Phyre2

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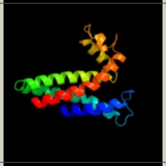
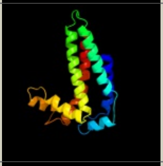
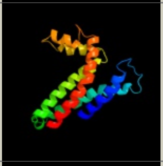
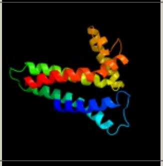
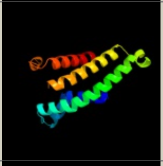
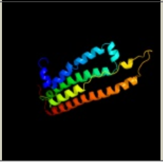
| Description | P0AEL0 |
| Date | Thu Jan 5 11:23:36 GMT 2012 |
| Unique Job ID | 424399b82e571ae4 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1kqfc_ | Alignment |  | 100.0 | 48 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Formate dehydrogenase N, cytochrome (gamma) subunit |
| 2 | c2qjkM_ | Alignment |  | 98.2 | 17 | **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 | d1q90b_ | Alignment |  | 98.1 | 19 | **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 | d3cx5c2 | Alignment |  | 98.1 | 14 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Transmembrane di-heme cytochromes<br>**Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) |
| 5 | c3cx5N_ | Alignment |  | 98.1 | 14 | **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. |
| 6 | c3cwbC_ | Alignment |  | 98.1 | 14 | **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 |
| 7 | d1bccc3 | Alignment |  | 98.0 | 14 | **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 | d1ppjc2 | Alignment |  | 98.0 | 13 | **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 | d2e74a1 | Alignment |  | 98.0 | 18 | **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 |  | 42.5 | 17 | **Fold:**Heme-binding four-helical bundle<br>**Superfamily:**Respiratory nitrate reductase 1 gamma chain<br>**Family:**Respiratory nitrate reductase 1 gamma chain |
| 11 | c3mk7K_ | Alignment |  | 33.4 | 14 | **PDB header:**oxidoreductase<br>**Chain:** K: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit n;<br>**PDBTitle:** the structure of cbb3 cytochrome oxidase |

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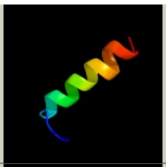
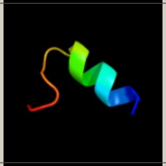
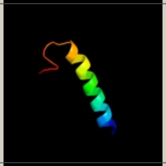
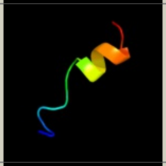
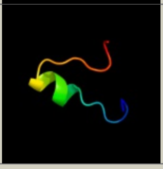
| 12 | c2kygC_ | Alignment |  | 33.3 | 27 | **PDB header:**protein binding<br>**Chain:** C: **PDB Molecule:**protein cbfa2t1;<br>**PDBTitle:** structure of the aml1-eto nervy domain - pka(riia) complex and its2 contribution to aml1-eto activity |
| 13 | c2levA_ | Alignment |  | 31.3 | 38 | **PDB header:**transcription regulator/dna<br>**Chain:** A: **PDB Molecule:**ler;<br>**PDBTitle:** structure of the dna complex of the c-terminal domain of ler |
| 14 | c3kmpA_ | Alignment |  | 14.0 | 21 | **PDB header:**transcription regulator/dna<br>**Chain:** A: **PDB Molecule:**smad1-mh1;<br>**PDBTitle:** crystal structure of smad1-mh1/dna complex |
| 15 | d1m56d_ | Alignment |  | 13.4 | 12 | **Fold:**Single transmembrane helix<br>**Superfamily:**Bacterial aa3 type cytochrome c oxidase subunit IV<br>**Family:**Bacterial aa3 type cytochrome c oxidase subunit IV |
| 16 | d1hnra_ | Alignment |  | 9.7 | 6 | **Fold:**H-NS histone-like proteins<br>**Superfamily:**H-NS histone-like proteins<br>**Family:**H-NS histone-like proteins |
| 17 | d2od6a1 | Alignment |  | 7.0 | 21 | **Fold:**Ferredoxin-like<br>**Superfamily:**Dimeric alpha+beta barrel<br>**Family:**Marine metagenome family DABB1 |
| 18 | c2l4gA_ | Alignment |  | 6.0 | 14 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**haemagglutinin;<br>**PDBTitle:** influenza haemagglutinin fusion peptide mutant g13a |
| 19 | c1fcuA_ | Alignment |  | 6.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase;<br>**PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase |
| 20 | d1rrza_ | Alignment |  | 5.9 | 27 | **Fold:**Spectrin repeat-like<br>**Superfamily:**Glycogen synthesis protein GlgS<br>**Family:**Glycogen synthesis protein GlgS |
| 21 | c1rrzA_ | Alignment | not modelled | 5.9 | 27 | **PDB header:**structural genomics,biosynthetic protein<br>**Chain:** A: **PDB Molecule:**glycogen synthesis protein glgs;<br>**PDBTitle:** solution structure of glgs protein from e. coli |
| 22 | d1v0da_ | Alignment | not modelled | 5.8 | 15 | **Fold:**His-Me finger endonucleases<br>**Superfamily:**His-Me finger endonucleases<br>**Family:**Caspase-activated DNase, CAD (DffB, DFF40) |
| 23 | c1v0dA_ | Alignment | not modelled | 5.8 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dna fragmentation factor 40 kda subunit;<br>**PDBTitle:** crystal structure of caspase-activated dnase (cad) |
| 24 | d1fcqa_ | Alignment | not modelled | 5.4 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Bee venom hyaluronidase |
| 25 | c3nrtC_ | Alignment | not modelled | 5.3 | 14 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**putative ryanodine receptor;<br>**PDBTitle:** the crystal strucutre of putative ryanodine receptor from bacteroides2 thetaiotaomicron vpi-5482 |
| 26 | c1m46B_ | Alignment | not modelled | 5.2 | 17 | **PDB header:**cell cycle protein<br>**Chain:** B: **PDB Molecule:**iq4 motif from myo2p, a class v myosin;<br>**PDBTitle:** crystal structure of mlc1p bound to iq4 of myo2p, a class v2 myosin |
| 27 | d1ecfa1 | Alignment | not modelled | 5.1 | 10 | **Fold:**PRTase-like<br>**Superfamily:**PRTase-like<br>**Family:**Phosphoribosyltransferases (PRTases) |
| 28 | c1xooA_ | Alignment | not modelled | 5.0 | 15 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**hemagglutinin;<br>**PDBTitle:** nmr structure of g1s mutant of influenza hemagglutinin2 fusion peptide in dpc micelles at ph 5 |