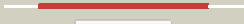



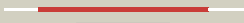








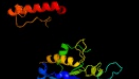

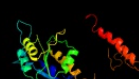








# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD2906c\_trmD\_3215675\_3216367  
 Date Thu Aug 8 16:20:06 BST 2019  
 Unique Job ID 7f1c5de52a34165b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3quvB_</a>	 Alignment		100.0	76	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (guanine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of a trna-guanine-n1-methyltransferase from2 mycobacterium abscessus
2	<a href="#">c4h3zA_</a>	 Alignment		100.0	42	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of a symmetric dimer of a trna (guanine-(n(1)-)-2 methyltransferase from burkholderia phymatum bound to s-adenosyl3 homocystein in both half-sites
3	<a href="#">c5wyrA_</a>	 Alignment		100.0	46	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure and catalytic mechanism of the essential m1g37 trna2 methyltransferase trmd from pseudomonas aeruginosa
4	<a href="#">d1uala_</a>	 Alignment		100.0	42	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> tRNA(m1G37)-methyltransferase TrmD
5	<a href="#">d1p9pa_</a>	 Alignment		100.0	44	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> tRNA(m1G37)-methyltransferase TrmD
6	<a href="#">c3iefA_</a>	 Alignment		100.0	45	<b>PDB header:</b> transferase, rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of trna guanine-n1-methyltransferase from bartonella2 henselae using mpcs.
7	<a href="#">c3ky7A_</a>	 Alignment		100.0	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(1)-)-methyltransferase; <b>PDBTitle:</b> 2.35 angstrom resolution crystal structure of a putative trna2 (guanine-7-)-methyltransferase (trmd) from staphylococcus aureus3 subsp. aureus mrsa252
8	<a href="#">c1oy5B_</a>	 Alignment		100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> trna (guanine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of trna (m1g37) methyltransferase from aquifex2 aeolicus
9	<a href="#">d1oy5a_</a>	 Alignment		100.0	38	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> tRNA(m1G37)-methyltransferase TrmD
10	<a href="#">c3knuD_</a>	 Alignment		100.0	50	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> trna (guanine-n(1)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
11	<a href="#">d1to0a_</a>	 Alignment		95.2	23	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like

12	<a href="#">d1vh0a_</a>	Alignment		94.9	22	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like
13	<a href="#">d1ns5a_</a>	Alignment		94.1	13	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like
14	<a href="#">c2v3jA_</a>	Alignment		94.0	8	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> essential for mitotic growth 1; <b>PDBTitle:</b> the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
15	<a href="#">d2v3ka1</a>	Alignment		93.2	8	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> EMG1/NEP1-like
16	<a href="#">d1o6da_</a>	Alignment		92.8	13	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YbeA-like
17	<a href="#">c3o7bA_</a>	Alignment		82.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome biogenesis nep1 rna methyltransferase; <b>PDBTitle:</b> crystal structure of archaeoglobus fulgidus nep1 bound to s-2 adenosylhomocysteine
18	<a href="#">c6aytD_</a>	Alignment		45.4	16	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 5'-methylthioadenosine/s-adenosylhomocysteine nucleosidase; <b>PDBTitle:</b> crystal structure of campylobacter jejuni 5'-methylthioadenosine/s-2 adenosyl homocysteine nucleosidase (mtan) complexed with3 pyrazinylthio-dadme-immucillin-a
19	<a href="#">c5faiA_</a>	Alignment		40.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase nep1; <b>PDBTitle:</b> emg1 n1-specific pseudouridine methyltransferase
20	<a href="#">c3d3ra_</a>	Alignment		40.7	54	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase assembly chaperone hupc/hupf; <b>PDBTitle:</b> crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
21	<a href="#">d3d3ra1</a>	Alignment	not modelled	38.7	54	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
22	<a href="#">c4k30B_</a>	Alignment	not modelled	31.6	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylglutamate synthase, mitochondrial; <b>PDBTitle:</b> structure of the n-acetyltransferase domain of human n-acetylglutamate2 synthase
23	<a href="#">c3ai9X_</a>	Alignment	not modelled	31.5	14	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> upf0217 protein mj1640; <b>PDBTitle:</b> crystal structure of duf358 protein reveals a putative spout-class2 rna methyltransferase
24	<a href="#">c6hnuA_</a>	Alignment	not modelled	31.1	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aromatic amino acid aminotransferase i; <b>PDBTitle:</b> crystal structure of the aminotransferase aro8 from c. albicans with2 ligands
25	<a href="#">c5zyoD_</a>	Alignment	not modelled	29.6	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal rna large subunit methyltransferase h; <b>PDBTitle:</b> crystal structure of domain-swapped circular-permuted ybea (cp74) from2 escherichia coli
26	<a href="#">d2ot2a1</a>	Alignment	not modelled	29.5	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
27	<a href="#">c1zosE_</a>	Alignment	not modelled	29.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> 5'-methylthioadenosine / s-adenosylhomocysteine <b>PDBTitle:</b> structure of 5'-methylthioadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state inhibitor mt-3 imma <b>PDB header:</b> transferase

28	<a href="#">c5n9mA_</a>	Alignment	not modelled	27.9	17	<b>Chain:</b> A; <b>PDB Molecule:</b> cobyric acid synthase; <b>PDBTitle:</b> crystal structure of gatd - a glutamine amidotransferase from <i>Staphylococcus aureus</i> involved in peptidoglycan amidation
29	<a href="#">c4m38A_</a>	Alignment	not modelled	27.0	13	<b>PDB header:</b> transferase/transferase substrate <b>Chain:</b> A; <b>PDB Molecule:</b> protein arginine n-methyltransferase 7; <b>PDBTitle:</b> crystal structure of trypanosoma brucei protein arginine2 methyltransferase 7 complex with adohcy and histone h4 peptide
30	<a href="#">d2z1ca1</a>	Alignment	not modelled	25.9	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> HupF/HypC-like <b>Family:</b> HupF/HypC-like
31	<a href="#">c1rcuB_</a>	Alignment	not modelled	23.6	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> conserved hypothetical protein vt76; <b>PDBTitle:</b> x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
32	<a href="#">c4l69A_</a>	Alignment	not modelled	23.4	19	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase e; <b>PDBTitle:</b> rv2372c of mycobacterium tuberculosis is rsmE like methyltransferase
33	<a href="#">d1rcua_</a>	Alignment	not modelled	23.0	9	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
34	<a href="#">c3kw2A_</a>	Alignment	not modelled	21.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> probable r-rna methyltransferase; <b>PDBTitle:</b> crystal structure of probable rRNA-methyltransferase from <i>Porphyromonas gingivalis</i>
35	<a href="#">d1fdja_</a>	Alignment	not modelled	21.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
36	<a href="#">c6h4kA_</a>	Alignment	not modelled	21.0	29	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase 25; <b>PDBTitle:</b> structure of the usp25 c-terminal domain
37	<a href="#">c3bl6A_</a>	Alignment	not modelled	20.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> 5'-methylthioadenosine nucleosidase/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
38	<a href="#">c4ljkA_</a>	Alignment	not modelled	20.0	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dna processing chain a (dpra); <b>PDBTitle:</b> structural insights into the unique single-stranded dna binding mode2 of dna processing protein a from <i>Helicobacter pylori</i>
39	<a href="#">c3r7tA_</a>	Alignment	not modelled	19.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> crystal structure of adenylosuccinate synthetase from <i>Campylobacter jejuni</i>
40	<a href="#">c5vm8A_</a>	Alignment	not modelled	19.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ribosomal rna small subunit methyltransferase e; <b>PDBTitle:</b> crystal structure of a ribosomal rna small subunit methyltransferase e2 from <i>Neisseria gonorrhoeae</i> bound to s-adenosyl methionine
