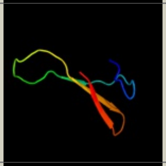
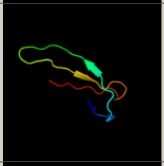
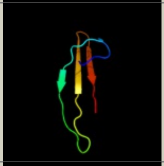
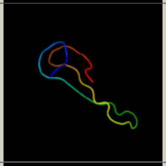
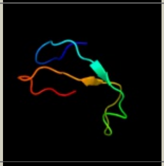
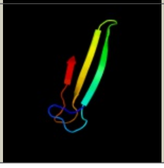
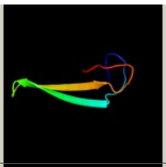
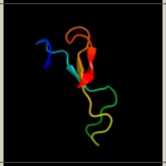
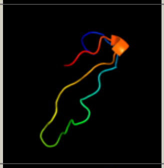
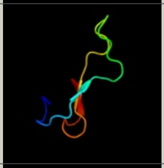
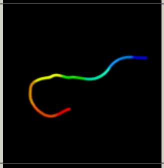
# Phyre$^2$

| | |
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P37057 |
| Date | Thu Jan 5 11:54:46 GMT 2012 |
| Unique Job ID | a8d3a0d2c1370a53 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1tfia_ | Alignment |  | 96.0 | 18 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 2 | d1twfi2 | Alignment |  | 95.7 | 24 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 3 | d1qypa_ | Alignment |  | 95.6 | 19 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 4 | c1pqvS_ | Alignment |  | 94.4 | 15 | **PDB header:**transferase/transcription<br>**Chain:** S: **PDB Molecule:**transcription elongation factor s-ii;<br>**PDBTitle:** rna polymerase ii-tfiis complex |
| 5 | c1y1yS_ | Alignment |  | 93.7 | 15 | **PDB header:**transferase/transcription/dna-rna hybrid<br>**Chain:** S: **PDB Molecule:**transcription elongation factor s-ii;<br>**PDBTitle:** rna polymerase ii-tfiis-dna/rna complex |
| 6 | c1i3qI_ | Alignment |  | 93.4 | 24 | **PDB header:**transcription<br>**Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd<br>**PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution |
| 7 | c3h0gI_ | Alignment |  | 93.2 | 22 | **PDB header:**transcription<br>**Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9;<br>**PDBTitle:** rna polymerase ii from schizosaccharomyces pombe |
| 8 | c2hu9B_ | Alignment |  | 92.0 | 16 | **PDB header:**metal transport<br>**Chain:** B: **PDB Molecule:**mercuric transport protein periplasmic component;<br>**PDBTitle:** x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain |
| 9 | d1dgsa1 | Alignment |  | 87.8 | 35 | **Fold:**SAM domain-like<br>**Superfamily:**RuvA domain 2-like<br>**Family:**NAD+-dependent DNA ligase, domain 3 |
| 10 | c4a17Y_ | Alignment |  | 79.6 | 30 | **PDB header:**ribosome<br>**Chain:** Y: **PDB Molecule:**rpl37a;<br>**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2. |
| 11 | d1wiia_ | Alignment |  | 79.0 | 29 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Putative zinc binding domain |

| | | | | | | |
|---|---|---|---|---|---|---|
| 12 | d2fiya1 | Alignment |  | 77.6 | 39 | **Fold:**FdhE-like<br>**Superfamily:**FdhE-like<br>**Family:**FdhE-like |
| 13 | c3cc4Z_ | Alignment |  | 75.8 | 33 | **PDB header:**ribosome<br>**Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae;<br>**PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit |
| 14 | c1dgsB_ | Alignment |  | 75.0 | 35 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**dna ligase;<br>**PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis |
| 15 | c1yshD_ | Alignment |  | 74.3 | 27 | **PDB header:**structural protein/rna<br>**Chain:** D: **PDB Molecule:**ribosomal protein l37a;<br>**PDBTitle:** localization and dynamic behavior of ribosomal protein l30e |
| 16 | c2zkrz_ | Alignment |  | 74.0 | 27 | **PDB header:**ribosomal protein/rna<br>**Chain:** Z: **PDB Molecule:**e site t-rna;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 17 | d1vqoz1 | Alignment |  | 73.7 | 35 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L37ae |
| 18 | d2ctda2 | Alignment |  | 72.5 | 50 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 19 | c2qa4Z_ | Alignment |  | 72.3 | 35 | **PDB header:**ribosome<br>**Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae;<br>**PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit |
| 20 | d1jj2y_ | Alignment |  | 71.2 | 27 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L37ae |
| 21 | d1ffkw_ | Alignment | not modelled | 71.0 | 31 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L37ae |
| 22 | c3cngC_ | Alignment | not modelled | 70.7 | 29 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**nudix hydrolase;<br>**PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea |
| 23 | c3gn5B_ | Alignment | not modelled | 64.3 | 25 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021);<br>**PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021) |
| 24 | c2kpiA_ | Alignment | not modelled | 63.1 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein sco3027;<br>**PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58 |
| 25 | c2jr6A_ | Alignment |  | 61.0 | 3 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0434 protein nma0874;<br>**PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32 |
| 26 | c3ndjA_ | Alignment | not modelled | 59.7 | 15 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**methyltransferase;<br>**PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product |
| 27 | c2f9iD_ | Alignment | not modelled | 59.5 | 28 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl<br>**PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 28 | c1v9pB_ | Alignment | not modelled | 59.3 | 35 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**dna ligase;<br>**PDBTitle:** crystal structure of nad+-dependent dna ligase |
| 29 | c2owoA_ | Alignment | not modelled | 59.2 | 28 | **PDB header:**ligase/dna<br>**Chain:** A: **PDB Molecule:**dna ligase;<br>**PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate |
| 30 | c1x31D_ | Alignment | not modelled | 58.6 | 30 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**sarcosine oxidase delta subunit;<br>**PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96 |
| 31 | c2js4A_ | Alignment | not modelled | 58.0 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0434 protein bb2007;<br>**PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54 |
| 32 | c1s1i9_ | Alignment | not modelled | 57.9 | 27 | **PDB header:**ribosome<br>**Chain:** 9: **PDB Molecule:**60s ribosomal protein l43;<br>**PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h. |
| 33 | c2qkdA_ | Alignment | not modelled | 57.9 | 24 | **PDB header:**signaling protein, cell cycle<br>**Chain:** A: **PDB Molecule:**zinc finger protein zpr1;<br>**PDBTitle:** crystal structure of tandem zpr1 domains |
| 34 | d2jnya1 | Alignment | not modelled | 55.4 | 14 | **Fold:**Trm112p-like<br>**Superfamily:**Trm112p-like<br>**Family:**Trm112p-like |
| 35 | d1p91a_ | Alignment | not modelled | 50.3 | 28 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA methyltransferase RlmA |
| 36 | c3jyw9_ | Alignment | not modelled | 46.7 | 27 | **PDB header:**ribosome<br>**Chain:** 9: **PDB Molecule:**60s ribosomal protein l43;<br>**PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution |
| 37 | c2k5cA_ | Alignment | not modelled | 45.8 | 36 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**uncharacterized protein pf0385;<br>**PDBTitle:** nmr structure for pf0385 |
| 38 | c3a44D_ | Alignment | not modelled | 44.2 | 38 | **PDB header:**metal binding protein<br>**Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa;<br>**PDBTitle:** crystal structure of hypa in the dimeric form |
| 39 | d2fu5a1 | Alignment | not modelled | 41.0 | 17 | **Fold:**Mss4-like<br>**Superfamily:**Mss4-like<br>**Family:**RabGEF Mss4 |
| 40 | c2gajA_ | Alignment | not modelled | 40.1 | 27 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**dna topoisomerase i;<br>**PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form |
| 41 | d1hxra_ | Alignment | not modelled | 39.9 | 17 | **Fold:**Mss4-like<br>**Superfamily:**Mss4-like<br>**Family:**RabGEF Mss4 |
| 42 | c2gb5B_ | Alignment | not modelled | 38.8 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**nadh pyrophosphatase;<br>**PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution |
| 43 | d1dl6a_ | Alignment | not modelled | 38.6 | 25 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 44 | d2cona1 | Alignment | not modelled | 38.5 | 22 | **Fold:**Rubredoxin-like<br>**Superfamily:**NOB1 zinc finger-like<br>**Family:**NOB1 zinc finger-like |
| 45 | c2f9yB_ | Alignment | not modelled | 37.3 | 20 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit<br>**PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli |
| 46 | d2f9yb1 | Alignment | not modelled | 37.3 | 20 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Biotin dependent carboxylase carboxyltransferase domain |
| 47 | c2kdxA_ | Alignment | not modelled | 34.4 | 11 | **PDB header:**metal-binding protein<br>**Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein<br>**PDBTitle:** solution structure of hypa protein |
| 48 | c1dvbA_ | Alignment | not modelled | 32.7 | 24 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**rubrerythrin;<br>**PDBTitle:** rubrerythrin |
| 49 | c2adrA_ | Alignment | not modelled | 31.1 | 25 | **PDB header:**transcription regulation<br>**Chain:** A: **PDB Molecule:**adr1;<br>**PDBTitle:** adr1 dna-binding domain from saccharomyces cerevisiae, nmr,2 25 structures |
| 50 | d2pk7a1 | Alignment | not modelled | 30.9 | 14 | **Fold:**Trm112p-like<br>**Superfamily:**Trm112p-like<br>**Family:**Trm112p-like |
| 51 | d2hf1a1 | Alignment | not modelled | 29.5 | 31 | **Fold:**Trm112p-like<br>**Superfamily:**Trm112p-like<br>**Family:**Trm112p-like |
| 52 | c3k7aM_ | Alignment | not modelled | 29.1 | 33 | **PDB header:**transcription<br>**Chain:** M: **PDB Molecule:**transcription initiation factor iib;<br>**PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex |
| 53 | c1llmC_ | Alignment | not modelled | 28.2 | 16 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**chimera of zif23-gcn4; |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | | | | | **PDBTitle:** crystal structure of a zif23-gcn4 chimera bound to dna |
| 54 | c2ghfA_ | Alignment | not modelled | 28.1 | 14 | **PDB header:**transcription, metal binding protein<br>**Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1;<br>**PDBTitle:** solution structure of the complete zinc-finger region of2 human zinc-fingers and homeoboxes 1 (zhx1) |
| 55 | c2cotA_ | Alignment | not modelled | 27.6 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**zinc finger protein 435;<br>**PDBTitle:** solution structure of the first and second zf-c2h2 domain2 of zinc finger protein 435 |
| 56 | d1wj2a_ | Alignment | not modelled | 26.6 | 21 | **Fold:**WRKY DNA-binding domain<br>**Superfamily:**WRKY DNA-binding domain<br>**Family:**WRKY DNA-binding domain |
| 57 | c1wjvA_ | Alignment | not modelled | 26.3 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**cell growth regulating nucleolar protein lyar;<br>**PDBTitle:** solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar |
| 58 | d1pfva3 | Alignment | not modelled | 26.0 | 30 | **Fold:**Rubredoxin-like<br>**Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain<br>**Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain |
| 59 | c2d9kA_ | Alignment | not modelled | 25.9 | 21 | **PDB header:**immune system<br>**Chain:** A: **PDB Molecule:**fln29 gene product;<br>**PDBTitle:** solution structure of the zf-traf domain of fln29 gene2 product |
| 60 | c1x5wA_ | Alignment | not modelled | 25.2 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**zinc finger protein 64, isoforms 1;<br>**PDBTitle:** solution structure of the c2h2 type zinc-binding domain of2 human zinc finger protein 64, isoforms 1 and 2 |
| 61 | d2ct1a1 | Alignment | not modelled | 25.0 | 71 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 62 | d2dlqa2 | Alignment | not modelled | 24.7 | 57 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 63 | c2ct1A_ | Alignment | not modelled | 24.6 | 14 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional repressor ctcf;<br>**PDBTitle:** solution structure of the zinc finger domain of2 transcriptional repressor ctcf protein |
| 64 | c2hr5B_ | Alignment | not modelled | 24.3 | 25 | **PDB header:**metal binding protein<br>**Chain:** B: **PDB Molecule:**rubrerythrin;<br>**PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form |
| 65 | d1pvma3 | Alignment | not modelled | 23.3 | 21 | **Fold:**Rubredoxin-like<br>**Superfamily:**Hypothetical protein Ta0289 C-terminal domain<br>**Family:**Hypothetical protein Ta0289 C-terminal domain |
| 66 | c2yreA_ | Alignment | not modelled | 22.0 | 17 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**f-box only protein 30;<br>**PDBTitle:** solution structure of the zinc finger domains (1-87) from2 human f-box only protein |
| 67 | c1x6eA_ | Alignment | not modelled | 21.7 | 13 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**zinc finger protein 24;<br>**PDBTitle:** solution structures of the c2h2 type zinc finger domain of2 human zinc finger protein 24 |
| 68 | d1nuia2 | Alignment | not modelled | 21.6 | 22 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**DNA primase zinc finger |
| 69 | d1twfi1 | Alignment | not modelled | 21.6 | 19 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 70 | c2aydA_ | Alignment | not modelled | 21.2 | 21 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**wrky transcription factor 1;<br>**PDBTitle:** crystal structure of the c-terminal wrky domainof atwrky1,2 an sa-induced and partially npr1-dependent transcription3 factor |
| 71 | d1pfta_ | Alignment | not modelled | 20.2 | 40 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 72 | d2ey4e1 | Alignment | not modelled | 19.9 | 16 | **Fold:**Rubredoxin-like<br>**Superfamily:**Nop10-like SnoRNP<br>**Family:**Nucleolar RNA-binding protein Nop10-like |
| 73 | c1yuzB_ | Alignment | not modelled | 19.7 | 21 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nigerythrin;<br>**PDBTitle:** partially reduced state of nigerythrin |
| 74 | c3hctA_ | Alignment | not modelled | 19.1 | 13 | **PDB header:**signaling protein/ligase<br>**Chain:** A: **PDB Molecule:**tnf receptor-associated factor 6;<br>**PDBTitle:** crystal structure of traf6 in complex with ubc13 in the p12 space group |
| 75 | c2ja6L_ | Alignment | not modelled | 18.4 | 30 | **PDB header:**transferase<br>**Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 7.7<br>**PDBTitle:** cpd lesion containing rna polymerase ii elongation complex2 b |
| 76 | c1wjpA_ | Alignment | not modelled | 18.4 | 19 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**zinc finger protein 295;<br>**PDBTitle:** solution structure of zf-c2h2 domains from human zinc2 finger protein 295 |
| 77 | d1aaya1 | Alignment | not modelled | 17.9 | 25 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 78 | c2wbtA_ | Alignment | not modelled | 16.4 | 28 | **PDB header:**dna-binding protein<br>**Chain:** A: **PDB Molecule:**b-129;<br>**PDBTitle:** the structure of a double c2h2 zinc finger protein from a2 hyperthermophilic archaeal virus in the absence of dna |
| | | | | | | **Fold:**Rubredoxin-like |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| 79 | d2apob1 | Alignment | not modelled | 15.5 | 16 | **Superfamily:**Nop10-like SnoRNP<br>**Family:**Nucleolar RNA-binding protein Nop10-like |
| 80 | d6rxna_ | Alignment | not modelled | 15.2 | 33 | **Fold:**Rubredoxin-like<br>**Superfamily:**Rubredoxin-like<br>**Family:**Rubredoxin |
| 81 | d1a1ia1 | Alignment | not modelled | 15.1 | 25 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 82 | d2qam01 | Alignment | not modelled | 15.0 | 0 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L32p |
| 83 | c3htkC_ | Alignment | not modelled | 15.0 | 22 | **PDB header:**recombination/replication/ligase<br>**Chain:** C: **PDB Molecule:**e3 sumo-protein ligase mms21;<br>**PDBTitle:** crystal structure of mms21 and smc5 complex |
| 84 | c2yu4A_ | Alignment | not modelled | 14.9 | 33 | **PDB header:**apoptosis<br>**Chain:** A: **PDB Molecule:**e3 sumo-protein ligase nse2;<br>**PDBTitle:** solution structure of the sp-ring domain in non-smc element2 2 homolog (mms21, s. cerevisiae) |
| 85 | d1a1ha1 | Alignment | not modelled | 14.8 | 25 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 86 | c1nltA_ | Alignment | not modelled | 14.3 | 15 | **PDB header:**protein transport<br>**Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5;<br>**PDBTitle:** the crystal structure of hsp40 ydj1 |
| 87 | c3lpeF_ | Alignment | not modelled | 14.3 | 25 | **PDB header:**transferase<br>**Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e'';<br>**PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii |
| 88 | c2d9hA_ | Alignment | not modelled | 14.1 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**zinc finger protein 692;<br>**PDBTitle:** solution structure of the forth and fifth zf-c2h2 domains2 of zinc finger protein 692 |
| 89 | d1f2ig1 | Alignment | not modelled | 14.0 | 27 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 90 | d1lv3a_ | Alignment | not modelled | 13.9 | 30 | **Fold:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Superfamily:**Glucocorticoid receptor-like (DNA-binding domain)<br>**Family:**Hypothetical zinc finger protein YacG |
| 91 | c3h0gL_ | Alignment | not modelled | 13.3 | 33 | **PDB header:**transcription<br>**Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii<br>**PDBTitle:** rna polymerase ii from schizosaccharomyces pombe |
| 92 | c3iz5p_ | Alignment | not modelled | 13.3 | 23 | **PDB header:**ribosome<br>**Chain:** P: **PDB Molecule:**60s ribosomal protein l15 (l15e);<br>**PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 93 | d2j0151 | Alignment | not modelled | 12.9 | 33 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L32p |
| 94 | d1nnqa2 | Alignment | not modelled | 12.6 | 21 | **Fold:**Rubredoxin-like<br>**Superfamily:**Rubredoxin-like<br>**Family:**Rubredoxin |
| 95 | d2zjrz1 | Alignment | not modelled | 12.5 | 30 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L32p |
| 96 | d1a1ga1 | Alignment | not modelled | 12.4 | 25 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 97 | c2bx9J_ | Alignment | not modelled | 12.2 | 27 | **PDB header:**transcription regulation<br>**Chain:** J: **PDB Molecule:**tryptophan rna-binding attenuator protein-inhibitory<br>**PDBTitle:** crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions |
| 98 | d1yuza2 | Alignment | not modelled | 12.1 | 38 | **Fold:**Rubredoxin-like<br>**Superfamily:**Rubredoxin-like<br>**Family:**Rubredoxin |
| 99 | c3alrA_ | Alignment | not modelled | 12.1 | 50 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**nanos protein;<br>**PDBTitle:** crystal structure of nanos |