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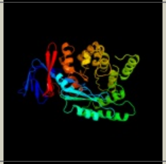
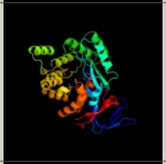
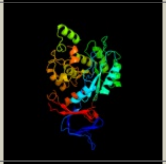
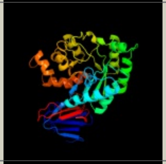
|---|---|
| Email | l.a.kelley@imperial.ac.uk |
| Description | P16689 |
| Date | Thu Jan 5 11:35:39 GMT 2012 |
| Unique Job ID | 9f328b722b71a9ec |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c3nqbB_ | Alignment |  | 100.0 | 20 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**adenine deaminase 2;<br>**PDBTitle:** crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58) |
| 2 | c1nfgA_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**d-hydantoinase;<br>**PDBTitle:** structure of d-hydantoinase |
| 3 | c1gkpD_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**hydantoinase;<br>**PDBTitle:** d-hydantoinase (dihydropyrimidinase) from thermus sp. in2 space group c2221 |
| 4 | c2pajA_ | Alignment |  | 100.0 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative cytosine/guanine deaminase;<br>**PDBTitle:** crystal structure of an amidohydrolase from an environmental sample of2 sargasso sea |
| 5 | c3be7B_ | Alignment |  | 100.0 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**zn-dependent arginine carboxypeptidase;<br>**PDBTitle:** crystal structure of zn-dependent arginine carboxypeptidase |
| 6 | c2vr2A_ | Alignment |  | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydropyrimidinase;<br>**PDBTitle:** human dihydropyrimidinase |
| 7 | c2gseC_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**dihydropyrimidinase-related protein 2;<br>**PDBTitle:** crystal structure of human dihydropyrimidinease-like 2 |
| 8 | c2ftwA_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydropyrimidine amidohydrolase;<br>**PDBTitle:** crystal structure of dihydropyrimidinase from dictyostelium discoideum |
| 9 | c3hpaB_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**amidohydrolase;<br>**PDBTitle:** crystal structure of an amidohydrolase gi:44264246 from an2 evironmental sample of sargasso sea |
| 10 | c2bb0A_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**imidazolonepropionase;<br>**PDBTitle:** structure of imidazolonepropionase from bacillus subtilis |
| 11 | c1k1dF_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** F: **PDB Molecule:**d-hydantoinase;<br>**PDBTitle:** crystal structure of d-hydantoinase |

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| 12 | c3ooqC_ | Alignment |  | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**amidohydrolase;<br>**PDBTitle:** crystal structure of amidohydrolase from thermotoga maritima msb8 |
| 13 | c3gnhA_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**l-lysine, l-arginine carboxypeptidase cc2672;<br>**PDBTitle:** crystal structure of l-lysine, l-arginine carboxypeptidase cc2672 from2 caulobacter crescentus cb15 complexed with n-methyl phosphonate3 derivative of l-arginine. |
| 14 | c3hm7A_ | Alignment |  | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**allantoinase;<br>**PDBTitle:** crystal structure of allantoinase from bacillus halodurans c-125 |
| 15 | c2fvmA_ | Alignment |  | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydropyrimidinase;<br>**PDBTitle:** crystal structure of dihydropyrimidinase from saccharomyces kluyveri2 in complex with the reaction product n-carbamyl-beta-alanine |
| 16 | c3dc8B_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**dihydropyrimidinase;<br>**PDBTitle:** crystal structure of dihydropyrimidinase from sinorhizobium meliloti |
| 17 | c1gkrA_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**non-atp dependent l-selective hydantoinase;<br>**PDBTitle:** l-hydantoinase (dihydropyrimidinase) from arthrobacter2 aurescens |
| 18 | c3lsbA_ | Alignment |  | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**triazine hydrolase;<br>**PDBTitle:** crystal structure of the mutant e241q of atrazine chlorohydrolase trzn2 from arthrobacter aurescens tc1 complexed with zinc and ametrin |
| 19 | c3e74D_ | Alignment |  | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**allantoinase;<br>**PDBTitle:** crystal structure of e. coli allantoinase with iron ions at2 the metal center |
| 20 | c2i9uA_ | Alignment |  | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cytosine/guanine deaminase related protein;<br>**PDBTitle:** crystal structure of guanine deaminase from c. acetobutylicum with2 bound guanine in the active site |
| 21 | c3griB_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** the crystal structure of a dihydroorotase from staphylococcus aureus |
| 22 | c2q09A_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**imidazolonepropionase;<br>**PDBTitle:** crystal structure of imidazolonepropionase from environmental sample2 with bound inhibitor 3-(2,5-dioxo-imidazolidin-4-yl)-propionic acid |
| 23 | c3d6nA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase/transferase<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase |
| 24 | c2gwnA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** the structure of putative dihydroorotase from porphyromonas2 gingivalis. |
| 25 | c3lnpA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**amidohydrolase family protein olei01672_1_465;<br>**PDBTitle:** crystal structure of amidohydrolase family protein2 olei01672_1_465 from oleispira antarctica |
| 26 | c1p1mA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein tm0936;<br>**PDBTitle:** structure of thermotoga maritima amidohydrolase tm09362 bound to ni and methionine |
| 27 | c2gokA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**imidazolonepropionase;<br>**PDBTitle:** crystal structure of the imidazolonepropionase from agrobacterium2 tumefaciens at 1.87 a resolution |
| 28 | c1xrfA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydroorotase; |

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| 28 | c1xrtA_ | Alignment | not modelled | 100.0 | 16 | **PDBTitle:** the crystal structure of a novel, latent dihydroorotase from aquifex2 aeolicus at 1.7 a resolution |
| 29 | c2r8cB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative amidohydrolase;<br>**PDBTitle:** crystal structure of uncharacterized protein eaj56179 |
| 30 | c2vhlB_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase;<br>**PDBTitle:** the three-dimensional structure of the n-acetylglucosamine-2 6-phosphate deacetylase from bacillus subtilis |
| 31 | c3mpgB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** dihydroorotase from bacillus anthracis |
| 32 | c2aqoB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**isoaspartyl dipeptidase;<br>**PDBTitle:** crystal structure of e. coli isoaspartyl dipeptidase mutant e77q |
| 33 | c2z00A_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** crystal structure of dihydroorotase from thermus thermophilus |
| 34 | c3e0lB_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**guanine deaminase;<br>**PDBTitle:** computationally designed ammelide deaminase |
| 35 | c2qs8A_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**xaa-pro dipeptidase;<br>**PDBTitle:** crystal structure of a xaa-pro dipeptidase with bound2 methionine in the active site |
| 36 | c3v7pA_ | Alignment | not modelled | 100.0 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**amidohydrolase family protein;<br>**PDBTitle:** crystal structure of amidohydrolase nis_0429 (target efi-500396) from2 nitratiruptor sp. sb155-2 |
| 37 | c2p50C_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase;<br>**PDBTitle:** crystal structure of n-acetyl-d-glucosamine-6-phosphate deacetylase2 liganded with zn |
| 38 | c3feqB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative amidohydrolase;<br>**PDBTitle:** crystal structure of uncharacterized protein eah89906 |
| 39 | c1r9yA_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**cytosine deaminase;<br>**PDBTitle:** bacterial cytosine deaminase d314a mutant. |
| 40 | c2ubpC_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**protein (urease alpha subunit);<br>**PDBTitle:** structure of native urease from bacillus pasteurii |
| 41 | c2qt3A_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-isopropylammelide isopropyl amidohydrolase;<br>**PDBTitle:** crystal structure of n-isopropylammelide isopropylaminohydrolase atzc2 from pseudomonas sp. strain adp complexed with zn |
| 42 | c1e9yB_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**urease subunit beta;<br>**PDBTitle:** crystal structure of helicobacter pylori urease in complex with2 acetohydroxamic acid |
| 43 | c2p9bA_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**possible prolidase;<br>**PDBTitle:** crystal structure of putative prolidase from2 bifidobacterium longum |
| 44 | c3gipB_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**n-acyl-d-glutamate deacylase;<br>**PDBTitle:** crystal structure of n-acyl-d-glutamate deacylase from2 bordetella bronchiseptica complexed with zinc, acetate and3 formate ions. |
| 45 | c2oodA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**blr3880 protein;<br>**PDBTitle:** crystal structure of guanine deaminase from bradyrhizobium japonicum |
| 46 | c2vunC_ | Alignment | not modelled | 100.0 | 17 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**enamidase;<br>**PDBTitle:** the crystal structure of enamidase at 1.9 a resolution - a2 new member of the amidohydrolase superfamily |
| 47 | c3egjA_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase;<br>**PDBTitle:** n-acetylglucosamine-6-phosphate deacetylase from vibrio cholerae. |
| 48 | c1o12B_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**n-acetylglucosamine-6-phosphate deacetylase;<br>**PDBTitle:** crystal structure of n-acetylglucosamine-6-phosphate2 deacetylase (tm0814) from thermotoga maritima at 2.5 a3 resolution |
| 49 | c1fwcC_ | Alignment | not modelled | 100.0 | 15 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**urease;<br>**PDBTitle:** klebsiella aerogenes urease, c319a variant at ph 8.5 |
| 50 | c3la4A_ | Alignment | not modelled | 100.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**urease;<br>**PDBTitle:** crystal structure of the first plant urease from jack bean (canavalia2 ensiformis) |
| 51 | c2icsA_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**adenine deaminase;<br>**PDBTitle:** crystal structure of an adenine deaminase |
| 52 | c1rjqA_ | Alignment | not modelled | 100.0 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**d-aminoacylase;<br>**PDBTitle:** the crystal structure of the d-aminoacylase mutant d366a |

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| 53 | c3mduA_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**n-formimino-l-glutamate iminohydrolase;<br>**PDBTitle:** the structure of n-formimino-l-glutamate iminohydrolase from2 pseudomonas aeruginosa complexed with n-guanidino-l-glutamate |
| 54 | c2ogjB_ | Alignment | not modelled | 100.0 | 19 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** crystal structure of a dihydroorotase |
| 55 | c3etkA_ | Alignment | not modelled | 100.0 | 11 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uncharacterized metal-dependent hydrolase;<br>**PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus furiosus |
| 56 | c3ighX_ | Alignment | not modelled | 100.0 | 12 | **PDB header:**hydrolase<br>**Chain:** X: **PDB Molecule:**uncharacterized metal-dependent hydrolase;<br>**PDBTitle:** crystal structure of an uncharacterized metal-dependent2 hydrolase from pyrococcus horikoshii ot3 |
| 57 | c2imrA_ | Alignment | not modelled | 100.0 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein dr_0824;<br>**PDBTitle:** crystal structure of amidohydrolase dr_0824 from2 deinococcus radiodurans |
| 58 | d2uz9a2 | Alignment | not modelled | 99.8 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**SAH/MTA deaminase-like |
| 59 | c3msrA_ | Alignment | not modelled | 99.8 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**amidohydrolases;<br>**PDBTitle:** the crystal structure of an amidohydrolase from mycoplasma synoviae |
| 60 | d1gkpa2 | Alignment | not modelled | 99.7 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 61 | d3be7a2 | Alignment | not modelled | 99.7 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Zn-dependent arginine carboxypeptidase-like |
| 62 | d2paja2 | Alignment | not modelled | 99.7 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**SAH/MTA deaminase-like |
| 63 | d2i9ua2 | Alignment | not modelled | 99.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**SAH/MTA deaminase-like |
| 64 | d4ubpc2 | Alignment | not modelled | 99.7 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**alpha-subunit of urease, catalytic domain |
| 65 | d2r8ca2 | Alignment | not modelled | 99.7 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Zn-dependent arginine carboxypeptidase-like |
| 66 | d2ooda2 | Alignment | not modelled | 99.7 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**SAH/MTA deaminase-like |
| 67 | d2qs8a2 | Alignment | not modelled | 99.7 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Zn-dependent arginine carboxypeptidase-like |
| 68 | d2bb0a2 | Alignment | not modelled | 99.7 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Imidazolonepropionase-like |
| 69 | d1ra0a2 | Alignment | not modelled | 99.6 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Cytosine deaminase catalytic domain |
| 70 | d1kcxa2 | Alignment | not modelled | 99.6 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 71 | d2puza2 | Alignment | not modelled | 99.6 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Imidazolonepropionase-like |
| 72 | c3pnuA_ | Alignment | not modelled | 99.6 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni. |
| 73 | d2ftwa2 | Alignment | not modelled | 99.6 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 74 | d2imra2 | Alignment | not modelled | 99.6 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**DR0824-like |
| 75 | d2q09a2 | Alignment | not modelled | 99.6 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Imidazolonepropionase-like |
| 76 | d2p9ba2 | Alignment | not modelled | 99.6 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Imidazolonepropionase-like |
| 77 | d1p1ma2 | Alignment | not modelled | 99.6 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**SAH/MTA deaminase-like |
| 78 | d1un7a2 | Alignment | not modelled | 99.6 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain |
| | | | | | | **Fold:**TIM beta/alpha-barrel |

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| 79 | d1ynya2 | Alignment | not modelled | 99.6 | 13 | **Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 80 | d1ejxc1 | Alignment | not modelled | 99.5 | 21 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**alpha-Subunit of urease |
| 81 | c3jzeC_ | Alignment | not modelled | 99.5 | 11 | **PDB header:**hydrolase<br>**Chain:** C: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** 1.8 angstrom resolution crystal structure of dihydroorotase (pyrc)2 from salmonella enterica subsp. enterica serovar typhimurium str. lt2 |
| 82 | d2fvka1 | Alignment | not modelled | 99.5 | 26 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase) |
| 83 | d1nfga2 | Alignment | not modelled | 99.5 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 84 | d2eg6a1 | Alignment | not modelled | 99.5 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Dihydroorotase |
| 85 | d1e9yb1 | Alignment | not modelled | 99.5 | 22 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**alpha-Subunit of urease |
| 86 | d1xrta2 | Alignment | not modelled | 99.5 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 87 | d1yrra2 | Alignment | not modelled | 99.5 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain |
| 88 | d1onwa2 | Alignment | not modelled | 99.5 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Isoaspartyl dipeptidase, catalytic domain |
| 89 | d1k1da2 | Alignment | not modelled | 99.5 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 90 | d1onwa1 | Alignment | not modelled | 99.5 | 19 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Isoaspartyl dipeptidase |
| 91 | d1gkra2 | Alignment | not modelled | 99.5 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 92 | c3ggmB_ | Alignment | not modelled | 99.4 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein bt9727_2919;<br>**PDBTitle:** crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b |
| 93 | d1i0da_ | Alignment | not modelled | 99.4 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Phosphotriesterase-like |
| 94 | d2p9ba1 | Alignment | not modelled | 99.4 | 14 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Imidazolonepropionase-like |
| 95 | d1yrra1 | Alignment | not modelled | 99.4 | 17 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA |
| 96 | d2r8ca1 | Alignment | not modelled | 99.4 | 21 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Zn-dependent arginine carboxypeptidase-like |
| 97 | d2icsa2 | Alignment | not modelled | 99.4 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Adenine deaminase-like |
| 98 | d2fvka2 | Alignment | not modelled | 99.4 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 99 | d2d2ja1 | Alignment | not modelled | 99.3 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Phosphotriesterase-like |
| 100 | d1k1da1 | Alignment | not modelled | 99.3 | 21 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase) |
| 101 | c1pscA_ | Alignment | not modelled | 99.2 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphotriesterase;<br>**PDBTitle:** phosphotriesterase from pseudomonas diminuta |
| 102 | d2ftwa1 | Alignment | not modelled | 99.2 | 17 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase) |
| 103 | d1ynya1 | Alignment | not modelled | 99.2 | 15 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase) |
| 104 | d1o12a2 | Alignment | not modelled | 99.2 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain |
| 105 | d1gkpa1 | Alignment | not modelled | 99.1 | 15 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase) |
| 106 | c3pnzD | Alignment | not modelled | 99.0 | 14 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**phosphotriesterase family protein; |

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|---|---|---|---|---|---|---|
| 106 | c3pnzD_ | Alignment | not modelled | 99.0 | 14 | **PDBTitle:** crystal structure of the lactonase lmo2620 from listeria monocytogenes |
| 107 | c2zc1A_ | Alignment | not modelled | 99.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphotriesterase;<br>**PDBTitle:** organophosphorus hydrolase from deinococcus radiodurans |
| 108 | c3f4cA_ | Alignment | not modelled | 99.0 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**organophosphorus hydrolase;<br>**PDBTitle:** crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound |
| 109 | d1kcxa1 | Alignment | not modelled | 99.0 | 11 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase) |
| 110 | d1bf6a_ | Alignment | not modelled | 99.0 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Phosphotriesterase-like |
| 111 | c3ou8B_ | Alignment | not modelled | 98.9 | 12 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**adenosine deaminase;<br>**PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa |
| 112 | d1m7ja1 | Alignment | not modelled | 98.9 | 18 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**D-aminoacylase |
| 113 | c3ou8A_ | Alignment | not modelled | 98.8 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**adenosine deaminase;<br>**PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa |
| 114 | d1m7ja3 | Alignment | not modelled | 98.8 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**D-aminoacylase, catalytic domain |
| 115 | c2vc7A_ | Alignment | not modelled | 98.7 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**aryldialkylphosphatase;<br>**PDBTitle:** structural basis for natural lactonase and promiscuous2 phosphotriesterase activities |
| 116 | d3be7a1 | Alignment | not modelled | 98.7 | 20 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Zn-dependent arginine carboxypeptidase-like |
| 117 | d2paja1 | Alignment | not modelled | 98.6 | 15 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**SAH/MTA deaminase-like |
| 118 | d2bb0a1 | Alignment | not modelled | 98.6 | 20 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Imidazolonepropionase-like |
| 119 | d1nfga1 | Alignment | not modelled | 98.4 | 21 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase) |
| 120 | d1p1ma1 | Alignment | not modelled | 98.2 | 23 | **Fold:**Composite domain of metallo-dependent hydrolases<br>**Superfamily:**Composite domain of metallo-dependent hydrolases<br>**Family:**SAH/MTA deaminase-like |