Phyre2

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Description	RVBD2202c_(cbhK)_2467061_2468035
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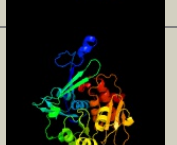
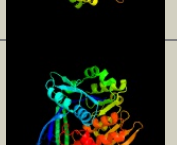
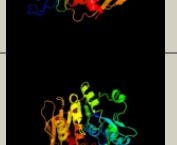
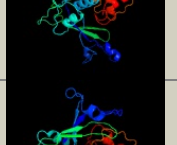
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pkkA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluro adenosine
2	c3b1qD_	Alignment		100.0	35	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase, putative; **PDBTitle:** structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
3	c2c49A_	Alignment		100.0	28	**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	c2rbcA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sugar kinase; **PDBTitle:** crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
5	c4x8fD_	Alignment		100.0	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribokinase; **PDBTitle:** vibrio cholerae o395 ribokinase in apo form
6	c6ilsB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribokinase; **PDBTitle:** structure of arabidopsis thaliana ribokinase complexed with ribose and2 atp
7	d1rkda_	Alignment		100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
8	c6cw5A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribokinase; **PDBTitle:** crystal structure of ribokinase from cryptococcus neoformans var.2 grubii serotype a
9	c3in1A_	Alignment		100.0	19	**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
10	c3pl2D_	Alignment		100.0	17	**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
11	d2fv7a1	Alignment		100.0	20	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like

12	c3kzhA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable sugar kinase; **PDBTitle:** crystal structure of a putative sugar kinase from2 clostridium perfringens
13	c2qcvA_	Alignment		100.0	14	**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
14	c3go6B_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribokinase rbsk; **PDBTitle:** crystal structure of m. tuberculosis ribokinase (rv2436) in complex2 with ribose and amp-pnp
15	c2nwhA_	Alignment		100.0	19	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** carbohydrate kinase from agrobacterium tumefaciens
16	c4e3aB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sugar kinase protein; **PDBTitle:** crystal structure of probable sugar kinase protein from rhizobium etli2 cfn 42
17	d1v19a_	Alignment		100.0	24	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
18	c3iq0B_	Alignment		100.0	15	**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
19	d1vm7a_	Alignment		100.0	21	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
20	c3i3yB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
21	c5zwyB_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribokinase; **PDBTitle:** ribokinase from leishmania donovani
22	c2xtbA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator
23	c2varB_	Alignment	not modelled	100.0	20	**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
24	c3ry7A_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribokinase; **PDBTitle:** crystal structure of sa239
25	c4gm6C_	Alignment	not modelled	100.0	14	**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
26	d2dcna1	Alignment	not modelled	100.0	21	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
27	d2f02a1	Alignment	not modelled	100.0	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
28	d1bx4a_	Alignment	not modelled	100.0	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
						Fold: Ribokinase-like

29	d2absa1	Alignment	not modelled	100.0	20	**Superfamily:**Ribokinase-like **Family:**Ribokinase-like
30	c2absA_	Alignment	not modelled	100.0	20	**PDB header:**signaling protein,transferase **Chain:** A: **PDB Molecule:**adenosine kinase; **PDBTitle:** crystal structure of t. gondii adenosine kinase complexed with amp-pcp
31	c5eynA_	Alignment	not modelled	100.0	21	**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
32	c3cqdB_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase isozyme 2; **PDBTitle:** structure of the tetrameric inhibited form of phosphofructokinase-22 from escherichia coli
33	c3ktnA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase, pfkb family; **PDBTitle:** crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
34	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
35	c3bf5A_	Alignment	not modelled	100.0	23	**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
36	d2abqa1	Alignment	not modelled	100.0	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
37	c2jg5B_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructose 1-phosphate kinase; **PDBTitle:** crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
38	c3looC_	Alignment	not modelled	100.0	18	**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
39	c3uq6B_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosine kinase, putative; **PDBTitle:** adenosine kinase from schistosoma mansoni in complex with adenosine2 and amp
40	c2jg1C_	Alignment	not modelled	100.0	15	**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
41	d2afba1	Alignment	not modelled	100.0	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
42	c4ebuA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxygluconokinase; **PDBTitle:** crystal structure of a sugar kinase (target efi-502312) from2 oceanicola granulosus, with bound amp/adp crystal form i
43	c3julA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lin2199 protein; **PDBTitle:** crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
44	c3b3lC_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ketohexokinase; **PDBTitle:** crystal structures of alternatively-spliced isoforms of human2 ketohexokinase
45	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
46	c4du5B_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pfkb; **PDBTitle:** crystal structure of pfkb protein from polaromonas sp. js666
47	d1tyya_	Alignment	not modelled	100.0	21	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
48	c4e8wA_	Alignment	not modelled	100.0	21	**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
49	c4u7xA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribokinase:carbohydrate kinase, pfkb; **PDBTitle:** crystal structure of fructokinase from brucella abortus 2308
50	c3lhxA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ketodeoxygluconokinase; **PDBTitle:** crystal structure of a ketodeoxygluconokinase (kdgk) from shigella2 flexneri
51	d2ajra1	Alignment	not modelled	100.0	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
52	c1tz6B_	Alignment	not modelled	100.0	21	**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
53	c3lkiA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of fructokinase with bound atp from2 xylella fastidiosa
54	c2qhpA_	Alignment	not modelled	100.0	17	**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

55	d1vk4a_	Alignment	not modelled	100.0	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Ribokinase-like
56	c3hj6B_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fructokinase; **PDBTitle:** structure of halothermothrix orenii fructokinase (frk)
57	c3w4sB_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate/pyrimidine kinase, pfkb family; **PDBTitle:** myo-inositol kinase from thermococcus kodakarensis
58	c2ddmA_	Alignment	not modelled	99.9	19	**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	18	**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	15	**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	19	**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	c3ibqA_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from lactobacillus plantarum in2 complex with atp
64	c3mbjA_	Alignment	not modelled	99.7	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)
65	c2i5bC_	Alignment	not modelled	99.6	15	**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	d1vi9a_	Alignment	not modelled	99.6	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
67	d1ub0a_	Alignment	not modelled	99.6	12	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
68	c3zs7A_	Alignment	not modelled	99.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxal kinase; **PDBTitle:** crystal structure of pyridoxal kinase from trypanosoma brucei
69	c4c5lC_	Alignment	not modelled	99.6	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphomethylpyrimidine kinase; **PDBTitle:** structure of the pyridoxal kinase from staphylococcus2 aureus in complex with pyridoxal
70	c6jyyC_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hydroxyethylthiazole kinase; **PDBTitle:** crystal structure of the 5-(hydroxyethyl)-methylthiazole kinase thim2 from klebsiella pneumonia
71	d1lhpa_	Alignment	not modelled	99.5	20	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**PfkB-like kinase
72	c3rm5B_	Alignment	not modelled	99.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hydroxymethylpyrimidine/phosphomethylpyrimidine kinase **PDBTitle:** structure of trifunctional thi20 from yeast
73	c4jjpB_	Alignment	not modelled	99.4	16	**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	c3dzvB_	Alignment	not modelled	99.3	12	**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
75	d1jxha_	Alignment	not modelled	99.3	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
76	d2ax3a1	Alignment	not modelled	99.0	13	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
77	d1kyha_	Alignment	not modelled	98.9	14	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**YjeF C-terminal domain-like
78	d1v8aa_	Alignment	not modelled	98.9	18	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
79	c5cgaC_	Alignment	not modelled	98.9	11	**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
80	c4yl5A_	Alignment	not modelled	98.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphomethylpyrimidine kinase; **PDBTitle:** structure of a putative phosphomethylpyrimidine kinase from2 acinetobacter baumannii
81	d1ekqa_	Alignment	not modelled	98.6	12	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
82	c2ax3A_	Alignment	not modelled	98.6	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
83	c5k27B_	Alignment	not modelled	98.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ancmt; **PDBTitle:** crystal structure of ancestral protein ancmt of adp-dependent sugar2 kinases family.
84	d1gc5a_	Alignment	not modelled	98.5	17	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
85	c5od2B_	Alignment	not modelled	98.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional adp-specific glucokinase/phosphofructokinase; **PDBTitle:** crystal structure of adp-dependent glucokinase from methanocaldococcus2 jannaschii
86	c2r3bA_	Alignment	not modelled	98.4	8	**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
87	c3nm3D_	Alignment	not modelled	98.3	11	**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 biosyhthesis of eukaryotes
88	d1u2xa_	Alignment	not modelled	98.2	12	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
89	c3bgkA_	Alignment	not modelled	98.0	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of hypothetic protein smu.573 from streptococcus2 mutans
90	d1ua4a_	Alignment	not modelled	97.9	15	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
91	c3k5wA_	Alignment	not modelled	97.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbohydrate kinase; **PDBTitle:** crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
92	c3drwA_	Alignment	not modelled	97.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adp-specific phosphofructokinase; **PDBTitle:** crystal structure of a phosphofructokinase from pyrococcus horikoshii2 ot3 with amp
93	d1l2la_	Alignment	not modelled	97.6	16	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**ADP-specific Phosphofructokinase/Glucokinase
94	c6c8zA_	Alignment	not modelled	97.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adp-dependent phosphofructokinase; **PDBTitle:** last common ancestor of adp-dependent phosphofructokinases from2 methanosarcinales
95	c6efwA_	Alignment	not modelled	96.6	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**atp-dependent (s)-nad(p)h-hydrate dehydratase; **PDBTitle:** crystal structure of a yjef family protein from cryptococcus2 neoformans var. grubii serotype a
96	c5ccfA_	Alignment	not modelled	96.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adp-dependent glucokinase; **PDBTitle:** structure of mouse adp-dependent glucokinase
97	c2yx6C_	Alignment	not modelled	73.1	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein ph0822; **PDBTitle:** crystal structure of ph0822
98	c2wfbA_	Alignment	not modelled	56.6	20	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein orp; **PDBTitle:** high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
99	d1rq2a1	Alignment	not modelled	53.9	18	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
100	c6ahwB_	Alignment	not modelled	52.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**circular-permutated trna (cytidine(34)-2'-o)- **PDBTitle:** crystal structure of circular-permutated yibk methyltransferase from2 haemophilus influenzae
101	d2jfga1	Alignment	not modelled	51.4	17	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
102	c1w59B_	Alignment	not modelled	50.2	20	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
103	c1vi2B_	Alignment	not modelled	49.8	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
104	d1rdua_	Alignment	not modelled	47.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
105	d1j6ua1	Alignment	not modelled	43.6	17	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain

						Family: MurCD N-terminal domain
106	d1xi8a3	Alignment	not modelled	43.6	25	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
107	d1t3va_	Alignment	not modelled	40.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Nitrogenase accessory factor-like **Family:**MTH1175-like
108	c2f00A_	Alignment	not modelled	37.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
109	c2vawA_	Alignment	not modelled	37.2	21	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
110	c4e6eA_	Alignment	not modelled	36.9	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of a putative cell division protein ftsz (tfu_1113)2 from thermobifida fusca yx-er1 at 2.22 a resolution (psi community3 target, van wezel g.p.)
111	c2q1yB_	Alignment	not modelled	36.7	17	**PDB header:**cell cycle, signaling protein **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
112	d2vapa1	Alignment	not modelled	36.2	21	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
113	d1p3da1	Alignment	not modelled	35.1	11	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
114	d2a7va1	Alignment	not modelled	34.7	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
115	c2a7vA_	Alignment	not modelled	34.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** human mitochondrial serine hydroxymethyltransferase 2
116	c2cduB_	Alignment	not modelled	32.6	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph oxidase; **PDBTitle:** the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
117	c6cauA_	Alignment	not modelled	32.2	13	**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 amppnp
118	c4b2oB_	Alignment	not modelled	31.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ymdb phosphodiesterase; **PDBTitle:** crystal structure of bacillus subtilis ymdb, a global2 regulator of late adaptive responses.
119	d1vkza2	Alignment	not modelled	31.2	38	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
120	c4qjiB_	Alignment	not modelled	30.9	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphopantothenate--cysteine ligase; **PDBTitle:** crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis