# Phyre2

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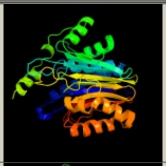
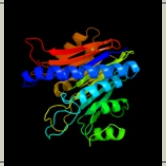
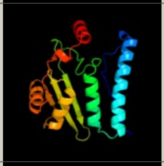
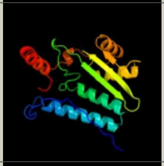
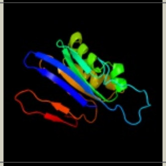
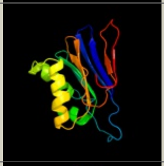
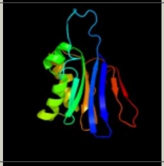
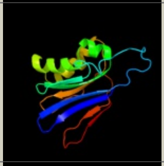
| Email | l.a.kelley@imperial.ac.uk |
| Description | P37595 |
| Date | Thu Jan 5 11:55:41 GMT 2012 |
| Unique Job ID | bdb45a0974b871d2 |

## Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2zakB_ | Alignment |  | 100.0 | 99 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**l-asparaginase precursor;<br>**PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation |
| 2 | c1p4vA_ | Alignment |  | 100.0 | 34 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n(4)-(beta-n-acetylglucosaminyl)-l-asparaginase<br>**PDBTitle:** crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine |
| 3 | c2a8lB_ | Alignment |  | 100.0 | 36 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**threonine aspartase 1;<br>**PDBTitle:** crystal structure of human taspase1 (t234a mutant) |
| 4 | c1t3mA_ | Alignment |  | 100.0 | 100 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative l-asparaginase;<br>**PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli |
| 5 | c2gezE_ | Alignment |  | 100.0 | 40 | **PDB header:**hydrolase<br>**Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit;<br>**PDBTitle:** crystal structure of potassium-independent plant asparaginase |
| 6 | c2zalD_ | Alignment |  | 100.0 | 99 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**l-asparaginase;<br>**PDBTitle:** crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate |
| 7 | c2zalB_ | Alignment |  | 100.0 | 99 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**l-asparaginase;<br>**PDBTitle:** crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate |
| 8 | c1k2xB_ | Alignment |  | 100.0 | 100 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative l-asparaginase;<br>**PDBTitle:** crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene |
| 9 | c1k2xD_ | Alignment |  | 100.0 | 100 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**putative l-asparaginase;<br>**PDBTitle:** crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene |
| 10 | c1jn9D_ | Alignment |  | 100.0 | 100 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**putative l-asparaginase;<br>**PDBTitle:** structure of putative asparaginase encoded by escherichia coli ybik2 gene |
| 11 | c1t3mD_ | Alignment |  | 100.0 | 100 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**putative l-asparaginase;<br>**PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli |

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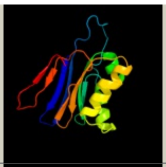
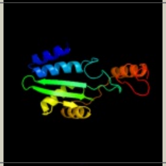
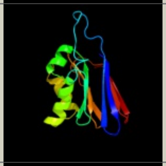
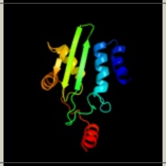
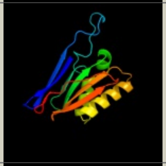
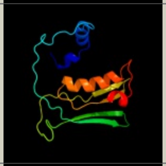
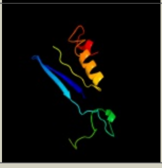
|---|---|---|---|---|---|---|
| 12 | c1jn9B_ | Alignment |  | 100.0 | 100 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative l-asparaginase;<br>**PDBTitle:** structure of putative asparaginase encoded by escherichia coli ybik2 gene |
| 13 | c1t3mB_ | Alignment |  | 100.0 | 100 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**putative l-asparaginase;<br>**PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli |
| 14 | c1apyA_ | Alignment |  | 100.0 | 26 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aspartylglucosaminidase;<br>**PDBTitle:** human aspartylglucosaminidase |
| 15 | c2gezF_ | Alignment |  | 100.0 | 55 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**l-asparaginase beta subunit;<br>**PDBTitle:** crystal structure of potassium-independent plant asparaginase |
| 16 | c2gacA_ | Alignment |  | 100.0 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**glycosylasparaginase;<br>**PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum |
| 17 | c2gacD_ | Alignment |  | 100.0 | 34 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**glycosylasparaginase;<br>**PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum |
| 18 | c1apzB_ | Alignment |  | 100.0 | 32 | **PDB header:**complex (hydrolase/peptide)<br>**Chain:** B: **PDB Molecule:**aspartylglucosaminidase;<br>**PDBTitle:** human aspartylglucosaminidase complex with reaction product |
| 19 | c2e0wA_ | Alignment |  | 97.0 | 19 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase;<br>**PDBTitle:** t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli |
| 20 | c2e0yB_ | Alignment |  | 95.0 | 37 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase;<br>**PDBTitle:** crystal structure of the samarium derivative of mature gamma-2 glutamyltranspeptidase from escherichia coli |
| 21 | d2nlza1 | Alignment | not modelled | 94.6 | 26 | **Fold:**Ntn hydrolase-like<br>**Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases)<br>**Family:**Gamma-glutamyltranspeptidase-like |
| 22 | c2z8jA_ | Alignment | not modelled | 94.5 | 14 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase;<br>**PDBTitle:** crystal structure of escherichia coli gamma-2 glutamyltranspeptidase in complex with azaserine prepared3 in the dark |
| 23 | c2qm6C_ | Alignment | not modelled | 93.3 | 32 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**gamma-glutamyltranspeptidase;<br>**PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase2 in complex with glutamate |
| 24 | c2v36A_ | Alignment | not modelled | 92.9 | 25 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase large chain;<br>**PDBTitle:** crystal structure of gamma-glutamyl transferase from2 bacillus subtilis |
| 25 | c3g9kD_ | Alignment | not modelled | 92.8 | 35 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**capsule biosynthesis protein capd;<br>**PDBTitle:** crystal structure of bacillus anthracis transpeptidase enzyme capd |
| 26 | d2i3oa1 | Alignment | not modelled | 92.6 | 14 | **Fold:**Ntn hydrolase-like<br>**Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases)<br>**Family:**Gamma-glutamyltranspeptidase-like |
| 27 | c3ga9S_ | Alignment | not modelled | 91.9 | 24 | **PDB header:**hydrolase<br>**Chain:** S: **PDB Molecule:**capsule biosynthesis protein capd;<br>**PDBTitle:** crystal structure of bacillus anthracis transpeptidase enzyme capd,2 crystal form ii |
| 28 | d2imha1 | Alignment | not modelled | 91.7 | 20 | **Fold:**Ntn hydrolase-like<br>**Superfamily:**N-terminal nucleophile aminohydrolases (Ntn |

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| 28 | d2fmna1 | Alignment | not modelled | 91.7 | 20 | hydrolases)<br>**Family:**SPO2555-like |
| 29 | c2v36D_ | Alignment | not modelled | 88.3 | 22 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**gamma-glutamyltranspeptidase small chain;<br>**PDBTitle:** crystal structure of gamma-glutamyl transferase from2 bacillus subtilis |
| 30 | c2nqoB_ | Alignment | not modelled | 78.9 | 22 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase;<br>**PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase |
| 31 | d1k4ia_ | Alignment | not modelled | 48.1 | 17 | **Fold:**YrdC/RibB<br>**Superfamily:**YrdC/RibB<br>**Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB |
| 32 | c2otdC_ | Alignment | not modelled | 31.1 | 26 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**glycerophosphodiester phosphodiesterase;<br>**PDBTitle:** the crystal structure of the glycerophosphodiester phosphodiesterase2 from shigella flexneri 2a |
| 33 | d1hw8a2 | Alignment | not modelled | 23.7 | 27 | **Fold:**Substrate-binding domain of HMG-CoA reductase<br>**Superfamily:**Substrate-binding domain of HMG-CoA reductase<br>**Family:**Substrate-binding domain of HMG-CoA reductase |
| 34 | c3mioA_ | Alignment | not modelled | 23.2 | 13 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase;<br>**PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00 |
| 35 | c1yy3A_ | Alignment | not modelled | 21.5 | 22 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase-<br>**PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea) |
| 36 | d1tqha_ | Alignment | not modelled | 21.0 | 22 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Carboxylesterase/lipase |
| 37 | c3cdkD_ | Alignment | not modelled | 19.0 | 32 | **PDB header:**transferase<br>**Chain:** D: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase<br>**PDBTitle:** crystal structure of the co-expressed succinyl-coa2 transferase a and b complex from bacillus subtilis |
| 38 | d1tksa_ | Alignment | not modelled | 19.0 | 11 | **Fold:**YrdC/RibB<br>**Superfamily:**YrdC/RibB<br>**Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB |
| 39 | d1g57a_ | Alignment | not modelled | 18.5 | 19 | **Fold:**YrdC/RibB<br>**Superfamily:**YrdC/RibB<br>**Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB |
| 40 | d2nn6h2 | Alignment | not modelled | 16.6 | 20 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Ribosomal L27 protein-like<br>**Family:**ECR1 N-terminal domain-like |
| 41 | d2djia1 | Alignment | not modelled | 16.6 | 21 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 42 | d1k25a4 | Alignment | not modelled | 16.2 | 13 | **Fold:**beta-lactamase/transpeptidase-like<br>**Superfamily:**beta-lactamase/transpeptidase-like<br>**Family:**beta-Lactamase/D-ala carboxypeptidase |
| 43 | c3m1eA_ | Alignment | not modelled | 16.1 | 18 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**hth-type transcriptional regulator benm;<br>**PDBTitle:** crystal structure of benm_dbd |
| 44 | d2ihta1 | Alignment | not modelled | 15.8 | 25 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 45 | d1azwa_ | Alignment | not modelled | 15.4 | 54 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Proline iminopeptidase-like |
| 46 | d1t9ba1 | Alignment | not modelled | 15.3 | 19 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 47 | d1dqaa4 | Alignment | not modelled | 15.2 | 27 | **Fold:**Substrate-binding domain of HMG-CoA reductase<br>**Superfamily:**Substrate-binding domain of HMG-CoA reductase<br>**Family:**Substrate-binding domain of HMG-CoA reductase |
| 48 | d2phna1 | Alignment | not modelled | 14.8 | 25 | **Fold:**CofE-like<br>**Superfamily:**CofE-like<br>**Family:**CofE-like |
| 49 | d1kyqa2 | Alignment | not modelled | 14.8 | 30 | **Fold:**Siroheme synthase middle domains-like<br>**Superfamily:**Siroheme synthase middle domains-like<br>**Family:**Siroheme synthase middle domains-like |
| 50 | c2qruA_ | Alignment | not modelled | 14.7 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis |
| 51 | c1qgeD_ | Alignment | not modelled | 14.6 | 46 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase);<br>**PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase |
| 52 | c3hxkB_ | Alignment | not modelled | 14.5 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**sugar hydrolase;<br>**PDBTitle:** crystal structure of a sugar hydrolase (yeeb) from2 lactococcus lactis, northeast structural genomics3 consortium target kr108 |
|  |  |  |  |  |  | **PDB header:**hydrolase |

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| 53 | c3fnbB_ | Alignment | not modelled | 14.3 | 18 | **Chain:** B: **PDB Molecule:**acylaminoacyl peptidase smu_737;<br>**PDBTitle:** crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159 |
| 54 | d1n9ba_ | Alignment | not modelled | 14.0 | 19 | **Fold:**beta-lactamase/transpeptidase-like<br>**Superfamily:**beta-lactamase/transpeptidase-like<br>**Family:**beta-Lactamase/D-ala carboxypeptidase |
| 55 | c3ms6A_ | Alignment | not modelled | 13.9 | 27 | **PDB header:**protein binding<br>**Chain:** A: **PDB Molecule:**hepatitis b virus x-interacting protein;<br>**PDBTitle:** crystal structure of hepatitis b x-interacting protein (hbxip) |
| 56 | d1zpda1 | Alignment | not modelled | 13.8 | 19 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 57 | d2nn6i2 | Alignment | not modelled | 13.8 | 25 | **Fold:**Barrel-sandwich hybrid<br>**Superfamily:**Ribosomal L27 protein-like<br>**Family:**ECR1 N-terminal domain-like |
| 58 | d1hw8c2 | Alignment | not modelled | 13.7 | 27 | **Fold:**Substrate-binding domain of HMG-CoA reductase<br>**Superfamily:**Substrate-binding domain of HMG-CoA reductase<br>**Family:**Substrate-binding domain of HMG-CoA reductase |
| 59 | c3bitA_ | Alignment | not modelled | 13.6 | 19 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**fact complex subunit spt16;<br>**PDBTitle:** crystal structure of yeast spt16 n-terminal domain |
| 60 | d2ez9a1 | Alignment | not modelled | 13.5 | 16 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 61 | d1wjsa_ | Alignment | not modelled | 13.3 | 13 | **Fold:**SH3-like barrel<br>**Superfamily:**Tudor/PWWP/MBT<br>**Family:**MBT repeat |
| 62 | c3ue3A_ | Alignment | not modelled | 13.3 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**septum formation, penicillin binding protein 3,<br>**PDBTitle:** crystal structure of acinetobacter baumanni pbp3 |
| 63 | c2op8A_ | Alignment | not modelled | 13.2 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**probable tautomerase ywhb;<br>**PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase |
| 64 | c2gzqA_ | Alignment | not modelled | 13.0 | 12 | **PDB header:**lipid binding protein<br>**Chain:** A: **PDB Molecule:**phosphatidylethanolamine-binding protein;<br>**PDBTitle:** phosphatidylethanolamine-binding protein from plasmodium vivax |
| 65 | c1kyqC_ | Alignment | not modelled | 12.9 | 28 | **PDB header:**oxidoreductase, lyase<br>**Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8;<br>**PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis. |
| 66 | c1w7vD_ | Alignment | not modelled | 12.9 | 24 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**xaa-pro aminopeptidase;<br>**PDBTitle:** znmg substituted aminopeptidase p from e. coli |
| 67 | c1alnA_ | Alignment | not modelled | 12.6 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cytidine deaminase;<br>**PDBTitle:** crystal structure of cytidine deaminase complexed with 3-deazacytidine |
| 68 | d1qlwa_ | Alignment | not modelled | 12.5 | 27 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**A novel bacterial esterase |
| 69 | c1hwjB_ | Alignment | not modelled | 12.3 | 27 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**hmg-coa reductase;<br>**PDBTitle:** complex of the catalytic portion of human hmg-coa reductase2 with cerivastatin |
| 70 | c3dclC_ | Alignment | not modelled | 12.2 | 27 | **PDB header:**structural genomics, unknown function<br>**Chain:** C: **PDB Molecule:**tm1086;<br>**PDBTitle:** crystal structure of tm1086 |
| 71 | c3cd0B_ | Alignment | not modelled | 12.2 | 27 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**3-hydroxy-3-methylglutaryl-coenzyme a reductase;<br>**PDBTitle:** thermodynamic and structure guided design of statin hmg-coa2 reductase inhibitors |
| 72 | d1pvda1 | Alignment | not modelled | 12.1 | 13 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 73 | d2ji7a1 | Alignment | not modelled | 12.0 | 34 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 74 | c2l09A_ | Alignment | not modelled | 12.0 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**asr4154 protein;<br>**PDBTitle:** solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143 |
| 75 | d2bgra2 | Alignment | not modelled | 11.8 | 9 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**DPP6 catalytic domain-like |
| 76 | d1dosa_ | Alignment | not modelled | 11.7 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Aldolase<br>**Family:**Class II FBP aldolase |
| 77 | c3cb5A_ | Alignment | not modelled | 11.7 | 14 | **PDB header:**transcription<br>**Chain:** A: **PDB Molecule:**fact complex subunit spt16;<br>**PDBTitle:** crystal structure of the s. pombe peptidase homology domain of fact2 complex subunit spt16 (form a) |
| 78 | c3h04A_ | Alignment | not modelled | 11.4 | 50 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50 |
| | | | | | | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; |

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| 79 | c2x4kB_ | Alignment | not modelled | 11.3 | 25 | **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa) |
| 80 | d1bjpa_ | Alignment | not modelled | 11.0 | 23 | **Fold:**Tautomerase/MIF<br>**Superfamily:**Tautomerase/MIF<br>**Family:**4-oxalocrotonate tautomerase-like |
| 81 | c2g6pA_ | Alignment | not modelled | 11.0 | 2 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**methionine aminopeptidase 1;<br>**PDBTitle:** crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative |
| 82 | c2gz5A_ | Alignment | not modelled | 11.0 | 2 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**methionine aminopeptidase 1;<br>**PDBTitle:** human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang |
| 83 | d1alna1 | Alignment | not modelled | 10.7 | 19 | **Fold:**Cytidine deaminase-like<br>**Superfamily:**Cytidine deaminase-like<br>**Family:**Cytidine deaminase |
| 84 | d1pjaa_ | Alignment | not modelled | 10.6 | 42 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Thioesterases |
| 85 | c1pjaA_ | Alignment | not modelled | 10.6 | 42 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**palmitoyl-protein thioesterase 2 precursor;<br>**PDBTitle:** the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2) |
| 86 | d1snna_ | Alignment | not modelled | 10.4 | 16 | **Fold:**YrdC/RibB<br>**Superfamily:**YrdC/RibB<br>**Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB |
| 87 | c3oc2A_ | Alignment | not modelled | 10.3 | 23 | **PDB header:**penicillin-binding protein<br>**Chain:** A: **PDB Molecule:**penicillin-binding protein 3;<br>**PDBTitle:** crystal structure of penicillin-binding protein 3 from pseudomonas2 aeruginosa |
| 88 | d1oxwa_ | Alignment | not modelled | 10.3 | 45 | **Fold:**FabD/lysophospholipase-like<br>**Superfamily:**FabD/lysophospholipase-like<br>**Family:**Patatin |
| 89 | d2pmra1 | Alignment | not modelled | 10.2 | 14 | **Fold:**immunoglobulin/albumin-binding domain-like<br>**Superfamily:**AF1782-like<br>**Family:**AF1782-like |
| 90 | c3llcA_ | Alignment | not modelled | 10.0 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative hydrolase;<br>**PDBTitle:** crystal structure of putative hydrolase (yp_002548124.1) from2 agrobacterium vitis s4 at 1.80 a resolution |
| 91 | d1q6za1 | Alignment | not modelled | 9.9 | 9 | **Fold:**DHS-like NAD/FAD-binding domain<br>**Superfamily:**DHS-like NAD/FAD-binding domain<br>**Family:**Pyruvate oxidase and decarboxylase, middle domain |
| 92 | c2jz5A_ | Alignment | not modelled | 9.8 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein vpa0419;<br>**PDBTitle:** nmr solution structure of protein vpa0419 from vibrio2 parahaemolyticus. northeast structural genomics target3 vpr68 |
| 93 | c3dgsA_ | Alignment | not modelled | 9.6 | 31 | **PDB header:**viral protein<br>**Chain:** A: **PDB Molecule:**coat protein a;<br>**PDBTitle:** changing the determinants of protein stability from2 covalent to non-covalent interactions by in-vitro3 evolution: a structural and energetic analysis |
| 94 | c1chmA_ | Alignment | not modelled | 9.6 | 22 | **PDB header:**creatinase<br>**Chain:** A: **PDB Molecule:**creatine amidinohydrolase;<br>**PDBTitle:** enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures |
| 95 | c2kdvA_ | Alignment | not modelled | 9.6 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase;<br>**PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli |
| 96 | d2nn6c2 | Alignment | not modelled | 9.6 | 17 | **Fold:**Ribonuclease PH domain 2-like<br>**Superfamily:**Ribonuclease PH domain 2-like<br>**Family:**Ribonuclease PH domain 2-like |
| 97 | c3gy9A_ | Alignment | not modelled | 9.6 | 21 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase;<br>**PDBTitle:** crystal structure of putative acetyltransferase (yp_001815201.1) from2 exiguobacterium sp. 255-15 at 1.52 a resolution |
| 98 | c2z0rA_ | Alignment | not modelled | 9.5 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0547;<br>**PDBTitle:** crystal structure of hypothetical protein ttha0547 |
| 99 | d1xkla_ | Alignment | not modelled | 9.5 | 31 | **Fold:**alpha/beta-Hydrolases<br>**Superfamily:**alpha/beta-Hydrolases<br>**Family:**Hydroxynitrile lyase-like |