# Phyre$^2$

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| Description | P39363 |
| Date | Thu Jan 5 11:59:54 GMT 2012 |
| Unique Job ID | 95bb96de30f4905b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3oxpB_ | Alignment |  | 100.0 | 37 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**phosphotransferase enzyme ii, a component;<br>**PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution |
| 2 | c3oxpA_ | Alignment |  | 100.0 | 37 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**phosphotransferase enzyme ii, a component;<br>**PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution |
| 3 | c2oq3A_ | Alignment |  | 100.0 | 34 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**mannitol-specific cryptic phosphotransferase<br>**PDBTitle:** solution structure of the mannitol- specific cryptic2 phosphotransferase enzyme iia cmtb from escherichia coli |
| 4 | c3bjvA_ | Alignment |  | 100.0 | 35 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rmpa;<br>**PDBTitle:** the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans |
| 5 | c2oqtD_ | Alignment |  | 100.0 | 29 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**hypothetical protein spy0176;<br>**PDBTitle:** structural genomics, the crystal structure of a putative2 pts iia domain from streptococcus pyogenes m1 gas |
| 6 | d1a3aa_ | Alignment |  | 100.0 | 25 | **Fold:**Phoshotransferase/anion transport protein<br>**Superfamily:**Phoshotransferase/anion transport protein<br>**Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII |
| 7 | d1xiza_ | Alignment |  | 100.0 | 17 | **Fold:**Phoshotransferase/anion transport protein<br>**Superfamily:**Phoshotransferase/anion transport protein<br>**Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII |
| 8 | c3urrB_ | Alignment |  | 99.9 | 19 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**pts iia-like nitrogen-regulatory protein ptsn;<br>**PDBTitle:** structure of pts iia-like nitrogen-regulatory protein ptsn (bth_i0484)2 (ptsn) |
| 9 | d1a6ja_ | Alignment |  | 99.9 | 20 | **Fold:**Phoshotransferase/anion transport protein<br>**Superfamily:**Phoshotransferase/anion transport protein<br>**Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII |
| 10 | c2a0jA_ | Alignment |  | 99.9 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**pts system, nitrogen regulatory iia protein;<br>**PDBTitle:** crystal structure of nitrogen regulatory protein iia-ntr from2 neisseria meningitidis |
| 11 | c1hynQ_ | Alignment |  | 96.9 | 12 | **PDB header:**membrane protein<br>**Chain:** Q: **PDB Molecule:**band 3 anion transport protein;<br>**PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein |

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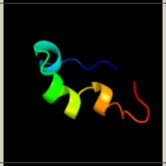
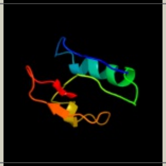
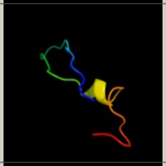
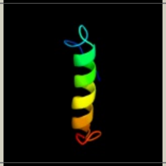
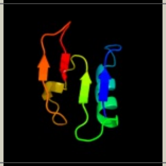
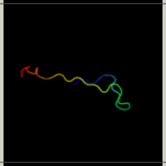
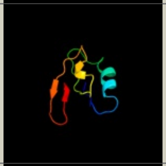
| 12 | d1hynp_ | Alignment |  | 96.1 | 13 | **Fold:**Phoshotransferase/anion transport protein<br>**Superfamily:**Phoshotransferase/anion transport protein<br>**Family:**Anion transport protein, cytoplasmic domain |
| 13 | d1gtda_ | Alignment |  | 22.2 | 10 | **Fold:**PurS-like<br>**Superfamily:**PurS-like<br>**Family:**PurS subunit of FGAM synthetase |
| 14 | d1susa1 | Alignment |  | 19.9 | 9 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**COMT-like |
| 15 | d1vq3a_ | Alignment |  | 15.9 | 19 | **Fold:**PurS-like<br>**Superfamily:**PurS-like<br>**Family:**PurS subunit of FGAM synthetase |
| 16 | d1a3xa3 | Alignment |  | 14.6 | 7 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**Pyruvate kinase, C-terminal domain |
| 17 | d2avda1 | Alignment |  | 13.3 | 13 | **Fold:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases<br>**Family:**COMT-like |
| 18 | c1eptB_ | Alignment |  | 12.5 | 14 | **PDB header:**hydrolase (serine protease)<br>**Chain:** B: **PDB Molecule:**porcine e-trypsin;<br>**PDBTitle:** refined 1.8 angstroms resolution crystal structure of2 porcine epsilon-trypsin |
| 19 | c3ntvB_ | Alignment |  | 10.7 | 20 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**mw1564 protein;<br>**PDBTitle:** crystal structure of a putative caffeoyl-coa o-methyltransferase from2 staphylococcus aureus |
| 20 | d1vlfm2 | Alignment |  | 10.3 | 20 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 21 | c2hntE_ | Alignment | not modelled | 9.6 | 25 | **PDB header:**serine protease<br>**Chain:** E: **PDB Molecule:**gamma-thrombin;<br>**PDBTitle:** crystallographic structure of human gamma-thrombin |
| 22 | c1tmoA_ | Alignment | not modelled | 9.4 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**trimethylamine n-oxide reductase;<br>**PDBTitle:** trimethylamine n-oxide reductase from shewanella massilia |
| 23 | d2i5ua1 | Alignment | not modelled | 9.2 | 21 | **Fold:**DnaD domain-like<br>**Superfamily:**DnaD domain-like<br>**Family:**DnaD domain |
| 24 | d1g8ka2 | Alignment | not modelled | 9.0 | 13 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 25 | c2dxbR_ | Alignment | not modelled | 8.9 | 11 | **PDB header:**hydrolase<br>**Chain:** R: **PDB Molecule:**thiocyanate hydrolase subunit gamma;<br>**PDBTitle:** recombinant thiocyanate hydrolase comprising partially-modified cobalt2 centers |
| 26 | c2fugC_ | Alignment | not modelled | 8.7 | 18 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3;<br>**PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus |
| 27 | d2jioa2 | Alignment | not modelled | 7.6 | 13 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 28 | d1dmra2 | Alignment | not modelled | 7.5 | 20 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| | | | | | | **PDB header:**oxidoreductase |

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| 29 | c1h5nC_ | Alignment | not modelled | 7.5 | 20 | **Chain:** C: **PDB Molecule:**dmso reductase;<br>**PDBTitle:** dmso reductase modified by the presence of dms and air |
| 30 | c2zw2B_ | Alignment | not modelled | 7.4 | 6 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178;<br>**PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs) |
| 31 | c1g8jC_ | Alignment | not modelled | 7.1 | 13 | **PDB header:**oxidoreductase<br>**Chain:** C: **PDB Molecule:**arsenite oxidase;<br>**PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis |
| 32 | d1tmoa2 | Alignment | not modelled | 7.0 | 20 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 33 | c1vlfQ_ | Alignment | not modelled | 7.0 | 20 | **PDB header:**oxidoreductase<br>**Chain:** Q: **PDB Molecule:**pyrogallol hydroxytransferase large subunit;<br>**PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici complexed3 with inhibitor 1,2,4,5-tetrahydroxy-benzene |
| 34 | d1uhwa_ | Alignment | not modelled | 7.0 | 14 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**DEP domain |
| 35 | d1e0ta3 | Alignment | not modelled | 6.9 | 14 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**Pyruvate kinase, C-terminal domain |
| 36 | d1sxjb1 | Alignment | not modelled | 6.7 | 13 | **Fold:**post-AAA+ oligomerization domain-like<br>**Superfamily:**post-AAA+ oligomerization domain-like<br>**Family:**DNA polymerase III clamp loader subunits, C-terminal domain |
| 37 | d1eu1a2 | Alignment | not modelled | 6.7 | 27 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 38 | c2yx5A_ | Alignment | not modelled | 6.6 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**upf0062 protein mj1593;<br>**PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway |
| 39 | c3c3pC_ | Alignment | not modelled | 6.5 | 13 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**methyltransferase;<br>**PDBTitle:** crystal structure of a methyltransferase (np_951602.1) from geobacter2 sulfurreducens at 1.90 a resolution |
| 40 | c3e3vA_ | Alignment | not modelled | 6.5 | 7 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**regulatory protein recx;<br>**PDBTitle:** crystal structure of recx from lactobacillus salivarius |
| 41 | d2csoa1 | Alignment | not modelled | 6.3 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**DEP domain |
| 42 | d1kqfa2 | Alignment | not modelled | 6.3 | 20 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 43 | d1v3fa_ | Alignment | not modelled | 6.1 | 18 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**DEP domain |
| 44 | d2iv2x2 | Alignment | not modelled | 6.1 | 27 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 45 | d1ogya2 | Alignment | not modelled | 6.0 | 13 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 46 | c1h0hA_ | Alignment | not modelled | 6.0 | 7 | **PDB header:**dehydrogenase<br>**Chain:** A: **PDB Molecule:**formate dehydrogenase (large subunit);<br>**PDBTitle:** tungsten containing formate dehydrogenase from2 desulfovibrio gigas |
| 47 | c3cbgA_ | Alignment | not modelled | 6.0 | 16 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**o-methyltransferase;<br>**PDBTitle:** functional and structural characterization of a2 cationdependent o-methyltransferase from the3 cyanobacterium synechocystis sp. strain pcc 6803 |
| 48 | c1eu1A_ | Alignment | not modelled | 5.9 | 27 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**dimethyl sulfoxide reductase;<br>**PDBTitle:** the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments. |
| 49 | d1y5ia2 | Alignment | not modelled | 5.9 | 20 | **Fold:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Superfamily:**Formate dehydrogenase/DMSO reductase, domains 1-3<br>**Family:**Formate dehydrogenase/DMSO reductase, domains 1-3 |
| 50 | c1ogyA_ | Alignment | not modelled | 5.9 | 13 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**periplasmic nitrate reductase;<br>**PDBTitle:** crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides |
| 51 | c1kqgA_ | Alignment | not modelled | 5.9 | 20 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, major subunit;<br>**PDBTitle:** formate dehydrogenase n from e. coli |
| 52 | d2cs7a1 | Alignment | not modelled | 5.7 | 19 | **Fold:**IL8-like<br>**Superfamily:**PhtA domain-like<br>**Family:**PhtA domain-like |
| 53 | c3dfgA_ | Alignment | not modelled | 5.6 | 17 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**regulatory protein recx;<br>**PDBTitle:** crystal structure of recx: a potent inhibitor protein of2 reca from xanthomonas campestris |
| | | | | | | **PDB header:**oxidoreductase |

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| 54 | c2ivfA_ | Alignment | not modelled | 5.6 | 13 | **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit;<br>**PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum |
| 55 | d2g50a3 | Alignment | not modelled | 5.6 | 25 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**Pyruvate kinase, C-terminal domain |
| 56 | c2e7zA_ | Alignment | not modelled | 5.5 | 27 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**acetylene hydratase ahy;<br>**PDBTitle:** acetylene hydratase from pelobacter acetylenicus |
| 57 | d1w4ma_ | Alignment | not modelled | 5.5 | 11 | **Fold:**DNA/RNA-binding 3-helical bundle<br>**Superfamily:**"Winged helix" DNA-binding domain<br>**Family:**DEP domain |