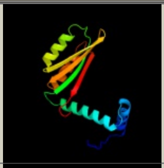
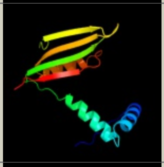
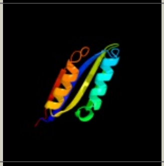
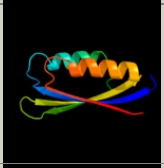
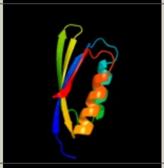
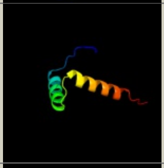
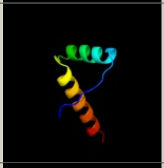
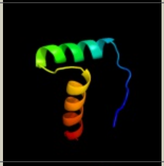
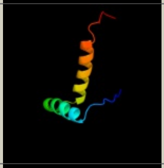
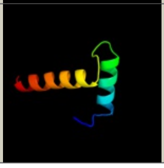
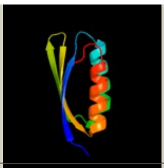
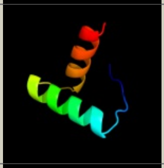
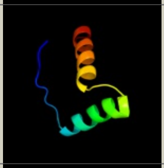
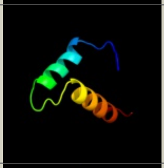
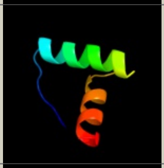
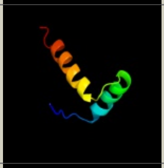
Email	l.a.kelley@imperial.ac.uk
Description	P0A6Z6
Date	Thu Jan 5 11:04:18 GMT 2012
Unique Job ID	dc5a952b7c58d9a0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ca9B_	Alignment		100.0	29	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
2	c2bj3D_	Alignment		100.0	32	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
3	c1q5vB_	Alignment		100.0	100	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
4	d1q5ya_	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Nickel responsive regulator NikR, C-terminal domain
5	d2bj7a2	Alignment		100.0	29	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Nickel responsive regulator NikR, C-terminal domain
6	c2y3yC_	Alignment		100.0	29	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** holo-ni(ii) hpnikr is a symmetric tetramer containing four2 canonic square-planar ni(ii) ions at physiological ph
7	d2bj7a1	Alignment		99.6	35	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
8	d2hzaa1	Alignment		99.6	98	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
9	d2hzab1	Alignment		99.5	98	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
10	c2k5jB_	Alignment		97.8	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
11	c3kxeD_	Alignment		97.3	31	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex

12	d2nzca1	Alignment		97.0	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**TM1266-like
13	d2cpga_	Alignment		93.2	32	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
14	c2k29A_	Alignment		91.5	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
15	c2kelB_	Alignment		90.2	20	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
16	c3h87D_	Alignment		77.8	44	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
17	d1y9ba1	Alignment		64.2	16	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VCA0319-like
18	c2k9iB_	Alignment		59.3	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
19	c3gxqB_	Alignment		55.8	31	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**putative regulator of transfer genes arta; **PDBTitle:** structure of arta and dna complex
20	d1p94a_	Alignment		55.1	14	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
21	d1ygya3	Alignment	not modelled	36.6	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
22	d1vioa2	Alignment	not modelled	34.4	29	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Pseudouridine synthase RsuA N-terminal domain
23	c2rbfB_	Alignment	not modelled	32.3	26	**PDB header:**oxidoreductase/dna **Chain:** B: **PDB Molecule:**bifunctional protein puta; **PDBTitle:** structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
24	d2cyya2	Alignment	not modelled	31.9	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
25	c2knjA_	Alignment	not modelled	31.7	21	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**microplusin preprotein; **PDBTitle:** nmr structure of microplusin a antimicrobial peptide from2 rhipicephalus (boophilus) microplus
26	c2e1cA_	Alignment	not modelled	25.9	15	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
27	d1c06a_	Alignment	not modelled	25.2	36	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Ribosomal protein S4
28	d1sc6a3	Alignment	not modelled	24.9	7	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain

29	c2vixB_	Alignment	not modelled	24.5	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**protein mxic; **PDBTitle:** methylated shigella flexneri mxic
30	d1l3la1	Alignment	not modelled	24.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
31	d1p9ka_	Alignment	not modelled	23.6	22	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
32	c2exuA_	Alignment	not modelled	23.0	3	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation protein spt4/spt5; **PDBTitle:** crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
33	c2q2kA_	Alignment	not modelled	21.1	36	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of nucleic-acid binding protein
34	d1u8sa1	Alignment	not modelled	20.7	3	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
35	c3m8jA_	Alignment	not modelled	20.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**focb protein; **PDBTitle:** crystal structure of e.coli focb at 1.4 a resolution
36	c2qhoF_	Alignment	not modelled	19.2	27	**PDB header:**protein binding/ligase **Chain:** F: **PDB Molecule:**e3 ubiquitin-protein ligase edd1; **PDBTitle:** crystal structure of the uba domain from edd ubiquitin2 ligase in complex with ubiquitin
37	c2kpoA_	Alignment	not modelled	17.3	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x2 fold protein; **PDBTitle:** solution nmr structure of de novo designed rossmann 2x2 fold protein,2 northeast structural genomics consortium target or16
38	c1u8sB_	Alignment	not modelled	16.6	5	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
39	c2cqjA_	Alignment	not modelled	16.2	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u3 small nucleolar ribonucleoprotein protein **PDBTitle:** solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
40	c2nyiB_	Alignment	not modelled	16.1	5	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
41	c2rnjA_	Alignment	not modelled	15.7	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
42	c2k6lA_	Alignment	not modelled	15.5	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the solution structure of xacb0070 from xanthonomas2 axonopodis pv citri reveals this new protein is a member of3 the rhh family of transcriptional repressors
43	d2gnoa1	Alignment	not modelled	15.3	11	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
44	d1vhwa_	Alignment	not modelled	15.0	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
45	d1xdia2	Alignment	not modelled	14.5	25	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
46	d2ac7a1	Alignment	not modelled	14.5	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
47	d1f06a2	Alignment	not modelled	14.5	32	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
48	c2x3dC_	Alignment	not modelled	12.6	18	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**sso6206; **PDBTitle:** crystal structure of sso6206 from sulfolobus solfataricus p2
49	d1k9sa_	Alignment	not modelled	12.5	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
50	c2krfB_	Alignment	not modelled	12.5	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
51	c3kk4B_	Alignment	not modelled	12.4	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
52	c3mntA_	Alignment	not modelled	11.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucine carboxyl methyltransferase 1; **PDBTitle:** crystal structure of human leucine carboxyl methyltransferase 1
53	c2y9jt_	Alignment	not modelled	11.8	12	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**protein prgh; **PDBTitle:** three-dimensional model of salmonella's needle complex at2 subnanometer resolution
54	c2jpcA_	Alignment	not modelled	11.5	7	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb;

						PDBTitle: ssrb dna binding protein
55	c1zljE_	Alignment	not modelled	11.3	12	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
56	d1sxjd1	Alignment	not modelled	10.9	10	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
57	c3b47A_	Alignment	not modelled	10.5	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0582
58	d2nwua1	Alignment	not modelled	10.5	30	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**SSO1042-like
59	c1yj7A_	Alignment	not modelled	9.9	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
60	d1uyla_	Alignment	not modelled	9.7	17	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**Heat shock protein 90, HSP90, N-terminal domain
61	c2fwyA_	Alignment	not modelled	9.7	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hsp 90-alpha; **PDBTitle:** structure of human hsp90-alpha bound to the potent water2 soluble inhibitor pu-h64
62	c1x3uA_	Alignment	not modelled	9.6	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
63	c3ieiD_	Alignment	not modelled	9.4	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**leucine carboxyl methyltransferase 1; **PDBTitle:** crystal structure of human leucine carboxylmethyltransferase-1 in2 complex with s-adenosyl homocysteine
64	d2qy9a1	Alignment	not modelled	9.4	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
65	d1sr9a1	Alignment	not modelled	9.3	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
66	d2raqa1	Alignment	not modelled	9.3	18	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
67	c2hwyB_	Alignment	not modelled	9.2	25	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein smg5; **PDBTitle:** structure of pin domain of human smg5.
68	c2nysA_	Alignment	not modelled	9.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**agr_c_3712p; **PDBTitle:** x-ray crystal structure of protein agr_c_3712 from2 agrobacterium tumefaciens. northeast structural genomics3 consortium target atr88.
69	d2nysa1	Alignment	not modelled	9.2	18	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**AGR C 3712p-like
70	c2kebA_	Alignment	not modelled	9.2	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
71	c3dh3C_	Alignment	not modelled	8.8	31	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
72	d1rjda_	Alignment	not modelled	8.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Leucine carboxy methyltransferase Ppm1
73	d2cg4a2	Alignment	not modelled	8.2	10	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
74	c3ggzH_	Alignment	not modelled	8.1	36	**PDB header:**protein transport, endocytosis **Chain:** H: **PDB Molecule:**vacuolar protein-sorting-associated protein 46; **PDBTitle:** crystal structure of s.cerevisiae ist1 n-terminal domain in2 complex with did2 mim motif
75	c2e1aD_	Alignment	not modelled	8.1	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
76	d1ebda3	Alignment	not modelled	8.1	19	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
77	c3b42B_	Alignment	not modelled	8.0	22	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** periplasmic sensor domain of chemotaxis protein gsu0935
78	d1lvla3	Alignment	not modelled	8.0	25	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain

79	c3ggzF_	Alignment	not modelled	8.0	36	**PDB header:**protein transport, endocytosis **Chain:** F: **PDB Molecule:**vacuolar protein-sorting-associated protein 46; **PDBTitle:** crystal structure of s.cerevisiae ist1 n-terminal domain in2 complex with did2 mim motif
80	c3ggzE_	Alignment	not modelled	8.0	36	**PDB header:**protein transport, endocytosis **Chain:** E: **PDB Molecule:**vacuolar protein-sorting-associated protein 46; **PDBTitle:** crystal structure of s.cerevisiae ist1 n-terminal domain in2 complex with did2 mim motif
81	c3ggzG_	Alignment	not modelled	7.9	36	**PDB header:**protein transport, endocytosis **Chain:** G: **PDB Molecule:**vacuolar protein-sorting-associated protein 46; **PDBTitle:** crystal structure of s.cerevisiae ist1 n-terminal domain in2 complex with did2 mim motif
82	d1mnta_	Alignment	not modelled	7.8	14	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
83	d1qxpa2	Alignment	not modelled	7.8	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Penta-EF-hand proteins
84	d3bpda1	Alignment	not modelled	7.8	18	**Fold:**Ferredoxin-like **Superfamily:**MTH889-like **Family:**MTH889-like
85	c2ia0A_	Alignment	not modelled	7.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator pf0864; **PDBTitle:** transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
86	c2c45F_	Alignment	not modelled	7.5	36	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor; **PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase
87	d1zpva1	Alignment	not modelled	7.4	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
88	d1cjya2	Alignment	not modelled	7.3	13	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase
89	d1nm2a2	Alignment	not modelled	7.3	16	**Fold:**Ferredoxin-like **Superfamily:**Probable ACP-binding domain of malonyl-CoA ACP transacylase **Family:**Probable ACP-binding domain of malonyl-CoA ACP transacylase
90	d1odka_	Alignment	not modelled	7.2	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
91	d2pzza1	Alignment	not modelled	7.2	21	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**SSO1042-like
92	c3m6jD_	Alignment	not modelled	7.2	28	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of unknown function protein from leptospirillum2 rubarum
93	c3h7hB_	Alignment	not modelled	7.2	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
94	c2zwaA_	Alignment	not modelled	7.1	48	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucine carboxyl methyltransferase 2; **PDBTitle:** crystal structure of trna wybutosine synthesizing enzyme2 tyw4
95	c2qasA_	Alignment	not modelled	7.1	16	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of caulobacter crescentus sspb ortholog
96	c2qazC_	Alignment	not modelled	7.0	16	**PDB header:**hydrolase activator **Chain:** C: **PDB Molecule:**sspb protein; **PDBTitle:** structure of c. crescentus sspb ortholog
97	c3qv0A_	Alignment	not modelled	7.0	38	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**mitochondrial acidic protein mam33; **PDBTitle:** crystal structure of saccharomyces cerevisiae mam33
98	d1zrra1	Alignment	not modelled	6.9	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Acireductone dioxygenase
99	d2hs5a1	Alignment	not modelled	6.9	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators