Phyre^2

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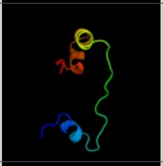
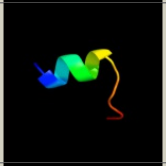
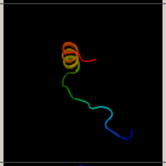
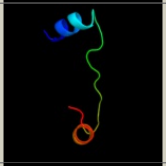
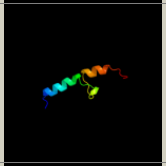
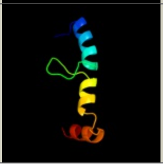
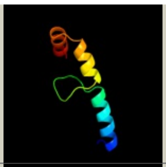
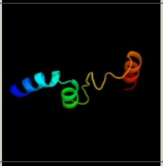
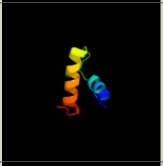
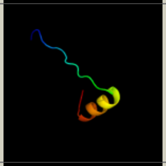
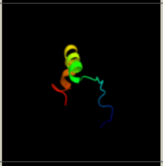
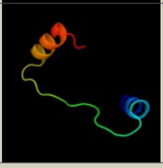
Description	P76097
Date	Thu Jan 5 12:18:52 GMT 2012
Unique Job ID	8ecf7f5bd09ea167

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rjbD_	Alignment		100.0	95	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein ydcj (sf1787)2 from shigella flexneri which includes domain duf1338.3 northeast structural genomics consortium target sfr276
2	c3iuzA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative glyoxalase superfamily protein; **PDBTitle:** crystal structure of putative glyoxalase superfamily protein2 (yp_299723.1) from ralstonia eutropha jmp134 at 1.90 a resolution
3	c3lhoA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative hydrolase (yp_751971.1) from shewanella2 frigidimarina ncimb 400 at 1.80 a resolution
4	c3rmuD_	Alignment		72.5	6	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**methylmalonyl-coa epimerase, mitochondrial; **PDBTitle:** crystal structure of human methylmalonyl-coa epimerase, mcee
5	d1v54i_	Alignment		61.9	57	**Fold:**Single transmembrane helix **Superfamily:**Mitochondrial cytochrome c oxidase subunit VIc **Family:**Mitochondrial cytochrome c oxidase subunit VIc
6	c1cjxC_	Alignment		60.7	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** crystal structure of pseudomonas fluorescens hppd
7	c3gm5A_	Alignment		58.3	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**lactoylglutathione lyase and related lyases; **PDBTitle:** crystal structure of a putative methylmalonyl-coenzyme a2 epimerase from thermoanaerobacter tengcongensis at 2.0 a3 resolution
8	d1sqia2	Alignment		56.0	26	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
9	c2nyxB_	Alignment		54.7	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
10	c3oa4A_	Alignment		54.3	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase; **PDBTitle:** crystal structure of hypothetical protein bh1468 from bacillus2 halodurans c-125
11	c3boqB_	Alignment		54.3	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi

12	d2etha1	Alignment		53.3	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
13	c3bjaA_	Alignment		51.9	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
14	c3o2iB_	Alignment		51.9	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein from2 leptospirillum sp. group ii uba
15	d1cjxa2	Alignment		51.9	21	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
16	d1jc4a_	Alignment		51.6	29	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Methylmalonyl-CoA epimerase
17	c3bj6B_	Alignment		50.9	22	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
18	d1t47a2	Alignment		50.6	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
19	d2fbia1	Alignment		47.0	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
20	c1t47A_	Alignment		46.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** structure of fe2-hppd bound to ntbc
21	d1sqia1	Alignment	not modelled	45.7	12	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
22	c2r5vA_	Alignment	not modelled	45.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pcza361.1; **PDBTitle:** hydroxymandelate synthase crystal structure
23	c3jw4C_	Alignment	not modelled	43.4	15	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, marr/emrr family; **PDBTitle:** the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
24	c3bpxB_	Alignment	not modelled	41.2	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of marr
25	d1s3ja_	Alignment	not modelled	40.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
26	c3nrvC_	Alignment	not modelled	40.2	20	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**putative transcriptional regulator (marr/emrr family); **PDBTitle:** crystal structure of marr/emrr family transcriptional regulator from2 acinetobacter sp. adp1
27	c3k0lA_	Alignment	not modelled	38.8	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
28	c3o6mD_	Alignment	not modelled	38.6	20	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**marr family transcriptional regulator;

28	c3e0mD_	Alignment	not modelled	38.6	20	**PDBTitle:** the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
29	c2qqzB_	Alignment	not modelled	38.2	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase family protein, putative; **PDBTitle:** crystal structure of putative glyoxalase family protein from bacillus2 anthracis
30	d1lnwa_	Alignment	not modelled	38.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
31	c3nqoB_	Alignment	not modelled	37.5	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**marr-family transcriptional regulator; **PDBTitle:** crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
32	c3l7tB_	Alignment	not modelled	35.0	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1112c
33	c2fa5B_	Alignment	not modelled	35.0	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator marr/emrr family; **PDBTitle:** the crystal structure of an unliganded multiple antibiotic-2 resistance repressor (marr) from xanthomonas campestris
34	d1t47a1	Alignment	not modelled	35.0	20	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
35	c1sqiA_	Alignment	not modelled	34.7	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvic acid dioxygenase; **PDBTitle:** structural basis for inhibitor selectivity revealed by2 crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
36	c2l1nA_	Alignment	not modelled	34.5	43	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of the protein yp_399305.1
37	c3kp3B_	Alignment	not modelled	34.1	17	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
38	d2pjsa1	Alignment	not modelled	33.5	14	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
39	c2rk0B_	Alignment	not modelled	32.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase domain; **PDBTitle:** crystal structure of glyoxylase/bleomycin resistance2 protein/dioxygenase domain from frankia sp. ean1pec
40	d1sqda2	Alignment	not modelled	32.3	21	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
41	c3ecoB_	Alignment	not modelled	32.0	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mepr; **PDBTitle:** crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
42	c3fm5D_	Alignment	not modelled	31.7	27	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator; **PDBTitle:** x-ray crystal structure of transcriptional regulator (marr family)2 from rhodococcus sp. rha1
43	d1ss4a_	Alignment	not modelled	31.1	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Hypothetical protein BC1747
44	c3hhgF_	Alignment	not modelled	31.0	31	**PDB header:**transcription regulator **Chain:** F: **PDB Molecule:**transcriptional regulator, lysr family; **PDBTitle:** structure of crga, a lysr-type transcriptional regulator from2 neisseria meningitidis.
45	d3broa1	Alignment	not modelled	29.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
46	d1cjxa1	Alignment	not modelled	29.5	16	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
47	c3g3zA_	Alignment	not modelled	29.3	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
48	c3oajA_	Alignment	not modelled	28.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative ring-cleaving dioxygenase mhqo; **PDBTitle:** crystal structure of putative dioxygenase from bacillus subtilis2 subsp. subtilis str. 168
49	c2zjsE_	Alignment	not modelled	28.1	33	**PDB header:**protein transport/immune system **Chain:** E: **PDB Molecule:**preprotein translocase sece subunit; **PDBTitle:** crystal structure of secye translocon from thermus thermophilus with a2 fab fragment
50	c3m1eA_	Alignment	not modelled	27.9	30	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm; **PDBTitle:** crystal structure of benm_dbd
51	d1qipa_	Alignment	not modelled	27.9	15	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase

						Family: Glyoxalase I (lactoylglutathione lyase)
52	d2fbha1	Alignment	not modelled	27.8	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
53	d1sqda1	Alignment	not modelled	27.6	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
54	c2nnnB_	Alignment	not modelled	26.7	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
55	d1lj9a_	Alignment	not modelled	26.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
56	c3nzpA_	Alignment	not modelled	24.9	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
57	d1s0pa_	Alignment	not modelled	23.9	13	**Fold:**N-terminal domain of adenylylcyclase associated protein, CAP **Superfamily:**N-terminal domain of adenylylcyclase associated protein, CAP **Family:**N-terminal domain of adenylylcyclase associated protein, CAP
58	c2gxgA_	Alignment	not modelled	23.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**146aa long hypothetical transcriptional regulator; **PDBTitle:** crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
59	d2p8ta1	Alignment	not modelled	23.3	45	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PH0730 N-terminal domain-like
60	d1sp8a2	Alignment	not modelled	23.1	18	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
61	d1kw3b1	Alignment	not modelled	22.9	6	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
62	d2fbka1	Alignment	not modelled	22.4	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
63	d1q1va_	Alignment	not modelled	22.3	12	**Fold:**Another 3-helical bundle **Superfamily:**DEK C-terminal domain **Family:**DEK C-terminal domain
64	d1xg8a_	Alignment	not modelled	22.3	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**YuzD-like
65	c1g3wA_	Alignment	not modelled	22.2	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
66	c3pkwA_	Alignment	not modelled	22.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**toxoflavin lyase (tfla); **PDBTitle:** crystal structure of toxoflavin lyase (tfla) bound to mn(ii)
67	c3cjnA_	Alignment	not modelled	22.2	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
68	c3fzjC_	Alignment	not modelled	21.9	38	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**lysr type regulator of tsambcd; **PDBTitle:** tsar low resolution crystal structure, tetragonal form
69	c2fxaB_	Alignment	not modelled	21.6	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protease production regulatory protein hpr; **PDBTitle:** structure of the protease production regulatory protein hpr from2 bacillus subtilis.
70	d1ni3a2	Alignment	not modelled	21.1	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
71	c3g12A_	Alignment	not modelled	21.0	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
72	c3b59A_	Alignment	not modelled	21.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** crystal structure of the mn(ii)-bound glyoxalase from novosphingobium2 aromaticivorans
73	c1fx7C_	Alignment	not modelled	20.9	26	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of the iron-dependent regulator (ider)2 from mycobacterium tuberculosis
74	c3ijmA_	Alignment	not modelled	20.7	41	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized restriction endonuclease-like fold **PDBTitle:** the structure of a restriction endonuclease-like fold superfamily2 protein from spirosoma linguale.
75	d1jgsa_	Alignment	not modelled	19.7	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators

76	c3ecjC_	Alignment	not modelled	18.9	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**protein (homoprotocatechuate 2,3-dioxygenase); **PDBTitle:** structure of e323l mutant of homoprotocatechuate 2,3-dioxygenase from2 brevibacterium fuscum at 1.65a resolution
77	c3m2oB_	Alignment	not modelled	18.7	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein; **PDBTitle:** crystal structure of a putative glyoxalase/bleomycin resistance2 protein from rhodopseudomonas palustris cga009
78	c2oczA_	Alignment	not modelled	18.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** the structure of a putative 3-dehydroquinate dehydratase from2 streptococcus pyogenes.
79	d1jala2	Alignment	not modelled	18.4	47	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
80	c2f5jA_	Alignment	not modelled	17.6	33	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**mortality factor 4-like protein 1; **PDBTitle:** crystal structure of mrg domain from human mrg15
81	d2esna1	Alignment	not modelled	17.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LysR-like transcriptional regulators
82	c1f5tA_	Alignment	not modelled	17.3	37	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
83	d2csua2	Alignment	not modelled	17.1	22	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
84	c3fwbB_	Alignment	not modelled	16.5	28	**PDB header:**cell cycle, transcription **Chain:** B: **PDB Molecule:**nuclear mrna export protein sac3; **PDBTitle:** sac3:sus1:cdc31 complex
85	d1nkia_	Alignment	not modelled	16.3	7	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
86	c1iz1B_	Alignment	not modelled	16.3	38	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**lysr-type regulatory protein; **PDBTitle:** crystal structure of cbnr, a lysr family transcriptional2 regulator
87	c2esnC_	Alignment	not modelled	15.7	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** the crystal structure of probable transcriptional regulator pa04772 from pseudomonas aeruginosa
88	c2x4hA_	Alignment	not modelled	15.7	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
89	d2bv6a1	Alignment	not modelled	15.5	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
90	d1q0oa2	Alignment	not modelled	15.5	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
91	d1sp8a1	Alignment	not modelled	15.4	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
92	c2rdpA_	Alignment	not modelled	14.9	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
93	d1yhta1	Alignment	not modelled	14.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
94	d1rv9a_	Alignment	not modelled	14.8	40	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
95	d1914a2	Alignment	not modelled	14.7	39	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
96	d1hsja1	Alignment	not modelled	14.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
97	c1zswA_	Alignment	not modelled	14.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glyoxalase family protein; **PDBTitle:** crystal structure of bacillus cereus metallo protein from glyoxalase2 family
98	c2y0nE_	Alignment	not modelled	14.1	30	**PDB header:**transcription **Chain:** E: **PDB Molecule:**male-specific lethal 1 homolog; **PDBTitle:** crystal structure of the complex between dosage2 compensation factors msl1 and msl3
99	d1xqaa_	Alignment	not modelled	14.0	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins