# Phyre2

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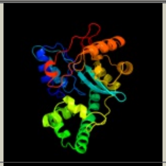
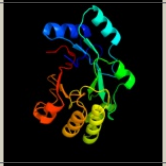
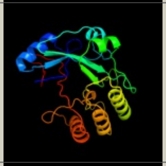
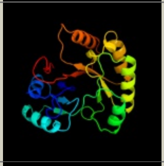
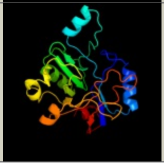
| Email | l.a.kelley@imperial.ac.uk |
| Description | P77766 |
| Date | Thu Jan 5 12:32:40 GMT 2012 |
| Unique Job ID | fdeb84a6611a7770 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | c2yb1A_ | Alignment |  | 100.0 | 40 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**amidohydrolase;<br>**PDBTitle:** structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate. |
| 2 | c3e0fA_ | Alignment |  | 100.0 | 28 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative metal-dependent phosphoesterase;<br>**PDBTitle:** crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution |
| 3 | c3dcpB_ | Alignment |  | 100.0 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**histidinol-phosphatase;<br>**PDBTitle:** crystal structure of the putative histidinol phosphatase2 hisk from listeria monocytogenes. northeast structural3 genomics consortium target lmr141. |
| 4 | c2yz5B_ | Alignment |  | 100.0 | 22 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**histidinol phosphatase;<br>**PDBTitle:** histidinol phosphate phosphatase complexed with phosphate |
| 5 | c2w9mB_ | Alignment |  | 99.9 | 19 | **PDB header:**dna replication<br>**Chain:** B: **PDB Molecule:**polymerase x;<br>**PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans |
| 6 | d1m65a_ | Alignment |  | 99.9 | 25 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**PHP domain-like<br>**Family:**PHP domain |
| 7 | c3qy6A_ | Alignment |  | 99.9 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase ywqe;<br>**PDBTitle:** crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases |
| 8 | c2wjeA_ | Alignment |  | 99.9 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb;<br>**PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4. |
| 9 | c3e38A_ | Alignment |  | 99.9 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**two-domain protein containing predicted php-like metal-<br>**PDBTitle:** crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution |
| 10 | c2hnhA_ | Alignment |  | 99.9 | 20 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit;<br>**PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii |
| 11 | c2anuA_ | Alignment |  | 99.9 | 28 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**hypothetical protein tm0559;<br>**PDBTitle:** crystal structure of predicted metal-dependent phosphoesterase (php2 family) (tm0559) from thermotoga maritima at 2.40 a resolution |

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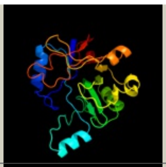
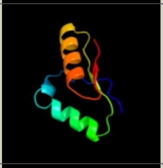
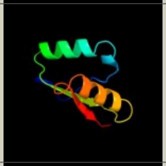
| 12 | d2anua1 | Alignment |  | 99.9 | 28 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**PHP domain-like<br>**Family:**PHP domain |
| 13 | c3e0dA_ | Alignment |  | 99.8 | 23 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha;<br>**PDBTitle:** insights into the replisome from the crystal structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit |
| 14 | c3f2cA_ | Alignment |  | 99.8 | 18 | **PDB header:**transferase/dna<br>**Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc;<br>**PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn |
| 15 | d1v77a_ | Alignment |  | 89.7 | 10 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**PHP domain-like<br>**Family:**RNase P subunit p30 |
| 16 | d1yixa1 | Alignment |  | 89.2 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**TatD Mg-dependent DNase-like |
| 17 | d1xwya1 | Alignment |  | 87.6 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**TatD Mg-dependent DNase-like |
| 18 | c3ipwA_ | Alignment |  | 87.4 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**hydrolase tatd family protein;<br>**PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica |
| 19 | c2y1hA_ | Alignment |  | 87.0 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn3;<br>**PDBTitle:** crystal structure of the human tatd-domain protein 3 (tatdn3) |
| 20 | c2xioA_ | Alignment |  | 85.7 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1;<br>**PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a |
| 21 | c3e2vA_ | Alignment | not modelled | 85.7 | 27 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**3'-5'-exonuclease;<br>**PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae |
| 22 | c2gzxB_ | Alignment | not modelled | 84.4 | 20 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative tatd related dnase;<br>**PDBTitle:** crystal structure of the tatd deoxyribonuclease mw0446 from2 staphylococcus aureus. northeast structural genomics consortium3 target zr237. |
| 23 | d1xrta2 | Alignment | not modelled | 83.7 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 24 | d1zzma1 | Alignment | not modelled | 83.3 | 26 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**TatD Mg-dependent DNase-like |
| 25 | c3a24A_ | Alignment | not modelled | 82.0 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-galactosidase;<br>**PDBTitle:** crystal structure of bt1871 retaining glycosidase |
| 26 | d1j6oa_ | Alignment | not modelled | 81.2 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**TatD Mg-dependent DNase-like |
| 27 | c3rcmA_ | Alignment | not modelled | 79.4 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**tatd family hydrolase;<br>**PDBTitle:** crystal structure of efi target 500140:tatd family hydrolase from2 pseudomonas putida |
| 28 | d1bf6a_ | Alignment | not modelled | 78.9 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Phosphotriesterase-like |

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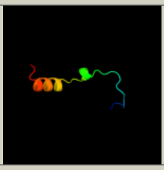
| 29 | d1qwga_ | Alignment | not modelled | 78.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA<br>**Family:**(2r)-phospho-3-sulfolactate synthase ComA |
| 30 | d2ffia1 | Alignment | not modelled | 78.0 | 9 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**PP1699/LP2961-like |
| 31 | d1gkra2 | Alignment | not modelled | 74.5 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 32 | d2icsa2 | Alignment | not modelled | 73.2 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Adenine deaminase-like |
| 33 | d1ynya2 | Alignment | not modelled | 72.1 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 34 | d1k1da2 | Alignment | not modelled | 71.5 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 35 | d1oi7a1 | Alignment | not modelled | 69.5 | 6 | **Fold:**NAD(P)-binding Rossmann-fold domains<br>**Superfamily:**NAD(P)-binding Rossmann-fold domains<br>**Family:**CoA-binding domain |
| 36 | d2fvka2 | Alignment | not modelled | 68.8 | 26 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 37 | d1vfla1 | Alignment | not modelled | 68.7 | 23 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Adenosine/AMP deaminase |
| 38 | c2zq0B_ | Alignment | not modelled | 68.5 | 8 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb);<br>**PDBTitle:** crystal structure of susb complexed with acarbose |
| 39 | d1a4ma_ | Alignment | not modelled | 68.5 | 27 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Adenosine/AMP deaminase |
| 40 | d1o12a2 | Alignment | not modelled | 67.6 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain |
| 41 | d2amxa1 | Alignment | not modelled | 67.1 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Adenosine/AMP deaminase |
| 42 | c3rysA_ | Alignment |  | 66.0 | 30 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**adenosine deaminase 1;<br>**PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens |
| 43 | d1nfga2 | Alignment | not modelled | 64.6 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 44 | c3ogrA_ | Alignment | not modelled | 64.6 | 11 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose |
| 45 | d1yx1a1 | Alignment | not modelled | 64.3 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**KguE-like |
| 46 | d2ftwa2 | Alignment | not modelled | 63.3 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 47 | d1gkpa2 | Alignment | not modelled | 63.0 | 20 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 48 | d1qtwa_ | Alignment | not modelled | 62.5 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Endonuclease IV |
| 49 | c3ktcB_ | Alignment | not modelled | 62.5 | 7 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**xylose isomerase;<br>**PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution |
| 50 | c2yv2A_ | Alignment | not modelled | 61.6 | 13 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain;<br>**PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1 |
| 51 | c2x7vA_ | Alignment | not modelled | 61.0 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable endonuclease 4;<br>**PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc |
| 52 | d1onwa2 | Alignment | not modelled | 60.8 | 27 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Isoaspartyl dipeptidase, catalytic domain |
| 53 | c3aamA_ | Alignment | not modelled | 60.5 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**endonuclease iv;<br>**PDBTitle:** crystal structure of endonuclease iv from thermus thermophilus hb8 |
| 54 | c3gg7A_ | Alignment | not modelled | 60.4 | 29 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized metalloprotein;<br>**PDBTitle:** crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans |

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| 55 | d1i0da_ | Alignment | not modelled | 59.7 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Phosphotriesterase-like |
| 56 | c3dmyA_ | Alignment | not modelled | 59.0 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**protein fdra;<br>**PDBTitle:** crystal structure of a predicated acyl-coa synthetase from e.coli |
| 57 | d1foba_ | Alignment | not modelled | 58.1 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-glycanases |
| 58 | d2p9ba2 | Alignment | not modelled | 56.4 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Imidazolonepropionase-like |
| 59 | c2zvrA_ | Alignment | not modelled | 52.5 | 15 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein tm_0416;<br>**PDBTitle:** crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima |
| 60 | c3cjpA_ | Alignment | not modelled | 51.7 | 24 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**predicted amidohydrolase, dihydroorotase family;<br>**PDBTitle:** crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum |
| 61 | d1x92a_ | Alignment | not modelled | 50.9 | 17 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 62 | c2x3yA_ | Alignment | not modelled | 50.8 | 13 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**phosphoheptose isomerase;<br>**PDBTitle:** crystal structure of gmha from burkholderia pseudomallei |
| 63 | d1un7a2 | Alignment | not modelled | 50.1 | 23 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain |
| 64 | c2ou4C_ | Alignment | not modelled | 50.1 | 20 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase;<br>**PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii |
| 65 | c3ju2A_ | Alignment | not modelled | 49.4 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein smc04130;<br>**PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021 |
| 66 | d2d2ja1 | Alignment | not modelled | 47.4 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Phosphotriesterase-like |
| 67 | c3msrA_ | Alignment | not modelled | 47.1 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**amidohydrolases;<br>**PDBTitle:** the crystal structure of an amidohydrolase from mycoplasma synoviae |
| 68 | c1oi7A_ | Alignment | not modelled | 47.1 | 6 | **PDB header:**synthetase<br>**Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain;<br>**PDBTitle:** the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus |
| 69 | c3pnuA_ | Alignment | not modelled | 46.8 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** 2.4 angstrom crystal structure of dihydroorotase (pyrc) from2 campylobacter jejuni. |
| 70 | c2yv1A_ | Alignment | not modelled | 46.3 | 10 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha;<br>**PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661 |
| 71 | c3jzeC_ | Alignment | not modelled | 45.8 | 17 | **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 |
| 72 | c3f4cA_ | Alignment | not modelled | 45.5 | 21 | **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 |
| 73 | c3shoA_ | Alignment | not modelled | 45.1 | 30 | **PDB header:**transcription regulator<br>**Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family;<br>**PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain) |
| 74 | c1o12B_ | Alignment | not modelled | 43.8 | 15 | **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 |
| 75 | c3pnzD_ | Alignment | not modelled | 43.0 | 11 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**phosphotriesterase family protein;<br>**PDBTitle:** crystal structure of the lactonase lmo2620 from listeria monocytogenes |
| 76 | c3ou8A_ | Alignment | not modelled | 43.0 | 33 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**adenosine deaminase;<br>**PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa |
| 77 | c3thdD_ | Alignment | not modelled | 42.9 | 12 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin |
| 78 | d1vkya_ | Alignment | not modelled | 42.8 | 15 | **Fold:**QueA-like<br>**Superfamily:**QueA-like<br>**Family:**QueA-like |
| 79 | d2eg6a1 | Alignment | not modelled | 42.2 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Dihydroorotase |
| | | | | | | **PDB header:**hydrolase |

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| 80 | c3lggA_ | Alignment | not modelled | 42.1 | 25 | **Chain:** A: **PDB Molecule:**adenosine deaminase cecr1;<br>**PDBTitle:** crystal structure of human adenosine deaminase growth factor,2 adenosine deaminase type 2 (ada2) complexed with transition state3 analogue, coformycin |
| 81 | c3cnyA_ | Alignment | not modelled | 41.5 | 17 | **PDB header:**biosynthetic protein<br>**Chain:** A: **PDB Molecule:**inositol catabolism protein iole;<br>**PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution |
| 82 | c3nqbB_ | Alignment | not modelled | 41.3 | 29 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**adenine deaminase 2;<br>**PDBTitle:** crystal structure of adenine deaminase from agrobacterium tumefaciens2 (str. c 58) |
| 83 | c3ou8B_ | Alignment | not modelled | 41.3 | 33 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**adenosine deaminase;<br>**PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa |
| 84 | c2nu8D_ | Alignment | not modelled | 40.9 | 4 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha;<br>**PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase |
| 85 | c1pscA_ | Alignment | not modelled | 40.1 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**phosphotriesterase;<br>**PDBTitle:** phosphotriesterase from pseudomonas diminuta |
| 86 | c2xhzC_ | Alignment | not modelled | 39.1 | 20 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase;<br>**PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography |
| 87 | c3trjC_ | Alignment | not modelled | 38.9 | 17 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**phosphoheptose isomerase;<br>**PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis |
| 88 | c1xrfA_ | Alignment | not modelled | 38.2 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** the crystal structure of a novel, latent dihydroorotase from aquifex2 aeolicus at 1.7 a resolution |
| 89 | c2je8B_ | Alignment | not modelled | 37.8 | 11 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**beta-mannosidase;<br>**PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron |
| 90 | d1rd5a_ | Alignment | not modelled | 37.1 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Ribulose-phoshate binding barrel<br>**Family:**Tryptophan biosynthesis enzymes |
| 91 | c2z00A_ | Alignment | not modelled | 37.1 | 22 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** crystal structure of dihydroorotase from thermus thermophilus |
| 92 | c2hmcA_ | Alignment | not modelled | 36.8 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;<br>**PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens |
| 93 | c2vunC_ | Alignment | not modelled | 36.7 | 18 | **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 |
| 94 | c3dx5A_ | Alignment | not modelled | 36.7 | 19 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**uncharacterized protein asbf;<br>**PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis |
| 95 | d2je8a5 | Alignment | not modelled | 36.0 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-glycanases |
| 96 | c3fxaA_ | Alignment | not modelled | 35.8 | 7 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**sis domain protein;<br>**PDBTitle:** crystal structure of a putative sugar-phosphate isomerase2 (lmof2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution |
| 97 | c3kwsB_ | Alignment | not modelled | 35.6 | 5 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**putative sugar isomerase;<br>**PDBTitle:** crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution |
| 98 | d1tg7a5 | Alignment | not modelled | 35.4 | 3 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Glycosyl hydrolases family 35 catalytic domain |
| 99 | c2hk1D_ | Alignment | not modelled | 35.2 | 18 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**d-psicose 3-epimerase;<br>**PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose |
| 100 | c3cqkB_ | Alignment | not modelled | 35.1 | 11 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**l-ribulose-5-phosphate 3-epimerase ulae;<br>**PDBTitle:** crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate |
| 101 | d1vima_ | Alignment | not modelled | 34.6 | 15 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 102 | c3e0vB_ | Alignment | not modelled | 34.3 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions |
| 103 | c2zdsB_ | Alignment | not modelled | 34.2 | 17 | **PDB header:**dna binding protein<br>**Chain:** B: **PDB Molecule:**putative dna-binding protein;<br>**PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2) |
| 104 | c2vr2A_ | Alignment | not modelled | 34.0 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**dihydropyrimidinase;<br>**PDBTitle:** human dihydropyrimidinase |

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| 105 | c1pklB_ | Alignment | not modelled | 33.8 | 12 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**protein (pyruvate kinase);<br>**PDBTitle:** the structure of leishmania pyruvate kinase |
| 106 | c2gwnA_ | Alignment | not modelled | 33.5 | 18 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** the structure of putative dihydroorotase from porphyromonas2 gingivalis. |
| 107 | d1ezwa_ | Alignment | not modelled | 32.9 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**F420 dependent oxidoreductases |
| 108 | c3guwB_ | Alignment | not modelled | 32.6 | 19 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**uncharacterized protein af_1765;<br>**PDBTitle:** crystal structure of the tatd-like protein (af1765) from2 archaeoglobus fulgidus, northeast structural genomics3 consortium target gr121 |
| 109 | d3bula2 | Alignment | not modelled | 32.4 | 16 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 110 | c3obeB_ | Alignment | not modelled | 32.2 | 9 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase;<br>**PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution |
| 111 | d2imra2 | Alignment | not modelled | 31.5 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**DR0824-like |
| 112 | c3d6nA_ | Alignment | not modelled | 31.4 | 20 | **PDB header:**hydrolase/transferase<br>**Chain:** A: **PDB Molecule:**dihydroorotase;<br>**PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase |
| 113 | d1xrsb1 | Alignment | not modelled | 31.3 | 24 | **Fold:**Flavodoxin-like<br>**Superfamily:**Cobalamin (vitamin B12)-binding domain<br>**Family:**Cobalamin (vitamin B12)-binding domain |
| 114 | d2ohwa1 | Alignment | not modelled | 30.9 | 13 | **Fold:**Bacillus chorismate mutase-like<br>**Superfamily:**YueI-like<br>**Family:**YueI-like |
| 115 | c3khdC_ | Alignment | not modelled | 30.5 | 16 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**pyruvate kinase;<br>**PDBTitle:** crystal structure of pff1300w. |
| 116 | c2wm1A_ | Alignment | not modelled | 30.3 | 26 | **PDB header:**lyase<br>**Chain:** A: **PDB Molecule:**2-amino-3-carboxymuconate-6-semialdehyde<br>**PDBTitle:** the crystal structure of human alpha-amino-beta-2 carboxymuconate-epsilon-semialdehyde decarboxylase in3 complex with 1,3- dihydroxyacetonephosphate suggests a4 regulatory link between nad synthesis and glycolysis |
| 117 | c1xc6A_ | Alignment | not modelled | 30.2 | 8 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**beta-galactosidase;<br>**PDBTitle:** native structure of beta-galactosidase from penicillium sp. in complex2 with galactose |
| 118 | d1tk9a_ | Alignment | not modelled | 30.0 | 15 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |
| 119 | d4ubpc2 | Alignment | not modelled | 29.8 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**alpha-subunit of urease, catalytic domain |
| 120 | d1jeoa_ | Alignment | not modelled | 29.7 | 14 | **Fold:**SIS domain<br>**Superfamily:**SIS domain<br>**Family:**mono-SIS domain |