# Phyre2

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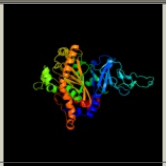
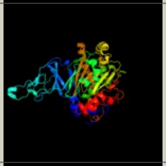
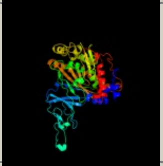
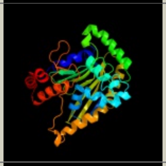
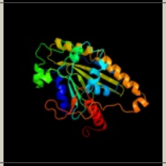
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ABR5 |
| Date | Thu Jan 5 11:16:07 GMT 2012 |
| Unique Job ID | 39a095706115e165 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2gbxE_ | Alignment |  | 100.0 | 38 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**biphenyl 2,3-dioxygenase alpha subunit;<br>**PDBTitle:** crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl |
| 2 | c2hmnA_ | Alignment |  | 100.0 | 36 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase alpha subunit;<br>**PDBTitle:** crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene. |
| 3 | c1wqlA_ | Alignment |  | 100.0 | 44 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**iron-sulfur protein large subunit of cumene dioxygenase;<br>**PDBTitle:** cumene dioxygenase (cuma1a2) from pseudomonas fluorescens ip01 |
| 4 | c1uljA_ | Alignment |  | 100.0 | 48 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**biphenyl dioxygenase large subunit;<br>**PDBTitle:** biphenyl dioxygenase (bpha1a2) in complex with the substrate |
| 5 | c2b1xE_ | Alignment |  | 100.0 | 39 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**naphthalene dioxygenase large subunit;<br>**PDBTitle:** crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp. |
| 6 | c3n0qA_ | Alignment |  | 100.0 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**putative aromatic-ring hydroxylating dioxygenase;<br>**PDBTitle:** crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution |
| 7 | d1o7na2 | Alignment |  | 100.0 | 30 | **Fold:**TBP-like<br>**Superfamily:**Bet v1-like<br>**Family:**Ring hydroxylating alpha subunit catalytic domain |
| 8 | d1wqla2 | Alignment |  | 100.0 | 38 | **Fold:**TBP-like<br>**Superfamily:**Bet v1-like<br>**Family:**Ring hydroxylating alpha subunit catalytic domain |
| 9 | d2bmoa2 | Alignment |  | 100.0 | 30 | **Fold:**TBP-like<br>**Superfamily:**Bet v1-like<br>**Family:**Ring hydroxylating alpha subunit catalytic domain |
| 10 | d1ulia2 | Alignment |  | 100.0 | 44 | **Fold:**TBP-like<br>**Superfamily:**Bet v1-like<br>**Family:**Ring hydroxylating alpha subunit catalytic domain |
| 11 | d2b1xa2 | Alignment |  | 100.0 | 34 | **Fold:**TBP-like<br>**Superfamily:**Bet v1-like<br>**Family:**Ring hydroxylating alpha subunit catalytic domain |

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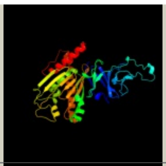
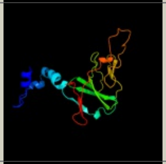
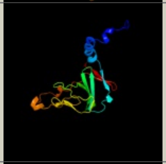
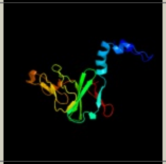
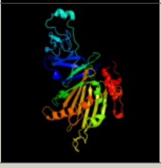
|---|---|---|---|---|---|---|
| 12 | c3gteB_ | Alignment |  | 100.0 | 16 | **PDB header:**electron transport, oxidoreductase<br>**Chain:** B: **PDB Molecule:**ddmc;<br>**PDBTitle:** crystal structure of dicamba monooxygenase with non-heme2 iron |
| 13 | c3gkqB_ | Alignment |  | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a-<br>**PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 novosphingobium sp. ka1 |
| 14 | c3gcfC_ | Alignment |  | 100.0 | 18 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a-<br>**PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioides aromaticivorans ic177 |
| 15 | d1wqla1 | Alignment |  | 100.0 | 56 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 16 | c1z01D_ | Alignment |  | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** D: **PDB Molecule:**2-oxo-1,2-dihydroquinoline 8-monooxygenase,<br>**PDBTitle:** 2-oxoquinoline 8-monooxygenase component: active site2 modulation by rieske-[2fe-2s] center oxidation/reduction |
| 17 | d2b1xa1 | Alignment |  | 100.0 | 48 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 18 | d1ulia1 | Alignment |  | 100.0 | 58 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 19 | d2bmoa1 | Alignment |  | 100.0 | 47 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 20 | c2zylA_ | Alignment |  | 100.0 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**possible oxidoreductase;<br>**PDBTitle:** crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis |
| 21 | c2de7B_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole;<br>**PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase |
| 22 | d1o7na1 | Alignment | not modelled | 100.0 | 46 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 23 | d1z01a1 | Alignment | not modelled | 100.0 | 21 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 24 | d2de6a1 | Alignment | not modelled | 100.0 | 25 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Ring hydroxylating alpha subunit ISP domain |
| 25 | c3d89A_ | Alignment | not modelled | 99.9 | 16 | **PDB header:**electron transport<br>**Chain:** A: **PDB Molecule:**rieske domain-containing protein;<br>**PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus |
| 26 | d1vm9a_ | Alignment | not modelled | 99.8 | 21 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 27 | c2de7E_ | Alignment | not modelled | 99.8 | 21 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**ferredoxin component of carbazole;<br>**PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase |
| 28 | d2jzaa1 | Alignment | not modelled | 99.8 | 14 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**NirD-like |
| | | | | | | **PDB header:**oxidoreductase |

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| 29 | c3dqyA_ | Alignment | not modelled | 99.8 | 20 | **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin<br>**PDBTitle:** crystal structure of toluene 2,3-dioxygenase ferredoxin |
| 30 | d3c0da1 | Alignment | not modelled | 99.8 | 12 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**NirD-like |
| 31 | c3gceA_ | Alignment | not modelled | 99.8 | 22 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ferredoxin component of carbazole 1,9a-<br>**PDBTitle:** ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177 |
| 32 | d1fqta_ | Alignment | not modelled | 99.8 | 16 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 33 | c2qpzA_ | Alignment | not modelled | 99.8 | 22 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase system ferredoxin<br>**PDBTitle:** naphthalene 1,2-dioxygenase rieske ferredoxin |
| 34 | d2jo6a1 | Alignment | not modelled | 99.8 | 14 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**NirD-like |
| 35 | c2i7fB_ | Alignment | not modelled | 99.7 | 22 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase;<br>**PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin |
| 36 | d1q90c_ | Alignment | not modelled | 99.6 | 23 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 37 | d1rfsa_ | Alignment | not modelled | 99.6 | 24 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 38 | d3cx5e1 | Alignment | not modelled | 99.4 | 28 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 39 | d2e74d1 | Alignment | not modelled | 99.4 | 22 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 40 | d1g8kb_ | Alignment | not modelled | 99.4 | 18 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 41 | d1riea_ | Alignment | not modelled | 99.4 | 23 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 42 | c2nvgA_ | Alignment | not modelled | 99.3 | 19 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit;<br>**PDBTitle:** soluble domain of rieske iron sulfur protein. |
| 43 | c2e76D_ | Alignment | not modelled | 99.0 | 23 | **PDB header:**photosynthesis<br>**Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit;<br>**PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus |
| 44 | c2fynO_ | Alignment | not modelled | 99.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur<br>**PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex |
| 45 | d1nyka_ | Alignment | not modelled | 98.9 | 24 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 46 | c2fyuE_ | Alignment | not modelled | 98.8 | 22 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit,<br>**PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor |
| 47 | c1p84E_ | Alignment | not modelled | 98.3 | 25 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur<br>**PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex |
| 48 | d1z01a2 | Alignment | not modelled | 97.7 | 13 | **Fold:**TBP-like<br>**Superfamily:**Bet v1-like<br>**Family:**Ring hydroxylating alpha subunit catalytic domain |
| 49 | d1jm1a_ | Alignment | not modelled | 97.3 | 25 | **Fold:**ISP domain<br>**Superfamily:**ISP domain<br>**Family:**Rieske iron-sulfur protein (ISP) |
| 50 | d2de6a2 | Alignment | not modelled | 96.3 | 17 | **Fold:**TBP-like<br>**Superfamily:**Bet v1-like<br>**Family:**Ring hydroxylating alpha subunit catalytic domain |
| 51 | d1uhva1 | Alignment | not modelled | 31.4 | 28 | **Fold:**Glycosyl hydrolase domain<br>**Superfamily:**Glycosyl hydrolase domain<br>**Family:**Composite domain of glycosyl hydrolase families 5, 30, 39 and 51 |
| 52 | c3fcgB_ | Alignment | not modelled | 29.7 | 27 | **PDB header:**membrane protein, protein transport<br>**Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein;<br>**PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher |
| 53 | c3kv0A_ | Alignment | not modelled | 28.3 | 43 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**het-c2;<br>**PDBTitle:** crystal structure of het-c2: a fungal glycolipid transfer protein2 (gltp) |
| 54 | d1mkna_ | Alignment | not modelled | 24.1 | 67 | **Fold:**Midkine<br>**Superfamily:**Midkine<br>**Family:**Midkine, a heparin-binding growth factor, N-terminal domain |
| | | | | | | **Fold:**Galactose-binding domain-like |

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| 55 | d1wmxa_ | Alignment | not modelled | 23.9 | 22 | **Superfamily:**Galactose-binding domain-like<br>**Family:**Family 30 carbohydrate binding module, CBM30 (PKD repeat) |
| 56 | d2fu5a1 | Alignment | not modelled | 23.8 | 25 | **Fold:**Mss4-like<br>**Superfamily:**Mss4-like<br>**Family:**RabGEF Mss4 |
| 57 | d1pwka_ | Alignment | not modelled | 23.7 | 13 | **Fold:**DLC<br>**Superfamily:**DLC<br>**Family:**DLC |
| 58 | c1ddzA_ | Alignment | not modelled | 23.2 | 42 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1 |
| 59 | c1lshB_ | Alignment | not modelled | 22.3 | 19 | **PDB header:**lipid binding protein<br>**Chain:** B: **PDB Molecule:**lipovitellin (lv-2);<br>**PDBTitle:** lipid-protein interactions in lipovitellin |
| 60 | d1lshb_ | Alignment | not modelled | 22.3 | 19 | **Fold:**Lipovitellin-phosvitin complex; beta-sheet shell regions<br>**Superfamily:**Lipovitellin-phosvitin complex; beta-sheet shell regions<br>**Family:**Lipovitellin-phosvitin complex; beta-sheet shell regions |
| 61 | d1w91a1 | Alignment | not modelled | 22.2 | 50 | **Fold:**Glycosyl hydrolase domain<br>**Superfamily:**Glycosyl hydrolase domain<br>**Family:**Composite domain of glycosyl hydrolase families 5, 30, 39 and 51 |
| 62 | d1hxra_ | Alignment | not modelled | 21.5 | 25 | **Fold:**Mss4-like<br>**Superfamily:**Mss4-like<br>**Family:**RabGEF Mss4 |
| 63 | d3brda2 | Alignment | not modelled | 18.6 | 35 | **Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f<br>**Superfamily:**p53-like transcription factors<br>**Family:**DNA-binding protein LAG-1 (CSL) |
| 64 | d1ddza2 | Alignment | not modelled | 18.6 | 42 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 65 | c2x3mA_ | Alignment | not modelled | 18.4 | 33 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein orf239;<br>**PDBTitle:** crystal structure of hypothetical protein orf239 from pyrobaculum2 spherical virus |
| 66 | c2wb6A_ | Alignment | not modelled | 18.0 | 16 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**afv1-102;<br>**PDBTitle:** crystal structure of afv1-102, a protein from the acidianus2 filamentous virus 1 |
| 67 | d3orca_ | Alignment | not modelled | 16.7 | 24 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 68 | c2c3yA_ | Alignment | not modelled | 16.3 | 27 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase;<br>**PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus |
| 69 | c3lasA_ | Alignment | not modelled | 15.5 | 29 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**putative carbonic anhydrase;<br>**PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution |
| 70 | d1nr3a_ | Alignment | not modelled | 15.3 | 19 | **Fold:**DNA-binding protein Tfx<br>**Superfamily:**DNA-binding protein Tfx<br>**Family:**DNA-binding protein Tfx |
| 71 | c1ylkA_ | Alignment | not modelled | 14.4 | 29 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein rv1284/mt1322;<br>**PDBTitle:** crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate |
| 72 | d1swxa_ | Alignment | not modelled | 14.1 | 80 | **Fold:**Glycolipid transfer protein, GLTP<br>**Superfamily:**Glycolipid transfer protein, GLTP<br>**Family:**Glycolipid transfer protein, GLTP |
| 73 | c2i3fA_ | Alignment | not modelled | 13.5 | 40 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**glycolipid transfer-like protein;<br>**PDBTitle:** crystal structure of a glycolipid transfer-like protein2 from galdieria sulphuraria |
| 74 | d1cmia_ | Alignment | not modelled | 13.5 | 13 | **Fold:**DLC<br>**Superfamily:**DLC<br>**Family:**DLC |
| 75 | d1e1oa1 | Alignment | not modelled | 13.1 | 20 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 76 | c2lm4A_ | Alignment | not modelled | 13.0 | 38 | **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 |
| 77 | d2c42a2 | Alignment | not modelled | 13.0 | 27 | **Fold:**Thiamin diphosphate-binding fold (THDP-binding)<br>**Superfamily:**Thiamin diphosphate-binding fold (THDP-binding)<br>**Family:**PFOR PP module |
| 78 | c2jz8A_ | Alignment | not modelled | 12.6 | 33 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein bh09830;<br>**PDBTitle:** solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55 |
| 79 | c2vpyB_ | Alignment | not modelled | 12.4 | 27 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nrfc protein;<br>**PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp) |
| 80 | c3brgC_ | Alignment | not modelled | 12.2 | 35 | **PDB header:**dna binding protein/dna<br>**Chain:** C: **PDB Molecule:**recombining binding protein suppressor of |

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| | | | | | | **PDBTitle:** csl (rbp-jk) bound to dna |
| 81 | d3cdda1 | Alignment | not modelled | 12.2 | 17 | **Fold:**Phage tail proteins<br>**Superfamily:**Phage tail proteins<br>**Family:**Baseplate protein-like |
| 82 | c3izbP_ | Alignment | not modelled | 12.1 | 60 | **PDB header:**ribosome<br>**Chain:** P: **PDB Molecule:**40s ribosomal protein rps11 (s17p);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 83 | c2a8cE_ | Alignment | not modelled | 11.9 | 50 | **PDB header:**lyase<br>**Chain:** E: **PDB Molecule:**carbonic anhydrase 2;<br>**PDBTitle:** haemophilus influenzae beta-carbonic anhydrase |
| 84 | c3iz6P_ | Alignment | not modelled | 11.8 | 60 | **PDB header:**ribosome<br>**Chain:** P: **PDB Molecule:**40s ribosomal protein s11 (s17p);<br>**PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome |
| 85 | d3e2ba1 | Alignment | not modelled | 11.8 | 13 | **Fold:**DLC<br>**Superfamily:**DLC<br>**Family:**DLC |
| 86 | c2fo1A_ | Alignment | not modelled | 11.6 | 35 | **PDB header:**gene regulation/signalling protein/dna<br>**Chain:** A: **PDB Molecule:**lin-12 and glp-1 phenotype protein 1, isoform b;<br>**PDBTitle:** crystal structure of the csl-notch-mastermind ternary2 complex bound to dna |
| 87 | d1bbua1 | Alignment | not modelled | 11.4 | 20 | **Fold:**OB-fold<br>**Superfamily:**Nucleic acid-binding proteins<br>**Family:**Anticodon-binding domain |
| 88 | d1kt0a2 | Alignment | not modelled | 11.2 | 26 | **Fold:**FKBP-like<br>**Superfamily:**FKBP-like<br>**Family:**FKBP immunophilin/proline isomerase |
| 89 | d1ddza1 | Alignment | not modelled | 10.9 | 43 | **Fold:**Resolvase-like<br>**Superfamily:**beta-carbonic anhydrase, cab<br>**Family:**beta-carbonic anhydrase, cab |
| 90 | c2yrtA_ | Alignment | not modelled | 10.8 | 25 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**chord containing protein-1;<br>**PDBTitle:** solution structure of the chord domain of human chord-2 containing protein 1 |
| 91 | c2w3nA_ | Alignment | not modelled | 10.8 | 32 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**carbonic anhydrase 2;<br>**PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans |
| 92 | d1nfga1 | Alignment | not modelled | 10.6 | 22 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase) |
| 93 | d1ubdc4 | Alignment | not modelled | 10.5 | 44 | **Fold:**beta-beta-alpha zinc fingers<br>**Superfamily:**beta-beta-alpha zinc fingers<br>**Family:**Classic zinc finger, C2H2 |
| 94 | d1vmka_ | Alignment | not modelled | 10.4 | 20 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**Purine and uridine phosphorylases<br>**Family:**Purine and uridine phosphorylases |
| 95 | c3eyxB_ | Alignment | not modelled | 10.2 | 27 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**carbonic anhydrase;<br>**PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae |
| 96 | d2abxa_ | Alignment | not modelled | 10.2 | 42 | **Fold:**Snake toxin-like<br>**Superfamily:**Snake toxin-like<br>**Family:**Snake venom toxins |
| 97 | d1d1la_ | Alignment | not modelled | 10.2 | 24 | **Fold:**lambda repressor-like DNA-binding domains<br>**Superfamily:**lambda repressor-like DNA-binding domains<br>**Family:**Phage repressors |
| 98 | c2ivfB_ | Alignment | not modelled | 9.6 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit;<br>**PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum |
| 99 | c2xznQ_ | Alignment | not modelled | 9.6 | 40 | **PDB header:**ribosome<br>**Chain:** Q: **PDB Molecule:**ribosomal protein s17 containing protein;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2 |