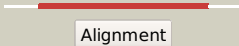



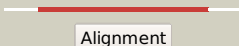

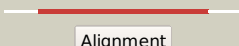

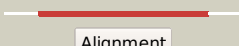

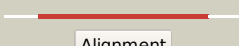

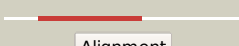











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2726c_(dapF)_3038941_3039810
Date	Wed Aug 7 12:50:38 BST 2019
Unique Job ID	d68ffc5e037a3359

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3fveA_</a>	 Alignment		100.0	96	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate epimerase; <b>PDBTitle:</b> crystal structure of diaminopimelate epimerase mycobacterium2 tuberculosis dapf
2	<a href="#">c5m47A_</a>	 Alignment		100.0	53	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate epimerase; <b>PDBTitle:</b> crystal structure of dapf from corynebacterium glutamicum in complex2 with d,l-diaminopimelate
3	<a href="#">c2gkjA_</a>	 Alignment		100.0	28	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate epimerase; <b>PDBTitle:</b> crystal structure of diaminopimelate epimerase in complex2 with an irreversible inhibitor dl-azidap
4	<a href="#">c5ha4A_</a>	 Alignment		100.0	31	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate epimerase; <b>PDBTitle:</b> structure of a diaminopimelate epimerase from acinetobacter baumannii
5	<a href="#">c2otnB_</a>	 Alignment		100.0	31	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate epimerase; <b>PDBTitle:</b> crystal structure of the catalytically active form of diaminopimelate2 epimerase from bacillus anthracis
6	<a href="#">c3ekmE_</a>	 Alignment		100.0	35	<b>PDB header:</b> isomerase <b>Chain:</b> E: <b>PDB Molecule:</b> diaminopimelate epimerase, chloroplastic; <b>PDBTitle:</b> crystal structure of diaminopimelate epimerase form2 arabidopsis thaliana in complex with irreversible inhibitor3 dl-azidap
7	<a href="#">d2gkea1</a>	 Alignment		100.0	32	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> Diaminopimelate epimerase
8	<a href="#">c4juuA_</a>	 Alignment		100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> epimerase; <b>PDBTitle:</b> crystal structure of a putative hydroxyproline epimerase from2 xanthomonas campestris (target efi-506516) with bound phosphate and3 unknown ligand
9	<a href="#">c3ednB_</a>	 Alignment		100.0	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> phenazine biosynthesis protein, phzf family; <b>PDBTitle:</b> crystal structure of the bacillus anthracis phenazine2 biosynthesis protein, phzf family
10	<a href="#">c1qy9B_</a>	 Alignment		100.0	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ydde; <b>PDBTitle:</b> crystal structure of e. coli se-met protein ydde
11	<a href="#">d1s7ja_</a>	 Alignment		100.0	15	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like

12	<a href="#">c1ym5A_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical 32.6 kda protein in dap2-slt2 <b>PDBTitle:</b> crystal structure of yhi9, the yeast member of the2 phenazine biosynthesis phzf enzyme superfamily.
13	<a href="#">c4dunA_</a>	Alignment		100.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative phenazine biosynthesis phzc/phzf protein; <b>PDBTitle:</b> 1.76a x-ray crystal structure of a putative phenazine biosynthesis2 phzc/phzf protein from clostridium difficile (strain 630)
14	<a href="#">c2azpA_</a>	Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa1268; <b>PDBTitle:</b> crystal structure of pa1268 solved by sulfur sad
15	<a href="#">c1u1wA_</a>	Alignment		100.0	15	<b>PDB header:</b> isomerase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phenazine biosynthesis protein phzf; <b>PDBTitle:</b> structure and function of phenazine-biosynthesis protein phzf from2 pseudomonas fluorescens 2-79
16	<a href="#">c1u0kA_</a>	Alignment		100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gene product pa4716; <b>PDBTitle:</b> the structure of a predicted epimerase pa4716 from pseudomonas2 aeruginosa
17	<a href="#">c4jd7D_</a>	Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> proline racemase; <b>PDBTitle:</b> crystal structure of pput_1285, a putative hydroxyproline epimerase2 from pseudomonas putida f1 (target efi-506500), open form, space3 group p212121, bound sulfate
18	<a href="#">c6r77B_</a>	Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> proline racemase; <b>PDBTitle:</b> crystal structure of trans-3-hydroxy-l-proline dehydratase in complex2 with substrate - closed conformation
19	<a href="#">d1tm0a_</a>	Alignment		100.0	13	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> Proline racemase
20	<a href="#">c6hjgB_</a>	Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> proline racemase a; <b>PDBTitle:</b> trypanosoma cruzi proline racemase in complex with inhibitor oxopa
21	<a href="#">c1w62B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> racemase <b>Chain:</b> B: <b>PDB Molecule:</b> proline racemase a; <b>PDBTitle:</b> proline racemase in complex with one molecule of pyrrole-2-carboxylic2 acid (hemi form)
22	<a href="#">c6j7cA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> proline racemase; <b>PDBTitle:</b> crystal structure of proline racemase-like protein from thermococcus2 litoralis in complex with proline
23	<a href="#">c4lb0B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hydroxyproline epimerase from agrobacterium2 vitis, target efi-506420, with bound trans-4-oh-l-proline
24	<a href="#">d2gkea2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> Diaminopimelate epimerase
25	<a href="#">c4k7gD_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-hydroxyproline dehydratse; <b>PDBTitle:</b> crystal structure of a 3-hydroxyproline dehydratse from agrobacterium2 vitis, target efi-506470, with bound pyrrole 2-carboxylate, ordered3 active site
26	<a href="#">d1qy9a1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
27	<a href="#">d1xuba1</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
28	<a href="#">d1xuba2</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like

29	<a href="#">d1qy9a2</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
30	<a href="#">d1u0ka2</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
31	<a href="#">d1u0ka1</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
32	<a href="#">c6p3hB</a>	Alignment	not modelled	98.4	21	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> (4e)-oxalomesaconate delta-isomerase; <b>PDBTitle:</b> crystal structure of ligu(k66m) bound to substrate
33	<a href="#">c6otvA</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative isomerase ybhh; <b>PDBTitle:</b> crystal structure of putative isomerase ec2056
34	<a href="#">c3g7kD</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-methylitaconate isomerase; <b>PDBTitle:</b> crystal structure of methylitaconate-delta-isomerase
35	<a href="#">c2pw0A</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> prpf methylaconitate isomerase; <b>PDBTitle:</b> crystal structure of trans-aconitate bound to methylaconitate2 isomerase prpf from shewanella oneidensis
36	<a href="#">d1sr8a</a>	Alignment	not modelled	56.4	39	<b>Fold:</b> CbiD-like <b>Superfamily:</b> CbiD-like <b>Family:</b> CbiD-like
37	<a href="#">d2h9fa2</a>	Alignment	not modelled	55.6	23	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PA0793-like
38	<a href="#">c3axtA</a>	Alignment	not modelled	31.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable n(2),n(2)-dimethylguanosine trna methyltransferase <b>PDBTitle:</b> complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
39	<a href="#">d2h9fa1</a>	Alignment	not modelled	25.8	13	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PA0793-like
40	<a href="#">d2dula1</a>	Alignment	not modelled	23.2	33	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> TRM1-like
41	<a href="#">c5jvoA</a>	Alignment	not modelled	20.9	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine repressor; <b>PDBTitle:</b> crystal structure of the arginine repressor from the pathogenic2 bacterium corynebacterium pseudotuberculosis
42	<a href="#">c5hr4J</a>	Alignment	not modelled	20.6	17	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> J: <b>PDB Molecule:</b> mmei; <b>PDBTitle:</b> structure of type iii restriction-modification enzyme mmei in complex2 with dna has implications for engineering of new specificities
43	<a href="#">d1vema1</a>	Alignment	not modelled	19.5	11	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Starch-binding domain
44	<a href="#">d2ih2a1</a>	Alignment	not modelled	19.2	18	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> DNA methylase TaqI, N-terminal domain
45	<a href="#">c4o1hA</a>	Alignment	not modelled	19.0	27	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator glnr; <b>PDBTitle:</b> crystal structure of the regulatory domain of ameglNr
46	<a href="#">d1q7sa</a>	Alignment	not modelled	18.7	16	<b>Fold:</b> Peptidyl-tRNA hydrolase II <b>Superfamily:</b> Peptidyl-tRNA hydrolase II <b>Family:</b> Peptidyl-tRNA hydrolase II
47	<a href="#">d2ar0a1</a>	Alignment	not modelled	18.7	9	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N-6 DNA Methylase-like
48	<a href="#">c5ybbA</a>	Alignment	not modelled	18.5	17	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> structural basis underlying complex assembly and conformational2 transition of the type i r-m system
49	<a href="#">c1vzhB</a>	Alignment	not modelled	16.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> desulfoferrodoxin; <b>PDBTitle:</b> structure of superoxide reductase bound to ferrocyanide and active2 site expansion upon x-ray induced photoreduction
50	<a href="#">c3khkA</a>	Alignment	not modelled	15.1	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methylation subunit; <b>PDBTitle:</b> crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazei.
51	<a href="#">c2waqG</a>	Alignment	not modelled	14.6	25	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> dna-directed rna polymerase rpo8 subunit; <b>PDBTitle:</b> the complete structure of the archaeal 13-subunit dna-directed rna2 polymerase
52	<a href="#">d2ayxa2</a>	Alignment	not modelled	14.2	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> RcsC linker domain-like
53	<a href="#">c2l3bA</a>	Alignment	not modelled	14.1	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein found in conjugate transposon; <b>PDBTitle:</b> solution nmr structure of the bt_0084 lipoprotein from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr376

54	<a href="#">d1jwya1</a>	Alignment	not modelled	14.0	28	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Myosin S1 fragment, N-terminal domain <b>Family:</b> Myosin S1 fragment, N-terminal domain
55	<a href="#">c3lkdB</a>	Alignment	not modelled	13.9	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> crystal structure of the type i restriction-modification system2 methyltransferase subunit from streptococcus thermophilus, northeast3 structural genomics consortium target sur80
56	<a href="#">c3ufbA</a>	Alignment	not modelled	13.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type i restriction-modification system methyltransferase <b>PDBTitle:</b> crystal structure of a modification subunit of a putative type i2 restriction enzyme from vibrio vulnificus yj016
57	<a href="#">c2l7qA</a>	Alignment	not modelled	13.3	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved protein found in conjugate transposon; <b>PDBTitle:</b> solution nmr structure of conjugate transposon protein bvu_1572(27-2 141) from bacteroides vulgatus, northeast structural genomics3 consortium target bvr155
58	<a href="#">c3p9nA</a>	Alignment	not modelled	13.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible methyltransferase (methylase); <b>PDBTitle:</b> rv2966c of m. tuberculosis is a rsmd-like methyltransferase
59	<a href="#">c3j3bU</a>	Alignment	not modelled	12.7	7	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein l22; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
60	<a href="#">c4qxIA</a>	Alignment	not modelled	12.2	20	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein flhe; <b>PDBTitle:</b> crystal structure of flhe
61	<a href="#">c5hfjF</a>	Alignment	not modelled	12.1	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> adenine specific dna methyltransferase (dpna); <b>PDBTitle:</b> crystal structure of m1.hpyavi-sam complex
62	<a href="#">c3j39U</a>	Alignment	not modelled	12.1	7	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 60s ribosomal protein l22; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
63	<a href="#">c1aqjB</a>	Alignment	not modelled	12.0	21	<b>PDB header:</b> methyltransferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenine-n6-dna-methyltransferase taqi; <b>PDBTitle:</b> structure of adenine-n6-dna-methyltransferase taqi
64	<a href="#">c4lbaB</a>	Alignment	not modelled	11.5	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conjugative transposon lipoprotein; <b>PDBTitle:</b> crystal structure of a conjugative transposon lipoprotein2 (bacegg_03088) from bacteroides eggerthii dsm 20697 at 1.70 a3 resolution
65	<a href="#">d2okca1</a>	Alignment	not modelled	11.3	22	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N-6 DNA Methylase-like
66	<a href="#">c4zyeA</a>	Alignment	not modelled	10.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus o6-methylguanine2 methyltransferase
67	<a href="#">c6h2uA</a>	Alignment	not modelled	10.8	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methyltransferase-like protein 5; <b>PDBTitle:</b> crystal structure of human mettl5-trmt112 complex, the 18s rna2 m6a1832 methyltransferase at 1.6a resolution
68	<a href="#">d2f8la1</a>	Alignment	not modelled	10.6	17	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> N-6 DNA Methylase-like
69	<a href="#">c4qh0D</a>	Alignment	not modelled	10.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dna-entry nuclease (competence-specific nuclease); <b>PDBTitle:</b> crystal structure of nuca from streptococcus agalactiae with magnesium2 ion bound
70	<a href="#">c1xtyD</a>	Alignment	not modelled	10.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus peptidyl-trna hydrolase
71	<a href="#">c3ldgA</a>	Alignment	not modelled	9.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein smu.472; <b>PDBTitle:</b> crystal structure of smu.472, a putative methyltransferase complexed2 with sah
72	<a href="#">d1dkua1</a>	Alignment	not modelled	9.8	17	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosylpyrophosphate synthetase-like
73	<a href="#">d1rka</a>	Alignment	not modelled	9.7	15	<b>Fold:</b> Peptidyl-tRNA hydrolase II <b>Superfamily:</b> Peptidyl-tRNA hydrolase II <b>Family:</b> Peptidyl-tRNA hydrolase II
74	<a href="#">c2zv3E</a>	Alignment	not modelled	9.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
75	<a href="#">c2vwtA</a>	Alignment	not modelled	9.5	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> yfau, 2-keto-3-deoxy sugar aldolase; <b>PDBTitle:</b> crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
76	<a href="#">c1g38A</a>	Alignment	not modelled	9.5	21	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> modification methylase taqi; <b>PDBTitle:</b> adenine-specific methyltransferase m. taq i/dna complex
77	<a href="#">d1ne2a</a>	Alignment	not modelled	9.5	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like <b>PDB header:</b> transferase

78	<a href="#">c2g7hA</a>	Alignment	not modelled	9.3	17	<b>Chain:</b> A: <b>PDB Molecule:</b> methylated-dna--protein-cysteine <b>PDBTitle:</b> structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
79	<a href="#">c4tv6A</a>	Alignment	not modelled	9.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyglucarate aldolase; <b>PDBTitle:</b> crystal structure of citrate synthase variant sbng e151q
80	<a href="#">c6b3oB</a>	Alignment	not modelled	9.0	31	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
81	<a href="#">c3hvvB</a>	Alignment	not modelled	8.8	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the tgs domain of the cleop_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
82	<a href="#">c5fgwA</a>	Alignment	not modelled	8.6	24	<b>PDB header:</b> metal binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular streptodornase d; <b>PDBTitle:</b> structure of sda1 nuclease with bound zinc ion
83	<a href="#">c3owvA</a>	Alignment	not modelled	8.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-entry nuclease; <b>PDBTitle:</b> structural insights into catalytic and substrate binding mechanisms of2 the strategic endo nuclease from streptococcus pneumoniae
84	<a href="#">d1wy7a1</a>	Alignment	not modelled	8.4	21	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Ta1320-like
85	<a href="#">c5e72A</a>	Alignment	not modelled	8.3	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n2, n2-dimethylguanosine trna methyltransferase; <b>PDBTitle:</b> crystal structure of the archaeal trna m2g/m22g10 methyltransferase2 (atrm11) in complex with s-adenosyl-l-methionine (sam) from3 thermococcus kodakarensis
86	<a href="#">d1xo8a</a>	Alignment	not modelled	8.3	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> LEA14-like <b>Family:</b> LEA14-like
87	<a href="#">c5egpB</a>	Alignment	not modelled	8.3	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ubie/coq5 family methyltransferase, putative; <b>PDBTitle:</b> crystal structure of the s-methyltransferase tmta
88	<a href="#">d1mgt1</a>	Alignment	not modelled	7.8	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain <b>Family:</b> Methylated DNA-protein cysteine methyltransferase, C-terminal domain
89	<a href="#">d1bf2a2</a>	Alignment	not modelled	7.7	10	<b>Fold:</b> Glycosyl hydrolase domain <b>Superfamily:</b> Glycosyl hydrolase domain <b>Family:</b> alpha-Amylases, C-terminal beta-sheet domain
90	<a href="#">d2esra1</a>	Alignment	not modelled	7.5	20	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
91	<a href="#">d1ws6a1</a>	Alignment	not modelled	7.5	27	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like
92	<a href="#">c3qz6A</a>	Alignment	not modelled	7.4	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
93	<a href="#">d2p92a1</a>	Alignment	not modelled	7.4	16	<b>Fold:</b> eIF1-like <b>Superfamily:</b> TM1457-like <b>Family:</b> TM1457-like
94	<a href="#">c3cioA</a>	Alignment	not modelled	7.4	27	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase etk; <b>PDBTitle:</b> the kinase domain of escherichia coli tyrosine kinase etk
95	<a href="#">c2xh3B</a>	Alignment	not modelled	7.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> spd1 nuclease; <b>PDBTitle:</b> extracellular nuclease
96	<a href="#">c4he5A</a>	Alignment	not modelled	7.1	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase family u32; <b>PDBTitle:</b> crystal structure of the selenomethionine variant of the c-terminal2 domain of geobacillus thermoleovorans putative u32 peptidase
97	<a href="#">c2d3kA</a>	Alignment	not modelled	7.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> structural study on project id ph1539 from pyrococcus2 horikoshii ot3
98	<a href="#">c2p35A</a>	Alignment	not modelled	7.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trans-aconitate 2-methyltransferase; <b>PDBTitle:</b> crystal structure of trans-aconitate methyltransferase from2 agrobacterium tumefaciens
99	<a href="#">d2fpoa1</a>	Alignment	not modelled	7.0	13	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> YhhF-like