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: pyridoxine kinase; PDBTitle: crystal structure of pyridoxal kinase from the escherichia coli pdxk2 gene at 2.1 a resolution
59	c5b6aA_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase pdxy; PDBTitle: structure of pyridoxal kinasefrom pseudomonas aeruginosa
60	c4s1hA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: pyridoxal kinase of entamoeba histolytica with adp
61	c5trwA_	Alignment	not modelled	99.7	20	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase pdxy; PDBTitle: crystal structure of pyridoxamine kinase pdxy from burkholderia2 xenovorans
62	c5zwbB_	Alignment	not modelled	99.7	20	PDB header: transferase Chain: B: PDB Molecule: pyridoxine/pyridoxal/pyridoxamine kinase; PDBTitle: crystal structure of pyridoxal kinase (pdxk) from salmonella2 typhimurium in complex with adp, pl-linked to lys233 via a schiff3 base
63	c3mbjA_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A: PDB Molecule: putative phosphomethylpyrimidine kinase; PDBTitle: crystal structure of a putative phosphomethylpyrimidine kinase2 (bt_4458) from bacteroides thetaiotaomicron vpi-5482 at 2.10 a3 resolution (rhombohedral form)
64	d1vi9a_	Alignment	not modelled	99.6	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
65	c2i5bC_	Alignment	not modelled	99.5	21	PDB header: transferase Chain: C: PDB Molecule: phosphomethylpyrimidine kinase; PDBTitle: the crystal structure of an adp complex of bacillus subtilis pyridoxal2 kinase provides evidence for the parralel emergence of enzyme3 activity during evolution
66	c3ibqA_	Alignment	not modelled	99.5	18	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: crystal structure of pyridoxal kinase from lactobacillus plantarum in2 complex with atp
67	d1ub0a_	Alignment	not modelled	99.5	23	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
68	d1hpa_	Alignment	not modelled	99.4	23	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
69	c3zs7A_	Alignment	not modelled	99.4	18	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: crystal structure of pyridoxal kinase from trypanosoma brucei
70	c6jyyC_	Alignment	not modelled	99.3	16	PDB header: hydrolase Chain: C: PDB Molecule: hydroxyethylthiazole kinase; PDBTitle: crystal structure of the 5-(hydroxyethyl)-methylthiazole kinase thim2 from klebsiella pneumonia
71	c4c51C_	Alignment	not modelled	99.3	24	PDB header: transferase Chain: C: PDB Molecule: phosphomethylpyrimidine kinase; PDBTitle: structure of the pyridoxal kinase from staphylococcus2 aureus in complex with pyridoxal
72	d1jxha_	Alignment	not modelled	99.1	19	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
73	c4jipB_	Alignment	not modelled	99.1	13	PDB header: transferase Chain: B: PDB Molecule: phosphomethylpyrimidine kinase; PDBTitle: 2.06 angstrom resolution crystal structure of phosphomethylpyrimidine2 kinase (thid)from clostridium difficile 630
74	c3rm5B_	Alignment	not modelled	99.0	18	PDB header: transferase Chain: B: PDB Molecule: hydroxymethylpyrimidine/phosphomethylpyrimidine kinase PDBTitle: structure of trifunctional thi20 from yeast
75	c3dzvB_	Alignment	not modelled	99.0	20	PDB header: transferase Chain: B: PDB Molecule: 4-methyl-5-(beta-hydroxyethyl)thiazole kinase; PDBTitle: crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole kinase2 (np_816404.1) from enterococcus faecalis v583 at 2.57 a resolution
76	c5cgaC_	Alignment	not modelled	98.8	22	PDB header: transferase Chain: C: PDB Molecule: hydroxyethylthiazole kinase; PDBTitle: structure of hydroxyethylthiazole kinase thim from staphylococcus2 aureus in complex with substrate analog 2-(1,3,5-trimethyl-1h-3 pyrazole-4-yl)ethanol
77	d1v8aa_	Alignment	not modelled	98.6	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
78	d1kyha_	Alignment	not modelled	98.4	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: YjeF C-terminal domain-like
79	c4yl5A_	Alignment	not modelled	98.4	13	PDB header: transferase Chain: A: PDB Molecule: putative phosphomethylpyrimidine kinase; PDBTitle: structure of a putative phosphomethylpyrimidine kinase

						from2 acinetobacter baumannii
80	d2ax3a1	Alignment	not modelled	98.1	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: YjeF C-terminal domain-like
81	d1lekqa	Alignment	not modelled	98.0	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
82	c6c8zA	Alignment	not modelled	97.7	15	PDB header: transferase Chain: A: PDB Molecule: adp-dependent phosphofructokinase; PDBTitle: last common ancestor of adp-dependent phosphofructokinases from2 methanosarcinales
83	c5k27B	Alignment	not modelled	97.7	17	PDB header: transferase Chain: B: PDB Molecule: ancmt; PDBTitle: crystal structure of ancestral protein ancmt of adp-dependent sugar2 kinases family.