41	<a href="#">c1zggA_</a>	Alignment	not modelled	19.0	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative low molecular weight protein-tyrosine-phosphatase from <i>Bacillus subtilis</i>
42	<a href="#">c2mxfA_</a>	Alignment	not modelled	18.8	23	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A; <b>PDB Molecule:</b> mvat; <b>PDBTitle:</b> structure of the dna complex of the c-terminal domain of mvat
43	<a href="#">c1egpA_</a>	Alignment	not modelled	18.7	27	<b>PDB header:</b> proteinase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> eglin-c; <b>PDBTitle:</b> proteinase inhibitor eglin c with hydrolysed reactive center
44	<a href="#">c5t87D_</a>	Alignment	not modelled	18.2	35	<b>PDB header:</b> toxin <b>Chain:</b> D; <b>PDB Molecule:</b> cdi immunity protein; <b>PDBTitle:</b> crystal structure of cdi complex from <i>Cupriavidus taiwanensis</i> lmg2 19424
45	<a href="#">d2z1aa2</a>	Alignment	not modelled	17.9	17	<b>Fold:</b> Metallo-dependent phosphatases <b>Superfamily:</b> Metallo-dependent phosphatases <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
46	<a href="#">c6acvA_</a>	Alignment	not modelled	17.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> methyl-cpg-binding domain-containing protein 11; <b>PDBTitle:</b> the solution nmr structure of mbd domain
47	<a href="#">c4etiA_</a>	Alignment	not modelled	17.4	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> low molecular weight protein-tyrosine-phosphatase ywle; <b>PDBTitle:</b> crystal structure of ywle from <i>Bacillus subtilis</i>
48	<a href="#">c2xhzC_</a>	Alignment	not modelled	16.7	16	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> arabinose 5-phosphate isomerase; <b>PDBTitle:</b> probing the active site of the sugar isomerase domain from <i>E. coli</i> 2 arabinose-5-phosphate isomerase via x-ray crystallography
49	<a href="#">c3fxaA_</a>	Alignment	not modelled	16.7	11	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> sis domain protein; <b>PDBTitle:</b> crystal structure of a putative sugar-phosphate isomerase2 (lmoF2365_0531) from <i>Listeria monocytogenes</i> str. 4b f2365 at 1.60 a3 resolution
50	<a href="#">c1w4zA_</a>	Alignment	not modelled	16.3	18	<b>PDB header:</b> antibiotic biosynthesis <b>Chain:</b> A; <b>PDB Molecule:</b> ketoacyl reductase; <b>PDBTitle:</b> structure of actinorhodin polyketide (actiii) reductase
51	<a href="#">c3uqzB_</a>	Alignment	not modelled	16.1	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> dna processing protein dpra; <b>PDBTitle:</b> x-ray structure of dna processing protein a (dpra) from <i>Streptococcus pneumoniae</i>
52	<a href="#">c4dowA_</a>	Alignment	not modelled	16.0	30	<b>PDB header:</b> replication <b>Chain:</b> A; <b>PDB Molecule:</b> origin recognition complex subunit 1;

						<b>PDBTitle:</b> structure of mouse orc1 bah domain bound to h4k20me2
53	<a href="#">d1p9ba_</a>	Alignment	not modelled	15.5	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
54	<a href="#">d1ixrc1</a>	Alignment	not modelled	15.4	34	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Helicase DNA-binding domain
55	<a href="#">c5i34B_</a>	Alignment	not modelled	15.3	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylosuccinate synthetase; <b>PDBTitle:</b> adenylosuccinate synthetase from cryptococcus neoformans complexed2 with gdp and imp
56	<a href="#">c2pyhB_</a>	Alignment	not modelled	15.3	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 4; <b>PDBTitle:</b> azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
57	<a href="#">c2ky8A_</a>	Alignment	not modelled	15.1	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-cpg-binding domain protein 2; <b>PDBTitle:</b> solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
58	<a href="#">d1zcza1</a>	Alignment	not modelled	15.0	26	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Inosicase
59	<a href="#">c4txkA_</a>	Alignment	not modelled	14.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-methionine sulfoxide oxidase mical1; <b>PDBTitle:</b> construct of mical-1 containing the monooxygenase and calponin2 homology domains
60	<a href="#">c3vxvA_</a>	Alignment	not modelled	14.9	27	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-cpg-binding domain protein 4; <b>PDBTitle:</b> crystal structure of methyl cpb binding domain of mbd4 in complex with2 the 5mcg/tg sequence
61	<a href="#">c5z3mB_</a>	Alignment	not modelled	14.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphotyrosine protein phosphatase; <b>PDBTitle:</b> crystal structure of low molecular weight phosphotyrosine phosphatase2 (vclmwptp-2) from vibrio choleraeo395
62	<a href="#">d1m2ka_</a>	Alignment	not modelled	14.7	15	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Sir2 family of transcriptional regulators
63	<a href="#">c4xruE_</a>	Alignment	not modelled	14.4	30	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> rrn1; <b>PDBTitle:</b> structure of pnkp1/rrn1/hen1 complex
64	<a href="#">d1dj3a_</a>	Alignment	not modelled	14.2	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
65	<a href="#">c1xi4O_</a>	Alignment	not modelled	14.1	22	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> O: <b>PDB Molecule:</b> clathrin light chain a; <b>PDBTitle:</b> clathrin d6 coat
66	<a href="#">c3a8tA_</a>	Alignment	not modelled	13.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate isopentenyltransferase; <b>PDBTitle:</b> plant adenylyl isopentenyltransferase in complex with atp
67	<a href="#">d3dl3a1</a>	Alignment	not modelled	13.9	21	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminate synthase-like <b>Family:</b> TehB-like
68	<a href="#">d1a5ca_</a>	Alignment	not modelled	13.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
69	<a href="#">d1nxza2</a>	Alignment	not modelled	13.6	13	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> YggJ C-terminal domain-like
70	<a href="#">c2ehdB_</a>	Alignment	not modelled	13.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, short-chain dehydrogenase/reductase family; <b>PDBTitle:</b> crystal structure analysis of oxidoreductase
71	<a href="#">d3bb6a1</a>	Alignment	not modelled	13.5	8	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> Clavaminate synthase-like <b>Family:</b> TehB-like
72	<a href="#">c5agqA_</a>	Alignment	not modelled	13.5	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bromodomain adjacent to zinc finger domain protein 2a; <b>PDBTitle:</b> solution structure of the tam domain of human tip5 baz2a2 involved in epigenetic regulation of rrna genes
73	<a href="#">c3h7aC_</a>	Alignment	not modelled	13.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short chain dehydrogenase; <b>PDBTitle:</b> crystal structure of short-chain dehydrogenase from rhodospseudomonas2 palustris
74	<a href="#">c4p6iD_</a>	Alignment	not modelled	13.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> crispr-associated endonuclease cas1; <b>PDBTitle:</b> crystal structure of the cas1-cas2 complex from escherichia coli
75	<a href="#">c1zmrA_</a>	Alignment	not modelled	13.0	5	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of the e. coli phosphoglycerate kinase
76	<a href="#">c2pc4B_</a>	Alignment	not modelled	12.9	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> fructose-bisphosphate aldolase; <b>PDBTitle:</b> crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
77	<a href="#">c4da9C_</a>	Alignment	not modelled	12.9	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from2 sinorhizobium meliloti 1021
						<b>PDB header:</b> transferase

78	<a href="#">c4dg5A_</a>	Alignment	not modelled	12.8	7	<b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate kinase; <b>PDBTitle:</b> crystal structure of staphylococcal phosphoglycerate kinase
79	<a href="#">c4e6nC_</a>	Alignment	not modelled	12.5	67	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> metallophosphoesterase; <b>PDBTitle:</b> crystal structure of bacterial pnkp-c/hen1-n heterodimer
80	<a href="#">c4go1A_</a>	Alignment	not modelled	12.5	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lsrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrr from e.2 coli.
81	<a href="#">d1gxha_</a>	Alignment	not modelled	12.4	30	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Colicin E immunity proteins <b>Family:</b> Colicin E immunity proteins
82	<a href="#">d2qmma1</a>	Alignment	not modelled	12.4	18	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> AF1056-like
83	<a href="#">c2k1B_</a>	Alignment	not modelled	12.4	55	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
84	<a href="#">c2k1kA_</a>	Alignment	not modelled	12.4	55	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
85	<a href="#">c2k1kB_</a>	Alignment	not modelled	12.4	55	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 4.3
86	<a href="#">c2k1IA_</a>	Alignment	not modelled	12.4	55	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ephrin type-a receptor 1; <b>PDBTitle:</b> nmr structures of dimeric transmembrane domain of the2 receptor tyrosine kinase epha1 in lipid bicelles at ph 6.3
87	<a href="#">c5b7pB_</a>	Alignment	not modelled	12.4	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mta/sah nucleosidase; <b>PDBTitle:</b> structures and functional analysis of periplasmic 5-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase from3 aeromonas hydrophila
88	<a href="#">c2no8A_</a>	Alignment	not modelled	12.3	30	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> colicin-e2 immunity protein; <b>PDBTitle:</b> nmr structure analysis of the colicin immunity protein im2
89	<a href="#">c6ixjK_</a>	Alignment	not modelled	12.2	18	<b>PDB header:</b> cytosolic protein <b>Chain:</b> K: <b>PDB Molecule:</b> sulfoacetaldehyde reductase; <b>PDBTitle:</b> the crystal structure of sulfoacetaldehyde reductase from klebsiella2 oxytoca
90	<a href="#">c4qkoA_</a>	Alignment	not modelled	12.2	20	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> pyocin-s2 immunity protein; <b>PDBTitle:</b> the crystal structure of the pyocin s2 nuclease domain, immunity2 protein complex at 1.8 angstroms
91	<a href="#">d1xfba1</a>	Alignment	not modelled	12.1	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
92	<a href="#">c6fqbE_</a>	Alignment	not modelled	12.1	15	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> cobyrinic acid synthase; <b>PDBTitle:</b> murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
93	<a href="#">d2vlqa1</a>	Alignment	not modelled	12.0	20	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Colicin E immunity proteins <b>Family:</b> Colicin E immunity proteins
94	<a href="#">c3ty8A_</a>	Alignment	not modelled	12.0	67	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide 2',3'-cyclic phosphate phosphodiesterase / <b>PDBTitle:</b> crystal structure of c. thermocellum pnkp ligase domain apo form
95	<a href="#">c5fwaA_</a>	Alignment	not modelled	11.8	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arginine n-methyltransferase 2; <b>PDBTitle:</b> crystal structure of mus musculus protein arginine methyltransferase 22 with cp1
96	<a href="#">d3bbda1</a>	Alignment	not modelled	11.8	12	<b>Fold:</b> alpha/beta knot <b>Superfamily:</b> alpha/beta knot <b>Family:</b> EMG1/NEP1-like
97	<a href="#">d1ayia_</a>	Alignment	not modelled	11.8	30	<b>Fold:</b> Acyl carrier protein-like <b>Superfamily:</b> Colicin E immunity proteins <b>Family:</b> Colicin E immunity proteins
98	<a href="#">d1zaia1</a>	Alignment	not modelled	11.7	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
99	<a href="#">c1gshA_</a>	Alignment	not modelled	11.5	20	<b>PDB header:</b> glutathione biosynthesis ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthetic ligase; <b>PDBTitle:</b> structure of escherichia coli glutathione synthetase at ph 7.5