# Phyre2

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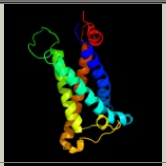
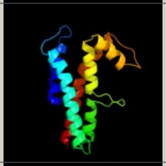
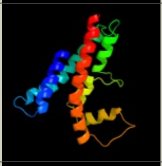
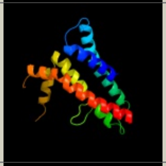
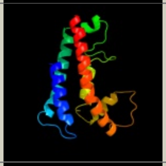
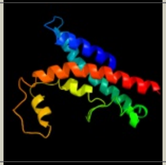
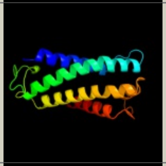
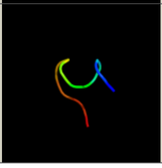
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ABE5 |
| Date | Thu Jan 5 11:15:18 GMT 2012 |
| Unique Job ID | 03c84cf8074adacf |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1kqfc_ | Alignment |  | 99.9 | 16 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Formate dehydrogenase N, cytochrome (gamma) subunit |
| 2 | c2qjkM_ | Alignment |  | 95.5 | 15 | **PDB header:**electron transport<br>**Chain:** M: **PDB Molecule:**cytochrome b;<br>**PDBTitle:** crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin |
| 3 | d3cx5c2 | Alignment |  | 95.1 | 16 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 4 | c3cx5N_ | Alignment |  | 94.5 | 16 | **PDB header:**oxidoreductase<br>**Chain:** N: **PDB Molecule:**cytochrome b;<br>**PDBTitle:** structure of complex iii with bound cytochrome c in reduced2 state and definition of a minimal core interface for3 electron transfer. |
| 5 | c3cwbC_ | Alignment |  | 94.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**cytochrome b;<br>**PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d |
| 6 | d2e74a1 | Alignment |  | 92.7 | 15 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 7 | d1ppjc2 | Alignment |  | 91.8 | 16 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 8 | d1q90b_ | Alignment |  | 91.1 | 15 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 9 | d1bccc3 | Alignment |  | 90.0 | 16 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 10 | d1y5ic1 | Alignment |  | 81.3 | 11 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Respiratory nitrate reductase 1 gamma chain<br>**Family:**Respiratory nitrate reductase 1 gamma chain |
| 11 | c2ftcQ_ | Alignment |  | 23.0 | 36 | **PDB header:**ribosome<br>**Chain:** Q: **PDB Molecule:**39s ribosomal protein l34, mitochondrial;<br>**PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome |

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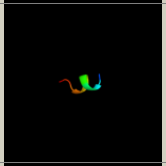
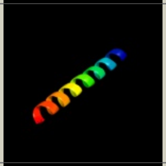
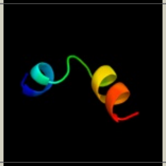
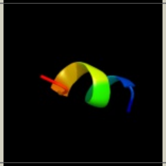
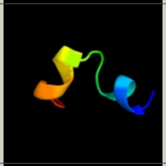
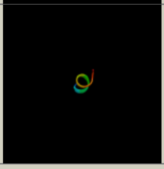
| 12 | d1t33a1 | Alignment |  | 15.8 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 13 | d2ieca1 | Alignment |  | 12.6 | 20 | **Fold:**MK0786-like<br>**Superfamily:**MK0786-like<br>**Family:**MK0786-like |
| 14 | d1m56d_ | Alignment |  | 10.5 | 14 | **Fold:**Single transmembrane helix<br>**Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV<br>**Family:**Bacterial aa3 type cytochrome c oxidase subunit IV |
| 15 | c3nnrA_ | Alignment |  | 10.4 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family;<br>**PDBTitle:** crystal structure of a tetr-family transcriptional regulator2 (maqu_3571) from marinobacter aquaeolei vt8 at 2.49 a resolution |
| 16 | c2ogfD_ | Alignment |  | 10.3 | 30 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**hypothetical protein mj0408;<br>**PDBTitle:** crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372 |
| 17 | d2id6a1 | Alignment |  | 10.2 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 18 | c2yvhA_ | Alignment |  | 10.1 | 22 | **PDB header:**transcription/dna<br>**Chain:** A: **PDB Molecule:**transcriptional regulator;<br>**PDBTitle:** crystal structure of the operator-binding form of the multi-drug2 binding transcriptional repressor cgmr |
| 19 | c2raeA_ | Alignment |  | 9.8 | 11 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, acrr family protein;<br>**PDBTitle:** crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1 |
| 20 | d2i52a1 | Alignment |  | 9.7 | 30 | **Fold:**MK0786-like<br>**Superfamily:**MK0786-like<br>**Family:**MK0786-like |
| 21 | c1z0xA_ | Alignment | not modelled | 9.6 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family;<br>**PDBTitle:** crystal structure of transcriptional regulator, tetr family from2 enterococcus faecalis v583 |
| 22 | c2guhA_ | Alignment | not modelled | 9.4 | 6 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator;<br>**PDBTitle:** crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1 |
| 23 | d2d6ya1 | Alignment | not modelled | 9.2 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 24 | c2qibA_ | Alignment | not modelled | 8.7 | 11 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator;<br>**PDBTitle:** crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor |
| 25 | d2gfna1 | Alignment | not modelled | 8.5 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 26 | c2dg8D_ | Alignment | not modelled | 8.4 | 11 | **PDB header:**gene regulation<br>**Chain:** D: **PDB Molecule:**putative tetr-family transcriptional regulatory protein;<br>**PDBTitle:** crystal structure of the putative trasncriptional regulator sco75182 from streptomyces coelicolor a3(2) |
| 27 | d1z0xa1 | Alignment | not modelled | 8.3 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 28 | c2wgbB_ | Alignment | not modelled | 7.7 | 11 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**tetr family transcriptional repressor lfrr;<br>**PDBTitle:** crystal structure of the tetr-like transcriptional2 |

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|  |  |  |  |  |  | regulator lfrr from mycobacterium smegmatis |
| 29 | d1uf2c2 | Alignment | not modelled | 7.6 | 33 | **Fold:**Viral protein domain<br>**Superfamily:**Viral protein domain<br>**Family:**Top domain of virus capsid protein |
| 30 | d2g3ba1 | Alignment | not modelled | 7.5 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 31 | c2hxiA_ | Alignment | not modelled | 7.5 | 22 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator from streptomyces coelicolor a3(2) |
| 32 | d2fx0a1 | Alignment | not modelled | 7.5 | 17 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 33 | d2vkea1 | Alignment | not modelled | 7.3 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 34 | c2fbqA_ | Alignment | not modelled | 7.2 | 22 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**probable transcriptional regulator;<br>**PDBTitle:** the crystal structure of transcriptional regulator pa3006 |
| 35 | d2j7ja2 | Alignment | not modelled | 7.1 | 10 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 36 | d2o7ta1 | Alignment | not modelled | 7.1 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 37 | d2hkua1 | Alignment | not modelled | 6.7 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 38 | d2id3a1 | Alignment | not modelled | 6.6 | 0 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 39 | c3fiwB_ | Alignment | not modelled | 6.5 | 17 | **PDB header:**transcription regulator<br>**Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator;<br>**PDBTitle:** structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor |
| 40 | d1vi0a1 | Alignment | not modelled | 6.3 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 41 | d2g7ga1 | Alignment | not modelled | 6.3 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 42 | d2vkva1 | Alignment | not modelled | 6.2 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 43 | c2g7sA_ | Alignment | not modelled | 6.2 | 22 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family;<br>**PDBTitle:** the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens |
| 44 | d1v7ba1 | Alignment | not modelled | 6.1 | 28 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 45 | c3efdK_ | Alignment | not modelled | 6.1 | 33 | **PDB header:**immune system<br>**Chain:** K: **PDB Molecule:**kcsa;<br>**PDBTitle:** the crystal structure of the cytoplasmic domain of kcsa |
| 46 | c2id3A_ | Alignment | not modelled | 6.1 | 0 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** crystal structure of transcriptional regulator sco5951 from2 streptomyces coelicolor a3(2) |
| 47 | d2i10a1 | Alignment | not modelled | 6.1 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 48 | d1qled_ | Alignment | not modelled | 6.1 | 7 | **Fold:**Single transmembrane helix<br>**Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV<br>**Family:**Bacterial aa3 type cytochrome c oxidase subunit IV |
| 49 | c3c2bA_ | Alignment | not modelled | 6.0 | 17 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family;<br>**PDBTitle:** crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens |
| 50 | d2axti1 | Alignment | not modelled | 6.0 | 14 | **Fold:**Single transmembrane helix<br>**Superfamily:**Photosystem II reaction center protein I, PsbI<br>**Family:**PsbI-like |
| 51 | c3rh2A_ | Alignment | not modelled | 6.0 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**hypothetical tetr-like transcriptional regulator;<br>**PDBTitle:** crystal structure of a hypothetical tetr-like transcriptional2 regulator (sama_0099) from shewanella amazonensis sb2b at 2.42 a3 resolution |
| 52 | c2g3bB_ | Alignment | not modelled | 5.9 | 17 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator;<br>**PDBTitle:** crystal structure of putative tetr-family transcriptional regulator2 from rhodococcus sp. |
| 53 | c3cwrA_ | Alignment | not modelled | 5.9 | 6 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family;<br>**PDBTitle:** crystal structure of transcriptional regulator of tetr2 family (yp_425770.1) from rhodospirillum rubrum atcc 111703 at 1.50 a resolution |
|  |  |  |  |  |  | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**putative tetr-family transcriptional |

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|---|---|---|---|---|---|---|
| 54 | c3bniA_ | Alignment | not modelled | 5.9 | 6 | regulator;<br>**PDBTitle:** crystal structure of tetr-family transcriptional regulator from2 streptomyces coelicolor |
| 55 | d2axtb1 | Alignment | not modelled | 5.8 | 22 | **Fold:**Photosystem II antenna protein-like<br>**Superfamily:**Photosystem II antenna protein-like<br>**Family:**Photosystem II antenna protein-like |
| 56 | d2axtc1 | Alignment | not modelled | 5.8 | 22 | **Fold:**Photosystem II antenna protein-like<br>**Superfamily:**Photosystem II antenna protein-like<br>**Family:**Photosystem II antenna protein-like |
| 57 | c2axtc_ | Alignment | not modelled | 5.8 | 22 | **PDB header:**electron transport<br>**Chain:** C: **PDB Molecule:**photosystem ii cp43 protein;<br>**PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus |
| 58 | c2d6yA_ | Alignment | not modelled | 5.8 | 11 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**putative tetr family regulatory protein;<br>**PDBTitle:** crystal structure of transcriptional factor sco4008 from streptomyces2 coelicolor a3(2) |
| 59 | c2zcxA_ | Alignment | not modelled | 5.7 | 17 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**tetr-family transcriptional regulator;<br>**PDBTitle:** crystal structure of tetr family transcriptional regulator2 sco7815 |
| 60 | c2dg7A_ | Alignment | not modelled | 5.5 | 11 | **PDB header:**gene regulation<br>**Chain:** A: **PDB Molecule:**putative transcriptional regulator;<br>**PDBTitle:** crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2) |
| 61 | c2o7tA_ | Alignment | not modelled | 5.4 | 11 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**transcriptional regulator;<br>**PDBTitle:** crystal structure of a tetr family transcriptional regulator2 (ncgl1578, cgl1640) from corynebacterium glutamicum at 2.10 a3 resolution |
| 62 | d2g7sa1 | Alignment | not modelled | 5.4 | 22 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 63 | c1t33B_ | Alignment | not modelled | 5.4 | 22 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**putative transcriptional repressor (tetr/acrr family);<br>**PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional repressor (tetr/acrr family) from salmonella3 typhimurim lt2 |
| 64 | d1pb6a1 | Alignment | not modelled | 5.3 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |
| 65 | c3o60A_ | Alignment | not modelled | 5.2 | 11 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**lin0861 protein;<br>**PDBTitle:** the crystal structure of lin0861 from listeria innocua to 2.8a |
| 66 | c3egqB_ | Alignment | not modelled | 5.2 | 17 | **PDB header:**transcription<br>**Chain:** B: **PDB Molecule:**tetr family transcriptional regulator;<br>**PDBTitle:** crystal structure of a tetr-family transcriptional regulator (af_1817)2 from archaeoglobus fulgidus at 2.55 a resolution |
| 67 | d1jt6a1 | Alignment | not modelled | 5.2 | 28 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**Homeodomain-like<br>**Family:**Tetracyclin repressor-like, N-terminal domain |