# Phyre2

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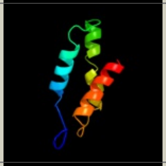
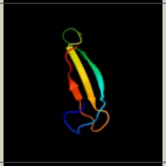
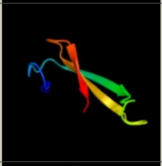
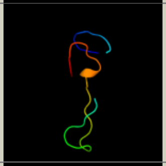
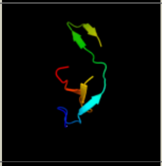
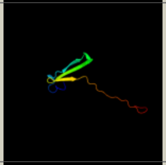
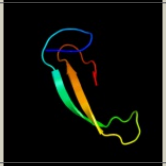
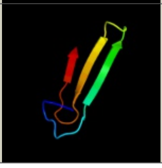
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0A8D0 |
| Date | Thu Jan 5 11:07:30 GMT 2012 |
| Unique Job ID | 8d0bfbaea44db975 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3r1rB_ | Alignment |  | 98.4 | 19 | **PDB header:**complex (oxidoreductase/peptide)<br>**Chain:** B: **PDB Molecule:**ribonucleotide reductase r1 protein;<br>**PDBTitle:** ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli |
| 2 | d1rlra1 | Alignment |  | 97.7 | 15 | **Fold:**R1 subunit of ribonucleotide reductase, N-terminal domain<br>**Superfamily:**R1 subunit of ribonucleotide reductase, N-terminal domain<br>**Family:**R1 subunit of ribonucleotide reductase, N-terminal domain |
| 3 | d1qypa_ | Alignment |  | 95.4 | 21 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 4 | d1twfi2 | Alignment |  | 94.6 | 29 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 5 | c3k7aM_ | Alignment |  | 93.8 | 31 | **PDB header:**transcription<br>**Chain:** M: **PDB Molecule:**transcription initiation factor iib;<br>**PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex |
| 6 | c1i3ql_ | Alignment |  | 93.3 | 29 | **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 | d1tfia_ | Alignment |  | 93.0 | 23 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 8 | c3gn5B_ | Alignment |  | 92.9 | 24 | **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) |
| 9 | c2gb5B_ | Alignment |  | 91.6 | 14 | **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 |
| 10 | c3h0gI_ | Alignment |  | 91.3 | 22 | **PDB header:**transcription<br>**Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9;<br>**PDBTitle:** rna polymerase ii from schizosaccharomyces pombe |
| 11 | d1wiia_ | Alignment |  | 89.8 | 29 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Putative zinc binding domain |

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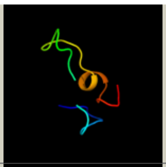
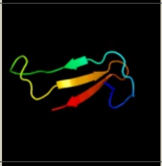
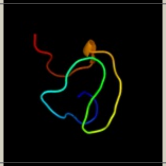
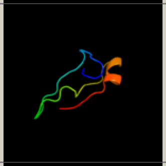
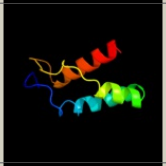
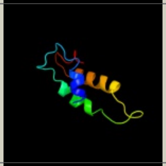
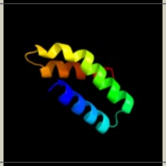
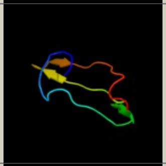
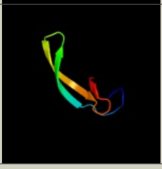
| 12 | d1dl6a_ | Alignment |  | 86.9 | 27 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 13 | d2fiya1 | Alignment |  | 83.6 | 20 | **Fold:**FdhE-like<br>**Superfamily:**FdhE-like<br>**Family:**FdhE-like |
| 14 | d1pfva3 | Alignment |  | 78.2 | 29 | **Fold:**Rubredoxin-like<br>**Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain<br>**Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain |
| 15 | c2e9hA_ | Alignment |  | 76.6 | 31 | **PDB header:**translation<br>**Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5;<br>**PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5 |
| 16 | d1rj9b1 | Alignment |  | 75.9 | 18 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Domain of the SRP/SRP receptor G-proteins<br>**Family:**Domain of the SRP/SRP receptor G-proteins |
| 17 | c3hnfA_ | Alignment |  | 75.2 | 18 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large subunit;<br>**PDBTitle:** crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp |
| 18 | d1ls1a1 | Alignment |  | 74.6 | 21 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Domain of the SRP/SRP receptor G-proteins<br>**Family:**Domain of the SRP/SRP receptor G-proteins |
| 19 | c1nuiA_ | Alignment |  | 73.6 | 29 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**dna primase/helicase;<br>**PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein |
| 20 | c3cngC_ | Alignment |  | 73.3 | 21 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**nudix hydrolase;<br>**PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea |
| 21 | c3ndjA_ | Alignment | not modelled | 73.2 | 21 | **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 |
| 22 | d1pfta_ | Alignment | not modelled | 72.7 | 31 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 23 | d1j8yf1 | Alignment | not modelled | 70.6 | 19 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Domain of the SRP/SRP receptor G-proteins<br>**Family:**Domain of the SRP/SRP receptor G-proteins |
| 24 | c2qkdA_ | Alignment | not modelled | 70.4 | 18 | **PDB header:**signaling protein, cell cycle<br>**Chain:** A: **PDB Molecule:**zinc finger protein zpr1;<br>**PDBTitle:** crystal structure of tandem zpr1 domains |
| 25 | c2elpA_ | Alignment | not modelled | 68.9 | 50 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**zinc finger protein 406;<br>**PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406 |
| 26 | d1wgwa_ | Alignment | not modelled | 68.7 | 21 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Domain of the SRP/SRP receptor G-proteins<br>**Family:**Domain of the SRP/SRP receptor G-proteins |
| 27 | d1vqoz1 | Alignment | not modelled | 67.7 | 46 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L37ae |
| 28 | c4a17Y_ | Alignment | not modelled | 66.5 | 39 | **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. |
| | | | | | | **PDB header:**ribosomal protein/rna |

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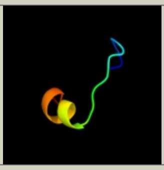
| 29 | c2zkrz_ | Alignment | not modelled | 65.9 | 33 | **Chain:** Z: **PDB Molecule:**e site t-rna;<br>**PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map |
| 30 | c2qa4Z_ | Alignment | not modelled | 65.5 | 46 | **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 |
| 31 | c1yshD_ | Alignment | not modelled | 65.3 | 33 | **PDB header:**structural protein/rna<br>**Chain:** D: **PDB Molecule:**ribosomal protein l37a;<br>**PDBTitle:** localization and dynamic behavior of ribosomal protein l30e |
| 32 | d2k4xa1 | Alignment | not modelled | 64.6 | 35 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein S27a |
| 33 | d1jj2y_ | Alignment | not modelled | 64.5 | 25 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L37ae |
| 34 | c2l7xA_ | Alignment | not modelled | 64.5 | 41 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**envelope glycoprotein;<br>**PDBTitle:** crimean congo hemorrhagic fever gn zinc finger |
| 35 | c3jyw9_ | Alignment | not modelled | 62.8 | 33 | **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 |
| 36 | c1s1i9_ | Alignment | not modelled | 62.6 | 33 | **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. |
| 37 | d1ffkw_ | Alignment | not modelled | 62.2 | 25 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L37ae |
| 38 | c3cc4Z_ | Alignment | not modelled | 61.4 | 48 | **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 |
| 39 | c2hu9B_ | Alignment | not modelled | 54.8 | 38 | **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 |
| 40 | d1vd4a_ | Alignment |  | 53.4 | 42 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zinc beta-ribbon<br>**Family:**Transcriptional factor domain |
| 41 | d1g2ra_ | Alignment | not modelled | 53.2 | 16 | **Fold:**YlxR-like<br>**Superfamily:**YlxR-like<br>**Family:**YlxR-like |
| 42 | c2f9iD_ | Alignment | not modelled | 53.0 | 27 | **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 |
| 43 | d1qzxa1 | Alignment | not modelled | 52.3 | 17 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**Domain of the SRP/SRP receptor G-proteins<br>**Family:**Domain of the SRP/SRP receptor G-proteins |
| 44 | c3eswA_ | Alignment | not modelled | 51.5 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine<br>**PDBTitle:** complex of yeast pngase with glcnac2-iac. |
| 45 | c2aklA_ | Alignment | not modelled | 50.5 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**phna-like protein pa0128;<br>**PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa |
| 46 | c2xigA_ | Alignment | not modelled | 50.1 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**ferric uptake regulation protein;<br>**PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites |
| 47 | d2cona1 | Alignment | not modelled | 50.0 | 19 | **Fold:**Rubredoxin-like<br>**Superfamily:**NOB1 zinc finger-like<br>**Family:**NOB1 zinc finger-like |
| 48 | c1x6eA_ | Alignment | not modelled | 48.9 | 15 | **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 |
| 49 | c2kvfA_ | Alignment | not modelled | 48.5 | 50 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32;<br>**PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein |
| 50 | d1x3za1 | Alignment | not modelled | 48.2 | 10 | **Fold:**Cysteine proteinases<br>**Superfamily:**Cysteine proteinases<br>**Family:**Transglutaminase core |
| 51 | c2jq5A_ | Alignment | not modelled | 46.6 | 40 | **PDB header:**structural genomics<br>**Chain:** A: **PDB Molecule:**sec-c motif;<br>**PDBTitle:** solution structure of rpa3114, a sec-c motif containing2 protein from rhodopseudomonas palustris; northeast3 structural genomics consortium target rpt5 / ontario4 center for structural proteomics target rp3097 |
| 52 | c2kaeA_ | Alignment | not modelled | 45.3 | 18 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**gata-type transcription factor; |

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| | | | | | | **PDBTitle:** data-driven model of med1:dna complex |
| 53 | c1meyG_ | Alignment | not modelled | 45.0 | 27 | **PDB header:**transferase/dna<br>**Chain:** G: **PDB Molecule:**consensus zinc finger;<br>**PDBTitle:** crystal structure of a designed zinc finger protein bound2 to dna |
| 54 | c2dmiA_ | Alignment | not modelled | 43.9 | 7 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**teashirt homolog 3;<br>**PDBTitle:** solution structure of the first and the second zf-c2h2 like2 domains of human teashirt homolog 3 |
| 55 | c2jneA_ | Alignment | not modelled | 43.4 | 40 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**hypothetical protein yfgj;<br>**PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317. |
| 56 | d2jnea1 | Alignment | not modelled | 43.4 | 40 | **Fold:**Rubredoxin-like<br>**Superfamily:**YfgJ-like<br>**Family:**YfgJ-like |
| 57 | c2f9yB_ | Alignment | not modelled | 43.3 | 21 | **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 |
| 58 | d2f9yb1 | Alignment | not modelled | 43.3 | 21 | **Fold:**ClpP/crotonase<br>**Superfamily:**ClpP/crotonase<br>**Family:**Biotin dependent carboxylase carboxyltransferase domain |
| 59 | c2ctdA_ | Alignment | not modelled | 42.9 | 23 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**zinc finger protein 512;<br>**PDBTitle:** solution structure of two zf-c2h2 domains from human zinc2 finger protein 512 |
| 60 | c2cotA_ | Alignment | not modelled | 42.4 | 15 | **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 |
| 61 | d1tlqa_ | Alignment | not modelled | 42.4 | 20 | **Fold:**YutG-like<br>**Superfamily:**YutG-like<br>**Family:**YutG-like |
| 62 | c1tlqA_ | Alignment | not modelled | 42.4 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein ypjq;<br>**PDBTitle:** crystal structure of protein ypjq from bacillus subtilis, pfam duf64 |
| 63 | d2cota1 | Alignment | not modelled | 42.2 | 30 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 64 | d1x6ea2 | Alignment | not modelled | 42.1 | 40 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 65 | c3hi2C_ | Alignment | not modelled | 41.6 | 57 | **PDB header:**dna binding protein/toxin<br>**Chain:** C: **PDB Molecule:**hth-type transcriptional regulator mqsa(ygit);<br>**PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022) |
| 66 | c3c8fA_ | Alignment | not modelled | 41.2 | 45 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyruvate formate-lyase 1-activating enzyme;<br>**PDBTitle:** 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet |
| 67 | c3g9yA_ | Alignment | not modelled | 41.0 | 30 | **PDB header:**transcription/rna<br>**Chain:** A: **PDB Molecule:**zinc finger ran-binding domain-containing protein 2;<br>**PDBTitle:** crystal structure of the second zinc finger from zranb2/znf265 bound2 to 6 nt ssrna sequence agguaa |
| 68 | d1a1ia2 | Alignment | not modelled | 40.8 | 40 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 69 | c1jocA_ | Alignment | not modelled | 40.8 | 36 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**early endosomal autoantigen 1;<br>**PDBTitle:** eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate |
| 70 | d1llmc2 | Alignment | not modelled | 40.8 | 30 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 71 | d1srka_ | Alignment | not modelled | 39.5 | 45 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 72 | c3zyqA_ | Alignment | not modelled | 39.2 | 25 | **PDB header:**signaling<br>**Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase<br>**PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution |
| 73 | d1u85a1 | Alignment | not modelled | 38.6 | 36 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 74 | c2gqjA_ | Alignment | not modelled | 38.1 | 20 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**zinc finger protein kiaa1196;<br>**PDBTitle:** solution structure of the two zf-c2h2 like domains(493-575)2 of human zinc finger protein kiaa1196 |
| 75 | c1rikA_ | Alignment | not modelled | 38.0 | 40 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**e6apc1 peptide;<br>**PDBTitle:** e6-binding zinc finger (e6apc1) |
| 76 | d1p91a_ | Alignment | not modelled | 37.6 | 16 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**rRNA methyltransferase RlmA |
| | | | | | | **Fold:**beta-beta-alpha zinc fingers |

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| 77 | d1xf7a_ | Alignment | not modelled | 37.4 | 40 | **Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 78 | c1xf7A_ | Alignment | not modelled | 37.4 | 40 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**wilms' tumor protein;<br>**PDBTitle:** high resolution nmr structure of the wilms' tumor2 suppressor protein (wt1) finger 3 |
| 79 | c2k2dA_ | Alignment | not modelled | 36.7 | 33 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain-<br>**PDBTitle:** solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c |
| 80 | d1m2ka_ | Alignment | not modelled | 36.3 | 14 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Sir2 family of transcriptional regulators |
| 81 | d1x6ea1 | Alignment | not modelled | 36.3 | 27 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 82 | c2elsA_ | Alignment | not modelled | 36.3 | 36 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**zinc finger protein 406;<br>**PDBTitle:** solution structure of the 2nd c2h2 zinc finger of human2 zinc finger protein 406 |
| 83 | c2lk0A_ | Alignment | not modelled | 36.0 | 37 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**rna-binding protein 5;<br>**PDBTitle:** solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5 |
| 84 | c1areA_ | Alignment | not modelled | 35.2 | 40 | **PDB header:**transcription regulation<br>**Chain:** A: **PDB Molecule:**yeast transcription factor adr1;<br>**PDBTitle:** structures of dna-binding mutant zinc finger domains:2 implications for dna binding |
| 85 | c3lpeF_ | Alignment | not modelled | 34.5 | 30 | **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 |
| 86 | d1p7aa_ | Alignment | not modelled | 34.3 | 36 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 87 | c2epsA_ | Alignment | not modelled | 33.9 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**poz-, at hook-, and zinc finger-containing<br>**PDBTitle:** solution structure of the 4th zinc finger domain of zinc2 finger protein 278 |
| 88 | d1a1ia3 | Alignment | not modelled | 33.6 | 30 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 89 | d1joca1 | Alignment | not modelled | 33.6 | 35 | **Fold:**FYVE/PHD zinc finger<br>**Superfamily:**FYVE/PHD zinc finger<br>**Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain |
| 90 | c2jrpA_ | Alignment | not modelled | 33.6 | 32 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative cytoplasmic protein;<br>**PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86 |
| 91 | c1dgsB_ | Alignment | not modelled | 33.0 | 48 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**dna ligase;<br>**PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis |
| 92 | c1ltlE_ | Alignment | not modelled | 32.9 | 16 | **PDB header:**replication<br>**Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54);<br>**PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum |
| 93 | c2ztgA_ | Alignment | not modelled | 32.9 | 22 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**alanyl-trna synthetase;<br>**PDBTitle:** crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa |
| 94 | d1lkoa2 | Alignment | not modelled | 32.8 | 24 | **Fold:**Rubredoxin-like<br>**Superfamily:**Rubredoxin-like<br>**Family:**Rubredoxin |
| 95 | c1va3A_ | Alignment | not modelled | 32.8 | 40 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription factor sp1;<br>**PDBTitle:** solution structure of transcription factor sp1 dna binding2 domain (zinc finger 3) |
| 96 | d2dula1 | Alignment | not modelled | 32.1 | 11 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**TRM1-like |
| 97 | c1sp1A_ | Alignment | not modelled | 32.0 | 40 | **PDB header:**zinc finger<br>**Chain:** A: **PDB Molecule:**sp1f3;<br>**PDBTitle:** nmr structure of a zinc finger domain from transcription2 factor sp1f3, minimized average structure |
| 98 | d1sp1a_ | Alignment | not modelled | 32.0 | 40 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 99 | c2hl7A_ | Alignment | not modelled | 31.9 | 40 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh;<br>**PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa |
| 100 | d2j0151 | Alignment | not modelled | 31.9 | 29 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L32p |
| 101 | c1v9pB_ | Alignment | not modelled | 31.8 | 48 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**dna ligase;<br>**PDBTitle:** crystal structure of nad+-dependent dna ligase |
| 102 | c2l8eA_ | Alignment | not modelled | 31.8 | 28 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**polyhomeotic-like protein 1;<br>**PDBTitle:** solution nmr structure of fcs domain of human polyhomeotic homolog 12 (hph1) |

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| 103 | c3f2cA_ | Alignment | not modelled | 31.6 | 25 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc;<br>**PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn |
| 104 | c3floD_ | Alignment | not modelled | 31.6 | 24 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**dna polymerase alpha catalytic subunit a;<br>**PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit |
| 105 | d2zjrz1 | Alignment | not modelled | 31.5 | 24 | **Fold:**Rubredoxin-like<br>**Superfamily:**Zn-binding ribosomal proteins<br>**Family:**Ribosomal protein L32p |
| 106 | c1z2qA_ | Alignment | not modelled | 31.4 | 31 | **PDB header:**membrane protein<br>**Chain:** A: **PDB Molecule:**lm5-1;<br>**PDBTitle:** high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major |
| 107 | c2kw0A_ | Alignment | not modelled | 31.4 | 30 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ccmh protein;<br>**PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli |
| 108 | c3pkiF_ | Alignment | not modelled | 31.3 | 21 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6;<br>**PDBTitle:** human sirt6 crystal structure in complex with adp ribose |
| 109 | c1rimA_ | Alignment | not modelled | 31.2 | 40 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**e6apc2 peptide;<br>**PDBTitle:** e6-binding zinc finger (e6apc2) |
| 110 | c2yteA_ | Alignment | not modelled | 31.1 | 36 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**zinc finger protein 473;<br>**PDBTitle:** solution structure of the c2h2 type zinc finger (region 484-2 512) of human zinc finger protein 473 |
| 111 | d2gmga1 | Alignment | not modelled | 31.0 | 24 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**PF0610-like |
| 112 | d1enwa_ | Alignment | not modelled | 31.0 | 10 | **Fold:**RuvA C-terminal domain-like<br>**Superfamily:**Elongation factor TFIIS domain 2<br>**Family:**Elongation factor TFIIS domain 2 |
| 113 | c1ardA_ | Alignment | not modelled | 30.8 | 40 | **PDB header:**transcription regulation<br>**Chain:** A: **PDB Molecule:**yeast transcription factor adr1;<br>**PDBTitle:** structures of dna-binding mutant zinc finger domains:2 implications for dna binding |
| 114 | d2adra1 | Alignment | not modelled | 30.6 | 40 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 115 | d2epqa1 | Alignment | not modelled | 30.4 | 33 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 116 | d1ltla_ | Alignment | not modelled | 30.2 | 17 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain |
| 117 | c2eltA_ | Alignment | not modelled | 30.1 | 18 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**zinc finger protein 406;<br>**PDBTitle:** solution structure of the 3rd c2h2 zinc finger of human2 zinc finger protein 406 |
| 118 | d1k81a_ | Alignment | not modelled | 29.8 | 50 | **Fold:**Zinc-binding domain of translation initiation factor 2 beta<br>**Superfamily:**Zinc-binding domain of translation initiation factor 2 beta<br>**Family:**Zinc-binding domain of translation initiation factor 2 beta |
| 119 | d2ct1a2 | Alignment | not modelled | 29.8 | 45 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 120 | d1ubdc2 | Alignment | not modelled | 29.2 | 31 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |