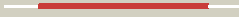




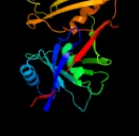


















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2716_(-)_3029182_3029868
Date	Wed Aug 7 12:50:37 BST 2019
Unique Job ID	0ebecc2600b32445

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ym5A_</a>	 Alignment		100.0	31	<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.
2	<a href="#">c3ednB_</a>	 Alignment		100.0	26	<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
3	<a href="#">c4dunA_</a>	 Alignment		100.0	23	<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)
4	<a href="#">d1s7ja_</a>	 Alignment		100.0	20	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
5	<a href="#">c1u0ka_</a>	 Alignment		100.0	29	<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
6	<a href="#">c1qy9B_</a>	 Alignment		100.0	24	<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
7	<a href="#">c1u1wA_</a>	 Alignment		100.0	31	<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
8	<a href="#">c5ha4A_</a>	 Alignment		100.0	23	<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
9	<a href="#">c3ekmE_</a>	 Alignment		100.0	18	<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
10	<a href="#">d1u0ka1</a>	 Alignment		100.0	26	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
11	<a href="#">c4juuA_</a>	 Alignment		100.0	22	<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

12	<a href="#">c6r77B_</a>	Alignment		100.0	18	<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
13	<a href="#">d1xuba1</a>	Alignment		100.0	26	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
14	<a href="#">c6j7cA_</a>	Alignment		100.0	16	<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
15	<a href="#">c4jd7D_</a>	Alignment		100.0	19	<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
16	<a href="#">c2azpA_</a>	Alignment		100.0	19	<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
17	<a href="#">c2gkja_</a>	Alignment		100.0	15	<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
18	<a href="#">d1qy9a1</a>	Alignment		100.0	25	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
19	<a href="#">c2otnB_</a>	Alignment		100.0	20	<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
20	<a href="#">c4k7gD_</a>	Alignment		100.0	21	<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
21	<a href="#">c1w62B_</a>	Alignment	not modelled	100.0	18	<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="#">c6hjbB_</a>	Alignment	not modelled	100.0	17	<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
23	<a href="#">c4lb0B_</a>	Alignment	not modelled	99.9	19	<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="#">d1qy9a2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
25	<a href="#">d1xuba2</a>	Alignment	not modelled	99.9	33	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
26	<a href="#">d1tm0a_</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> Proline racemase
27	<a href="#">d1u0ka2</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PhzC/PhzF-like
28	<a href="#">d2gkea1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> Diaminopimelate epimerase
						<b>PDB header:</b> isomerase

29	<a href="#">c5m47A_</a>	Alignment	not modelled	99.4	15	<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
30	<a href="#">c3fveA_</a>	Alignment	not modelled	99.3	18	<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
31	<a href="#">d2gkea2</a>	Alignment	not modelled	97.2	17	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> Diaminopimelate epimerase
32	<a href="#">c6p3hB_</a>	Alignment	not modelled	90.7	18	<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	86.5	18	<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="#">d2h9fa2</a>	Alignment	not modelled	82.7	21	<b>Fold:</b> Diaminopimelate epimerase-like <b>Superfamily:</b> Diaminopimelate epimerase-like <b>Family:</b> PA0793-like
35	<a href="#">c2pw0A_</a>	Alignment	not modelled	71.5	22	<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="#">c3g7kD_</a>	Alignment	not modelled	62.1	27	<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
37	<a href="#">c5hr4J_</a>	Alignment	not modelled	45.6	29	<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
38	<a href="#">c5z2tC_</a>	Alignment	not modelled	25.3	29	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> double homeobox protein 4; <b>PDBTitle:</b> crystal structure of dna-bound dux4-hd2
39	<a href="#">d1uhsa_</a>	Alignment	not modelled	22.8	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
40	<a href="#">d1up8a_</a>	Alignment	not modelled	21.9	16	<b>Fold:</b> Acid phosphatase/Vanadium-dependent haloperoxidase <b>Superfamily:</b> Acid phosphatase/Vanadium-dependent haloperoxidase <b>Family:</b> Haloperoxidase (bromoperoxidase)
41	<a href="#">d2cuea1</a>	Alignment	not modelled	18.8	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
42	<a href="#">d1yh5a1</a>	Alignment	not modelled	18.8	9	<b>Fold:</b> YggU-like <b>Superfamily:</b> YggU-like <b>Family:</b> YggU-like
43	<a href="#">c1x2mA_</a>	Alignment	not modelled	18.5	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lag1 longevity assurance homolog 6; <b>PDBTitle:</b> solution structure of the homeobox domain of mouse lag12 longevity assurance homolog 6
44	<a href="#">d1s7ea1</a>	Alignment	not modelled	17.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
45	<a href="#">c2da2A_</a>	Alignment	not modelled	17.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-fetoprotein enhancer binding protein; <b>PDBTitle:</b> solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
46	<a href="#">c2waqG_</a>	Alignment	not modelled	17.3	31	<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
47	<a href="#">c2dmuA_</a>	Alignment	not modelled	17.1	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein gooseoid; <b>PDBTitle:</b> solution structure of the homeobox domain of homeobox2 protein gooseoid
48	<a href="#">d2p81a1</a>	Alignment	not modelled	17.0	41	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
49	<a href="#">c6aziA_</a>	Alignment	not modelled	16.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-alanyl-d-alanine endopeptidase; <b>PDBTitle:</b> 1.75 angstrom resolution crystal structure of d-alanyl-d-alanine2 endopeptidase from enterobacter cloacae in complex with covalently3 bound boronic acid
50	<a href="#">d1ftza_</a>	Alignment	not modelled	16.3	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
51	<a href="#">c2l9rA_</a>	Alignment	not modelled	16.0	28	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein nkx-3.1; <b>PDBTitle:</b> solution nmr structure of homeobox domain of homeobox protein nkx-3.12 from homo sapiens, northeast structural genomics consortium target3 hr6470a
52	<a href="#">d1o4xa1</a>	Alignment	not modelled	15.9	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
53	<a href="#">d1e3oc1</a>	Alignment	not modelled	15.7	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
54	<a href="#">d2ar0a1</a>	Alignment	not modelled	15.6	36	<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
55	<a href="#">d1au7a1</a>	Alignment	not modelled	15.4	6	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
56	<a href="#">d1o9ga</a>	Alignment	not modelled	15.4	16	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> rRNA methyltransferase AviRa
57	<a href="#">d2craa1</a>	Alignment	not modelled	14.7	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
58	<a href="#">c3k0bA</a>	Alignment	not modelled	14.5	29	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted n6-adenine-specific dna methylase; <b>PDBTitle:</b> crystal structure of a predicted n6-adenine-specific dna methylase2 from listeria monocytogenes str. 4b f2365
59	<a href="#">d1p7ia</a>	Alignment	not modelled	14.2	41	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
60	<a href="#">d1le8a</a>	Alignment	not modelled	14.0	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
61	<a href="#">c3ufbA</a>	Alignment	not modelled	14.0	21	<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
62	<a href="#">c2da4A</a>	Alignment	not modelled	13.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein dkfzp686k21156; <b>PDBTitle:</b> solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
63	<a href="#">c2vi6F</a>	Alignment	not modelled	13.8	18	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> homeobox protein nanog; <b>PDBTitle:</b> crystal structure of the nanog homeodomain
64	<a href="#">c3khkA</a>	Alignment	not modelled	13.6	21	<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.
65	<a href="#">c3a01A</a>	Alignment	not modelled	13.5	17	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeodomain-containing protein; <b>PDBTitle:</b> crystal structure of aristaless and clawless homeodomains bound to dna
66	<a href="#">d1ig7a</a>	Alignment	not modelled	13.4	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
67	<a href="#">d2hi3a1</a>	Alignment	not modelled	13.3	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
68	<a href="#">c5hjfF</a>	Alignment	not modelled	13.3	14	<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
69	<a href="#">c2da1A</a>	Alignment	not modelled	13.2	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-fetoprotein enhancer binding protein; <b>PDBTitle:</b> solution structure of the first homeobox domain of at-2 binding transcription factor 1 (atbf1)
70	<a href="#">d1octc1</a>	Alignment	not modelled	13.2	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
71	<a href="#">d2cqxa1</a>	Alignment	not modelled	12.8	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
72	<a href="#">d1jgga</a>	Alignment	not modelled	12.8	41	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
73	<a href="#">d1fjlb</a>	Alignment	not modelled	12.5	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
74	<a href="#">d2okca1</a>	Alignment	not modelled	12.1	36	<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
75	<a href="#">c2dmsA</a>	Alignment	not modelled	12.0	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein otx2; <b>PDBTitle:</b> solution structure of the homeobox domain of homeobox2 protein otx2
76	<a href="#">c2e19A</a>	Alignment	not modelled	12.0	6	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor 8; <b>PDBTitle:</b> solution structure of the homeobox domain from human nil-2-2 a zinc finger protein, transcription factor 8
77	<a href="#">d1g60a</a>	Alignment	not modelled	11.9	14	<b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Type II DNA methylase
78	<a href="#">d1f43a</a>	Alignment	not modelled	11.9	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
79	<a href="#">c5ybbA</a>	Alignment	not modelled	11.8	29	<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 andconformational2 transition of the type i r-m system <b>PDB header:</b> unknown function

80	<a href="#">c4h4nA_</a>	Alignment	not modelled	11.8	29	<b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ba_2335; <b>PDBTitle:</b> 1.1 angstrom crystal structure of hypothetical protein ba_2335 from2 bacillus anthracis
81	<a href="#">d1zq3p1</a>	Alignment	not modelled	11.7	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
82	<a href="#">d2r5yb1</a>	Alignment	not modelled	11.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
83	<a href="#">c3itcA_</a>	Alignment	not modelled	11.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> renal dipeptidase; <b>PDBTitle:</b> crystal structure of sco3058 with bound citrate and glycerol
84	<a href="#">c2zifB_</a>	Alignment	not modelled	11.3	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative modification methylase; <b>PDBTitle:</b> crystal structure of ttha0409, putative dna modification methylase2 from thermus thermophilus hb8- complexed with s-adenosyl-l-methionine
85	<a href="#">d1bgva2</a>	Alignment	not modelled	11.0	13	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
86	<a href="#">d2hddb_</a>	Alignment	not modelled	10.9	41	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
87	<a href="#">d1b8ia_</a>	Alignment	not modelled	10.8	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
88	<a href="#">d9anta_</a>	Alignment	not modelled	10.6	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
89	<a href="#">c2k40A_</a>	Alignment	not modelled	10.6	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox expressed in es cells 1; <b>PDBTitle:</b> nmr structure of hexs-1 homeodomain double mutant r31l/e42l
90	<a href="#">c1g38A_</a>	Alignment	not modelled	10.5	7	<b>PDB header:</b> transferase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> modification methylase taqi; <b>PDBTitle:</b> adenine-specific methyltransferase m. taqi i/dna complex
91	<a href="#">d1vnda_</a>	Alignment	not modelled	10.4	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
92	<a href="#">c2i5gB_</a>	Alignment	not modelled	10.4	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> crystal strcuture of amidohydrolase from pseudomonas aeruginosa
93	<a href="#">c5cffE_</a>	Alignment	not modelled	10.4	13	<b>PDB header:</b> transcription/rna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> staufen; <b>PDBTitle:</b> crystal structure of miranda/staufen dsrbd5 complex
94	<a href="#">c3a03A_</a>	Alignment	not modelled	10.3	18	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> t-cell leukemia homeobox protein 2; <b>PDBTitle:</b> crystal structure of hox11l1 homeodomain
95	<a href="#">c3ldgA_</a>	Alignment	not modelled	10.1	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
96	<a href="#">c1aqjB_</a>	Alignment	not modelled	10.1	7	<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
97	<a href="#">d1du0a_</a>	Alignment	not modelled	10.0	41	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Homeodomain
98	<a href="#">c3lu2B_</a>	Alignment	not modelled	10.0	0	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lmo2462 protein; <b>PDBTitle:</b> structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
99	<a href="#">c2ragB_</a>	Alignment	not modelled	9.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidase; <b>PDBTitle:</b> crystal structure of aminohydrolase from caulobacter crescentus