84	c5od2B	Alignment	not modelled	97.6	13	PDB header: transferase Chain: B: PDB Molecule: bifunctional adp-specific glucokinase/phosphofructokinase; PDBTitle: crystal structure of adp-dependent glucokinase from methanocaldococcus2 jannaschii
85	d1gc5a	Alignment	not modelled	97.6	16	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
86	d1l2la	Alignment	not modelled	97.3	13	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
87	c5ccfA	Alignment	not modelled	97.2	17	PDB header: transferase Chain: A: PDB Molecule: adp-dependent glucokinase; PDBTitle: structure of mouse adp-dependent glucokinase
88	d1u2xa	Alignment	not modelled	97.2	16	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
89	c2ax3A	Alignment	not modelled	97.1	14	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tm0922; PDBTitle: crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
90	c3bgkA	Alignment	not modelled	96.9	13	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of hypothetic protein smu.573 from streptococcus2 mutans
91	c2r3bA	Alignment	not modelled	96.9	16	PDB header: transferase Chain: A: PDB Molecule: yjef-related protein; PDBTitle: crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution
92	d1ua4a	Alignment	not modelled	96.8	15	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
93	c3nm3D	Alignment	not modelled	96.2	18	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
94	c3k5wA	Alignment	not modelled	95.5	23	PDB header: transferase Chain: A: PDB Molecule: carbohydrate kinase; PDBTitle: crystal structure of a carbohydrate kinase (yjeF family)from2 helicobacter pylori
95	c3drwA	Alignment	not modelled	95.1	11	PDB header: transferase Chain: A: PDB Molecule: adp-specific phosphofructokinase; PDBTitle: crystal structure of a phosphofructokinase from pyrococcus horikoshii2 ot3 with amp
96	c6cauA	Alignment	not modelled	90.1	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with ampnpn
97	d1j6ua1	Alignment	not modelled	76.1	23	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
98	c2f00A	Alignment	not modelled	75.3	27	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
99	d1p3da1	Alignment	not modelled	71.8	16	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
100	d1wu2a3	Alignment	not modelled	59.6	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
101	c4wpgA	Alignment	not modelled	52.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmlD)
102	c5tukC	Alignment	not modelled	51.7	31	PDB header: oxidoreductase Chain: C: PDB Molecule: tetracycline destructase tet(51); PDBTitle: crystal structure of tetracycline destructase tet(51)
103	d1uz5a3	Alignment	not modelled	50.1	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
104	d2ftsa3	Alignment	not modelled	48.8	21	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
105	d1ofua1	Alignment	not modelled	43.3	20	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
						PDB header: cell cycle

106	c2rf6r1_	Alignment	not modelled	41.2	16	Chain: 1: PDB Molecule: cell division protein ftsz; PDBTitle: aquifex aeolicus ftsz
107	c2rhoB_	Alignment	not modelled	39.6	18	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: synthetic gene encoded bacillus subtilis ftsz ncs dimer with bound gdp2 and gtp-gamma-s
108	d1w5fa1	Alignment	not modelled	37.9	15	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
109	d2vapa1	Alignment	not modelled	36.5	18	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
110	c2vxyA_	Alignment	not modelled	35.1	18	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: the structure of ftsz from bacillus subtilis at 1.7a2 resolution
111	c1w5fA_	Alignment	not modelled	34.0	15	PDB header: cell division Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
112	d1rq2a1	Alignment	not modelled	34.0	19	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
113	d1djqa2	Alignment	not modelled	33.0	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: C-terminal domain of adrenodoxin reductase-like
114	c2vawA_	Alignment	not modelled	32.9	20	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz pseudomonas aeruginosa gdp
115	c3d8xB_	Alignment	not modelled	31.9	29	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of saccharomyces cerevisiae ndpph dependent2 thioredoxin reductase 1
116	c1w59B_	Alignment	not modelled	30.8	18	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
117	c3ay3C_	Alignment	not modelled	30.7	36	PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
118	c6bpyA_	Alignment	not modelled	28.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: aspergillus fumigatus thioredoxin reductase
119	c4jdrB_	Alignment	not modelled	27.4	34	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli
120	d1li4a1	Alignment	not modelled	27.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain