# Phyre$^2$

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|---|---|
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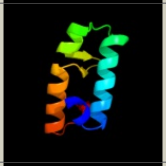
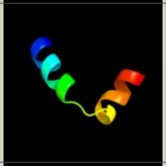
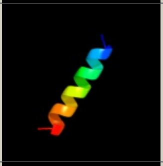
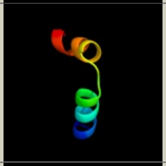
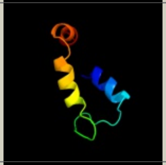
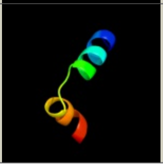
| Description | P75617 |
| Date | Thu Jan 5 12:12:48 GMT 2012 |
| Unique Job ID | 6c6d7768c1f55c96 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1oeya_ | Alignment |  | 77.0 | 37 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**CAD & PB1 domains<br>**Family:**PB1 domain |
| 2 | d2o3la1 | Alignment |  | 53.0 | 16 | **Fold:**Left-handed superhelix<br>**Superfamily:**BH3980-like<br>**Family:**BH3980-like |
| 3 | d1gt0d_ | Alignment |  | 50.3 | 26 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 4 | c2wvrB_ | Alignment |  | 49.8 | 11 | **PDB header:**replication<br>**Chain:** B: **PDB Molecule:**geminin;<br>**PDBTitle:** human cdt1:geminin complex |
| 5 | d1wgfa_ | Alignment |  | 47.1 | 22 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 6 | d2hh6a1 | Alignment |  | 46.6 | 14 | **Fold:**Left-handed superhelix<br>**Superfamily:**BH3980-like<br>**Family:**BH3980-like |
| 7 | c2e6oA_ | Alignment |  | 46.0 | 26 | **PDB header:**transcription, cell cycle<br>**Chain:** A: **PDB Molecule:**hmg box-containing protein 1;<br>**PDBTitle:** solution structure of the hmg box domain from human hmg-box2 transcription factor 1 |
| 8 | c2zxxA_ | Alignment |  | 44.4 | 11 | **PDB header:**cell cycle/replication<br>**Chain:** A: **PDB Molecule:**geminin;<br>**PDBTitle:** crystal structure of cdt1/geminin complex |
| 9 | c3u2bC_ | Alignment |  | 44.3 | 17 | **PDB header:**transcription/dna<br>**Chain:** C: **PDB Molecule:**transcription factor sox-4;<br>**PDBTitle:** structure of the sox4 hmg domain bound to dna |
| 10 | d2lefa_ | Alignment |  | 42.8 | 17 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 11 | c2eqzA_ | Alignment |  | 42.0 | 22 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**high mobility group protein b3;<br>**PDBTitle:** solution structure of the first hmg-box domain from high2 mobility group protein b3 |

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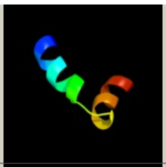
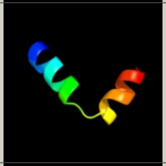
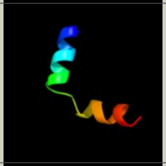
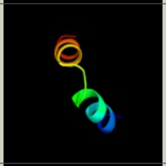
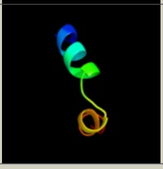
| 12 | c1j3xA_ | Alignment |  | 41.5 | 22 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**high mobility group protein 2;<br>**PDBTitle:** solution structure of the n-terminal domain of the hmgb2 |
| 13 | d1j3xa_ | Alignment |  | 41.5 | 22 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 14 | d2gzka2 | Alignment |  | 40.1 | 26 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 15 | c1hryA_ | Alignment |  | 40.1 | 26 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**human sry;<br>**PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multid-dimensional heteronuclear-edited and-filtered nmr |
| 16 | c1hrzA_ | Alignment |  | 40.1 | 26 | **PDB header:**dna binding protein/dna<br>**Chain:** A: **PDB Molecule:**human sry;<br>**PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multi-dimensional heteronuclear-edited and-filtered nmr |
| 17 | c2cs1A_ | Alignment |  | 39.3 | 22 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**pms1 protein homolog 1;<br>**PDBTitle:** solution structure of the hmg domain of human dna mismatch2 repair protein |
| 18 | d1j46a_ | Alignment |  | 39.2 | 26 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 19 | c2d7lA_ | Alignment |  | 38.3 | 4 | **PDB header:**gene regulation, dna binding protein<br>**Chain:** A: **PDB Molecule:**wd repeat and hmg-box dna binding protein 1;<br>**PDBTitle:** solution structure of the hmg box domain from human wd2 repeat and hmg-box dna binding protein 1 |
| 20 | c2yulA_ | Alignment |  | 38.3 | 26 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription factor sox-17;<br>**PDBTitle:** solution structure of the hmg box of human transcription2 factor sox-17 |
| 21 | c1wz6A_ | Alignment | not modelled | 37.4 | 22 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**hmg-box transcription factor bbx;<br>**PDBTitle:** solution structure of the hmg_box domain of murine bobby2 sox homolog |
| 22 | c3fghA_ | Alignment | not modelled | 35.7 | 13 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial;<br>**PDBTitle:** human mitochondrial transcription factor a box b |
| 23 | c2crjA_ | Alignment | not modelled | 33.0 | 26 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin-<br>**PDBTitle:** solution structure of the hmg domain of mouse hmg domain2 protein hmgx2 |
| 24 | c1hmfA_ | Alignment | not modelled | 31.5 | 17 | **PDB header:**dna-binding<br>**Chain:** A: **PDB Molecule:**high mobility group protein fragment-b;<br>**PDBTitle:** structure of the hmg box motif in the b-domain of hmg1 |
| 25 | d1hmfa_ | Alignment | not modelled | 31.5 | 17 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 26 | d1jhga_ | Alignment | not modelled | 30.5 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**TrpR-like<br>**Family:**Trp repressor, TrpR |
| 27 | d1lwma_ | Alignment | not modelled | 30.0 | 26 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 28 | c2co9A_ | Alignment | not modelled | 28.5 | 22 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox;<br>**PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse |
|  |  |  |  |  |  | **PDB header:**de novo protein |

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| 29 | c2jvfA_ | Alignment | not modelled | 28.2 | 28 | **Chain:** A: **PDB Molecule:**de novo protein m7;<br>**PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein |
| 30 | d1v54m_ | Alignment | not modelled | 28.0 | 18 | **Fold:**Single transmembrane helix<br>**Superfamily:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)<br>**Family:**Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) |
| 31 | c1qysA_ | Alignment | not modelled | 27.7 | 13 | **PDB header:**de novo protein<br>**Chain:** A: **PDB Molecule:**top7;<br>**PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold |
| 32 | d1i11a_ | Alignment | not modelled | 27.2 | 26 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 33 | c1aabA_ | Alignment | not modelled | 27.0 | 22 | **PDB header:**dna-binding<br>**Chain:** A: **PDB Molecule:**high mobility group protein;<br>**PDBTitle:** nmr structure of rat hmg1 hmga fragment |
| 34 | d1aaba_ | Alignment | not modelled | 27.0 | 22 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 35 | d1k99a_ | Alignment | not modelled | 26.0 | 22 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 36 | d1ckta_ | Alignment | not modelled | 26.0 | 22 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 37 | d2o4ta1 | Alignment | not modelled | 25.9 | 16 | **Fold:**Left-handed superhelix<br>**Superfamily:**BH3980-like<br>**Family:**BH3980-like |
| 38 | d1hsma_ | Alignment | not modelled | 24.2 | 17 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 39 | d1j3da_ | Alignment | not modelled | 22.5 | 17 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 40 | c2qguA_ | Alignment | not modelled | 22.4 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**probable signal peptide protein;<br>**PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89 |
| 41 | d1r8ja1 | Alignment | not modelled | 22.2 | 13 | **Fold:**KaiA/RbsU domain<br>**Superfamily:**KaiA/RbsU domain<br>**Family:**Circadian clock protein KaiA, C-terminal domain |
| 42 | c3cxjB_ | Alignment | not modelled | 21.7 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus |
| 43 | c3frwF_ | Alignment | not modelled | 20.8 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** F: **PDB Molecule:**putative trp repressor protein;<br>**PDBTitle:** crystal structure of putative trpr protein from ruminococcus obeum |
| 44 | d1puza_ | Alignment | not modelled | 20.8 | 16 | **Fold:**YgfY-like<br>**Superfamily:**YgfY-like<br>**Family:**YgfY-like |
| 45 | c1e1hD_ | Alignment | not modelled | 20.4 | 42 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**botulinum neurotoxin type a light chain;<br>**PDBTitle:** crystal structure of recombinant botulinum neurotoxin type2 a light chain, self-inhibiting zn endopeptidase. |
| 46 | d1cc5a_ | Alignment | not modelled | 20.0 | 19 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**monodomain cytochrome c |
| 47 | d1v64a_ | Alignment | not modelled | 19.2 | 13 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 48 | d1gl4a1 | Alignment | not modelled | 18.7 | 35 | **Fold:**GFP-like<br>**Superfamily:**GFP-like<br>**Family:**Domain G2 of nidogen-1 |
| 49 | d1v63a_ | Alignment | not modelled | 18.7 | 9 | **Fold:**HMG-box<br>**Superfamily:**HMG-box<br>**Family:**HMG-box |
| 50 | c1x6iB_ | Alignment | not modelled | 18.3 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical protein ygfy;<br>**PDBTitle:** crystal structure of ygfy from escherichia coli |
| 51 | d1sv1a_ | Alignment | not modelled | 18.0 | 13 | **Fold:**KaiA/RbsU domain<br>**Superfamily:**KaiA/RbsU domain<br>**Family:**Circadian clock protein KaiA, C-terminal domain |
| 52 | c2awyB_ | Alignment | not modelled | 17.7 | 11 | **PDB header:**oxygen storage/transport<br>**Chain:** B: **PDB Molecule:**hemerythrin-like domain protein dcrh;<br>**PDBTitle:** met-dcrh-hr |
| 53 | c2y69Z_ | Alignment | not modelled | 17.6 | 19 | **PDB header:**electron transport<br>**Chain:** Z: **PDB Molecule:**cytochrome c oxidase polypeptide 8h;<br>**PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen |
| 54 | c2l66B_ | Alignment | not modelled | 17.1 | 60 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**transcriptional regulator, abrb family;<br>**PDBTitle:** the dna-recognition fold of sso7c4 suggests a new member of spovt-abrb2 superfamily from archaea. |
| 55 | c1rh1A_ | Alignment | not modelled | 16.9 | 14 | **PDB header:**antibiotic<br>**Chain:** A: **PDB Molecule:**colicin b;<br>**PDBTitle:** crystal structure of the cytotoxic bacterial protein2 |

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| | | | | | | colicin b at 2.5 a resolution |
| 56 | c3lisB_ | Alignment | not modelled | 16.9 | 16 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**csp231i c protein;<br>**PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form) |
| 57 | c2rlwA_ | Alignment | not modelled | 16.6 | 30 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**plnf;<br>**PDBTitle:** three-dimensional structure of the two peptides that2 constitute the two-peptide bacteriocin plantaracin ef |
| 58 | c1h4uA_ | Alignment | not modelled | 16.5 | 35 | **PDB header:**extracellular matrix protein<br>**Chain:** A: **PDB Molecule:**nidogen-1;<br>**PDBTitle:** domain g2 of mouse nidogen-1 |
| 59 | d2je8a5 | Alignment | not modelled | 16.1 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-glycanases |
| 60 | d1vp8a_ | Alignment | not modelled | 16.1 | 21 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**MTH1675-like |
| 61 | c3korD_ | Alignment | not modelled | 16.0 | 19 | **PDB header:**transcription<br>**Chain:** D: **PDB Molecule:**possible trp repressor;<br>**PDBTitle:** crystal structure of a putative trp repressor from staphylococcus2 aureus |
| 62 | d2al3a1 | Alignment | not modelled | 15.7 | 14 | **Fold:**beta-Grasp (ubiquitin-like)<br>**Superfamily:**Ubiquitin-like<br>**Family:**UBX domain |
| 63 | d2akja1 | Alignment | not modelled | 15.5 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like<br>**Family:**Duplicated SiR/NiR-like domains 1 and 3 |
| 64 | d1kx7a_ | Alignment | not modelled | 14.9 | 11 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**monodomain cytochrome c |
| 65 | c2lm4A_ | Alignment | not modelled | 14.6 | 26 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**succinate dehydrogenase assembly factor 2, mitochondrial;<br>**PDBTitle:** solution nmr structure of mitochondrial succinate dehydrogenase2 assembly factor 2 from saccharomyces cerevisiae, northeast structural3 genomics consortium target yt682a |
| 66 | c2jr5A_ | Alignment | not modelled | 14.4 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0350 protein vc_2471;<br>**PDBTitle:** solution structure of upf0350 protein vc_2471. northeast2 structural genomics target vcr36 |
| 67 | d1ctda_ | Alignment | not modelled | 14.4 | 38 | **Fold:**EF Hand-like<br>**Superfamily:**EF-hand<br>**Family:**Calmodulin-like |
| 68 | d1tlha_ | Alignment | not modelled | 13.8 | 16 | **Fold:**Anti-sigma factor AsiA<br>**Superfamily:**Anti-sigma factor AsiA<br>**Family:**Anti-sigma factor AsiA |
| 69 | c1r8jB_ | Alignment | not modelled | 13.8 | 13 | **PDB header:**circadian clock protein<br>**Chain:** B: **PDB Molecule:**kaia;<br>**PDBTitle:** crystal structure of circadian clock protein kaia from2 synechococcus elongatus |
| 70 | c1ojhK_ | Alignment | not modelled | 13.7 | 17 | **PDB header:**protein binding<br>**Chain:** K: **PDB Molecule:**nbla;<br>**PDBTitle:** crystal structure of nbla from pcc 7120 |
| 71 | d1m47a_ | Alignment | not modelled | 13.7 | 24 | **Fold:**4-helical cytokines<br>**Superfamily:**4-helical cytokines<br>**Family:**Short-chain cytokines |
| 72 | c2nxbB_ | Alignment | not modelled | 13.1 | 13 | **PDB header:**signaling protein<br>**Chain:** B: **PDB Molecule:**bromodomain-containing protein 3;<br>**PDBTitle:** crystal structure of human bromodomain containing protein 3 (brd3) |
| 73 | d1ojha_ | Alignment | not modelled | 12.5 | 17 | **Fold:**NblA-like<br>**Superfamily:**NblA-like<br>**Family:**NblA-like |
| 74 | c3lpgA_ | Alignment | not modelled | 12.3 | 15 | **PDB header:**hydrolase/hydrolase inhibitor<br>**Chain:** A: **PDB Molecule:**beta-glucuronidase;<br>**PDBTitle:** structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3 2-dihydroquinolin-3-yl)methyl)urea |
| 75 | c2je8B_ | Alignment | not modelled | 11.8 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**beta-mannosidase;<br>**PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron |
| 76 | d1fcdc1 | Alignment | not modelled | 11.6 | 11 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**Two-domain cytochrome c |
| 77 | c3d0wD_ | Alignment | not modelled | 11.6 | 26 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**yflh protein;<br>**PDBTitle:** crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326 |
| 78 | c3bzjA_ | Alignment | not modelled | 11.6 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uv endonuclease;<br>**PDBTitle:** uvde k229l |
| 79 | d1pgja1 | Alignment | not modelled | 11.3 | 16 | **Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like<br>**Family:**Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain |
| 80 | c2zxyA_ | Alignment | not modelled | 11.2 | 22 | **PDB header:**oxygen binding, transport protein<br>**Chain:** A: **PDB Molecule:**cytochrome c552;<br>**PDBTitle:** crystal structure of cytochrome c555 from aquifex aeolicus |
| | | | | | | **Fold:**Cytochrome c |

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| 81 | d1ql3a_ | Alignment | not modelled | 11.2 | 28 | **Superfamily:**Cytochrome c<br>**Family:**monodomain cytochrome c |
| 82 | d1rh1a2 | Alignment | not modelled | 11.1 | 16 | **Fold:**Toxins' membrane translocation domains<br>**Superfamily:**Colicin<br>**Family:**Colicin |
| 83 | c1zb7A_ | Alignment | not modelled | 10.8 | 50 | **PDB header:**toxin<br>**Chain:** A: **PDB Molecule:**neurotoxin;<br>**PDBTitle:** crystal structure of botulinum neurotoxin type g light chain |
| 84 | d1dvha_ | Alignment | not modelled | 10.7 | 22 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**monodomain cytochrome c |
| 85 | d1pega1 | Alignment | not modelled | 10.5 | 7 | **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 |
| 86 | c2r7tA_ | Alignment | not modelled | 10.5 | 24 | **PDB header:**transferase/rna<br>**Chain:** A: **PDB Molecule:**rna-dependent rna polymerase;<br>**PDBTitle:** crystal structure of rotavirus sa11 vp1/rna (ugugaacc)2 complex |
| 87 | d1c53a_ | Alignment | not modelled | 10.5 | 17 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**monodomain cytochrome c |
| 88 | c3ogrA_ | Alignment | not modelled | 10.5 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose |
| 89 | d1v2za_ | Alignment | not modelled | 10.4 | 12 | **Fold:**KaiA/RbsU domain<br>**Superfamily:**KaiA/RbsU domain<br>**Family:**Circadian clock protein KaiA, C-terminal domain |
| 90 | d1txla_ | Alignment | not modelled | 10.1 | 20 | **Fold:**Lipocalins<br>**Superfamily:**Lipocalins<br>**Family:**Hypothetical protein YodA |
| 91 | c1txlA_ | Alignment | not modelled | 10.1 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**metal-binding protein yoda;<br>**PDBTitle:** crystal structure of metal-binding protein yoda from e.2 coli, pfam duf149 |
| 92 | d1zj8a1 | Alignment | not modelled | 10.1 | 18 | **Fold:**Ferredoxin-like<br>**Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like<br>**Family:**Duplicated SiR/NiR-like domains 1 and 3 |
| 93 | c2zonG_ | Alignment | not modelled | 9.9 | 13 | **PDB header:**oxidoreductase/electron transport<br>**Chain:** G: **PDB Molecule:**cytochrome c551;<br>**PDBTitle:** crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c |
| 94 | d1h9xa1 | Alignment | not modelled | 9.8 | 28 | **Fold:**Cytochrome c<br>**Superfamily:**Cytochrome c<br>**Family:**N-terminal (heme c) domain of cytochrome cd1-nitrite reductase |
| 95 | c3ivpD_ | Alignment | not modelled | 9.7 | 9 | **PDB header:**dna binding protein<br>**Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein;<br>**PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630. |
| 96 | c3op9A_ | Alignment | not modelled | 9.7 | 18 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**pli0006 protein;<br>**PDBTitle:** crystal structure of transcriptional regulator from listeria innocua |
| 97 | c2da4A_ | Alignment | not modelled | 9.6 | 10 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156;<br>**PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156 |
| 98 | c2xhlA_ | Alignment | not modelled | 9.6 | 50 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**botulinum neurotoxin b light chain;<br>**PDBTitle:** structure of a functional derivative of clostridium2 botulinum neurotoxin type b |
| 99 | c2xrhA_ | Alignment | not modelled | 9.4 | 17 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**protein hp0721;<br>**PDBTitle:** crystal structure of the truncated form of hp0721 |