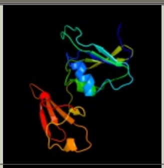
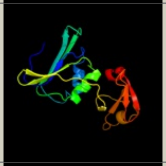
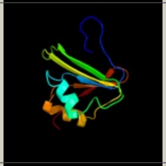
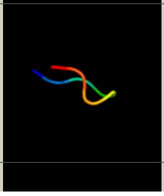
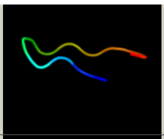
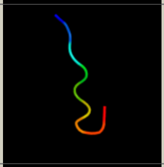
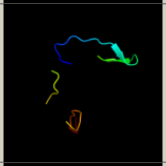
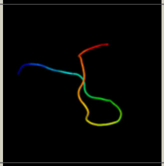
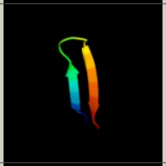
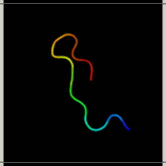
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A7F3
Date	Thu Jan 5 11:05:33 GMT 2012
Unique Job ID	8906af9600ed0ab5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h3eB_	Alignment		100.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** structure of wild-type e. coli aspartate transcarbamoylase in the2 presence of n-phosphonacetyl-l-isoasparagine at 2.3a resolution
2	c1pg5B_	Alignment		100.0	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius
3	c2ywwA_	Alignment		100.0	35	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of aspartate carbamoyltransferase2 regulatory chain from methanocaldococcus jannaschii
4	c2be7E_	Alignment		100.0	57	**PDB header:**transferase **Chain:** E: **PDB Molecule:**aspartate carbamoyltransferase regulatory chain; **PDBTitle:** crystal structure of the unliganded (t-state) aspartate2 transcarbamoylase of the psychrophilic bacterium moritella profunda
5	d2fzcb1	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain
6	d2atcb1	Alignment		100.0	88	**Fold:**Ferredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain
7	d1pg5b1	Alignment		100.0	42	**Fold:**Ferredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, N-terminal domain
8	d2fzcb2	Alignment		99.8	100	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
9	d2atcb2	Alignment		99.7	90	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
10	d1pg5b2	Alignment		99.7	23	**Fold:**Rubredoxin-like **Superfamily:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain **Family:**Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain
11	c1xrzA_	Alignment		51.4	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger y-chromosomal protein; **PDBTitle:** nmr structure of a zinc finger with cyclohexanylalanine2 substituted for the central aromatic residue

12	c7znfA_	Alignment		42.9	46	**PDB header:**zinc finger dna binding domain **Chain:** A: **PDB Molecule:**zinc finger; **PDBTitle:** alternating zinc fingers in the human male associated2 protein zfy: 2d nmr structure of an even finger and3 implications for "jumping-linker" dna recognition
13	d7znfa_	Alignment		42.9	46	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
14	d1pvma3	Alignment		41.1	44	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
15	c1dgsB_	Alignment		39.2	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
16	c2elpA_	Alignment		38.7	37	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
17	d1vq0a2	Alignment		38.3	18	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
18	c2l8eA_	Alignment		37.6	40	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**polyhomeotic-like protein 1; **PDBTitle:** solution nmr structure of fcs domain of human polyhomeotic homolog 12 (hph1)
19	c1rikA_	Alignment		37.4	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apc1 peptide; **PDBTitle:** e6-binding zinc finger (e6apc1)
20	c5znfA_	Alignment		37.3	57	**PDB header:**zinc finger dna binding domain **Chain:** A: **PDB Molecule:**zinc finger; **PDBTitle:** alternating zinc fingers in the human male associated2 protein zfy: 2d nmr structure of an even finger and3 implications for "jumping-linker" dna recognition
21	d1xjha_	Alignment	not modelled	35.6	29	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
22	c2jvmA_	Alignment	not modelled	35.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of rhodobacter sphaeroides protein2 rhos4_26430. northeast structural genomics consortium3 target rhr95
23	c1vzyA_	Alignment	not modelled	34.9	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of the bacillus subtilis hsp33
24	d1vzya2	Alignment	not modelled	34.1	12	**Fold:**HSP33 redox switch-like **Superfamily:**HSP33 redox switch-like **Family:**HSP33 redox switch-like
25	c3siqF_	Alignment	not modelled	33.4	17	**PDB header:**ligase **Chain:** F: **PDB Molecule:**apoptosis 1 inhibitor; **PDBTitle:** crystal structure of autoinhibited diap1-bir1 domain
26	c2jrrA_	Alignment	not modelled	32.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q5lls5 from silicibacter2 pomeroyi. northeast structural genomics consortium target3 sir90
27	c1vq0A_	Alignment	not modelled	32.1	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
28	c1klsA_	Alignment	not modelled	29.8	57	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger y-chromosomal protein; **PDBTitle:** nmr structure of the zfy-6t[y10l] zinc finger
						PDB header:transcription

29	c1klrA_	Alignment	not modelled	29.6	57	**Chain:** A: **PDB Molecule:**zinc finger y-chromosomal protein; **PDBTitle:** nmr structure of the zfy-6t[y10f] zinc finger
30	d1klra_	Alignment	not modelled	29.6	57	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
31	d1njqa_	Alignment	not modelled	28.0	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Plant C2H2 finger (QALGGH zinc finger)
32	c2elvA_	Alignment	not modelled	27.5	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 6th c2h2 zinc finger of human2 zinc finger protein 406
33	d2cota1	Alignment	not modelled	27.0	42	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
34	d1a1ia2	Alignment	not modelled	26.9	24	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
35	d1llmc2	Alignment	not modelled	26.6	18	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
36	c2eltA_	Alignment	not modelled	25.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 3rd c2h2 zinc finger of human2 zinc finger protein 406
37	d2ct1a2	Alignment	not modelled	25.2	20	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
38	c1arfA_	Alignment	not modelled	25.1	21	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**yeast transcription factor adr1; **PDBTitle:** structures of dna-binding mutant zinc finger domains:2 implications for dna binding
39	c2jz8A_	Alignment	not modelled	24.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bh09830; **PDBTitle:** solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
40	d1ncsa_	Alignment	not modelled	24.1	28	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
41	c1meyG_	Alignment	not modelled	23.9	38	**PDB header:**transferase/dna **Chain:** G: **PDB Molecule:**consensus zinc finger; **PDBTitle:** crystal structure of a designed zinc finger protein bound2 to dna
42	c2eprA_	Alignment	not modelled	22.8	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**poz-, at hook-, and zinc finger-containing **PDBTitle:** solution structure of the secound zinc finger domain of2 zinc finger protein 278
43	c3t6pA_	Alignment	not modelled	22.6	25	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 2; **PDBTitle:** iap antagonist-induced conformational change in ciap1 promotes e32 ligase activation via dimerization
44	d1u85a1	Alignment	not modelled	22.3	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
45	c2elqA_	Alignment	not modelled	21.7	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 14th c2h2 zinc finger of human2 zinc finger protein 406
46	c2drpD_	Alignment	not modelled	21.4	20	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**protein (tramtrack dna-binding domain); **PDBTitle:** the crystal structure of a two zinc-finger peptide reveals2 an extension to the rules for zinc-finger/dna recognition
47	d1m4ma_	Alignment	not modelled	21.2	22	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
48	d1tfqa_	Alignment	not modelled	21.1	19	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
49	c2el5A_	Alignment	not modelled	21.0	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 268; **PDBTitle:** solution structure of the 18th zf-c2h2 domain from human2 zinc finger protein 268
50	c3m0aD_	Alignment	not modelled	20.5	19	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**baculoviral iap repeat-containing protein 3; **PDBTitle:** crystal structure of traf2:ciap2 complex
51	d1i3oe_	Alignment	not modelled	20.3	10	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
52	d2raxa1	Alignment	not modelled	20.1	19	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
53	d1xb0a_	Alignment	not modelled	20.1	9	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
54	d1srka_	Alignment	not modelled	20.0	18	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
55	d2dkta1	Alignment	not modelled	20.0	23	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger

56	d2vsla1	Alignment	not modelled	19.7	12	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
57	d1a1ia3	Alignment	not modelled	19.3	18	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
58	d1se0a_	Alignment	not modelled	19.3	19	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
59	d1q4qa_	Alignment	not modelled	19.0	13	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
60	d1m4ka2	Alignment	not modelled	18.9	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
61	d2i3ha1	Alignment	not modelled	18.8	14	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
62	d1dgsa1	Alignment	not modelled	18.8	56	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
63	d1tf3a2	Alignment	not modelled	18.4	43	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
64	d3d9ta1	Alignment	not modelled	18.4	29	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
65	d2epsa1	Alignment	not modelled	18.1	42	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
66	d1xb0b_	Alignment	not modelled	18.1	14	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
67	d2epra1	Alignment	not modelled	18.1	36	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
68	c1v9pB_	Alignment	not modelled	17.9	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
69	d1x6ha2	Alignment	not modelled	17.4	26	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
70	c2poiA_	Alignment	not modelled	16.9	13	**PDB header:**signaling protein/apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 4; **PDBTitle:** crystal structure of xiap bir1 domain (i222 form)
71	c2elsA_	Alignment	not modelled	16.9	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 2nd c2h2 zinc finger of human2 zinc finger protein 406
72	d1g73d_	Alignment	not modelled	16.8	19	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
73	d1jd5a_	Alignment	not modelled	16.6	14	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
74	c1va3A_	Alignment	not modelled	16.5	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor sp1; **PDBTitle:** solution structure of transcription factor sp1 dna binding2 domain (zinc finger 3)
75	d2vrda1	Alignment	not modelled	16.5	27	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
76	d1oxna_	Alignment	not modelled	16.4	14	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
77	d1x6ea2	Alignment	not modelled	16.2	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
78	d1vd4a_	Alignment	not modelled	16.1	14	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
79	c1rimA_	Alignment	not modelled	16.0	27	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apc2 peptide; **PDBTitle:** e6-binding zinc finger (e6apc2)
80	c2yu5A_	Alignment	not modelled	15.7	31	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the zf-c2h2 domain (669-699aa) in2 zinc finger protein 473
81	c2eoxA_	Alignment	not modelled	15.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 315-2 345) of human zinc finger protein 473
82	d1xf7a_	Alignment	not modelled	15.7	45	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
						PDB header:transcription

83	c1xf7A_	Alignment	not modelled	15.7	45	**Chain:** A: **PDB Molecule:**wilms' tumor protein; **PDBTitle:** high resolution nmr structure of the wilms' tumor2 suppressor protein (wt1) finger 3
84	d2qfaa1	Alignment	not modelled	15.6	19	**Fold:**Inhibitor of apoptosis (IAP) repeat **Superfamily:**Inhibitor of apoptosis (IAP) repeat **Family:**Inhibitor of apoptosis (IAP) repeat
85	c2epcA_	Alignment	not modelled	15.6	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 32; **PDBTitle:** solution structure of zinc finger domain 7 in zinc finger2 protein 32
86	d1nkra2	Alignment	not modelled	15.6	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
87	c2eifA_	Alignment	not modelled	15.3	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (eukaryotic translation initiation factor 5a); **PDBTitle:** eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
88	d2drpa1	Alignment	not modelled	15.3	20	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
89	c2epuA_	Alignment	not modelled	15.1	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 32; **PDBTitle:** solution structure of the secound c2h2 type zinc finger2 domain of zinc finger protein 32
90	c1oy7C_	Alignment	not modelled	14.9	14	**PDB header:**apoptosis/peptide **Chain:** C: **PDB Molecule:**baculoviral iap repeat-containing protein 7; **PDBTitle:** structure and function analysis of peptide antagonists of melanoma2 inhibitor of apoptosis (ml-iap)
91	c2en3A_	Alignment	not modelled	14.6	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 95 homolog; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 796-2 828) of human zinc finger protein 95 homolog
92	c2vm5A_	Alignment	not modelled	14.5	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 1; **PDBTitle:** human bir2 domain of baculoviral inhibitor of apoptosis2 repeat-containing 1 (birc1)
93	d1ueba1	Alignment	not modelled	14.2	10	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
94	c3m1cA_	Alignment	not modelled	14.0	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein h; **PDBTitle:** crystal structure of the conserved herpesvirus fusion regulator2 complex gh-gl
95	d1ubdc3	Alignment	not modelled	14.0	42	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
96	d1sp1a_	Alignment	not modelled	13.9	29	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
97	c1sp1A_	Alignment	not modelled	13.9	29	**PDB header:**zinc finger **Chain:** A: **PDB Molecule:**sp1f3; **PDBTitle:** nmr structure of a zinc finger domain from transcription2 factor sp1f3, minimized average structure
98	d2dl2a1	Alignment	not modelled	13.2	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
99	c2en8A_	Alignment	not modelled	13.1	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 224; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 171-2 203) of human zinc finger protein 224