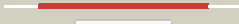



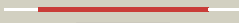

















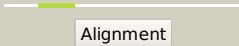




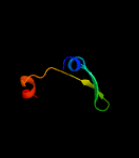
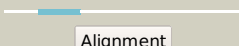

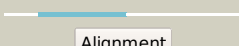

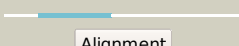

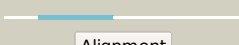







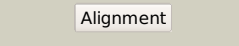
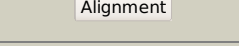
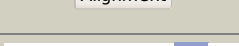

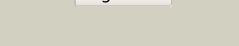
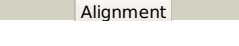


# Phyre2

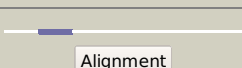
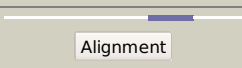
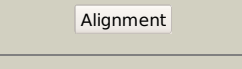
Email	mdejesus@rockefeller.edu
Description	RVBD1301_(-)_1457564_1458217
Date	Wed Jul 31 22:05:39 BST 2019
Unique Job ID	5954628397ffb6dc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6f87C_</a>	 Alignment		100.0	36	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> threonylcarbamoyl-amp synthase; <b>PDBTitle:</b> crystal structure of p. abyssi sua5 complexed with l-threonine and ppi
2	<a href="#">c2eqaA_</a>	 Alignment		100.0	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein st1526; <b>PDBTitle:</b> crystal structure of the hypothetical sua5 protein from2 sulfolobus tokodaii
3	<a href="#">d1k7ja_</a>	 Alignment		100.0	22	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
4	<a href="#">d1jcua_</a>	 Alignment		100.0	30	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
5	<a href="#">d1hrua_</a>	 Alignment		100.0	24	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> YrdC-like
6	<a href="#">c3vthA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
7	<a href="#">c3vthB_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
8	<a href="#">c3l7vA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.1377c; <b>PDBTitle:</b> crystal structure of a hypothetical protein smu.1377c from2 streptococcus mutans ua159
9	<a href="#">c4g9iA_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation protein hypf; <b>PDBTitle:</b> crystal structure of t.kodakarensis hypf
10	<a href="#">c3tsuA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
11	<a href="#">c3vewA_</a>	 Alignment		99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-carbamoyltransferase tobz; <b>PDBTitle:</b> crystal structure of the o-carbamoyltransferase tobz in complex with2 adp

12	<a href="#">c2m4mA_</a>	 Alignment		66.6	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata
13	<a href="#">c3p3dA_</a>	 Alignment		51.9	29	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoporin 53; <b>PDBTitle:</b> crystal structure of the nup53 rrm domain from pichia guilliermondii
14	<a href="#">c5uazB_</a>	 Alignment		51.1	23	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> nucleoporin nup53; <b>PDBTitle:</b> crystal structure of the yeast nucleoporin
15	<a href="#">c4fp9F_</a>	 Alignment		39.3	18	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> methyltransferase nsun4; <b>PDBTitle:</b> human mterf4-nsun4 protein complex
16	<a href="#">c2qs0A_</a>	 Alignment		38.2	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate synthetase a; <b>PDBTitle:</b> quinolinate synthase from pyrococcus furiosus
17	<a href="#">d1t5la1</a>	 Alignment		37.3	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
18	<a href="#">c5fmfY_</a>	 Alignment		34.8	9	<b>PDB header:</b> transcription <b>Chain:</b> Y: <b>PDB Molecule:</b> dna repair helicase rad3; <b>PDBTitle:</b> the p-lobe of rna polymerase ii pre-initiation complex
19	<a href="#">c2frxD_</a>	 Alignment		34.2	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein yebu; <b>PDBTitle:</b> crystal structure of yebu, a m5c rna methyltransferase from e.coli
20	<a href="#">c3m4xA_</a>	 Alignment		29.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> no11/nop2/sun family protein; <b>PDBTitle:</b> structure of a ribosomal methyltransferase
21	<a href="#">c4xqkB_</a>	 Alignment	not modelled	28.7	17	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> llabiii; <b>PDBTitle:</b> atp-dependent type isp restriction-modification enzyme llabiii bound2 to dna
22	<a href="#">c1solA_</a>	 Alignment	not modelled	27.9	36	<b>PDB header:</b> actin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gelsolin (150-169); <b>PDBTitle:</b> a pip2 and f-actin-binding site of gelsolin, residue 150-2169 (nmr, averaged structure)
23	<a href="#">c4c2IA_</a>	 Alignment	not modelled	25.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-xylogalacturonan hydrolase a; <b>PDBTitle:</b> crystal structure of endo-xylogalacturonan hydrolase from aspergillus2 tubingensis
24	<a href="#">d1hq0a_</a>	 Alignment	not modelled	25.7	33	<b>Fold:</b> CNF1/YfiH-like putative cysteine hydrolases <b>Superfamily:</b> CNF1/YfiH-like putative cysteine hydrolases <b>Family:</b> Type 1 cytotoxic necrotizing factor, catalytic domain
25	<a href="#">c3irsB_</a>	 Alignment	not modelled	25.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein bb4693; <b>PDBTitle:</b> crystal structure of uncharacterized tim-barrel protein bb4693 from2 bordetella bronchiseptica
26	<a href="#">d1r0ua_</a>	 Alignment	not modelled	24.7	35	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Hypothetical protein YwiB
27	<a href="#">c2oemA_</a>	 Alignment	not modelled	24.7	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; <b>PDBTitle:</b> crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohexane 1-phosphate
28	<a href="#">c3m6wA_</a>	 Alignment	not modelled	24.4	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> multi-site-specific 16s rrna methyltransferase rsmf from

						thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
29	<a href="#">d1d4oa_</a>	Alignment	not modelled	24.4	26	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
30	<a href="#">c1pt9B_</a>	Alignment	not modelled	24.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase, mitochondrial; <b>PDBTitle:</b> crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
31	<a href="#">d1ixka_</a>	Alignment	not modelled	24.1	15	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
32	<a href="#">c2dcqA_</a>	Alignment	not modelled	20.1	7	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative protein at4g01050; <b>PDBTitle:</b> fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
33	<a href="#">c3fk4A_</a>	Alignment	not modelled	19.7	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> rubisco-like protein; <b>PDBTitle:</b> crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
34	<a href="#">c3mioA_</a>	Alignment	not modelled	19.5	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase; <b>PDBTitle:</b> crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
35	<a href="#">d1rbla1</a>	Alignment	not modelled	19.4	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
36	<a href="#">d1sqga2</a>	Alignment	not modelled	19.3	23	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> NOL1/NOP2/sun
37	<a href="#">d1pnoa_</a>	Alignment	not modelled	18.7	21	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
38	<a href="#">c4p6dA_</a>	Alignment	not modelled	18.6	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase; <b>PDBTitle:</b> structure of ribb complexed with po4 ion
39	<a href="#">d1snna_</a>	Alignment	not modelled	18.3	15	<b>Fold:</b> YrdC/RibB <b>Superfamily:</b> YrdC/RibB <b>Family:</b> 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
40	<a href="#">c4nasD_</a>	Alignment	not modelled	17.9	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> ribulose-bisphosphate carboxylase; <b>PDBTitle:</b> the crystal structure of a rubisco-like protein (mtnw) from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
41	<a href="#">c3nwrA_</a>	Alignment	not modelled	17.7	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> a rubisco-like protein; <b>PDBTitle:</b> crystal structure of a rubisco-like protein from burkholderia fungorum
42	<a href="#">c6k1dB_</a>	Alignment	not modelled	17.4	3	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exonuclease 3'-5' domain-containing protein 2; <b>PDBTitle:</b> crystal structure of exd2 exonuclease domain soaked in mn and gmp
43	<a href="#">c3h1tA_</a>	Alignment	not modelled	17.4	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type i site-specific restriction-modification <b>PDBTitle:</b> the fragment structure of a putative hsdR subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
44	<a href="#">d1ej7l1</a>	Alignment	not modelled	16.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
45	<a href="#">d1c4oa1</a>	Alignment	not modelled	16.2	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
46	<a href="#">d1gk8a1</a>	Alignment	not modelled	15.7	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
47	<a href="#">d2d69a1</a>	Alignment	not modelled	15.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
48	<a href="#">d1ykwa1</a>	Alignment	not modelled	14.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
49	<a href="#">c2yxIA_</a>	Alignment	not modelled	14.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 450aa long hypothetical fmu protein; <b>PDBTitle:</b> crystal structure of ph0851
50	<a href="#">c3ckkA_</a>	Alignment	not modelled	14.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> crystal structure of human methyltransferase-like protein 1
51	<a href="#">c2e6mA_</a>	Alignment	not modelled	14.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> werner syndrome atp-dependent helicase homolog; <b>PDBTitle:</b> structure of mouse werner exonuclease domain
52	<a href="#">c3mtiA_</a>	Alignment	not modelled	14.5	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna methylase; <b>PDBTitle:</b> the crystal structure of a rrna methylase from streptococcus2 thermophilus to 1.95a
53	<a href="#">c3pfdD_</a>	Alignment	not modelled	14.5	9	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray crystal structure the n,n-dimethyltransferase tylm1 from2 streptomyces fradiae in complex with sah and dtdp-quip3n

54	<a href="#">c3id5F_</a>		Alignment	not modelled	14.3	21	<b>PDB header:</b> transferase/ribosomal protein/rna <b>Chain:</b> F: <b>PDB Molecule:</b> fibrillar-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus c/d rnp assembled with2 nop5, fibrillarln, l7ae and a split half c/d rna
55	<a href="#">c4mxnB_</a>		Alignment	not modelled	14.2	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative glycosyl hydrolase (parmer_00599) from2 parabacteroides merdae atcc 43184 at 1.95 a resolution
56	<a href="#">c1kevB_</a>		Alignment	not modelled	13.9	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> structure of nadp-dependent alcohol dehydrogenase
57	<a href="#">c2bruC_</a>		Alignment	not modelled	13.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
58	<a href="#">c4o9uB_</a>		Alignment	not modelled	13.7	21	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
59	<a href="#">d1zq1c2</a>		Alignment	not modelled	13.6	16	<b>Fold:</b> DCoH-like <b>Superfamily:</b> GAD domain-like <b>Family:</b> GAD domain
60	<a href="#">c1sqgA_</a>		Alignment	not modelled	13.6	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sun protein; <b>PDBTitle:</b> the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
61	<a href="#">c2qj8B_</a>		Alignment	not modelled	13.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mlr6093 protein; <b>PDBTitle:</b> crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
62	<a href="#">c4xpmA_</a>		Alignment	not modelled	13.5	16	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein meh1; <b>PDBTitle:</b> crystal structure of ego-tc
63	<a href="#">c4ffjA_</a>		Alignment	not modelled	13.4	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribba; <b>PDBTitle:</b> the crystal structure of spdhpbs from s.pneumoniae
64	<a href="#">c5knkB_</a>		Alignment	not modelled	13.3	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipid a biosynthesis lauroyl acyltransferase; <b>PDBTitle:</b> lipid a secondary acyltransferase lpxm from acinetobacter baumannii2 with catalytic residue substitution (e127a)
65	<a href="#">d1svda1</a>		Alignment	not modelled	12.6	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
66	<a href="#">c3qfwB_</a>		Alignment	not modelled	12.2	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose-1,5-bisphosphate carboxylase/oxygenase large <b>PDBTitle:</b> crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
67	<a href="#">c5c2xB_</a>		Alignment	not modelled	12.1	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> deoxyribose-phosphate aldolase; <b>PDBTitle:</b> crystal structure of deoxyribose-phosphate aldolase from colwellia2 psychrerythraea (tetragonal form)
68	<a href="#">c2ipxA_</a>		Alignment	not modelled	12.1	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rrna 2'-o-methyltransferase fibrillarln; <b>PDBTitle:</b> human fibrillarln
69	<a href="#">c5zvdB_</a>		Alignment	not modelled	11.9	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> 389aa long hypothetical nucleolar protein; <b>PDBTitle:</b> the crystal structure of nsun6 from pyrococcus horikoshii
70	<a href="#">c3cggB_</a>		Alignment	not modelled	11.5	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sam-dependent methyltransferase; <b>PDBTitle:</b> crystal structure of tehb-like sam-dependent methyltransferase2 (np_600671.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.00 a resolution
71	<a href="#">c3tfwB_</a>		Alignment	not modelled	11.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-methyltransferase; <b>PDBTitle:</b> crystal structure of a putative o-methyltransferase from klebsiella2 pneumoniae
72	<a href="#">c2g8nB_</a>		Alignment	not modelled	11.4	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phenylethanolamine n-methyltransferase; <b>PDBTitle:</b> structure of hpnmt with inhibitor 3-hydroxymethyl-7-(n-4-2 chlorophenylaminosulfonyl)-thiq and adohcy
73	<a href="#">c3zihB_</a>		Alignment	not modelled	11.3	13	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein sepf; <b>PDBTitle:</b> bacillus subtilis sepf, c-terminal domain
74	<a href="#">d1xcfa_</a>		Alignment	not modelled	11.3	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
75	<a href="#">d8ruca1</a>		Alignment	not modelled	11.2	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
76	<a href="#">c5bszA_</a>		Alignment	not modelled	11.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-methyltransferase; <b>PDBTitle:</b> x-ray structure of the sugar n-methyltransferase keds8 from2 streptoalloteichus sp atcc 53650
77	<a href="#">c4p3xA_</a>		Alignment	not modelled	11.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate synthase a; <b>PDBTitle:</b> structure of the fe4s4 quinolinate synthase nada from thermotoga2 maritima
78	<a href="#">c5jw9A_</a>		Alignment	not modelled	11.0	25	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> af4/fmr2 family member 4; <b>PDBTitle:</b> the crystal structure of ell2 ocludin domain and aff4 peptide
79	<a href="#">c4i14B_</a>		Alianment	not modelled	10.8	28	<b>PDB header:</b> hydrolase, lyase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribba;

						<b>PDBTitle:</b> crystal structure of mtb-riba2 (rv1415)
80	<a href="#">c6hunA</a>	Alignment	not modelled	10.7	18	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase; <b>PDBTitle:</b> dimeric archeal rubisco from hyperthermus butylicus
81	<a href="#">c1zwvA</a>	Alignment	not modelled	10.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipamide acyltransferase component of branched- <b>PDBTitle:</b> solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
82	<a href="#">c2vduE</a>	Alignment	not modelled	10.6	15	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> trna (guanine-n(7)-)-methyltransferase; <b>PDBTitle:</b> structure of trm8-trm82, the yeast trna m7g methylation2 complex
83	<a href="#">d1bhea</a>	Alignment	not modelled	10.3	18	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> Pectin lyase-like <b>Family:</b> Galacturonase
84	<a href="#">c2ouiB</a>	Alignment	not modelled	10.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica
85	<a href="#">c5ykaA</a>	Alignment	not modelled	10.2	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein kdo0; <b>PDBTitle:</b> crystal structure of the kdo hydroxylase kdo0, a non-heme fe(ii)2 alphaketoglutarate dependent dioxygenase in complex with cobalt(ii)
86	<a href="#">d1yb2a1</a>	Alignment	not modelled	10.1	19	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> tRNA(1-methyladenosine) methyltransferase-like
87	<a href="#">c1yb2A</a>	Alignment	not modelled	10.1	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ta0852; <b>PDBTitle:</b> structure of a putative methyltransferase from thermoplasma2 acidophilum.
88	<a href="#">c3p04A</a>	Alignment	not modelled	10.1	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized bcr; <b>PDBTitle:</b> crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
89	<a href="#">c1rldB</a>	Alignment	not modelled	10.0	14	<b>PDB header:</b> lyase(carbon-carbon) <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose 1,5 bisphosphate carboxylase/oxygenase (large <b>PDBTitle:</b> solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
90	<a href="#">c3cgxA</a>	Alignment	not modelled	10.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotide-diphospho-sugar transferase; <b>PDBTitle:</b> crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
91	<a href="#">c2hb0B</a>	Alignment	not modelled	10.0	45	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> cfa/i fimbrial subunit e; <b>PDBTitle:</b> crystal structure of cfae, the adhesive subunit of cfa/i2 fimbria of enterotoxigenic escherichia coli
92	<a href="#">c3w6kC</a>	Alignment	not modelled	9.9	7	<b>PDB header:</b> cell cycle <b>Chain:</b> C: <b>PDB Molecule:</b> scpb; <b>PDBTitle:</b> crystal structure of dimer of scpb n-terminal domain complexed with2 scpa peptide
93	<a href="#">c2zviB</a>	Alignment	not modelled	9.7	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-diketo-5-methylthiopentyl-1-phosphate <b>PDBTitle:</b> crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
94	<a href="#">c3ofkA</a>	Alignment	not modelled	9.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nodulation protein s; <b>PDBTitle:</b> crystal structure of n-methyltransferase nods from bradyrhizobium2 japonicum wm9 in complex with s-adenosyl-l-homocysteine (sah)
95	<a href="#">c3p04B</a>	Alignment	not modelled	9.6	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized bcr; <b>PDBTitle:</b> crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
96	<a href="#">c5wvrA</a>	Alignment	not modelled	9.5	26	<b>PDB header:</b> transferase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> putative methyltransferase nsun6; <b>PDBTitle:</b> crystal structure of human nsun6/trna/sfg
97	<a href="#">c2d69B</a>	Alignment	not modelled	9.5	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase; <b>PDBTitle:</b> crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
98	<a href="#">c4df3B</a>	Alignment	not modelled	9.5	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fibrillar-like rrna/trna 2'-o-methyltransferase; <b>PDBTitle:</b> crystal structure of aeropyrum pernix fibrillar in complex with2 natively bound s-adenosyl-l-methionine at 1.7a
99	<a href="#">c4obuG</a>	Alignment	not modelled	9.5	12	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> pyridoxal-dependent decarboxylase domain protein; <b>PDBTitle:</b> ruminococcus gnavus tryptophan decarboxylase rumgna_01526 (apo)