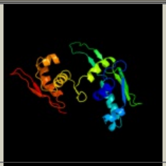
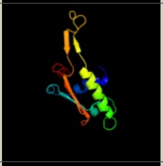
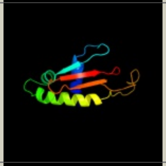
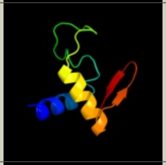
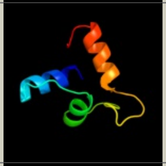
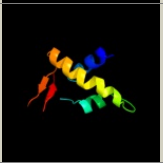
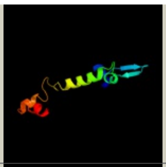
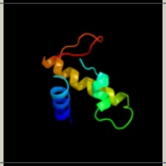
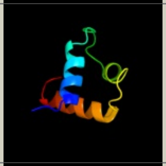
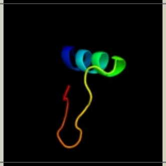
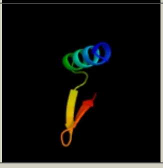
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q57154
Date	Thu Jan 5 12:37:14 GMT 2012
Unique Job ID	aa5e856751bb910e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z9oB_	Alignment		99.4	15	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**replication initiation protein; **PDBTitle:** crystal structure of the dimeric form of repe in complex with the repe2 operator dna
2	c2nraC_	Alignment		99.2	14	**PDB header:**replication/dna **Chain:** C: **PDB Molecule:**pi protein; **PDBTitle:** crystal structure of pi initiator protein in complex with iteron dna
3	d1repc2	Alignment		97.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
4	d1hkqa_	Alignment		97.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
5	d2nrac2	Alignment		96.9	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
6	d2nrac1	Alignment		96.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
7	d1repc1	Alignment		94.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Replication initiation protein
8	c2v79B_	Alignment		93.5	15	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
9	d2v7fa1	Alignment		91.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rps19E-like
10	d1stza1	Alignment		85.5	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
11	c2xznT_	Alignment		84.1	13	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**rps19e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2

12	c3ic7A_	Alignment		83.9	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron
13	c3iz6S_	Alignment		83.0	21	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**40s ribosomal protein s19 (s19e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
14	d1dpua_	Alignment		81.6	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
15	c1dpuA_	Alignment		81.6	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
16	c3neuA_	Alignment		73.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1836 protein; **PDBTitle:** the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
17	c2du9A_	Alignment		73.4	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
18	c3jyvT_	Alignment		70.7	23	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**s19e protein; **PDBTitle:** structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
19	c3by6C_	Alignment		69.9	17	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** crystal structure of a transcriptional regulator from oenococcus oeni
20	c3f8mA_	Alignment		64.8	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**gntr-family protein transcriptional regulator; **PDBTitle:** crystal structure of phnf from mycobacterium smegmatis
21	c2vn2B_	Alignment	not modelled	64.6	15	**PDB header:**replication **Chain:** B: **PDB Molecule:**chromosome replication initiation protein; **PDBTitle:** crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
22	c1stzB_	Alignment	not modelled	63.1	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
23	c3bwgA_	Alignment	not modelled	60.0	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**uncharacterized hth-type transcriptional regulator yydk; **PDBTitle:** the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
24	d1p4xa1	Alignment	not modelled	56.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
25	c3hrmA_	Alignment	not modelled	54.7	12	**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
26	d1okra_	Alignment	not modelled	53.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
27	c3edpB_	Alignment	not modelled	49.8	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lin2111 protein; **PDBTitle:** the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
						Fold:DNA/RNA-binding 3-helical bundle

28	d1jhfa1	Alignment	not modelled	48.7	19	**Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
29	c3ltiA_	Alignment	not modelled	48.4	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-betai4 domains
30	d2g9wa1	Alignment	not modelled	48.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
31	d1sata2	Alignment	not modelled	42.3	14	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
32	c3kp3B_	Alignment	not modelled	41.1	10	**PDB header:**transcription regulator/antibiotic **Chain:** B: **PDB Molecule:**transcriptional regulator tcar; **PDBTitle:** staphylococcus epidermidis in complex with ampicillin
33	c3eetA_	Alignment	not modelled	38.5	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative gntr-family transcriptional regulator; **PDBTitle:** crystal structure of putative gntr-family transcriptional2 regulator
34	c2y75F_	Alignment	not modelled	38.5	23	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
35	c2i5gB_	Alignment	not modelled	38.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal strcuture of amidohydrolase from pseudomonas2 aeruginosa
36	d1hw1a1	Alignment	not modelled	38.1	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
37	c2jtvA_	Alignment	not modelled	37.9	20	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
38	c3boqB_	Alignment	not modelled	37.8	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcriptional regulator from2 silicibacter pomeroyi
39	c3eqxB_	Alignment	not modelled	36.3	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**fic domain containing transcriptional regulator; **PDBTitle:** crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
40	c2k6xA_	Alignment	not modelled	36.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
41	d3bz6a1	Alignment	not modelled	35.8	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PSPTO2686-like
42	c3kfuJ_	Alignment	not modelled	35.5	29	**PDB header:**ligase/rna **Chain:** J: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c; **PDBTitle:** crystal structure of the transamidosome
43	d1o57a1	Alignment	not modelled	34.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**N-terminal domain of Bacillus PurR
44	c3edhA_	Alignment	not modelled	34.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bone morphogenetic protein 1; **PDBTitle:** crystal structure of bone morphogenetic protein 1 protease2 domain in complex with partially bound dmso
45	d1k7ia2	Alignment	not modelled	34.1	11	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
46	c1e2xA_	Alignment	not modelled	33.0	33	**PDB header:**transcriptional regulation **Chain:** A: **PDB Molecule:**fatty acid metabolism regulator protein; **PDBTitle:** fadr, fatty acid responsive transcription factor from e.2 coli
47	d2fbha1	Alignment	not modelled	32.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
48	c2k4bA_	Alignment	not modelled	32.4	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** copr repressor structure
49	d1m7va_	Alignment	not modelled	31.9	18	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
50	c3ff5B_	Alignment	not modelled	30.3	23	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 14; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
51	c3k2gA_	Alignment	not modelled	30.1	26	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
52	c2w85A_	Alignment	not modelled	29.8	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19
						Fold:DNA/RNA-binding 3-helical bundle

53	d2d1ha1	Alignment	not modelled	29.2	25	**Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
54	d1m9ma_	Alignment	not modelled	29.1	23	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
55	d1q2oa_	Alignment	not modelled	28.8	23	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
56	c3r0aB_	Alignment	not modelled	26.6	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
57	c3ihuA_	Alignment	not modelled	26.4	33	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
58	d2hs5a1	Alignment	not modelled	25.7	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
59	c3lu2B_	Alignment	not modelled	25.6	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2462 protein; **PDBTitle:** structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
60	d1ku9a_	Alignment	not modelled	25.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding protein Mj223
61	d2dk5a1	Alignment	not modelled	24.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RPO3F domain-like
62	c3bz6A_	Alignment	not modelled	24.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0502 protein pspto_2686; **PDBTitle:** crystal structure of a conserved protein of unknown function from2 pseudomonas syringae pv. tomato str. dc3000
63	d1p6ra_	Alignment	not modelled	24.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
64	c2krxA_	Alignment	not modelled	24.3	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asl3597 protein; **PDBTitle:** solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
65	c3b40A_	Alignment	not modelled	24.2	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable dipeptidase; **PDBTitle:** crystal structure of the probable dipeptidase pvdm from2 pseudomonas aeruginosa
66	c3itcA_	Alignment	not modelled	24.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
67	d1mzba_	Alignment	not modelled	23.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
68	c3fdgA_	Alignment	not modelled	23.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidase ac. metallo peptidase. merops family m19; **PDBTitle:** the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
69	d1a9xa1	Alignment	not modelled	23.2	22	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
70	d1v4ra1	Alignment	not modelled	22.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
71	c2ragB_	Alignment	not modelled	22.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dipeptidase; **PDBTitle:** crystal structure of aminohydrolase from caulobacter crescentus
72	d1mjta_	Alignment	not modelled	22.5	21	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
73	c3rhgA_	Alignment	not modelled	22.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
74	c2wv0H_	Alignment	not modelled	22.1	29	**PDB header:**transcription **Chain:** H: **PDB Molecule:**hth-type transcriptional repressor yvoa; **PDBTitle:** crystal structure of the gntr-hutc family member yvoa from2 bacillus subtilis
75	c1iojA_	Alignment	not modelled	21.4	38	**PDB header:**apolipoprotein **Chain:** A: **PDB Molecule:**apoc-i; **PDBTitle:** human apolipoprotein c-i, nmr, 18 structures
76	c1om8A_	Alignment	not modelled	21.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serralysin; **PDBTitle:** crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallyzed with 10 mm edta
77	d1j6ra_	Alignment	not modelled	20.8	7	**Fold:**Methionine synthase activation domain-like **Superfamily:**Methionine synthase activation domain-like **Family:**Hypothetical protein TM0269
78	d1kapp2	Alignment	not modelled	20.8	6	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain

79	d2oz6a1	Alignment	not modelled	20.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CAP C-terminal domain-like
80	c3o2pE_	Alignment	not modelled	20.6	29	**PDB header:**ligase, cell cycle **Chain:** E: **PDB Molecule:**cell division control protein 53; **PDBTitle:** a dual e3 mechanism for rub1 ligation to cdc53: dcn1(p)-cdc53(whb)
81	c3bj6B_	Alignment	not modelled	20.3	19	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
82	d2frha1	Alignment	not modelled	20.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
83	d1ub9a_	Alignment	not modelled	20.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
84	d1iuya_	Alignment	not modelled	20.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
85	d1mkma1	Alignment	not modelled	20.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
86	d1hova_	Alignment	not modelled	19.7	10	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
87	d3bwga1	Alignment	not modelled	18.8	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
88	c3nqoB_	Alignment	not modelled	18.7	20	**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
89	c1j5yA_	Alignment	not modelled	18.5	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, biotin repressor family; **PDBTitle:** crystal structure of transcriptional regulator (tm1602) from2 thermotoga maritima at 2.3 a resolution
90	d1lj9a_	Alignment	not modelled	18.3	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
91	c3c7jA_	Alignment	not modelled	18.1	22	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of transcriptional regulator (gntr family member)2 from pseudomonas syringae pv. tomato str. dc3000
92	d1i76a_	Alignment	not modelled	17.6	16	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
93	d3e7ga1	Alignment	not modelled	17.5	19	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
94	c1fooA_	Alignment	not modelled	17.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase; **PDBTitle:** bovine endothelial nitric oxide synthase heme domain complexed with l-2 arg and no(h4b-free)
95	d1itua_	Alignment	not modelled	17.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Renal dipeptidase
96	d3e7ma1	Alignment	not modelled	17.2	23	**Fold:**Nitric oxide (NO) synthase oxygenase domain **Superfamily:**Nitric oxide (NO) synthase oxygenase domain **Family:**Nitric oxide (NO) synthase oxygenase domain
97	d2ev0a1	Alignment	not modelled	17.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Iron-dependent repressor protein
98	d1uxja1	Alignment	not modelled	16.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
99	c2l4aA_	Alignment	not modelled	16.4	31	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp