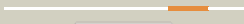
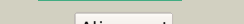
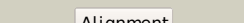
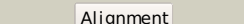
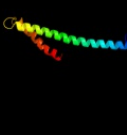
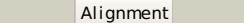
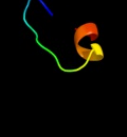
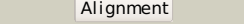
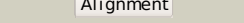
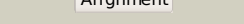
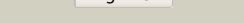
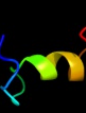


| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                                                |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3ax1A_</a> |  Alignment   |    | 98.2       | 11     | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> serrate rna effector molecule;<br><b>PDBTitle:</b> molecular insights into mirna processing by arabidopsis serrate                                                                                                      |
| 2  | <a href="#">dlzr9a1</a> |  Alignment   |    | 85.3       | 18     | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> HkH motif-containing C2H2 finger                                                                                                                                                    |
| 3  | <a href="#">clzr9A_</a> |  Alignment   |    | 85.3       | 18     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 593;<br><b>PDBTitle:</b> solution structure of a human c2h2-type zinc finger protein                                                                                                                  |
| 4  | <a href="#">clnafA_</a> |  Alignment   |   | 49.7       | 19     | <b>PDB header:</b> signaling protein, membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor binding protein gga1;<br><b>PDBTitle:</b> crystal structure of the human gga1 gat domain                                                                                    |
| 5  | <a href="#">dloxza_</a> |  Alignment |  | 46.6       | 15     | <b>Fold:</b> Spectrin repeat-like<br><b>Superfamily:</b> GAT-like domain<br><b>Family:</b> GAT domain                                                                                                                                                                                               |
| 6  | <a href="#">cloxzA_</a> |  Alignment |  | 46.6       | 15     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor binding protein gga1;<br><b>PDBTitle:</b> crystal structure of the human gga1 gat domain                                                                                                       |
| 7  | <a href="#">d2qlia1</a> |  Alignment |  | 41.2       | 41     | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                           |
| 8  | <a href="#">clzw8A_</a> |  Alignment |  | 37.5       | 23     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc-responsive transcriptional regulator zap1;<br><b>PDBTitle:</b> solution structure of a zap1 zinc-responsive domain2 provides insights into metalloregulatory transcriptional3 repression in saccharomyces cerevisiae |
| 9  | <a href="#">dlwira_</a> |  Alignment |  | 34.0       | 33     | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> variant C2H2 finger                                                                                                                                                                 |
| 10 | <a href="#">c2eluA_</a> |  Alignment |  | 30.1       | 29     | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406;<br><b>PDBTitle:</b> solution structure of the 5th c2h2 zinc finger of human2 zinc finger protein 406                                                                                             |
| 11 | <a href="#">clzu1A_</a> |  Alignment |  | 29.8       | 11     | <b>PDB header:</b> rna binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> rna binding protein zfa;<br><b>PDBTitle:</b> solution structure of the n-terminal zinc fingers of the2 xenopus laevis double stranded rna binding protein zfa                                                       |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                     |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c4znfA_</a> | Alignment |    | 24.8 | 22 | <b>PDB header:</b> zinc finger dna binding domain<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger;<br><b>PDBTitle:</b> high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution |
| 13 | <a href="#">d4znfa_</a> | Alignment |    | 24.8 | 22 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                           |
| 14 | <a href="#">c3znfA_</a> | Alignment |    | 24.8 | 22 | <b>PDB header:</b> zinc finger dna binding domain<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger;<br><b>PDBTitle:</b> high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution |
| 15 | <a href="#">d1x6ha1</a> | Alignment |    | 18.3 | 25 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                           |
| 16 | <a href="#">d2yrka1</a> | Alignment |    | 17.1 | 40 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> HkH motif-containing C2H2 finger                                                                                                    |
| 17 | <a href="#">c3a19B_</a> | Alignment |    | 16.8 | 29 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> plexin-a2;<br><b>PDBTitle:</b> mouse plexin a2 extracellular domain                                                                                                   |
| 18 | <a href="#">d1y0jb1</a> | Alignment |  | 16.7 | 32 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> C2HC finger                                                                                                                         |
| 19 | <a href="#">d2v4jb1</a> | Alignment |  | 16.1 | 40 | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> 4Fe-4S ferredoxins<br><b>Family:</b> Ferredoxin domains from multidomain proteins                                                                                                               |
| 20 | <a href="#">d1tfqa_</a> | Alignment |  | 16.0 | 30 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                   |
| 21 | <a href="#">c1wjpa_</a> | Alignment | not modelled                                                                        | 15.1 | 26 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 295;<br><b>PDBTitle:</b> solution structure of zf-c2h2 domains from human zinc2 finger protein 295                                            |
| 22 | <a href="#">c2ct1A_</a> | Alignment | not modelled                                                                        | 14.0 | 24 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor ctcf;<br><b>PDBTitle:</b> solution structure of the zinc finger domain of2 transcriptional repressor ctcf protein                               |
| 23 | <a href="#">d1qbha_</a> | Alignment | not modelled                                                                        | 13.4 | 20 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                   |
| 24 | <a href="#">d1xb0a_</a> | Alignment | not modelled                                                                        | 13.1 | 30 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                   |
| 25 | <a href="#">d3d9ta1</a> | Alignment | not modelled                                                                        | 12.2 | 18 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                   |
| 26 | <a href="#">d1i3oe_</a> | Alignment | not modelled                                                                        | 12.1 | 30 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                   |
| 27 | <a href="#">c1w1nA_</a> | Alignment | not modelled                                                                        | 12.1 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase tor1;<br><b>PDBTitle:</b> the solution structure of the fatc domain of the protein2 kinase tor1 from yeast                                    |
| 28 | <a href="#">d2qfaa1</a> | Alignment | not modelled                                                                        | 12.1 | 20 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                   |
| 29 | <a href="#">c1araA_</a> | Alignment | not modelled                                                                        | 11.6 | 26 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> yeast transcription factor adr1;                                                                                                                               |

|    |                         |           |              |      |    |                                                                                                                                                                                                                                                                                                                                              |
|----|-------------------------|-----------|--------------|------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c1a1eA_</a> | Alignment | not modelled | 11.0 | 20 | <b>PDBTitle:</b> structures of dna-binding mutant zinc finger domains:2 implications for dna binding<br><b>PDB header:</b> rna-binding protein/rna<br><b>Chain:</b> D: <b>PDB Molecule:</b> transcription factor iiiia;<br><b>PDBTitle:</b> the crystal structure of a zinc finger - rna complex2 reveals two modes of molecular recognition |
| 30 | <a href="#">c1un6D_</a> | Alignment | not modelled | 11.5 | 16 | <b>Fold:</b> Rubredoxin-like<br><b>Superfamily:</b> Zinc beta-ribbon<br><b>Family:</b> DNA primase zinc finger                                                                                                                                                                                                                               |
| 31 | <a href="#">d1nuia2</a> | Alignment | not modelled | 11.5 | 27 | <b>Fold:</b> Knottins (small inhibitors, toxins, lectins)<br><b>Superfamily:</b> Scorpion toxin-like<br><b>Family:</b> Short-chain scorpion toxins                                                                                                                                                                                           |
| 32 | <a href="#">d1pvza_</a> | Alignment | not modelled | 11.5 | 24 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                                                                            |
| 33 | <a href="#">d1jd5a_</a> | Alignment | not modelled | 11.2 | 30 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                                                                            |
| 34 | <a href="#">d1q4qa_</a> | Alignment | not modelled | 11.0 | 30 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                                                                    |
| 35 | <a href="#">d1aaya1</a> | Alignment | not modelled | 10.8 | 16 | <b>PDB header:</b> signaling protein/apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 4;<br><b>PDBTitle:</b> crystal structure of xiap bir1 domain (i222 form)                                                                                                                                   |
| 36 | <a href="#">c2poiA_</a> | Alignment | not modelled | 10.5 | 30 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                                                                    |
| 37 | <a href="#">d1zfdA_</a> | Alignment | not modelled | 10.2 | 29 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 224;<br><b>PDBTitle:</b> solution structure of the 11th c2h2 type zinc finger domain2 of zinc finger protein 224                                                                                                                               |
| 38 | <a href="#">c2eq4A_</a> | Alignment | not modelled | 10.2 | 24 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                                                                            |
| 39 | <a href="#">d2raxa1</a> | Alignment | not modelled | 10.0 | 20 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                                                                            |
| 40 | <a href="#">d1m4ma_</a> | Alignment | not modelled | 10.0 | 20 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of q5lls5 from silicibacter2 pomeroyi. northeast structural genomics consortium target3 sir90                                                                          |
| 41 | <a href="#">c2jrrA_</a> | Alignment | not modelled | 9.7  | 42 | <b>Fold:</b> Cysteine-rich domain<br><b>Superfamily:</b> Cysteine-rich domain<br><b>Family:</b> Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)                                                                                                                                                                           |
| 42 | <a href="#">d1r79a_</a> | Alignment | not modelled | 9.7  | 28 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> yeast transcription factor adr1;<br><b>PDBTitle:</b> structures of dna-binding mutant zinc finger domains:2 implications for dna binding                                                                                                                |
| 43 | <a href="#">c1arfA_</a> | Alignment | not modelled | 9.7  | 26 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                                                                            |
| 44 | <a href="#">d2i3ha1</a> | Alignment | not modelled | 9.6  | 30 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;<br><b>PDBTitle:</b> solution nmr structure of rhodobacter sphaeroides protein2 rhos4_26430. northeast structural genomics consortium3 target rhr95                                                                |
| 45 | <a href="#">c2jvmA_</a> | Alignment | not modelled | 9.6  | 50 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                                                                            |
| 46 | <a href="#">d2vsla1</a> | Alignment | not modelled | 9.5  | 30 | <b>PDB header:</b> apoptosis/peptide<br><b>Chain:</b> C: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 7;<br><b>PDBTitle:</b> structure and function analysis of peptide antagonists of melanoma2 inhibitor of apoptosis (ml-iap)                                                                                           |
| 47 | <a href="#">c1oy7C_</a> | Alignment | not modelled | 9.3  | 30 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 3;<br><b>PDBTitle:</b> crystal structure of traf2:ciap2 complex                                                                                                                                                      |
| 48 | <a href="#">c3m0aD_</a> | Alignment | not modelled | 9.1  | 40 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                                                                            |
| 49 | <a href="#">d1xb0b_</a> | Alignment | not modelled | 9.1  | 30 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> teashirt homolog 3;<br><b>PDBTitle:</b> solution structure of the first and the second zf-c2h2 like2 domains of human teashirt homolog 3                                                                                                                           |
| 50 | <a href="#">c2dmiA_</a> | Alignment | not modelled | 9.0  | 26 | <b>Fold:</b> HSP33 redox switch-like<br><b>Superfamily:</b> HSP33 redox switch-like<br><b>Family:</b> HSP33 redox switch-like                                                                                                                                                                                                                |
| 51 | <a href="#">d1vq0a2</a> | Alignment | not modelled | 8.8  | 38 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 473;<br><b>PDBTitle:</b> solution structure of the c2h2 type zinc finger (region 315-2 345) of human zinc finger protein 473                                                                                                                   |
| 52 | <a href="#">c2eoxA_</a> | Alignment | not modelled | 8.8  | 21 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> plexin-a2;<br><b>PDBTitle:</b> plexin a2 in complex with semaphorin 6a                                                                                                                                                                                         |
| 53 | <a href="#">c3okyA_</a> | Alignment | not modelled | 8.7  | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> F: <b>PDB Molecule:</b> apoptosis 1 inhibitor;<br><b>PDBTitle:</b> crystal structure of autoinhibited diap1-bir1 domain                                                                                                                                                                           |
| 54 | <a href="#">c3siqF_</a> | Alignment | not modelled | 8.6  | 40 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                                                                            |
| 55 | <a href="#">d1g73d_</a> | Alignment | not modelled | 8.5  | 30 |                                                                                                                                                                                                                                                                                                                                              |

|    |                         |           |              |     |    |                                                                                                                                                                                                                                                                                              |
|----|-------------------------|-----------|--------------|-----|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 56 | <a href="#">c2vm5A_</a> | Alignment | not modelled | 8.4 | 30 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 1;<br><b>PDBTitle:</b> human bir2 domain of baculoviral inhibitor of apoptosis2 repeat-containing 1 (birc1)                                                                  |
| 57 | <a href="#">d1se0a_</a> | Alignment | not modelled | 8.4 | 40 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                            |
| 58 | <a href="#">d1oqla_</a> | Alignment | not modelled | 8.2 | 12 | <b>Fold:</b> Concanavalin A-like lectins/glucanases<br><b>Superfamily:</b> Concanavalin A-like lectins/glucanases<br><b>Family:</b> Hypothetical protein YesU                                                                                                                                |
| 59 | <a href="#">c2qgpA_</a> | Alignment | not modelled | 8.2 | 36 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> hnh endonuclease;<br><b>PDBTitle:</b> x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.                                                 |
| 60 | <a href="#">d1oxna_</a> | Alignment | not modelled | 8.1 | 30 | <b>Fold:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Superfamily:</b> Inhibitor of apoptosis (IAP) repeat<br><b>Family:</b> Inhibitor of apoptosis (IAP) repeat                                                                                                                            |
| 61 | <a href="#">d2glia3</a> | Alignment | not modelled | 8.1 | 26 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                    |
| 62 | <a href="#">c2epcA_</a> | Alignment | not modelled | 8.1 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 32;<br><b>PDBTitle:</b> solution structure of zinc finger domain 7 in zinc finger2 protein 32                                                                                                  |
| 63 | <a href="#">d1a1ga1</a> | Alignment | not modelled | 7.6 | 16 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                    |
| 64 | <a href="#">c2elrA_</a> | Alignment | not modelled | 7.6 | 23 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406;<br><b>PDBTitle:</b> solution structure of the 15th c2h2 zinc finger of human2 zinc finger protein 406                                                                                     |
| 65 | <a href="#">d1zu1a2</a> | Alignment | not modelled | 7.5 | 24 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> HkH motif-containing C2H2 finger                                                                                                                                             |
| 66 | <a href="#">d1qmya_</a> | Alignment | not modelled | 7.5 | 22 | <b>Fold:</b> Cysteine proteinases<br><b>Superfamily:</b> Cysteine proteinases<br><b>Family:</b> FMDV leader protease                                                                                                                                                                         |
| 67 | <a href="#">c1ardA_</a> | Alignment | not modelled | 7.5 | 29 | <b>PDB header:</b> transcription regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> yeast transcription factor adr1;<br><b>PDBTitle:</b> structures of dna-binding mutant zinc finger domains:2 implications for dna binding                                                                |
| 68 | <a href="#">d1qola_</a> | Alignment | not modelled | 7.4 | 22 | <b>Fold:</b> Cysteine proteinases<br><b>Superfamily:</b> Cysteine proteinases<br><b>Family:</b> FMDV leader protease                                                                                                                                                                         |
| 69 | <a href="#">d2adra1</a> | Alignment | not modelled | 7.4 | 29 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                    |
| 70 | <a href="#">c2drpD_</a> | Alignment | not modelled | 7.3 | 18 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> protein (tramtrack dna-binding domain);<br><b>PDBTitle:</b> the crystal structure of a two zinc-finger peptide reveals2 an extension to the rules for zinc-finger/dna recognition                              |
| 71 | <a href="#">d1dt9a3</a> | Alignment | not modelled | 7.3 | 28 | <b>Fold:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1<br><b>Superfamily:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1<br><b>Family:</b> N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 |
| 72 | <a href="#">d1ubdc3</a> | Alignment | not modelled | 7.3 | 21 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                    |
| 73 | <a href="#">d1xjha_</a> | Alignment | not modelled | 7.2 | 75 | <b>Fold:</b> HSP33 redox switch-like<br><b>Superfamily:</b> HSP33 redox switch-like<br><b>Family:</b> HSP33 redox switch-like                                                                                                                                                                |
| 74 | <a href="#">d1p7aa_</a> | Alignment | not modelled | 7.1 | 18 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                    |
| 75 | <a href="#">d1xf7a_</a> | Alignment | not modelled | 7.0 | 18 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                    |
| 76 | <a href="#">c1xf7A_</a> | Alignment | not modelled | 7.0 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> wilms' tumor protein;<br><b>PDBTitle:</b> high resolution nmr structure of the wilms' tumor2 suppressor protein (wt1) finger 3                                                                                     |
| 77 | <a href="#">c1rika_</a> | Alignment | not modelled | 7.0 | 18 | <b>PDB header:</b> de novo protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> e6apc1 peptide;<br><b>PDBTitle:</b> e6-binding zinc finger (e6apc1)                                                                                                                                              |
| 78 | <a href="#">c2h0dB_</a> | Alignment | not modelled | 6.9 | 20 | <b>PDB header:</b> metal binding protein/ligase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin ligase protein ring2;<br><b>PDBTitle:</b> structure of a bmi-1-ring1b polycomb group ubiquitin ligase complex                                                                             |
| 79 | <a href="#">c2elsA_</a> | Alignment | not modelled | 6.9 | 24 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406;<br><b>PDBTitle:</b> solution structure of the 2nd c2h2 zinc finger of human2 zinc finger protein 406                                                                                      |
| 80 | <a href="#">c3hi2C_</a> | Alignment | not modelled | 6.9 | 29 | <b>PDB header:</b> dna binding protein/toxin<br><b>Chain:</b> C: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa(ygit);<br><b>PDBTitle:</b> structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)  |
|    |                         |           |              |     |    | <b>Fold:</b> beta-beta-alpha zinc fingers                                                                                                                                                                                                                                                    |

|    |                         |           |              |     |    |                                                                                                                                                                                                                                                                                           |
|----|-------------------------|-----------|--------------|-----|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 81 | <a href="#">d1a1ia3</a> | Alignment | not modelled | 6.9 | 14 | <b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                                                              |
| 82 | <a href="#">d1vzya2</a> | Alignment | not modelled | 6.9 | 38 | <b>Fold:</b> HSP33 redox switch-like<br><b>Superfamily:</b> HSP33 redox switch-like<br><b>Family:</b> HSP33 redox switch-like                                                                                                                                                             |
| 83 | <a href="#">c1va3A</a>  | Alignment | not modelled | 6.7 | 18 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor sp1;<br><b>PDBTitle:</b> solution structure of transcription factor sp1 dna binding2 domain (zinc finger 3)                                                                                |
| 84 | <a href="#">c1bi6H</a>  | Alignment | not modelled | 6.6 | 53 | <b>PDB header:</b> cysteine protease inhibitor<br><b>Chain:</b> H: <b>PDB Molecule:</b> bromelain inhibitor vi;<br><b>PDBTitle:</b> nmr structure of bromelain inhibitor vi from pineapple stem                                                                                           |
| 85 | <a href="#">d7znfa</a>  | Alignment | not modelled | 6.5 | 24 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                 |
| 86 | <a href="#">c7znfa</a>  | Alignment | not modelled | 6.5 | 24 | <b>PDB header:</b> zinc finger dna binding domain<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger;<br><b>PDBTitle:</b> alternating zinc fingers in the human male associated2 protein zfy: 2d nmr structure of an even finger and3 implications for "jumping-linker" dna recognition |
| 87 | <a href="#">c3cw19</a>  | Alignment | not modelled | 6.5 | 33 | <b>PDB header:</b> splicing<br><b>Chain:</b> 9: <b>PDB Molecule:</b> u1 small nuclear ribonucleoprotein c;<br><b>PDBTitle:</b> crystal structure of human spliceosomal u1 snrnp                                                                                                           |
| 88 | <a href="#">d2vrda1</a> | Alignment | not modelled | 6.5 | 33 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> HkH motif-containing C2H2 finger                                                                                                                                          |
| 89 | <a href="#">c2eoqA</a>  | Alignment | not modelled | 6.5 | 24 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 224;<br><b>PDBTitle:</b> solution structure of the c2h2 type zinc finger (region 283-2 315) of human zinc finger protein 224                                                                |
| 90 | <a href="#">d2i9be3</a> | Alignment | not modelled | 6.4 | 64 | <b>Fold:</b> Snake toxin-like<br><b>Superfamily:</b> Snake toxin-like<br><b>Family:</b> Extracellular domain of cell surface receptors                                                                                                                                                    |
| 91 | <a href="#">c1vzyA</a>  | Alignment | not modelled | 6.3 | 38 | <b>PDB header:</b> chaperone<br><b>Chain:</b> A: <b>PDB Molecule:</b> 33 kda chaperonin;<br><b>PDBTitle:</b> crystal structure of the bacillus subtilis hsp33                                                                                                                             |
| 92 | <a href="#">c3l11A</a>  | Alignment | not modelled | 6.3 | 20 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf168;<br><b>PDBTitle:</b> crystal structure of the ring domain of rnf168                                                                                                                 |
| 93 | <a href="#">d2cota1</a> | Alignment | not modelled | 6.2 | 29 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                 |
| 94 | <a href="#">d2fd6u3</a> | Alignment | not modelled | 6.1 | 64 | <b>Fold:</b> Snake toxin-like<br><b>Superfamily:</b> Snake toxin-like<br><b>Family:</b> Extracellular domain of cell surface receptors                                                                                                                                                    |
| 95 | <a href="#">c1va1A</a>  | Alignment | not modelled | 6.1 | 22 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor sp1;<br><b>PDBTitle:</b> solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)                                                                                |
| 96 | <a href="#">c3q7aB</a>  | Alignment | not modelled | 6.1 | 29 | <b>PDB header:</b> transferase/transferase inhibitor<br><b>Chain:</b> B: <b>PDB Molecule:</b> farnesyltransferase beta subunit;<br><b>PDBTitle:</b> cryptococcus neoformans protein farnesyltransferase in complex with2 fpp and l-778,123                                                |
| 97 | <a href="#">d1tf3a2</a> | Alignment | not modelled | 6.1 | 21 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                 |
| 98 | <a href="#">c2ej4A</a>  | Alignment | not modelled | 6.1 | 12 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein zic 3;<br><b>PDBTitle:</b> functional and structural basis of nuclear localization2 signal in zic3 zinc finger domain: a role of conserved3 tryptophan residue in the zinc finger domain  |
| 99 | <a href="#">d2ct1a2</a> | Alignment | not modelled | 6.1 | 12 | <b>Fold:</b> beta-beta-alpha zinc fingers<br><b>Superfamily:</b> beta-beta-alpha zinc fingers<br><b>Family:</b> Classic zinc finger, C2H2                                                                                                                                                 |