Phyre2

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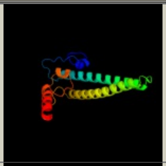
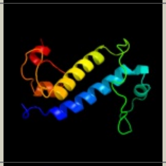
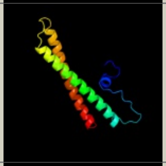
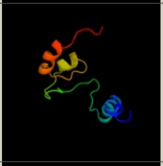
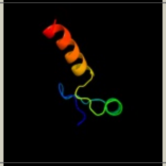
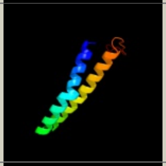
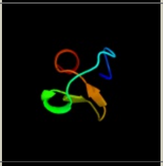
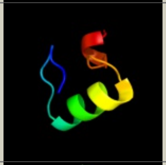
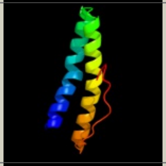
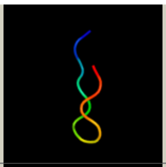
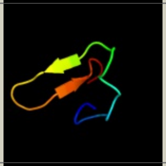
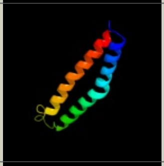
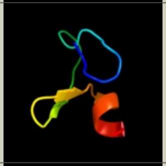
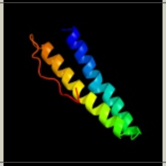
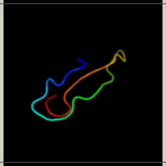
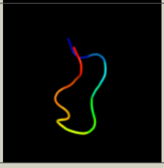
Description	P0ABS1
Date	Thu Jan 5 11:16:12 GMT 2012
Unique Job ID	6e6a8d698f5fce17

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tjlD_	Alignment		100.0	100	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
2	c2kq9A_	Alignment		99.9	21	**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
3	d1tjla1	Alignment		99.9	100	**Fold:**Long alpha-hairpin **Superfamily:**DnaK suppressor protein DksA, alpha-hairpin domain **Family:**DnaK suppressor protein DksA, alpha-hairpin domain
4	c2kgoA_	Alignment		99.7	25	**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
5	d1tjla2	Alignment		99.5	100	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Prokaryotic DksA/TraR C4-type zinc finger
6	c3mhsE_	Alignment		77.0	29	**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
7	c1dvbA_	Alignment		66.4	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
8	c2gviA_	Alignment		66.4	14	**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
9	c3d00A_	Alignment		60.7	27	**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
10	c2hr5B_	Alignment		58.6	14	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
11	d1x4ka1	Alignment		50.1	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain

12	d1xpaa2	Alignment		42.5	55	**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
13	d2cura1	Alignment		41.9	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
14	d1kjna_	Alignment		36.9	11	**Fold:**Hypothetical protein MTH777 (MT0777) **Superfamily:**Hypothetical protein MTH777 (MT0777) **Family:**Hypothetical protein MTH777 (MT0777)
15	c3u1dA_	Alignment		33.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the structure of a protein with a gntr superfamily winged-helix-turn-2 helix domain from halomicrobium mukohataei.
16	c1grjA_	Alignment		32.9	13	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
17	d1wyha1	Alignment		30.7	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
18	c1yuzB_	Alignment		28.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
19	c2f5qA_	Alignment		24.7	29	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
20	d1j2oa1	Alignment		23.7	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
21	d2czra1	Alignment	not modelled	22.9	50	**Fold:**Restriction endonuclease-like **Superfamily:**TBP-interacting protein-like **Family:**TBP-interacting protein-like
22	c2opfA_	Alignment	not modelled	22.7	32	**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
23	d1lpba2	Alignment	not modelled	22.7	27	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Colipase-like **Family:**Colipase-like
24	c1k82D_	Alignment	not modelled	22.6	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
25	d1weoa_	Alignment	not modelled	21.9	60	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
26	d1nf4a_	Alignment	not modelled	21.3	11	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
27	c2d8zA_	Alignment	not modelled	21.2	23	**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)
28	c2gb5B_	Alignment	not modelled	21.2	35	**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

29	d1rutx3	Alignment	not modelled	20.5	45	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
30	c1ee8A_	Alignment	not modelled	20.2	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
31	c2l3kA_	Alignment	not modelled	19.9	27	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**rhombotin-2, linker, lim domain-binding protein 1; **PDBTitle:** solution structure of lmo2(lim2)-ldb1(lid)
32	c2darA_	Alignment	not modelled	19.8	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	c1wjvA_	Alignment	not modelled	19.8	31	**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
34	c3a44D_	Alignment	not modelled	19.6	22	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
35	d1x63a2	Alignment	not modelled	19.4	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
36	c1nnjA_	Alignment	not modelled	18.7	32	**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	c1j2oA_	Alignment	not modelled	18.5	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
38	c2qgpA_	Alignment	not modelled	18.5	27	**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.
39	d2cupa3	Alignment	not modelled	18.1	44	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
40	d2ak3a2	Alignment	not modelled	17.9	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
41	c3cm6A_	Alignment	not modelled	17.4	31	**PDB header:**hydrolase, apoptosis **Chain:** A: **PDB Molecule:**cell death-related nuclease 4; **PDBTitle:** crystal structure of cell-death related nuclease 4 (crn-4)2 bound with er
42	d1rutx1	Alignment	not modelled	17.1	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
43	d1e4va2	Alignment	not modelled	16.9	30	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
44	c1x4lA_	Alignment	not modelled	16.6	25	**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
45	c2d8xA_	Alignment	not modelled	16.5	17	**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)
46	d2dara2	Alignment	not modelled	16.4	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
47	c1d4uA_	Alignment	not modelled	16.0	33	**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
48	c2cuqA_	Alignment	not modelled	16.0	17	**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
49	c1wyhA_	Alignment	not modelled	15.2	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
50	c2etnA_	Alignment	not modelled	15.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
51	c2i61A_	Alignment	not modelled	14.8	33	**PDB header:**toxin **Chain:** A: **PDB Molecule:**insect toxin 2; **PDBTitle:** depressant anti-insect neurotoxin, lqhit2 from leiurus2 quinquestriatus hebraeus
52	d1ee8a3	Alignment	not modelled	14.4	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
						PDB header:gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein

53	c2o03A_	Alignment	not modelled	14.3	57	furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
54	d1x4la2	Alignment	not modelled	14.2	44	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
55	c2curA_	Alignment	not modelled	13.9	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 1; **PDBTitle:** solution structure of skeletal muscle lim-protein 1
56	d1kx5b_	Alignment	not modelled	13.8	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
57	d1zina2	Alignment	not modelled	13.8	56	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
58	c3h0gL_	Alignment	not modelled	13.7	29	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
59	c2xigA_	Alignment	not modelled	13.6	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
60	d2cuqa1	Alignment	not modelled	13.6	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
61	c2a20A_	Alignment	not modelled	13.6	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**regulating synaptic membrane exocytosis protein **PDBTitle:** solution structure of rim2 zinc finger domain
62	d1id3b_	Alignment	not modelled	13.5	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
63	d1s3ga2	Alignment	not modelled	13.3	44	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
64	d1p3ja2	Alignment	not modelled	13.3	44	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
65	d1x3ha1	Alignment	not modelled	13.2	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
66	d1akya2	Alignment	not modelled	13.1	10	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
67	c1x63A_	Alignment	not modelled	13.0	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
68	d2b3ca_	Alignment	not modelled	12.6	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
69	c2fe3B_	Alignment	not modelled	12.6	43	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**peroxide operon regulator; **PDBTitle:** the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
70	c2ko5A_	Alignment	not modelled	12.5	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ring finger protein z; **PDBTitle:** nmr solution structure of lfv-z
71	d1bboa1	Alignment	not modelled	12.4	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
72	d1bmra_	Alignment	not modelled	12.2	33	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
73	d1xx6a2	Alignment	not modelled	12.1	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Type II thymidine kinase zinc finger
74	c3mwmA_	Alignment	not modelled	12.0	57	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
75	d1twfj_	Alignment	not modelled	11.9	56	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
76	c1x4kA_	Alignment	not modelled	11.8	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
77	c2i5oA_	Alignment	not modelled	11.6	40	**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
78	c2p4vA_	Alignment	not modelled	11.5	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution

79	d2i9ca1	Alignment	not modelled	11.1	30	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**RPA1889-like
80	c1x64A_	Alignment	not modelled	11.0	10	**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
81	d1jzaa_	Alignment	not modelled	11.0	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
82	c2egqA_	Alignment	not modelled	10.9	24	**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
83	c2a8vA_	Alignment	not modelled	10.9	23	**PDB header:**protein/rna **Chain:** A: **PDB Molecule:**rna binding domain of rho transcription **PDBTitle:** rho transcription termination factor/rna complex
84	c1x61A_	Alignment	not modelled	10.8	17	**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)
85	c2k5cA_	Alignment	not modelled	10.8	31	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
86	d1ef4a_	Alignment	not modelled	10.6	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**RNA polymerase subunit RPB10 **Family:**RNA polymerase subunit RPB10
87	c3jueA_	Alignment	not modelled	10.5	15	**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
88	d1cn2a_	Alignment	not modelled	10.4	33	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
89	d2huec1	Alignment	not modelled	10.4	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
90	d1a62a2	Alignment	not modelled	10.4	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
91	d1vnba_	Alignment	not modelled	10.3	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
92	d1nh5a_	Alignment	not modelled	10.3	25	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
93	c1x62A_	Alignment	not modelled	10.2	33	**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
94	d2sn3a_	Alignment	not modelled	10.2	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
95	d2yt9a2	Alignment	not modelled	10.1	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
96	d2cu8a1	Alignment	not modelled	10.0	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
97	c3gn5B_	Alignment	not modelled	10.0	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
98	c1x3hA_	Alignment	not modelled	9.9	10	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**leupaxin; **PDBTitle:** solution structure of the lim domain of human leupaxin
99	c2co8A_	Alignment	not modelled	9.9	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** solution structures of the lim domain of human nedd92 interacting protein with calponin homology and lim domains