Phyre2

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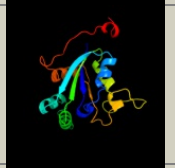
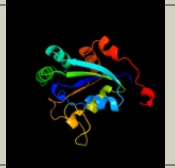
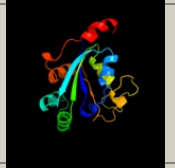
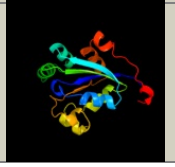
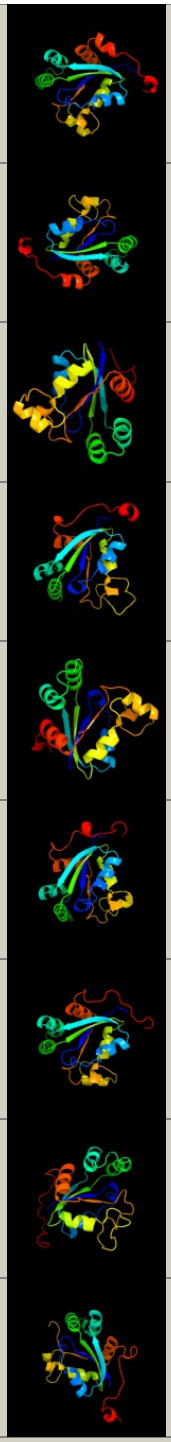
Description	P56597
Date	Thu Apr 26 09:17:35 BST 2012
Unique Job ID	1fd31c5614167232

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ztqC_	Alignment		100.0	39	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** hexagonal crystal form p61 of the aquifex aeolicus nucleoside2 diphosphate kinase
2	d1u8wa_	Alignment		100.0	28	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
3	c3mpdA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of nucleoside diphosphate kinase from2 encephalitozoon cuniculi, cubic form, apo
4	d3bbba1	Alignment		100.0	32	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
5	d1pkua1	Alignment		100.0	29	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
6	d1nhkl_	Alignment		100.0	32	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
7	c2hurF_	Alignment		100.0	39	**PDB header:**signaling protein,transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** escherichia coli nucleoside diphosphate kinase
8	c3ngtJ_	Alignment		100.0	32	**PDB header:**transferase **Chain:** J: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure of leishmania ndkb complexed with amp.
9	c3q89H_	Alignment		100.0	30	**PDB header:**transferase **Chain:** H: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of staphylococcus aureus nucleoside diphosphate2 kinase complexed with cdp
10	d1xiqa_	Alignment		100.0	28	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
11	d1s57a_	Alignment		100.0	29	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK

12	d1ucna_	Alignment		100.0	28	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
13	c3js9A_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase family protein; **PDBTitle:** crystal structure of nucleoside diphosphate kinase family protein from2 babesia bovis
14	c4dutA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** the structure of nucleoside diphosphate kinase (ndk) from burkholderia2 thailandensis
15	d1w7wa_	Alignment		100.0	27	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
16	d1ehwa_	Alignment		100.0	31	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
17	d1be4a_	Alignment		100.0	29	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
18	d1hlwa_	Alignment		100.0	29	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
19	d1nb2a_	Alignment		100.0	28	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
20	d2dyaa1	Alignment		100.0	31	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
21	c2vu5A_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of pndk from bacillus anthracis
22	c4di6F_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of nucleoside-diphosphate kinase from borrelia2 burgdorferi
23	d1k44a_	Alignment	not modelled	100.0	36	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
24	c1w7wF_	Alignment	not modelled	100.0	27	**PDB header:**transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure and mutational analysis of a plant mitochondrial2 nucleoside diphosphate kinase: identification of residues3 involved in serine phosphorylation and oligomerization.
25	d2az3a1	Alignment	not modelled	100.0	29	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
26	d1xqia1	Alignment	not modelled	100.0	39	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
27	d1zs6a1	Alignment	not modelled	100.0	29	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
28	d1wkja1	Alignment	not modelled	100.0	32	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
						Fold: Ferredoxin-like

29	d1nsqa_	Alignment	not modelled	100.0	30	**Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
30	d2b8qa1	Alignment	not modelled	100.0	29	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
31	c3b6bF_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of acanthamoeba polyphaga mimivirus2 nucleoside diphosphate kinase complexed with dgdp
32	c2az1B_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure of a halophilic nucleoside diphosphate kinase2 from halobacterium salinarum
33	c3b54A_	Alignment	not modelled	100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** saccharomyces cerevisiae nucleoside diphosphate kinase
34	c3r9lA_	Alignment	not modelled	100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of nucleoside diphosphate kinase from giardia2 lamblia featuring a disordered dinucleotide binding site
35	c3g36D_	Alignment		99.4	37	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**protein dpy-30 homolog; **PDBTitle:** crystal structure of the human dpy-30-like c-terminal domain
36	c2bx6A_	Alignment	not modelled	98.1	21	**PDB header:**transduction protein **Chain:** A: **PDB Molecule:**xrp2 protein; **PDBTitle:** crystal structure of the human retinitis pigmentosa2 protein 2 (rp2)
37	d2ezwa1	Alignment	not modelled	93.9	26	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
38	d2hwna1	Alignment	not modelled	60.3	31	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
39	d1r2aa_	Alignment	not modelled	58.0	31	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
40	c1y7pB_	Alignment	not modelled	57.1	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
41	c3p04A_	Alignment	not modelled	39.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
42	c2rd5D_	Alignment	not modelled	34.8	23	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pii protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
43	d1ukxa_	Alignment	not modelled	32.8	22	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**RWD domain
44	d2fgca1	Alignment	not modelled	27.0	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
45	c3bqsB_	Alignment	not modelled	25.3	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
46	d2fi0a1	Alignment	not modelled	17.1	12	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
47	d1nfpa_	Alignment	not modelled	16.2	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
48	c4dhdA_	Alignment	not modelled	15.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyprenyl synthetase; **PDBTitle:** crystal structure of isoprenoid synthase a3msh1 (target efi-501992)2 from pyrobaculum calidifontis
49	c2ebkA_	Alignment	not modelled	15.4	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rwd domain-containing protein 3; **PDBTitle:** solution structure of the rwd domain of human rwd domain2 containing protein 3
50	d1kvka2	Alignment	not modelled	13.4	18	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Mevalonate kinase
51	d1d8ja_	Alignment	not modelled	12.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**The central core domain of TFIIE beta
52	d1ydla1	Alignment	not modelled	12.3	11	**Fold:**TFB5-like **Superfamily:**TFB5-like **Family:**TFB5-like

53	d1wdcc_	Alignment	not modelled	12.2	27	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
54	c2z62A_	Alignment	not modelled	11.4	24	**PDB header:**immune system **Chain:** A: **PDB Molecule:**toll-like receptor 4, variable lymphocyte receptor b; **PDBTitle:** crystal structure of the tv3 hybrid of human tlr4 and hagfish vlrb.61
55	c1yfdA_	Alignment	not modelled	11.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase 1 beta **PDBTitle:** crystal structure of the y122h mutant of ribonucleotide2 reductase r2 protein from e. coli
56	c2qnfB_	Alignment	not modelled	10.8	23	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**recombination endonuclease vii; **PDBTitle:** crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
57	c4a1qB_	Alignment	not modelled	10.7	30	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**orf e73; **PDBTitle:** solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
58	c1go4F_	Alignment	not modelled	9.8	23	**PDB header:**cell cycle **Chain:** F: **PDB Molecule:**mad1 (mitotic arrest deficient)-like 1; **PDBTitle:** crystal structure of mad1-mad2 reveals a conserved mad22 binding motif in mad1 and cdc20.
59	d1whza_	Alignment	not modelled	9.8	25	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
60	d2dawa1	Alignment	not modelled	9.8	20	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**RWD domain
61	c3bq3A_	Alignment	not modelled	9.3	13	**PDB header:**cell cycle, ligase **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** crystal structure of s. cerevisiae dcn1
62	d2f06a1	Alignment	not modelled	9.2	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
63	c2a3lA_	Alignment	not modelled	9.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amp deaminase; **PDBTitle:** x-ray structure of adenosine 5'-monophosphate deaminase from2 arabidopsis thaliana in complex with coformycin 5'-phosphate
64	d2a3la1	Alignment	not modelled	9.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
65	d1d02a_	Alignment	not modelled	8.5	36	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease MunI
66	d2f1fa2	Alignment	not modelled	8.1	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
67	c4dbgB_	Alignment	not modelled	7.9	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ring finger protein 31; **PDBTitle:** crystal structure of hoil-1l-ubl complexed with a hoip-uba derivative
68	d1br1b_	Alignment	not modelled	7.8	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
69	d1bg6a2	Alignment	not modelled	7.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
70	c3dgpB_	Alignment	not modelled	7.3	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**rna polymerase ii transcription factor b subunit 5; **PDBTitle:** crystal structure of the complex between tfb5 and the c-terminal2 domain of tfb2
71	c2daeA_	Alignment	not modelled	7.3	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**kiaa0733 protein; **PDBTitle:** solution structure of the n-terminal cue domain in the2 human mitogen-activated protein kinase kinase kinase 73 interacting protein 2 (map3k7ip2)
72	d1dzfa1	Alignment	not modelled	7.3	14	**Fold:**Restriction endonuclease-like **Superfamily:**Eukaryotic RPB5 N-terminal domain **Family:**Eukaryotic RPB5 N-terminal domain
73	c3zvrA_	Alignment	not modelled	6.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of dynamin
74	d2i5nh2	Alignment	not modelled	6.3	33	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
75	d2nrqa1	Alignment	not modelled	6.3	19	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**SSO1042-like
76	d2daya1	Alignment	not modelled	6.2	18	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**RWD domain
77	c2yz0A_	Alignment	not modelled	6.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase gcn2; **PDBTitle:** solution structure of rwd/gi domain of saccharomyces2 cerevisiae gcn2

78	c3owpB_	Alignment	not modelled	6.1	45	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**camp-dependent protein kinase inhibitor alpha; **PDBTitle:** human camp-dependent protein kinase in complex with an inhibitor
79	c3fjqI_	Alignment	not modelled	6.1	45	**PDB header:**transferase **Chain:** I: **PDB Molecule:**camp-dependent protein kinase inhibitor alpha; **PDBTitle:** crystal structure of camp-dependent protein kinase catalytic2 subunit alpha in complex with peptide inhibitor pki alpha3 (6-25)
80	c3pooB_	Alignment	not modelled	6.1	45	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**camp-dependent protein kinase inhibitor alpha; **PDBTitle:** human camp-dependent protein kinase in complex with an inhibitor
81	c1svhB_	Alignment	not modelled	6.1	45	**PDB header:**transferase **Chain:** B: **PDB Molecule:**camp-dependent protein kinase inhibitor, alpha **PDBTitle:** crystal structure of protein kinase a in complex with2 azepane derivative 8
82	c3e8cJ_	Alignment	not modelled	6.1	45	**PDB header:**transferase **Chain:** J: **PDB Molecule:**camp-dependent protein kinase inhibitor peptide; **PDBTitle:** crystal structures of the kinase domain of pka in complex with atp-2 competitive inhibitors
83	c3p0mB_	Alignment	not modelled	6.1	45	**PDB header:**transferase **Chain:** B: **PDB Molecule:**camp-dependent protein kinase inhibitor alpha; **PDBTitle:** human camp-dependent protein kinase in complex with an inhibitor
84	c1sveB_	Alignment	not modelled	6.1	45	**PDB header:**transferase **Chain:** B: **PDB Molecule:**camp-dependent protein kinase inhibitor, alpha **PDBTitle:** crystal structure of protein kinase a in complex with2 azepane derivative 1
85	c1yg0A_	Alignment	not modelled	6.0	25	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cop associated protein; **PDBTitle:** solution structure of apo-copp from helicobacter pylori
86	d1g7sa3	Alignment	not modelled	5.9	15	**Fold:**Initiation factor IF2/eIF5b, domain 3 **Superfamily:**Initiation factor IF2/eIF5b, domain 3 **Family:**Initiation factor IF2/eIF5b, domain 3
87	c1kxfA_	Alignment	not modelled	5.8	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sindbis virus capsid protein; **PDBTitle:** sindbis virus capsid, (wild-type) residues 1-264,2 tetragonal crystal form (form ii)
88	c3odnA_	Alignment	not modelled	5.7	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dally-like protein; **PDBTitle:** the crystal structure of drosophila dally-like protein core domain
89	d2nlya1	Alignment	not modelled	5.7	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
90	d1ep5a_	Alignment	not modelled	5.7	24	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral proteases
91	d1ywxa1	Alignment	not modelled	5.6	20	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**Ribosomal protein S24e
92	c2xecD_	Alignment	not modelled	5.6	22	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
93	d1ufza_	Alignment	not modelled	5.6	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**HBS1-like domain **Family:**HBS1-like domain
94	c2yewG_	Alignment	not modelled	5.4	29	**PDB header:**virus **Chain:** G: **PDB Molecule:**capsid protein; **PDBTitle:** modeling barmah forest virus structural proteins
95	c3re1B_	Alignment	not modelled	5.3	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthetase; **PDBTitle:** crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
96	d1wgla_	Alignment	not modelled	5.3	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
97	d2g7oa1	Alignment	not modelled	5.3	23	**Fold:**TraM-like **Superfamily:**TraM-like **Family:**TraM-like
98	c3ceuA_	Alignment	not modelled	5.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamine phosphate pyrophosphorylase2 (bt_0647) from bacteroides thetaiotaomicron. northeast3 structural genomics consortium target btr268
99	c3h2bB_	Alignment	not modelled	5.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sam-dependent methyltransferase; **PDBTitle:** crystal structure of the sam-dependent methyltransferase2 cg3271 from corynebacterium glutamicum in complex with s-3 adenosyl-l-homocysteine and pyrophosphate. northeast4 structural genomics consortium target cgr113a