# Phyre$^2$

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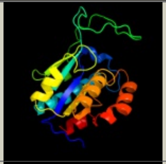
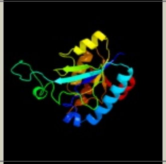
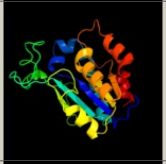
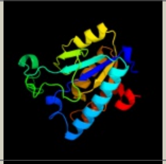
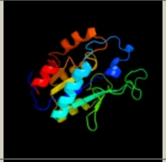
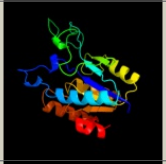
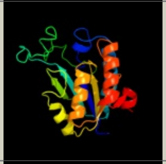
| Email | l.a.kelley@imperial.ac.uk |
| Description | P0ADI7 |
| Date | Thu Jan 5 11:21:06 GMT 2012 |
| Unique Job ID | bf4157d84899c692 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1j2ra_ | Alignment |  | 100.0 | 99 | **Fold:**Isochorismatase-like hydrolases<br>**Superfamily:**Isochorismatase-like hydrolases<br>**Family:**Isochorismatase-like hydrolases |
| 2 | d1nbaa_ | Alignment |  | 100.0 | 21 | **Fold:**Isochorismatase-like hydrolases<br>**Superfamily:**Isochorismatase-like hydrolases<br>**Family:**Isochorismatase-like hydrolases |
| 3 | c2fq1A_ | Alignment |  | 100.0 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**isochorismatase;<br>**PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains |
| 4 | c3irvA_ | Alignment |  | 100.0 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cysteine hydrolase;<br>**PDBTitle:** crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a |
| 5 | c3kl2K_ | Alignment |  | 100.0 | 30 | **PDB header:**structural genomics, unknown function<br>**Chain:** K: **PDB Molecule:**putative isochorismatase;<br>**PDBTitle:** crystal structure of a putative isochorismatase from streptomyces2 avermitilis |
| 6 | d1nf9a_ | Alignment |  | 100.0 | 21 | **Fold:**Isochorismatase-like hydrolases<br>**Superfamily:**Isochorismatase-like hydrolases<br>**Family:**Isochorismatase-like hydrolases |
| 7 | c3mcwA_ | Alignment |  | 100.0 | 30 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative hydrolase;<br>**PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution |
| 8 | c3hu5B_ | Alignment |  | 100.0 | 27 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**isochorismatase family protein;<br>**PDBTitle:** crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough |
| 9 | c3ot4F_ | Alignment |  | 100.0 | 21 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**putative isochorismatase;<br>**PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf |
| 10 | c3hb7G_ | Alignment |  | 100.0 | 21 | **PDB header:**hydrolase<br>**Chain:** G: **PDB Molecule:**isochorismatase hydrolase;<br>**PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a |
| 11 | c3oqpA_ | Alignment |  | 100.0 | 29 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative isochorismatase;<br>**PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution |

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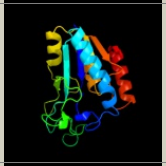
| 12 | c3oqpB_ | Alignment |  | 100.0 | 29 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative isochorismatase;<br>**PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution |
| 13 | c3eefA_ | Alignment |  | 100.0 | 27 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-carbamoylsarcosine amidase related protein;<br>**PDBTitle:** crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum |
| 14 | c3r2jC_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**alpha/beta-hydrolase-like protein;<br>**PDBTitle:** crystal structure of pnc1 from l. infantum in complex with nicotinate |
| 15 | c2wtaA_ | Alignment |  | 100.0 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nicotinamidase;<br>**PDBTitle:** acinetobacter baumanii nicotinamidase pyrazinamidease |
| 16 | d1im5a_ | Alignment |  | 100.0 | 22 | **Fold:**Isochorismatase-like hydrolases<br>**Superfamily:**Isochorismatase-like hydrolases<br>**Family:**Isochorismatase-like hydrolases |
| 17 | c3o93A_ | Alignment |  | 100.0 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**nicotinamidase;<br>**PDBTitle:** high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes |
| 18 | c3lqyA_ | Alignment |  | 100.0 | 28 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative isochorismatase hydrolase;<br>**PDBTitle:** crystal structure of putative isochorismatase hydrolase from2 oleispira antarctica |
| 19 | d1yaca_ | Alignment |  | 100.0 | 18 | **Fold:**Isochorismatase-like hydrolases<br>**Superfamily:**Isochorismatase-like hydrolases<br>**Family:**Isochorismatase-like hydrolases |
| 20 | c3gbcA_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**pyrazinamidase/nicotinamidas pnca;<br>**PDBTitle:** determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide |
| 21 | c2a67C_ | Alignment | not modelled | 100.0 | 24 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**isochorismatase family protein;<br>**PDBTitle:** crystal structure of isochorismatase family protein |
| 22 | c1yzvA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein;<br>**PDBTitle:** hypothetical protein from trypanosoma cruzi |
| 23 | c2b34C_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**mar1 ribonuclease;<br>**PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans |
| 24 | d1x9ga_ | Alignment | not modelled | 100.0 | 17 | **Fold:**Isochorismatase-like hydrolases<br>**Superfamily:**Isochorismatase-like hydrolases<br>**Family:**Isochorismatase-like hydrolases |
| 25 | c2h0rD_ | Alignment | not modelled | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**nicotinamidase;<br>**PDBTitle:** structure of the yeast nicotinamidase pnc1p |
| 26 | d1cmwa2 | Alignment | not modelled | 85.4 | 16 | **Fold:**PIN domain-like<br>**Superfamily:**PIN domain-like<br>**Family:**5' to 3' exonuclease catalytic domain |
| 27 | c1x1qA_ | Alignment | not modelled | 80.8 | 17 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**tryptophan synthase beta chain;<br>**PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8 |
| 28 | d1tfra2 | Alignment | not modelled | 66.9 | 5 | **Fold:**PIN domain-like<br>**Superfamily:**PIN domain-like<br>**Family:**5' to 3' exonuclease catalytic domain |
| 29 | c2ihnA_ | Alignment | not modelled | 66.7 | 7 | **PDB header:**hydrolase/dna<br>**Chain:** A: **PDB Molecule:**ribonuclease h;<br>**PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate |

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| 30 | c1ortD_ | Alignment | not modelled | 65.1 | 12 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**ornithine transcarbamoylase;<br>**PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa |
| 31 | d1xdpa3 | Alignment | not modelled | 65.0 | 9 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 32 | d1a9xa3 | Alignment | not modelled | 61.6 | 18 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 33 | c3bh0A_ | Alignment | not modelled | 60.7 | 15 | **PDB header:**replication<br>**Chain:** A: **PDB Molecule:**dnab-like replicative helicase;<br>**PDBTitle:** atpase domain of g40p |
| 34 | d1qopb_ | Alignment | not modelled | 57.8 | 18 | **Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes |
| 35 | c1cmwA_ | Alignment | not modelled | 54.1 | 17 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**protein (dna polymerase i);<br>**PDBTitle:** crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain |
| 36 | d1vp8a_ | Alignment | not modelled | 48.2 | 19 | **Fold:**Pyruvate kinase C-terminal domain-like<br>**Superfamily:**PK C-terminal domain-like<br>**Family:**MTH1675-like |
| 37 | c2w37A_ | Alignment | not modelled | 47.6 | 10 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic;<br>**PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii |
| 38 | c1xdoB_ | Alignment | not modelled | 47.6 | 9 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**polyphosphate kinase;<br>**PDBTitle:** crystal structure of escherichia coli polyphosphate kinase |
| 39 | c1f8sA_ | Alignment | not modelled | 45.6 | 28 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**l-amino acid oxidase;<br>**PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate. |
| 40 | c3bgwD_ | Alignment | not modelled | 43.4 | 15 | **PDB header:**replication<br>**Chain:** D: **PDB Molecule:**dnab-like replicative helicase;<br>**PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase |
| 41 | c1vlvA_ | Alignment | not modelled | 43.0 | 12 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase;<br>**PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution |
| 42 | d1szpa2 | Alignment | not modelled | 42.1 | 11 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**RecA protein-like (ATPase-domain) |
| 43 | c1xp8A_ | Alignment | not modelled | 40.0 | 17 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**reca protein;<br>**PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s" |
| 44 | d2ae2a_ | Alignment | not modelled | 39.1 | 19 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 45 | d1pv8a_ | Alignment | not modelled | 36.0 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) |
| 46 | c2rgoA_ | Alignment | not modelled | 35.3 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase;<br>**PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase |
| 47 | c3cbwA_ | Alignment | not modelled | 34.4 | 8 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**ydht protein;<br>**PDBTitle:** crystal structure of the ydht protein from bacillus subtilis |
| 48 | c3nugA_ | Alignment | not modelled | 32.4 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase;<br>**PDBTitle:** crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti |
| 49 | c1ipaA_ | Alignment | not modelled | 31.8 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**rna 2'-o-ribose methyltransferase;<br>**PDBTitle:** crystal structure of rna 2'-o ribose methyltransferase |
| 50 | d1xp8a1 | Alignment | not modelled | 30.2 | 19 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**RecA protein-like (ATPase-domain) |
| 51 | c2dflA_ | Alignment | not modelled | 29.9 | 10 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**dna repair and recombination protein rada;<br>**PDBTitle:** crystal structure of left-handed rada filament |
| 52 | d2iida1 | Alignment | not modelled | 29.0 | 24 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD-linked reductases, N-terminal domain |
| 53 | c1t4gA_ | Alignment | not modelled | 28.5 | 13 | **PDB header:**recombination<br>**Chain:** A: **PDB Molecule:**dna repair and recombination protein rada;<br>**PDBTitle:** atpase in complex with amp-pnp |
| 54 | d1duvg2 | Alignment | not modelled | 28.1 | 15 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/ornithine carbamoyltransferase<br>**Family:**Aspartate/ornithine carbamoyltransferase |

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| 55 | d1ae1a_ | Alignment | not modelled | 28.0 | 11 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 56 | d1dxha2 | Alignment | not modelled | 27.2 | 17 | **Fold:**ATC-like<br>**Superfamily:**Aspartate/ornithine carbamoyltransferase<br>**Family:**Aspartate/ornithine carbamoyltransferase |
| 57 | d1xsea_ | Alignment | not modelled | 26.9 | 23 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 58 | c1z2iA_ | Alignment | not modelled | 26.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**malate dehydrogenase;<br>**PDBTitle:** crystal structure of agrobacterium tumefaciens malate2 dehydrogenase, new york structural genomics consortium |
| 59 | d1xu9a_ | Alignment | not modelled | 26.5 | 25 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 60 | c3o26A_ | Alignment | not modelled | 26.2 | 14 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**salutaridine reductase;<br>**PDBTitle:** the structure of salutaridine reductase from papaver somniferum. |
| 61 | c2ha8A_ | Alignment | not modelled | 25.8 | 9 | **PDB header:**rna binding protein<br>**Chain:** A: **PDB Molecule:**tar (hiv-1) rna loop binding protein;<br>**PDBTitle:** methyltransferase domain of human tar (hiv-1) rna binding2 protein 1 |
| 62 | c3nklA_ | Alignment | not modelled | 25.8 | 13 | **PDB header:**oxidoreductase/lyase<br>**Chain:** A: **PDB Molecule:**udp-d-quinovosamine 4-dehydrogenase;<br>**PDBTitle:** crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri |
| 63 | c2vyeA_ | Alignment | not modelled | 25.4 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**replicative dna helicase;<br>**PDBTitle:** crystal structure of the dnac-ssdna complex |
| 64 | d1tyza_ | Alignment | not modelled | 25.4 | 22 | **Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes |
| 65 | d1f2da_ | Alignment | not modelled | 25.3 | 18 | **Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes |
| 66 | d1v8za1 | Alignment | not modelled | 25.0 | 16 | **Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes<br>**Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes |
| 67 | c2y8kA_ | Alignment | not modelled | 24.8 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**carbohydrate binding family 6;<br>**PDBTitle:** structure of ctgh5-cbm6, an arabinoxylan-specific xylanase. |
| 68 | c3g68A_ | Alignment | not modelled | 24.7 | 18 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative phosphosugar isomerase;<br>**PDBTitle:** crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution |
| 69 | c3ldaA_ | Alignment | not modelled | 24.7 | 12 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**dna repair protein rad51;<br>**PDBTitle:** yeast rad51 h352y filament interface mutant |
| 70 | c3euaD_ | Alignment | not modelled | 24.5 | 9 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase;<br>**PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution |
| 71 | c3fkjA_ | Alignment | not modelled | 24.4 | 7 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative phosphosugar isomerases;<br>**PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution |
| 72 | c2recB_ | Alignment | not modelled | 24.3 | 17 | **PDB header:**helicase<br>**PDB COMPND:** |
| 73 | d1ooea_ | Alignment | not modelled | 24.3 | 10 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 74 | c3ijrF_ | Alignment | not modelled | 24.2 | 20 | **PDB header:**oxidoreductase<br>**Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family;<br>**PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+ |
| 75 | c2nm0B_ | Alignment | not modelled | 24.0 | 23 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**probable 3-oxacyl-(acyl-carrier-protein) reductase;<br>**PDBTitle:** crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2) |
| 76 | c3updA_ | Alignment | not modelled | 23.9 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase;<br>**PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus |
| 77 | c3uoeB_ | Alignment | not modelled | 23.8 | 10 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**dehydrogenase;<br>**PDBTitle:** the crystal structure of dehydrogenase from sinorhizobium meliloti |
| 78 | d1qsga_ | Alignment | not modelled | 23.4 | 16 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |

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|---|---|---|---|---|---|---|
| 79 | c3toxG_ | Alignment | not modelled | 23.1 | 19 | **PDB header:**oxidoreductase<br>**Chain:** G: **PDB Molecule:**short chain dehydrogenase;<br>**PDBTitle:** crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021 |
| 80 | c2b4qB_ | Alignment | not modelled | 22.8 | 25 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**rhamnolipids biosynthesis 3-oxoacyl-[acyl-<br>**PDBTitle:** pseudomonas aeruginosa rhlg/nadp active-site complex |
| 81 | d1xrha_ | Alignment | not modelled | 22.6 | 8 | **Fold:**L-sulfolactate dehydrogenase-like<br>**Superfamily:**L-sulfolactate dehydrogenase-like<br>**Family:**L-sulfolactate dehydrogenase-like |
| 82 | d1c0pa1 | Alignment | not modelled | 22.4 | 21 | **Fold:**Nucleotide-binding domain<br>**Superfamily:**Nucleotide-binding domain<br>**Family:**D-aminoacid oxidase, N-terminal domain |
| 83 | d1onfa2 | Alignment | not modelled | 21.5 | 12 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD/NAD-linked reductases, N-terminal and central domains |
| 84 | c2rghA_ | Alignment | not modelled | 21.1 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase;<br>**PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase |
| 85 | d2o8ra3 | Alignment | not modelled | 21.0 | 11 | **Fold:**Phospholipase D/nuclease<br>**Superfamily:**Phospholipase D/nuclease<br>**Family:**Polyphosphate kinase C-terminal domain |
| 86 | d1reoa1 | Alignment | not modelled | 20.9 | 26 | **Fold:**FAD/NAD(P)-binding domain<br>**Superfamily:**FAD/NAD(P)-binding domain<br>**Family:**FAD-linked reductases, N-terminal domain |
| 87 | c2e4gB_ | Alignment | not modelled | 20.4 | 15 | **PDB header:**biosynthetic protein, flavoprotein<br>**Chain:** B: **PDB Molecule:**tryptophan halogenase;<br>**PDBTitle:** rebh with bound l-trp |
| 88 | d1xg5a_ | Alignment | not modelled | 20.3 | 20 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 89 | d1xq1a_ | Alignment | not modelled | 20.0 | 15 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |
| 90 | d2i1qa2 | Alignment | not modelled | 19.8 | 13 | **Fold:**P-loop containing nucleoside triphosphate hydrolases<br>**Superfamily:**P-loop containing nucleoside triphosphate hydrolases<br>**Family:**RecA protein-like (ATPase-domain) |
| 91 | c2v1dA_ | Alignment | not modelled | 19.5 | 32 | **PDB header:**oxidoreductase/repressor<br>**Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1;<br>**PDBTitle:** structural basis of lsd1-corest selectivity in histone h32 recognition |
| 92 | c2xagA_ | Alignment | not modelled | 19.5 | 32 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**lysine-specific histone demethylase 1;<br>**PDBTitle:** crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine |
| 93 | d1nxua_ | Alignment | not modelled | 19.1 | 12 | **Fold:**L-sulfolactate dehydrogenase-like<br>**Superfamily:**L-sulfolactate dehydrogenase-like<br>**Family:**L-sulfolactate dehydrogenase-like |
| 94 | d1a9xa4 | Alignment | not modelled | 19.1 | 18 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 95 | d1iz5a1 | Alignment | not modelled | 18.9 | 18 | **Fold:**DNA clamp<br>**Superfamily:**DNA clamp<br>**Family:**DNA polymerase processivity factor |
| 96 | d1rfma_ | Alignment | not modelled | 18.5 | 20 | **Fold:**L-sulfolactate dehydrogenase-like<br>**Superfamily:**L-sulfolactate dehydrogenase-like<br>**Family:**L-sulfolactate dehydrogenase-like |
| 97 | c2weuD_ | Alignment | not modelled | 18.3 | 14 | **PDB header:**antifungal protein<br>**Chain:** D: **PDB Molecule:**tryptophan 5-halogenase;<br>**PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan |
| 98 | d1plqa1 | Alignment | not modelled | 17.9 | 9 | **Fold:**DNA clamp<br>**Superfamily:**DNA clamp<br>**Family:**DNA polymerase processivity factor |
| 99 | d2c07a1 | Alignment | not modelled | 17.5 | 9 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**Tyrosine-dependent oxidoreductases |