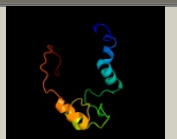
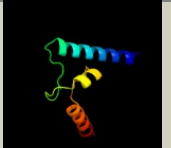
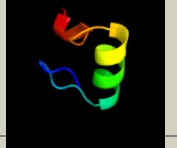
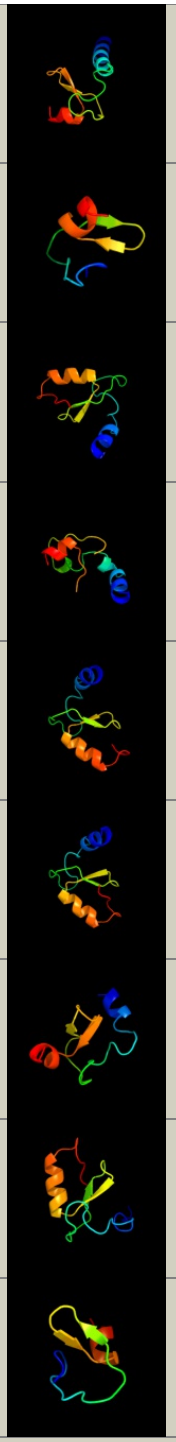
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P41039
Date	Thu Jan 5 12:01:20 GMT 2012
Unique Job ID	4ed97a43b2181352

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kgoA_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ybii; **PDBTitle:** solution nmr structure of zn finger protein ybil from escherichia2 coli. nesg target et107, ocsp target ec0402
2	c1tjlD_	Alignment		99.9	25	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
3	c2kq9A_	Alignment		99.7	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** solution structure of dnak suppressor protein from2 agrobacterium tumefaciens c58. northeast structural3 genomics consortium target att12/ontario center for4 structural proteomics target atc0888
4	d1tjla2	Alignment		99.5	34	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Prokaryotic DksA/TraR C4-type zinc finger
5	c2gviA_	Alignment		77.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a putative formylmethanofuran dehydrogenase2 subunit e (ta1109) from thermoplasma acidophilum at 1.87 a resolution
6	c2p57A_	Alignment		69.7	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**gtpase-activating protein znf289; **PDBTitle:** gap domain of znf289, an id1-regulated zinc finger protein
7	c3d00A_	Alignment		59.0	41	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase subunit e; **PDBTitle:** crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmde)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
8	d1dcqa2	Alignment		58.3	30	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**Pyk2-associated protein beta ARF-GAP domain
9	c2d9lA_	Alignment		55.9	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoporin-like protein rip; **PDBTitle:** solution structure of the arfgap domain of human rip
10	c3mhsE_	Alignment		55.8	45	**PDB header:**hydrolase/transcription regulator/protei **Chain:** E: **PDB Molecule:**saga-associated factor 73; **PDBTitle:** structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
11	c2b0oF_	Alignment		52.3	20	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**uplc1; **PDBTitle:** crystal structure of uplc1 gap domain

12	c3fehA_	Alignment		50.5	26	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**centaurin-alpha-1; **PDBTitle:** crystal structure of full length centaurin alpha-1
13	d1wyha1	Alignment		48.6	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
14	c1dcqA_	Alignment		48.5	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pyk2-associated protein beta; **PDBTitle:** crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.
15	c2iqjB_	Alignment		48.0	28	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**stromal membrane-associated protein 1-like; **PDBTitle:** crystal structure of the gap domain of smap1l (loc64744)2 stromal membrane-associated protein 1-like
16	c2owaB_	Alignment		47.7	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**arfgap-like finger domain containing protein; **PDBTitle:** crystal structure of putative gtpase activating protein for2 adp ribosylation factor from cryptosporidium parvum3 (cgd5_1040)
17	c3lvrE_	Alignment		47.6	20	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**arf-gap with sh3 domain, ank repeat and ph domain- **PDBTitle:** the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
18	c3dwdB_	Alignment		47.2	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1; **PDBTitle:** crystal structure of the arfgap domain of human arfgap1
19	c3jueA_	Alignment		45.6	19	**PDB header:**protein transport/endocytosis **Chain:** A: **PDB Molecule:**arfgap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of arfgap and ank repeat domain of acap1
20	d1x4ka1	Alignment		44.7	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
21	c3o47A_	Alignment	not modelled	40.3	19	**PDB header:**hydrolase, hydrolase activator **Chain:** A: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1, adp- **PDBTitle:** crystal structure of arfgap1-arf1 fusion protein
22	d1tjla1	Alignment	not modelled	39.7	5	**Fold:**Long alpha-hairpin **Superfamily:**DnaK suppressor protein DksA, alpha-hairpin domain **Family:**DnaK suppressor protein DksA, alpha-hairpin domain
23	d2cura1	Alignment	not modelled	39.5	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
24	d1rutx1	Alignment	not modelled	36.4	42	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
25	d1j2oa1	Alignment	not modelled	34.4	46	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
26	d1rutx3	Alignment	not modelled	26.4	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
27	d2dloa1	Alignment	not modelled	21.5	30	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
28	c2d8zA_	Alignment	not modelled	20.3	20	**PDB header:**signaling protein, structural protein **Chain:** A: **PDB Molecule:**four and a half lim domains 2; **PDBTitle:** solution structure of the third lim domain of four and a2 half lim domains protein 2 (fhl-2)
29	d1x3ha1	Alignment	not modelled	17.6	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)

						Family:LIM domain
30	c2curA_	Alignment	not modelled	17.0	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 1; **PDBTitle:** solution structure of skeletal muscle lim-protein 1
31	c2d8xA_	Alignment	not modelled	15.3	20	**PDB header:**structural protein, cell cycle **Chain:** A: **PDB Molecule:**protein pinch; **PDBTitle:** solution structure of the second lim domain of particularly2 interesting new cys-his protein (pinch)
32	c2darA_	Alignment	not modelled	15.0	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pdz and lim domain protein 5; **PDBTitle:** solution structure of first lim domain of enigma-like pdz2 and lim domains protein
33	d1xpaa2	Alignment	not modelled	14.5	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain
34	c2gb5B_	Alignment	not modelled	14.3	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
35	c1j2oA_	Alignment	not modelled	14.2	46	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**fusion of rhombotin-2 and lim domain-binding **PDBTitle:** structure of flin2, a complex containing the n-terminal lim2 domain of lmo2 and ldb1-lid
36	c1nnjA_	Alignment	not modelled	14.1	25	**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
37	d2cuqa1	Alignment	not modelled	13.7	19	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
38	d1x63a2	Alignment	not modelled	13.3	19	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
39	c1x4lA_	Alignment	not modelled	12.5	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 3; **PDBTitle:** solution structure of lim domain in four and a half lim2 domains protein 2
40	c1wyhA_	Alignment	not modelled	12.2	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 2; **PDBTitle:** solution structure of the lim domain from human skeletal2 muscle lim-protein 2
41	c1wjvA_	Alignment	not modelled	11.5	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cell growth regulating nucleolar protein lyar; **PDBTitle:** solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar
42	c2cuqA_	Alignment	not modelled	11.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**four and a half lim domains 3; **PDBTitle:** solution structure of second lim domain from human skeletal2 muscle lim-protein 2
43	d1ee8a3	Alignment	not modelled	11.3	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
44	c3f6qB_	Alignment	not modelled	11.2	24	**PDB header:**signaling protein/signaling protein **Chain:** B: **PDB Molecule:**lim and senescent cell antigen-like-containing **PDBTitle:** crystal structure of integrin-linked kinase ankyrin repeat2 domain in complex with pinch1 lim1 domain
45	c1x64A_	Alignment	not modelled	11.2	17	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**alpha-actinin-2 associated lim protein; **PDBTitle:** solution structure of the lim domain of alpha-actinin-22 associated lim protein
46	d2cupa3	Alignment	not modelled	11.1	56	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
47	d1jmxa5	Alignment	not modelled	11.1	45	**Fold:**Streptavidin-like **Superfamily:**Quinohemoprotein amine dehydrogenase A chain, domain 3 **Family:**Quinohemoprotein amine dehydrogenase A chain, domain 3
48	d2dara2	Alignment	not modelled	10.6	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
49	c1x63A_	Alignment	not modelled	10.3	21	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 1; **PDBTitle:** solution structure of the second lim domain of skeletal2 muscle lim protein 1
50	d1m3va1	Alignment	not modelled	10.2	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
51	c1d4uA_	Alignment	not modelled	9.8	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**nucleotide excision repair protein xpa (xpa-mbd); **PDBTitle:** interactions of human nucleotide excision repair protein2 xpa with rpa70 and dna: chemical shift mapping and 15n nmr3 relaxation studies
52	c2egqA_	Alignment	not modelled	9.3	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**fhl1 protein; **PDBTitle:** solution structure of the fourth lim domain from human four2 and a half lim domains 1
53	d1x4la2	Alignment	not modelled	9.2	44	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
54	c3na7A_	Alignment	not modelled	9.2	15	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from

						helicobacter pylori2 ccug 17874
55	d2d8za2	Alignment	not modelled	9.0	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
56	d2cora1	Alignment	not modelled	9.0	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
57	c2o10A_	Alignment	not modelled	8.3	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**muscle lim protein; **PDBTitle:** solution structure of the n-terminal lim domain of mlp/crp3
58	c2hyxA_	Alignment	not modelled	8.3	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
59	c1x4kA_	Alignment	not modelled	7.8	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 3; **PDBTitle:** solution structure of lim domain in lim-protein 3
60	c1x61A_	Alignment	not modelled	7.6	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thyroid receptor interacting protein 6; **PDBTitle:** solution structure of the first lim domain of thyroid2 receptor interacting protein 6 (trip6)
61	c1x3hA_	Alignment	not modelled	7.3	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**leupaxin; **PDBTitle:** solution structure of the lim domain of human leupaxin
62	d1twfj_	Alignment	not modelled	7.2	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
63	c2l4zA_	Alignment	not modelled	7.0	43	**PDB header:**hydrolase, metal binding protein **Chain:** A: **PDB Molecule:**dna endonuclease rbbp8, lim domain transcription factor **PDBTitle:** nmr structure of fusion of ctip (641-685) to lmo4-lim1 (18-82)
64	c2ko5A_	Alignment	not modelled	6.8	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein z; **PDBTitle:** nmr solution structure of lfv-z
65	d1pbya5	Alignment	not modelled	6.8	8	**Fold:**Streptavidin-like **Superfamily:**Quinohemoprotein amine dehydrogenase A chain, domain 3 **Family:**Quinohemoprotein amine dehydrogenase A chain, domain 3
66	c2d8yA_	Alignment	not modelled	6.8	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**eplin protein; **PDBTitle:** solution structure of the lim domain of epithelial protein2 lost in neoplasm
67	c1ibiA_	Alignment	not modelled	6.6	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cysteine-rich protein 2; **PDBTitle:** quail cysteine and glycine-rich protein, nmr, 15 minimized2 model structures
68	d1u5sb1	Alignment	not modelled	6.4	44	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
69	c1jmxA_	Alignment	not modelled	6.2	42	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amine dehydrogenase; **PDBTitle:** crystal structure of a quinohemoprotein amine dehydrogenase2 from pseudomonas putida
70	d1v6ga1	Alignment	not modelled	6.2	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
71	c2i5oA_	Alignment	not modelled	6.0	56	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta
72	c2qgpA_	Alignment	not modelled	6.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hnh endonuclease; **PDBTitle:** x-ray structure of the nhn endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.
73	d1ef4a_	Alignment	not modelled	5.9	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
74	d1i5ga_	Alignment	not modelled	5.9	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
75	c2a20A_	Alignment	not modelled	5.8	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**regulating synaptic membrane exocytosis protein **PDBTitle:** solution structure of rim2 zinc finger domain
76	c1rutX_	Alignment	not modelled	5.8	42	**PDB header:**protein binding **Chain:** X: **PDB Molecule:**fusion protein of lmo4 protein and lim domain- **PDBTitle:** complex of lmo4 lim domains 1 and 2 with the ldb1 lid domain
77	c2f9iD_	Alignment	not modelled	5.8	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
78	c1a7iA_	Alignment	not modelled	5.7	17	**PDB header:**lim domain containing proteins **Chain:** A: **PDB Molecule:**qcrp2 (lim1); **PDBTitle:** amino-terminal lim domain from quail cysteine and glycine-2 rich protein, nmr, minimized average structure
79	d1o73a_	Alignment	not modelled	5.6	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
80	c3a44D_	Alignment	not modelled	5.6	22	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation

80	c3a44D_	Alignment	not modelled	5.6	22	protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
81	c1u5kA_	Alignment	not modelled	5.6	33	**PDB header:**recombination,replication **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** recombinational repair protein reco
82	d2ak3a2	Alignment	not modelled	5.6	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
83	d1qo8a1	Alignment	not modelled	5.5	13	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
84	c1nypA_	Alignment	not modelled	5.5	20	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pinch protein; **PDBTitle:** 4th lim domain of pinch protein
85	c2dloA_	Alignment	not modelled	5.4	42	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**thyroid receptor-interacting protein 6; **PDBTitle:** solution structure of the second lim domain of human2 thyroid receptor-interacting protein 6
86	d1e4va2	Alignment	not modelled	5.4	10	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
87	c2pmzN_	Alignment	not modelled	5.3	50	**PDB header:**translation, transferase **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
88	c2o13A_	Alignment	not modelled	5.3	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**muscle lim protein; **PDBTitle:** solution structure of the c-terminal lim domain of mlp/crp3
89	c2cu8A_	Alignment	not modelled	5.2	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**cysteine-rich protein 2; **PDBTitle:** solution structure of the lim domain of human cysteine-rich2 protein 2
90	d1kcfa1	Alignment	not modelled	5.1	57	**Fold:**LEM/SAP HeH motif **Superfamily:**SAP domain **Family:**SAP domain
91	d1ibia2	Alignment	not modelled	5.1	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
92	c3hi2C_	Alignment	not modelled	5.1	33	**PDB header:**dna binding protein/toxin **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator mqsa(ygit); **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)