Phyre^2

Email	l.a.kelley@imperial.ac.uk
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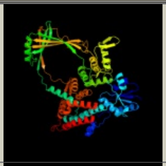
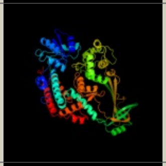
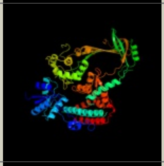
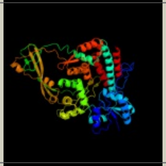
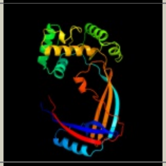
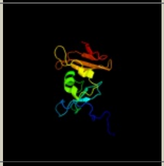
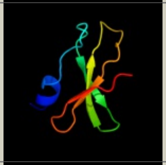
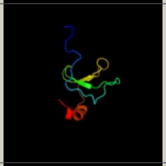
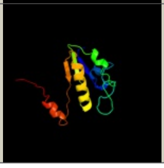
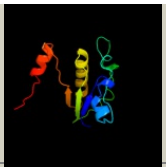
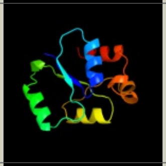
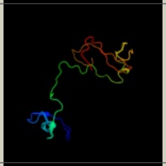
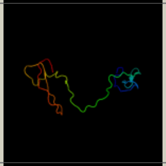
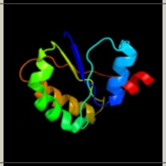
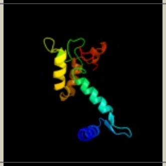
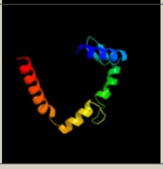
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mw9x_	Alignment		100.0	98	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
2	c2gajA_	Alignment		100.0	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
3	c2o59B_	Alignment		100.0	25	**PDB header:**isomerase/dna **Chain:** B: **PDB Molecule:**dna topoisomerase 3; **PDBTitle:** structure of e. coli topoisomerase iii in complex with an 8-2 base single stranded oligonucleotide. frozen in glycerol3 ph 8.0
4	d1i7da_	Alignment		100.0	25	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
5	c1gl9B_	Alignment		100.0	28	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
6	d1gkub3	Alignment		100.0	28	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
7	d1cy9a_	Alignment		100.0	98	**Fold:**Prokaryotic type I DNA topoisomerase **Superfamily:**Prokaryotic type I DNA topoisomerase **Family:**Prokaryotic type I DNA topoisomerase
8	c1yuaA_	Alignment		100.0	99	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**topoisomerase i; **PDBTitle:** c-terminal domain of escherichia coli topoisomerase i
9	d1yuaa2	Alignment		99.9	100	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
10	d1yuaa1	Alignment		99.4	98	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
11	d1vdda_	Alignment		99.2	25	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR

12	c1vddC_	Alignment		99.0	25	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
13	d2fcja1	Alignment		97.0	22	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
14	c1i3ql_	Alignment		96.5	13	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
15	d1nuia1	Alignment		95.8	21	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**Primase fragment of primase-helicase protein
16	c3h0gl_	Alignment		95.6	17	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
17	c1nuiA_	Alignment		95.2	21	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
18	c2x4hA_	Alignment		95.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
19	c1q57G_	Alignment		93.4	24	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
20	c3g3zA_	Alignment		92.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
21	c3hruA_	Alignment	not modelled	92.0	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metalloregulator scar; **PDBTitle:** crystal structure of scar with bound zn2+
22	c1g3wA_	Alignment	not modelled	90.9	9	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**diphtheria toxin repressor; **PDBTitle:** cd-cys102ser dtxr
23	c1f5tA_	Alignment	not modelled	90.5	9	**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
24	d2fxaa1	Alignment	not modelled	90.5	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
25	d2fbia1	Alignment	not modelled	90.1	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
26	c3nrvC_	Alignment	not modelled	90.0	12	**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	d2fiya1	Alignment	not modelled	89.9	18	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
28	d1pvma3	Alignment	not modelled	89.7	29	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
						PDB header:transcription regulator

29	c2pexA_	Alignment	not modelled	89.4	13	**Chain:** A: **PDB Molecule:**transcriptional regulator ohrr; **PDBTitle:** structure of reduced c22s ohrr from xanthamonas campestris
30	c1fx7C_	Alignment	not modelled	88.9	9	**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
31	c3s2wB_	Alignment	not modelled	88.7	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** the crystal structure of a marr transcriptional regulator from2 methanosarcina mazei go1
32	d1t6t1_	Alignment	not modelled	88.6	24	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
33	d2a61a1	Alignment	not modelled	88.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
34	d1lnwa_	Alignment	not modelled	88.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
35	d1dgsa1	Alignment	not modelled	88.1	36	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
36	c3boqB_	Alignment	not modelled	88.1	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
37	c3bjaA_	Alignment	not modelled	87.6	17	**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
38	d1lj9a_	Alignment	not modelled	87.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
39	c3jw4C_	Alignment	not modelled	87.2	13	**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
40	c2hr5B_	Alignment	not modelled	87.2	25	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
41	c2gxgA_	Alignment	not modelled	86.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**146aa long hypothetical transcriptional regulator; **PDBTitle:** crystal structure of emrr homolog from hyperthermophilic archaea2 sulfolobus tokodaii strain7
42	d1s3ja_	Alignment	not modelled	86.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
43	c3bj6B_	Alignment	not modelled	86.8	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
44	d3ctaa1	Alignment	not modelled	86.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
45	c2fxaB_	Alignment	not modelled	86.4	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protease production regulatory protein hpr; **PDBTitle:** structure of the protease production regulatory protein hpr from2 bacillus subtilis.
46	c2h09A_	Alignment	not modelled	86.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** crystal structure of diphtheria toxin repressor like protein2 from e. coli
47	c1v9pB_	Alignment	not modelled	86.4	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
48	c2f5qA_	Alignment	not modelled	86.3	29	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
49	c3kp3B_	Alignment	not modelled	86.3	5	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
50	c2qwwB_	Alignment	not modelled	86.1	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
51	c3bpxB_	Alignment	not modelled	86.0	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of marr
52	c1dgsB_	Alignment	not modelled	85.9	33	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
53	c2opfA_	Alignment	not modelled	85.4	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate

54	c2fa5B_	Alignment	not modelled	85.3	16	**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
55	c2it0A_	Alignment	not modelled	85.3	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
56	d1twfi2	Alignment	not modelled	85.2	14	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
57	c1k82D_	Alignment	not modelled	85.1	29	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
58	c1nnjA_	Alignment	not modelled	85.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
59	c2rdpA_	Alignment	not modelled	84.8	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator marr; **PDBTitle:** the structure of a marr family protein from bacillus2 stearothermophilus
60	d2hr3a1	Alignment	not modelled	84.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
61	d2bv6a1	Alignment	not modelled	84.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
62	d1p4xa1	Alignment	not modelled	84.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
63	c2nyxB_	Alignment	not modelled	84.3	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulatory protein, rv1404; **PDBTitle:** crystal structure of rv1404 from mycobacterium tuberculosis
64	c3floD_	Alignment	not modelled	84.3	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
65	d2fbha1	Alignment	not modelled	84.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
66	c1yuzB_	Alignment	not modelled	84.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
67	c1ee8A_	Alignment	not modelled	84.0	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
68	c3on1A_	Alignment	not modelled	83.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bh2414 protein; **PDBTitle:** the structure of a protein with unknown function from bacillus2 halodurans c
69	c3e6mD_	Alignment	not modelled	83.6	13	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**marr family transcriptional regulator; **PDBTitle:** the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
70	c3f3xA_	Alignment	not modelled	83.6	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of the transcriptional regulator bldr2 from sulfolobus solfataricus
71	d3broa1	Alignment	not modelled	83.4	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
72	d1r7ja_	Alignment	not modelled	83.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Archaeal DNA-binding protein
73	d1jgsa_	Alignment	not modelled	83.1	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
74	c3nqoB_	Alignment	not modelled	83.1	13	**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
75	c3cdhB_	Alignment	not modelled	82.6	24	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of the marr family transcriptional regulator spo14532 from silicibacter pomeroyi dss-3
76	d2etha1	Alignment	not modelled	82.2	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
77	d1p4xa2	Alignment	not modelled	81.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
78	c2owoA_	Alignment	not modelled	81.7	32	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
						Fold:DNA/RNA-binding 3-helical bundle

79	d1stza1	Alignment	not modelled	81.0	16	**Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
80	c3fm5D_	Alignment	not modelled	80.5	19	**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
81	c3cjnA_	Alignment	not modelled	79.9	25	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
82	c2nnnB_	Alignment	not modelled	79.4	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**probable transcriptional regulator; **PDBTitle:** crystal structure of probable transcriptional regulator from2 pseudomonas aeruginosa
83	c3hrmA_	Alignment	not modelled	79.4	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator sarz; **PDBTitle:** crystal structure of staphylococcus aureus protein sarz in sulfenic2 acid form
84	c3k0lA_	Alignment	not modelled	79.3	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
85	c1p4xA_	Alignment	not modelled	78.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**staphylococcal accessory regulator a homologue; **PDBTitle:** crystal structure of sars protein from staphylococcus aureus
86	d1ee8a3	Alignment	not modelled	78.0	28	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
87	d1ub9a_	Alignment	not modelled	76.9	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
88	d1tdza3	Alignment	not modelled	76.6	19	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
89	c3f2cA_	Alignment	not modelled	76.5	31	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
90	d1l1ta3	Alignment	not modelled	76.0	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
91	d1r2za3	Alignment	not modelled	75.4	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
92	d1k82a3	Alignment	not modelled	74.9	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
93	c3ecoB_	Alignment	not modelled	74.7	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**mepr; **PDBTitle:** crystal structure of mepr, a transcription regulator of the2 staphylococcus aureus multidrug efflux pump mepa
94	c2jrpA_	Alignment	not modelled	73.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
95	c2au3A_	Alignment	not modelled	73.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
96	c3oopA_	Alignment	not modelled	73.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2960 protein; **PDBTitle:** the structure of a protein with unknown function from listeria innocua2 clip11262
97	c3deuB_	Alignment	not modelled	73.0	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator slya; **PDBTitle:** crystal structure of transcription regulatory protein slya2 from salmonella typhimurium in complex with salicylate3 ligands
98	d1k3xa3	Alignment	not modelled	73.0	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
99	d2fbka1	Alignment	not modelled	72.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
100	d3deua1	Alignment	not modelled	72.6	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
101	c3tgnA_	Alignment	not modelled	72.4	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**adc operon repressor adcr; **PDBTitle:** crystal structure of the zinc-dependent marr family transcriptional2 regulator adcr in the zn(ii)-bound state
102	c3cngC_	Alignment	not modelled	71.6	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
103	c1dvbA_	Alignment	not modelled	71.0	24	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
104	c2ev5B_	Alignment	not modelled	70.7	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator mntr; **PDBTitle:** bacillus subtilis manganese transport regulator (mntr)2

						bound to calcium
105	c3nuhB_	Alignment	not modelled	70.7	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
106	c2wteB_	Alignment	not modelled	70.5	15	**PDB header:**antiviral protein **Chain:** B: **PDB Molecule:**csa3; **PDBTitle:** the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
107	d1olta_	Alignment	not modelled	69.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
108	c3ri2B_	Alignment	not modelled	68.7	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, padr-like family; **PDBTitle:** crystal structure of padr family transcriptional regulator from2 eggerthella lenta dsm 2243
109	c2hu9B_	Alignment	not modelled	67.4	25	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**mercuric transport protein periplasmic component; **PDBTitle:** x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
110	d1qypa_	Alignment	not modelled	67.2	33	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
111	d1z91a1	Alignment	not modelled	66.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
112	d2isya1	Alignment	not modelled	65.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
113	c3l09B_	Alignment	not modelled	65.0	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
114	c3ndjA_	Alignment	not modelled	64.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
115	c2jneA_	Alignment	not modelled	63.6	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein yfgj; **PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
116	d2jnea1	Alignment	not modelled	63.6	16	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
117	c2k4bA_	Alignment	not modelled	63.4	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** copr repressor structure
118	d1g3wa1	Alignment	not modelled	61.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
119	d1jhfa1	Alignment	not modelled	60.7	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
120	d2p6ra1	Alignment	not modelled	59.7	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like