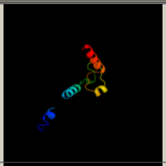
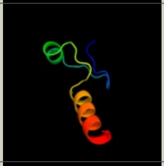
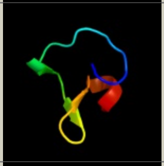
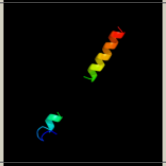
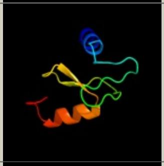
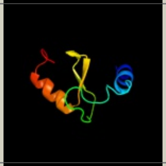
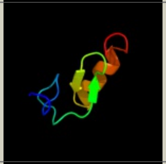
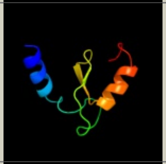
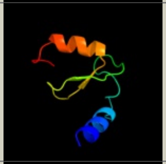
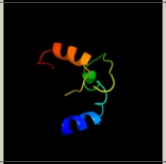
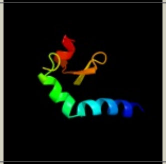
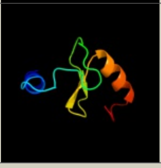
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P41065
Date	Thu Jan 5 12:01:22 GMT 2012
Unique Job ID	f9c61ee2af6d59b6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tjlD_	Alignment		99.8	27	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
2	c2kgoA_	Alignment		99.8	36	**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
3	c2kq9A_	Alignment		99.6	32	**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		99.6	33	**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		76.3	30	**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	d1tjla1	Alignment		72.4	20	**Fold:**Long alpha-hairpin **Superfamily:**DnaK suppressor protein DksA, alpha-hairpin domain **Family:**DnaK suppressor protein DksA, alpha-hairpin domain
7	c3mhsE_	Alignment		67.8	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
8	c2b0oF_	Alignment		67.0	19	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**uplc1; **PDBTitle:** crystal structure of uplc1 gap domain
9	c2owaB_	Alignment		66.5	15	**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)
10	c2p57A_	Alignment		66.3	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**gtpase-activating protein znf289; **PDBTitle:** gap domain of znf289, an id1-regulated zinc finger protein
11	c3jueA_	Alignment		64.5	29	**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

12	c3d00A_	Alignment		59.6	40	**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
13	c3lvrE_	Alignment		59.3	17	**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
14	d1dcqa2	Alignment		54.6	21	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**Pyk2-associated protein beta ARF-GAP domain
15	c1dcqA_	Alignment		48.6	21	**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.
16	c2iqjB_	Alignment		46.4	18	**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
17	c3fehA_	Alignment		43.2	21	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**centaurin-alpha-1; **PDBTitle:** crystal structure of full length centaurin alpha-1
18	d1rutx1	Alignment		39.3	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
19	c2d9lA_	Alignment		39.0	12	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoporin-like protein rip; **PDBTitle:** solution structure of the arfgap domain of human rip
20	c3dwdB_	Alignment		38.3	18	**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
21	c3o47A_	Alignment	not modelled	32.4	23	**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	d1j2oa1	Alignment	not modelled	31.3	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
23	d1rutx3	Alignment	not modelled	27.9	43	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
24	d1wyha1	Alignment	not modelled	27.6	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
25	d1x4ka1	Alignment	not modelled	27.5	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
26	d1xpaa2	Alignment	not modelled	26.4	33	**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
27	d2cura1	Alignment	not modelled	24.9	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
28	d1x3ha1	Alignment	not modelled	19.1	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
29	c2d8xA	Alignment	not modelled	17.9	21	**PDB header:**structural protein, cell cycle **Chain:** A: **PDB Molecule:**protein pinch;

29	c2d8xA_	Alignment	not modelled	17.9	21	**PDBTitle:** solution structure of the second lim domain of particularly2 interesting new cys-his protein (pinch)
30	d2cora1	Alignment	not modelled	16.9	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
31	c2curA_	Alignment	not modelled	16.4	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 1; **PDBTitle:** solution structure of skeletal muscle lim-protein 1
32	c2d8zA_	Alignment	not modelled	16.3	21	**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)
33	c3na7A_	Alignment	not modelled	16.3	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
34	d2cupa3	Alignment	not modelled	15.2	44	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
35	d2dloa1	Alignment	not modelled	13.3	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
36	c1x4lA_	Alignment	not modelled	13.1	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
37	c2cuqA_	Alignment	not modelled	12.9	24	**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
38	c3f6qB_	Alignment	not modelled	12.5	28	**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
39	d1twfj_	Alignment	not modelled	12.3	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
40	d1x4la2	Alignment	not modelled	12.3	56	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
41	c1wyhA_	Alignment	not modelled	12.3	24	**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
42	c1d4uA_	Alignment	not modelled	12.3	20	**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
43	c3h0gL_	Alignment	not modelled	12.2	36	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
44	d2dara2	Alignment	not modelled	11.9	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
45	c2darA_	Alignment	not modelled	11.8	21	**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
46	d1ef4a_	Alignment	not modelled	11.8	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
47	d1m3va1	Alignment	not modelled	11.6	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
48	c1j2oA_	Alignment	not modelled	11.4	23	**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
49	c2pmzN_	Alignment	not modelled	11.3	50	**PDB header:**translation, transferase **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
50	c2ja6L_	Alignment	not modelled	10.4	23	**PDB header:**transferase **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 7.7 **PDBTitle:** cpd lesion containing rna polymerase ii elongation complex2 b
51	c1x63A_	Alignment	not modelled	10.2	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
52	c2cu8A_	Alignment	not modelled	10.2	10	**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
53	d1ee8a3	Alignment	not modelled	9.7	36	**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
54	c2egqA_	Alignment	not modelled	9.1	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
55	c1x61A_	Alignment	not modelled	9.0	16	**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)
56	c1x64A_	Alignment	not modelled	8.9	14	**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
57	c2bzwB_	Alignment	not modelled	8.7	67	**PDB header:**transcription **Chain:** B: **PDB Molecule:**bcl2-antagonist of cell death; **PDBTitle:** the crystal structure of bcl-xl in complex with full-length2 bad
58	c1x62A_	Alignment	not modelled	8.6	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**c-terminal lim domain protein 1; **PDBTitle:** solution structure of the lim domain of carboxyl terminal2 lim domain protein 1
59	c1x4kA_	Alignment	not modelled	8.6	28	**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	c2l4zA_	Alignment	not modelled	8.3	31	**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)
61	c3a44D_	Alignment	not modelled	8.2	20	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
62	c2d8yA_	Alignment	not modelled	7.9	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**eplin protein; **PDBTitle:** solution structure of the lim domain of epithelial protein2 lost in neoplasm
63	c2o10A_	Alignment	not modelled	7.7	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
64	d1u5ka2	Alignment	not modelled	7.6	33	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**RecO C-terminal domain-like
65	c2iybG_	Alignment	not modelled	7.4	36	**PDB header:**metal-binding **Chain:** G: **PDB Molecule:**testin; **PDBTitle:** structure of complex between the 3rd lim domain of tes and2 the evh1 domain of mena
66	c2i5oA_	Alignment	not modelled	7.4	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
67	c1rutX_	Alignment	not modelled	7.3	33	**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
68	d2czra1	Alignment	not modelled	7.3	27	**Fold:**Restriction endonuclease-like **Superfamily:**TBP-interacting protein-like **Family:**TBP-interacting protein-like
69	d1xx6a2	Alignment	not modelled	7.3	63	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
70	c2dloA_	Alignment	not modelled	7.2	29	**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
71	c1ibiA_	Alignment	not modelled	6.8	24	**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
72	c3q8dB_	Alignment	not modelled	6.7	25	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair protein reco; **PDBTitle:** e. coli reco complex with ssb c-terminus
73	c1x68A_	Alignment	not modelled	6.6	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fhl5 protein; **PDBTitle:** solution structures of the c-terminal lim domain of human2 fhl5 protein
74	c1x3hA_	Alignment	not modelled	6.6	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**leupaxin; **PDBTitle:** solution structure of the lim domain of human leupaxin
75	c2qgpA_	Alignment	not modelled	6.4	33	**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.
76	d1v6ga1	Alignment	not modelled	6.4	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
77	c2ko5A_	Alignment	not modelled	6.4	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein z; **PDBTitle:** nmr solution structure of lfv-z
78	d2ak3a2	Alignment	not modelled	6.3	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
79	d2cuqa1	Alignment	not modelled	6.2	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
						PDB header:oncoprotein

80	c2xjyA_	Alignment	not modelled	6.2	25	**Chain:** A: **PDB Molecule:**rhombotin-2; **PDBTitle:** crystal structure of the lmo2:ldb1-lid complex, p21 crystal2 form
81	d2d8za2	Alignment	not modelled	6.0	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
82	d1e4va2	Alignment	not modelled	6.0	10	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
83	c2f9iD_	Alignment	not modelled	5.9	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
84	d1l1ta3	Alignment	not modelled	5.9	63	**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
85	d1x63a2	Alignment	not modelled	5.7	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
86	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
87	d1bboa1	Alignment	not modelled	5.6	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
88	d1k3xa3	Alignment	not modelled	5.6	63	**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	d1rzsa_	Alignment	not modelled	5.6	38	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
90	c1loiA_	Alignment	not modelled	5.5	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyclic 3',5'-amp specific phosphodiesterase rd1; **PDBTitle:** n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
91	c1m3vA_	Alignment	not modelled	5.5	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**fusion of the lim interacting domain of ldb1 and **PDBTitle:** flin4: fusion of the lim binding domain of ldb1 and the n-2 terminal lim domain of lmo4
92	d2d8ua1	Alignment	not modelled	5.5	33	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
93	c2l3kA_	Alignment	not modelled	5.4	33	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**rhombotin-2, linker, lim domain-binding protein 1; **PDBTitle:** solution structure of lmo2(lim2)-ldb1(lid)
94	d1k82a3	Alignment	not modelled	5.3	63	**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
95	c1b8tA_	Alignment	not modelled	5.3	16	**PDB header:**contractile **Chain:** A: **PDB Molecule:**protein (crp1); **PDBTitle:** solution structure of the chicken crp1
96	d1wjva2	Alignment	not modelled	5.2	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**C2HC finger
97	d1zina2	Alignment	not modelled	5.2	33	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
98	c2jtnA_	Alignment	not modelled	5.2	19	**PDB header:**protein binding/transcription **Chain:** A: **PDB Molecule:**lim domain-binding protein 1, lim/homeobox **PDBTitle:** nmr solution structure of a ldb1-lid:lhx3-lim complex
99	d1u5sb1	Alignment	not modelled	5.1	56	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain