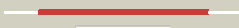














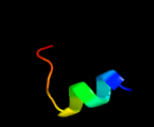

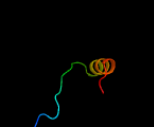






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3292_(-)_3672325_3673572
Date	Thu Aug 8 16:20:50 BST 2019
Unique Job ID	f873f818cfa55575

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2rjbD_</a>	 Alignment		100.0	43	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein ydcj (sf1787) from2 shigella flexneri which includes domain duf1338. northeast structural3 genomics consortium target sfr276
2	<a href="#">c3iuzA_</a>	 Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glyoxalase superfamily protein; <b>PDBTitle:</b> crystal structure of putative glyoxalase superfamily protein2 (yp_299723.1) from ralstonia eutropha jmp134 at 1.90 a resolution
3	<a href="#">c3lhoA_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative hydrolase (yp_751971.1) from shewanella2 frigidimarina ncimb 400 at 1.80 a resolution
4	<a href="#">c3rmuD_</a>	 Alignment		84.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> methylmalonyl-coa epimerase, mitochondrial; <b>PDBTitle:</b> crystal structure of human methylmalonyl-coa epimerase, mcee
5	<a href="#">d1jc4a_</a>	 Alignment		74.7	26	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Methylmalonyl-CoA epimerase
6	<a href="#">c3oa4A_</a>	 Alignment		65.7	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase; <b>PDBTitle:</b> crystal structure of hypothetical protein bh1468 from bacillus2 halodurans c-125
7	<a href="#">c4ro6A_</a>	 Alignment		60.9	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of glyoxalase i from zea mays
8	<a href="#">d1v54i_</a>	 Alignment		60.7	50	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIc <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIc
9	<a href="#">c1cjcC_</a>	 Alignment		60.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens hppd
10	<a href="#">c3gm5A_</a>	 Alignment		58.4	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase and related lyases; <b>PDBTitle:</b> crystal structure of a putative methylmalonyl-coenzyme a epimerase2 from thermoanaerobacter tengcongensis at 2.0 a resolution
11	<a href="#">d1sqia2</a>	 Alignment		55.4	26	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases

12	<a href="#">d1qipa_</a>	Alignment		54.0	20	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Glyoxalase I (lactoylglutathione lyase)
13	<a href="#">d1cxa2</a>	Alignment		51.4	14	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
14	<a href="#">c3oajA_</a>	Alignment		50.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative ring-cleaving dioxygenase mhqo; <b>PDBTitle:</b> crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
15	<a href="#">d1t47a2</a>	Alignment		50.5	21	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
16	<a href="#">c4g9qA_</a>	Alignment		48.7	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-carboxymuconolactone decarboxylase; <b>PDBTitle:</b> crystal structure of a 4-carboxymuconolactone decarboxylase
17	<a href="#">c6bu2A_</a>	Alignment		47.1	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase; <b>PDBTitle:</b> crystal structure of methylmalonyl-coa epimerase from mycobacterium2 tuberculosis
18	<a href="#">c1t47A_</a>	Alignment		46.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvate dioxygenase; <b>PDBTitle:</b> structure of fe2-hppd bound to ntbc
19	<a href="#">c2r5vA_</a>	Alignment		45.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pcza361.1; <b>PDBTitle:</b> hydroxymandelate synthase crystal structure
20	<a href="#">c2qqzB_</a>	Alignment		44.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase family protein, putative; <b>PDBTitle:</b> crystal structure of putative glyoxalase family protein from bacillus2 anthracis
21	<a href="#">d1q0oa2</a>	Alignment	not modelled	43.7	22	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
22	<a href="#">d1sqia1</a>	Alignment	not modelled	43.6	14	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
23	<a href="#">c3zw5A_</a>	Alignment	not modelled	41.6	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase domain-containing protein 5; <b>PDBTitle:</b> crystal structure of the human glyoxalase domain-containing protein 5
24	<a href="#">c2rk0B_</a>	Alignment	not modelled	40.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase domain; <b>PDBTitle:</b> crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase domain from frankia sp. ean1pec
25	<a href="#">c6ntwA_</a>	Alignment	not modelled	39.9	26	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> probable l,d-transpeptidase yccb; <b>PDBTitle:</b> crystal structure of e. coli yccb
26	<a href="#">d1kw3b1</a>	Alignment	not modelled	38.6	7	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
27	<a href="#">c2l1nA_</a>	Alignment	not modelled	36.4	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the protein yp_399305.1
28	<a href="#">c3l7tB_</a>	Alignment	not modelled	36.0	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein;

						<b>PDBTitle:</b> crystal structure of smu.1112c
29	<a href="#">c1sqiA_</a>	Alignment	not modelled	34.5	26	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvic acid dioxygenase; <b>PDBTitle:</b> structural basis for inhibitor selectivity revealed by 2 crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
30	<a href="#">d1t47a1</a>	Alignment	not modelled	34.1	18	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradial dioxygenases
31	<a href="#">c3zgiA_</a>	Alignment	not modelled	32.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxyphenylpyruvic acid dioxygenase; <b>PDBTitle:</b> s221m v223f y359a mutant of 4-hydroxymandelate synthase2 from streptomyces coelicolor
32	<a href="#">c1zswA_</a>	Alignment	not modelled	32.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase family protein; <b>PDBTitle:</b> crystal structure of bacillus cereus metallo protein from glyoxalase2 family
33	<a href="#">d2pjsa1</a>	Alignment	not modelled	32.5	18	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
34	<a href="#">c4pzjA_</a>	Alignment	not modelled	32.2	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of a transcriptional2 regulator of the lysr family from eggerthella lenta dsm 2243
35	<a href="#">c6o5cB_</a>	Alignment	not modelled	31.8	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative metal-dependent transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of metal-dependent transcriptional regulator2 mtsr
36	<a href="#">d1sqda2</a>	Alignment	not modelled	31.6	24	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradial dioxygenases
37	<a href="#">c4mtsA_</a>	Alignment	not modelled	31.5	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> ni- and zn-bound gloa2 at high resolution
38	<a href="#">c3o2iB_</a>	Alignment	not modelled	30.1	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba
39	<a href="#">d1zswa2</a>	Alignment	not modelled	29.7	16	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> BC1024-like
40	<a href="#">c3g05B_</a>	Alignment	not modelled	29.4	37	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of n-terminal domain (2-550) of e.coli mnmg
41	<a href="#">c5fo5A_</a>	Alignment	not modelled	29.4	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator metr; <b>PDBTitle:</b> structure of the dna-binding domain of escherichia coli methionine2 biosynthesis regulator metr
42	<a href="#">c3hhgF_</a>	Alignment	not modelled	28.0	31	<b>PDB header:</b> transcription regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulator, lysr family; <b>PDBTitle:</b> structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
43	<a href="#">c2qh0A_</a>	Alignment	not modelled	27.7	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of a glyoxalase from clostridium acetobutylicum
44	<a href="#">d1sqda1</a>	Alignment	not modelled	27.5	11	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradial dioxygenases
45	<a href="#">c5eriA_</a>	Alignment	not modelled	27.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> marr protein from peptoclostridium difficile da00132
46	<a href="#">c5cviB_</a>	Alignment	not modelled	26.7	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
47	<a href="#">d1ss4a_</a>	Alignment	not modelled	26.5	19	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Hypothetical protein BC1747
48	<a href="#">c3jw4C_</a>	Alignment	not modelled	26.2	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, marr/emrr family; <b>PDBTitle:</b> the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
49	<a href="#">d1nkia_</a>	Alignment	not modelled	26.2	9	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Antibiotic resistance proteins
50	<a href="#">c3cp2A_</a>	Alignment	not modelled	25.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from e. coli
51	<a href="#">c3m1eA_</a>	Alignment	not modelled	25.5	40	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of benm dbd

52	<a href="#">c3boqB</a>	Alignment	not modelled	25.2	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
53	<a href="#">c4b8xB</a>	Alignment	not modelled	24.9	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> possible marr-transcriptional regulator; <b>PDBTitle:</b> near atomic resolution crystal structure of sco5413, a marr family2 transcriptional regulator from streptomyces coelicolor
54	<a href="#">d1swxA</a>	Alignment	not modelled	24.6	23	<b>Fold:</b> Glycolipid transfer protein, GLTP <b>Superfamily:</b> Glycolipid transfer protein, GLTP <b>Family:</b> Glycolipid transfer protein, GLTP
55	<a href="#">c2nyxB</a>	Alignment	not modelled	24.6	33	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> probable transcriptional regulatory protein, rv1404; <b>PDBTitle:</b> crystal structure of rv1404 from mycobacterium tuberculosis
56	<a href="#">c1mpyD</a>	Alignment	not modelled	24.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catechol 2,3-dioxygenase; <b>PDBTitle:</b> structure of catechol 2,3-dioxygenase (metapyrocatechase)2 from pseudomonas putida mt-2
57	<a href="#">c5gsmB</a>	Alignment	not modelled	24.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exo-beta-d-glucosaminidase; <b>PDBTitle:</b> glycoside hydrolase b with product
58	<a href="#">c5e1xA</a>	Alignment	not modelled	23.3	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, marr family; <b>PDBTitle:</b> crystal structure of the organohalide sensing rdhr-cbdba16252 transcriptional regulator in the 3,4-dichlorophenol bound form
59	<a href="#">c3ey7B</a>	Alignment	not modelled	22.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> biphenyl-2,3-diol 1,2-dioxygenase iii-related <b>PDBTitle:</b> structure from the mobile metagenome of v. cholerae.2 integron cassette protein vch_cass1
60	<a href="#">c3bpxB</a>	Alignment	not modelled	22.8	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of marr
61	<a href="#">c5z4yB</a>	Alignment	not modelled	22.7	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cys regulon transcriptional activator; <b>PDBTitle:</b> crystal structure of pacysb ntd domain with space group p4
62	<a href="#">c3k1nB</a>	Alignment	not modelled	22.7	44	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator benm; <b>PDBTitle:</b> crystal structure of full-length benm
63	<a href="#">d1sp8a2</a>	Alignment	not modelled	22.6	21	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradial dioxygenases
64	<a href="#">c3hpyD</a>	Alignment	not modelled	22.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> catechol 2,3-dioxygenase; <b>PDBTitle:</b> crystal structure analysis of the 2,3-dioxygenase lapb from2 pseudomonas in the complex with 4-methylcatechol
65	<a href="#">d2vjma1</a>	Alignment	not modelled	22.5	33	<b>Fold:</b> CoA-transferase family III (CaiB/BaiF) <b>Superfamily:</b> CoA-transferase family III (CaiB/BaiF) <b>Family:</b> CoA-transferase family III (CaiB/BaiF)
66	<a href="#">d1jgsa</a>	Alignment	not modelled	22.3	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
67	<a href="#">c3nrvC</a>	Alignment	not modelled	22.0	44	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> putative transcriptional regulator (marr/emrr family); <b>PDBTitle:</b> crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
68	<a href="#">c3ecjC</a>	Alignment	not modelled	21.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> protein (homoprotocatechuate 2,3-dioxygenase); <b>PDBTitle:</b> structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
69	<a href="#">c3b59A</a>	Alignment	not modelled	21.9	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of the mn(ii)-bound glyoxalase from novosphingobium2 aromaticivorans
70	<a href="#">d2p8ta1</a>	Alignment	not modelled	21.8	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PH0730 N-terminal domain-like
71	<a href="#">d1s3ja</a>	Alignment	not modelled	21.6	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
72	<a href="#">c3k0A</a>	Alignment	not modelled	20.9	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> repressor protein; <b>PDBTitle:</b> crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
73	<a href="#">c2zxiC</a>	Alignment	not modelled	20.7	59	<b>PDB header:</b> fad-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> structure of aquifex aeolicus gida in the form ii crystal
74	<a href="#">c6a2uA</a>	Alignment	not modelled	20.6	21	<b>PDB header:</b> signaling protein/oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> twin-arginine translocation pathway signal; <b>PDBTitle:</b> crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase
75	<a href="#">c4mnuA</a>	Alignment	not modelled	20.5	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> slyA-like transcription regulator; <b>PDBTitle:</b> crystal structure of uncharacterized slyA-like transcription regulator2 from listeria monocytogenes
76	<a href="#">c6pzd</a>	Alignment	not modelled	20.2	12	<b>PDB header:</b> virus like particle <b>Chain:</b> I: <b>PDB Molecule:</b> afp11;

76	<a href="#">c1gaoI_</a>	Alignment	not modelled	20.2	43	<b>PDBTitle:</b> cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
77	<a href="#">c3fzjC_</a>	Alignment	not modelled	20.1	44	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> lysr type regulator of tsambcd; <b>PDBTitle:</b> tsar low resolution crystal structure, tetragonal form
78	<a href="#">c5umwA_</a>	Alignment	not modelled	19.7	22	<b>PDB header:</b> tiancimycin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of tnms2, an antibiotic binding protein from2 streptomyces sp. cb03234
79	<a href="#">c2zjsE_</a>	Alignment	not modelled	19.7	33	<b>PDB header:</b> protein transport/immune system <b>Chain:</b> E: <b>PDB Molecule:</b> preprotein translocase sece subunit; <b>PDBTitle:</b> crystal structure of sece translocon from thermus thermophilus with a2 fab fragment
80	<a href="#">d2frha1</a>	Alignment	not modelled	19.6	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
81	<a href="#">c6ivuB_</a>	Alignment	not modelled	19.4	32	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase sigma factor sigi1; <b>PDBTitle:</b> solution structure of the sigma-anti-sigma factor complex rsg1n-2 sigi1c from clostridium thermocellum
82	<a href="#">c3cp8C_</a>	Alignment	not modelled	19.3	71	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from chlorobium tepidum
83	<a href="#">c6g4rE_</a>	Alignment	not modelled	19.3	38	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> hydrogen peroxide-inducible genes activator; <b>PDBTitle:</b> corynebacterium glutamicum oxyr c206s mutant, h2o2-bound
84	<a href="#">c3e6mD_</a>	Alignment	not modelled	19.2	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> marr family transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
85	<a href="#">d1ygya1</a>	Alignment	not modelled	19.1	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
86	<a href="#">c3kp3B_</a>	Alignment	not modelled	19.0	23	<b>PDB header:</b> transcription regulator/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator tcar; <b>PDBTitle:</b> staphylococcus epidermidis in complex with ampicillin
87	<a href="#">d1l7ba_</a>	Alignment	not modelled	19.0	14	<b>Fold:</b> BRCT domain <b>Superfamily:</b> BRCT domain <b>Family:</b> DNA ligase
88	<a href="#">c5zc2B_</a>	Alignment	not modelled	18.7	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
89	<a href="#">c2mk6A_</a>	Alignment	not modelled	18.6	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> adapter protein meca; <b>PDBTitle:</b> structure determination of substrate binding domain of meca
90	<a href="#">c3ocrA_</a>	Alignment	not modelled	18.6	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> class ii aldolase/adducin domain protein; <b>PDBTitle:</b> crystal structure of aldolase ii superfamily protein from pseudomonas2 syringae
91	<a href="#">c3g12A_</a>	Alignment	not modelled	18.5	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lactoylglutathione lyase; <b>PDBTitle:</b> crystal structure of a putative lactoylglutathione lyase from2 bdellovibrio bacteriovorus
92	<a href="#">d1hsja1</a>	Alignment	not modelled	18.5	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
93	<a href="#">c5mu4A_</a>	Alignment	not modelled	18.4	52	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tail tubular protein a; <b>PDBTitle:</b> tail tubular protein a of klebsiella pneumoniae bacteriophage kp32
94	<a href="#">c5cb9A_</a>	Alignment	not modelled	18.3	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein/dioxygenase; <b>PDBTitle:</b> crystal structure of c-as lyase with mercaptoethonal
95	<a href="#">c3ecoB_</a>	Alignment	not modelled	18.2	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> mepR; <b>PDBTitle:</b> crystal structure of mepR, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
96	<a href="#">c3m2oB_</a>	Alignment	not modelled	18.2	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxalase/bleomycin resistance protein; <b>PDBTitle:</b> crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009
97	<a href="#">d1lnwa_</a>	Alignment	not modelled	18.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
98	<a href="#">c3wwyA_</a>	Alignment	not modelled	18.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
99	<a href="#">c1nytC_</a>	Alignment	not modelled	18.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> shikimate dehydrogenase aroe complexed with nadp+