Phyre2

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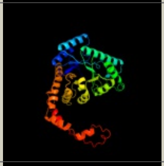
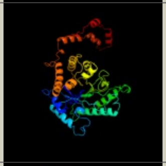
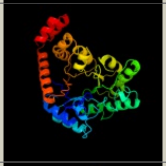
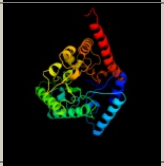
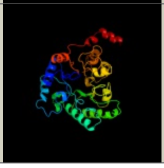
| Email | l.a.kelley@imperial.ac.uk |
| Description | P32170 |
| Date | Thu Jan 5 11:49:48 GMT 2012 |
| Unique Job ID | e491b94b05fd5204 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d1d8wa_ | Alignment |  | 100.0 | 98 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**L-rhamnose isomerase |
| 2 | c3p14C_ | Alignment |  | 100.0 | 59 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**l-rhamnose isomerase;<br>**PDBTitle:** crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans |
| 3 | c2i56A_ | Alignment |  | 100.0 | 19 | **PDB header:**isomerase, metal-binding protein<br>**Chain:** A: **PDB Molecule:**l-rhamnose isomerase;<br>**PDBTitle:** crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose |
| 4 | d1xlma_ | Alignment |  | 100.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 5 | d1bxca_ | Alignment |  | 100.0 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 6 | d1bxba_ | Alignment |  | 100.0 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 7 | c3ktcB_ | Alignment |  | 100.0 | 14 | **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 |
| 8 | d2glka1 | Alignment |  | 100.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 9 | d1muwa_ | Alignment |  | 100.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 10 | d1qt1a_ | Alignment |  | 100.0 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 11 | d1xima_ | Alignment |  | 100.0 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |

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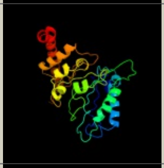
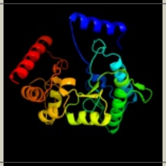
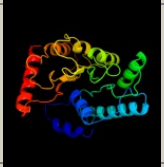
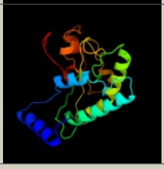
| 12 | d1a0ea_ | Alignment |  | 99.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 13 | d1a0da_ | Alignment |  | 99.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 14 | d1a0ca_ | Alignment |  | 99.7 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 15 | c3qxbB_ | Alignment |  | 98.7 | 13 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**putative xylose isomerase;<br>**PDBTitle:** crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution |
| 16 | c2qw5B_ | Alignment |  | 98.6 | 16 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel;<br>**PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution |
| 17 | c2zvrA_ | Alignment |  | 98.5 | 14 | **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 |
| 18 | c3cqkB_ | Alignment |  | 98.5 | 13 | **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 |
| 19 | c3kwsB_ | Alignment |  | 98.2 | 13 | **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 |
| 20 | c2hk1D_ | Alignment |  | 98.2 | 13 | **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 |
| 21 | d1i60a_ | Alignment | not modelled | 98.2 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**IolI-like |
| 22 | d1xp3a1 | Alignment | not modelled | 98.2 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Endonuclease IV |
| 23 | c2x7vA_ | Alignment | not modelled | 98.1 | 13 | **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 |
| 24 | d1qtwa_ | Alignment | not modelled | 98.0 | 9 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Endonuclease IV |
| 25 | c3ju2A_ | Alignment | not modelled | 97.9 | 18 | **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 |
| 26 | d1k77a_ | Alignment | not modelled | 97.8 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Hypothetical protein YgbM (EC1530) |
| 27 | c3bzjA_ | Alignment | not modelled | 97.7 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uv endonuclease;<br>**PDBTitle:** uvde k229l |
| 28 | c2zdsB_ | Alignment | not modelled | 97.7 | 11 | **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) |
| | | | | | | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase; |

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| 29 | c3obeB_ | Alignment | not modelled | 97.7 | 12 | **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution |
| 30 | c2ou4C_ | Alignment | not modelled | 97.5 | 14 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase;<br>**PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii |
| 31 | c3aamA_ | Alignment | not modelled | 97.3 | 13 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**endonuclease iv;<br>**PDBTitle:** crystal structure of endonuclease iv from thermus thermophilus hb8 |
| 32 | c3ngfA_ | Alignment | not modelled | 97.1 | 14 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**ap endonuclease, family 2;<br>**PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis |
| 33 | c3dx5A_ | Alignment | not modelled | 97.1 | 15 | **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 |
| 34 | c3l23A_ | Alignment | not modelled | 97.0 | 12 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase;<br>**PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution |
| 35 | c3lmzA_ | Alignment | not modelled | 96.7 | 11 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**putative sugar isomerase;<br>**PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution |
| 36 | d1tz9a_ | Alignment | not modelled | 96.7 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**UxuA-like |
| 37 | c3cnyA_ | Alignment | not modelled | 96.5 | 12 | **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 |
| 38 | c3bdkB_ | Alignment | not modelled | 96.4 | 16 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**d-mannonate dehydratase;<br>**PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue |
| 39 | d2g0wa1 | Alignment | not modelled | 96.0 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**IolI-like |
| 40 | d2q02a1 | Alignment | not modelled | 93.5 | 14 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**IolI-like |
| 41 | d1yx1a1 | Alignment | not modelled | 93.3 | 12 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**KguE-like |
| 42 | c3p6lA_ | Alignment | not modelled | 89.6 | 11 | **PDB header:**isomerase<br>**Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase;<br>**PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution |
| 43 | c2wvsD_ | Alignment | not modelled | 84.8 | 17 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**alpha-l-fucosidase;<br>**PDBTitle:** crystal structure of an alpha-l-fucosidase gh29 trapped2 covalent intermediate from bacteroides thetaiotaomicron in3 complex with 2-fluoro-fucosyl fluoride using an e288q4 mutant |
| 44 | d1x7fa2 | Alignment | not modelled | 73.7 | 27 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Outer surface protein, N-terminal domain |
| 45 | c2p0oA_ | Alignment | not modelled | 70.6 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**hypothetical protein duf871;<br>**PDBTitle:** crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function |
| 46 | c1uasA_ | Alignment | not modelled | 64.7 | 19 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-galactosidase;<br>**PDBTitle:** crystal structure of rice alpha-galactosidase |
| 47 | c2vpnB_ | Alignment | not modelled | 55.6 | 14 | **PDB header:**transport<br>**Chain:** B: **PDB Molecule:**periplasmic substrate binding protein;<br>**PDBTitle:** high-resolution structure of the periplasmic ectoine-2 binding protein from teaabc trap-transporter of halomonas3 elongata |
| 48 | c2by0A_ | Alignment | not modelled | 54.6 | 36 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**maltooligosyltrehalose trehalohydrolase;<br>**PDBTitle:** is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection |
| 49 | c3pt1A_ | Alignment | not modelled | 50.0 | 30 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**upf0364 protein ymr027w;<br>**PDBTitle:** structure of duf89 from saccharomyces cerevisiae co-crystallized with2 f6p. |
| 50 | d1ktba2 | Alignment | not modelled | 48.2 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 51 | c1x7fA_ | Alignment | not modelled | 48.0 | 32 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**outer surface protein;<br>**PDBTitle:** crystal structure of an uncharacterized b. cereus protein |
| 52 | c2d0gA_ | Alignment | not modelled | 45.5 | 20 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-amylase i;<br>**PDBTitle:** crystal structure of thermoactinomyces vulgaris r-47 alpha-2 amylase 1 (tvai) mutant d356n/e396q complexed with p5, a3 pullulan model oligosaccharide |
| 53 | d1uasa2 | Alignment | not modelled | 42.1 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |

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| 54 | c3lrmB_ | Alignment | not modelled | 41.3 | 11 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**alpha-galactosidase 1;<br>**PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose |
| 55 | c2ya0A_ | Alignment | not modelled | 38.2 | 21 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative alkaline amylopullulanase;<br>**PDBTitle:** catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua |
| 56 | c3emzA_ | Alignment | not modelled | 37.6 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**endo-1,4-beta-xylanase;<br>**PDBTitle:** crystal structure of xylanase xynb from paenibacillus2 barcinonensis complexed with a conduramine derivative |
| 57 | d1kwga2 | Alignment | not modelled | 37.6 | 9 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 58 | d1q2ha_ | Alignment | not modelled | 36.9 | 15 | **Fold:**Dimerisation interlock<br>**Superfamily:**Phenylalanine zipper<br>**Family:**Adapter protein APS, dimerisation domain |
| 59 | c3czkA_ | Alignment | not modelled | 36.4 | 9 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**sucrose hydrolase;<br>**PDBTitle:** crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex |
| 60 | c3k1dA_ | Alignment | not modelled | 34.3 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**1,4-alpha-glucan-branching enzyme;<br>**PDBTitle:** crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv |
| 61 | d2fywa1 | Alignment | not modelled | 33.7 | 26 | **Fold:**NIF3 (NGG1p interacting factor 3)-like<br>**Superfamily:**NIF3 (NGG1p interacting factor 3)-like<br>**Family:**NIF3 (NGG1p interacting factor 3)-like |
| 62 | d1bf2a3 | Alignment | not modelled | 33.6 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 63 | c3r66A_ | Alignment | not modelled | 33.2 | 20 | **PDB header:**viral protein/antiviral protein<br>**Chain:** A: **PDB Molecule:**non-structural protein 1;<br>**PDBTitle:** crystal structure of human isg15 in complex with ns1 n-terminal region2 from influenza virus b, northeast structural genomics consortium3 target ids hx6481, hr2873, and or2 |
| 64 | d1cyga4 | Alignment | not modelled | 33.1 | 32 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 65 | d1xeqa1 | Alignment | not modelled | 33.0 | 20 | **Fold:**S15/NS1 RNA-binding domain<br>**Superfamily:**S15/NS1 RNA-binding domain<br>**Family:**N-terminal, RNA-binding domain of nonstructural protein NS1 |
| 66 | c1h2aS_ | Alignment | not modelled | 32.5 | 24 | **PDB header:**oxidoreductase<br>**Chain:** S: **PDB Molecule:**hydrogenase;<br>**PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris |
| 67 | c2if8B_ | Alignment | not modelled | 32.2 | 16 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**inositol polyphosphate multikinase;<br>**PDBTitle:** crystal structure of inositol phosphate multikinase ipk2 in complex2 with adp and mn2+ from s. cerevisiae |
| 68 | c3m07A_ | Alignment | not modelled | 31.9 | 26 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**putative alpha amylase;<br>**PDBTitle:** 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium. |
| 69 | c3a23A_ | Alignment | not modelled | 31.7 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase;<br>**PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose |
| 70 | d1jvaa2 | Alignment | not modelled | 31.0 | 32 | **Fold:**Homing endonuclease-like<br>**Superfamily:**Homing endonucleases<br>**Family:**Intein endonuclease |
| 71 | d1wuis1 | Alignment | not modelled | 30.7 | 24 | **Fold:**HydA/Nqo6-like<br>**Superfamily:**HydA/Nqo6-like<br>**Family:**Nickel-iron hydrogenase, small subunit |
| 72 | c1ktbA_ | Alignment | not modelled | 30.7 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase;<br>**PDBTitle:** the structure of alpha-n-acetylgalactosaminidase |
| 73 | d1wzaa2 | Alignment | not modelled | 30.5 | 26 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 74 | c3rgwS_ | Alignment | not modelled | 30.3 | 23 | **PDB header:**oxidoreductase/oxidoreductase<br>**Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk;<br>**PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster |
| 75 | c2vncB_ | Alignment | not modelled | 29.9 | 25 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**glycogen operon protein glgx;<br>**PDBTitle:** crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus |
| 76 | d1e3da_ | Alignment | not modelled | 29.9 | 32 | **Fold:**HydA/Nqo6-like<br>**Superfamily:**HydA/Nqo6-like<br>**Family:**Nickel-iron hydrogenase, small subunit |
| 77 | d1y0na_ | Alignment | not modelled | 28.3 | 19 | **Fold:**YehU-like<br>**Superfamily:**YehU-like<br>**Family:**YehU-like |
| 78 | d2aaaa2 | Alignment | not modelled | 27.9 | 18 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 79 | d1uoza_ | Alignment | not modelled | 27.5 | 17 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycosyl hydrolases family 6, cellulases |

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|---|---|---|---|---|---|---|
| | | | | | | **Family:**Glycosyl hydrolases family 6, cellulases |
| 80 | c3myrE_ | Alignment | not modelled | 26.9 | 25 | **PDB header:**oxidoreductase<br>**Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda;<br>**PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state |
| 81 | c3a5vA_ | Alignment | not modelled | 26.9 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-galactosidase;<br>**PDBTitle:** crystal structure of alpha-galactosidase i from mortierella vinacea |
| 82 | d1eh9a3 | Alignment | not modelled | 26.3 | 31 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 83 | d1r46a2 | Alignment | not modelled | 26.3 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 84 | c2kelB_ | Alignment | not modelled | 25.6 | 17 | **PDB header:**transcription repressor<br>**Chain:** B: **PDB Molecule:**uncharacterized protein 56b;<br>**PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1 |
| 85 | c2e8yA_ | Alignment | not modelled | 25.2 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**amyx protein;<br>**PDBTitle:** crystal structure of pullulanase type i from bacillus subtilis str.2 168 |
| 86 | c1wzaA_ | Alignment | not modelled | 25.1 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-amylase a;<br>**PDBTitle:** crystal structure of alpha-amylase from h.orenii |
| 87 | d1tjoa_ | Alignment | not modelled | 25.1 | 11 | **Fold:**Ferritin-like<br>**Superfamily:**Ferritin-like<br>**Family:**Ferritin |
| 88 | d1frfs_ | Alignment | not modelled | 24.9 | 32 | **Fold:**HydA/Nqo6-like<br>**Superfamily:**HydA/Nqo6-like<br>**Family:**Nickel-iron hydrogenase, small subunit |
| 89 | c3uowB_ | Alignment | not modelled | 24.8 | 7 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**gmp synthetase;<br>**PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum |
| 90 | d1yq9a1 | Alignment | not modelled | 24.4 | 24 | **Fold:**HydA/Nqo6-like<br>**Superfamily:**HydA/Nqo6-like<br>**Family:**Nickel-iron hydrogenase, small subunit |
| 91 | c3qomA_ | Alignment | not modelled | 24.2 | 23 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase;<br>**PDBTitle:** crystal structure of 6-phospho-beta-glucosidase from lactobacillus2 plantarum |
| 92 | c2nydB_ | Alignment | not modelled | 23.7 | 13 | **PDB header:**unknown function<br>**Chain:** B: **PDB Molecule:**upf0135 protein sa1388;<br>**PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388 |
| 93 | c2kebA_ | Alignment | not modelled | 23.1 | 24 | **PDB header:**dna binding protein<br>**Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b;<br>**PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit |
| 94 | c1t0oA_ | Alignment | not modelled | 22.4 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**alpha-galactosidase;<br>**PDBTitle:** the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose |
| 95 | d1z8ma1 | Alignment | not modelled | 22.2 | 12 | **Fold:**RelE-like<br>**Superfamily:**RelE-like<br>**Family:**RelE-like |
| 96 | d1xyna_ | Alignment | not modelled | 22.0 | 33 | **Fold:**Concanavalin A-like lectins/glucanases<br>**Superfamily:**Concanavalin A-like lectins/glucanases<br>**Family:**Xylanase/endoglucanase 11/12 |
| 97 | c3civA_ | Alignment | not modelled | 21.3 | 12 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase;<br>**PDBTitle:** crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius |
| 98 | c3uj2C_ | Alignment | not modelled | 20.9 | 15 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**enolase 1;<br>**PDBTitle:** crystal structure of an enolase from anaerostipes caccae (efi target2 efi-502054) with bound mg and sulfate |
| 99 | c2cncA_ | Alignment | not modelled | 20.8 | 10 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**endoxylanase;<br>**PDBTitle:** family 10 xylanase |
| 100 | c3eypB_ | Alignment | not modelled | 20.8 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase;<br>**PDBTitle:** crystal structure of putative alpha-l-fucosidase from bacteroides2 thetaiotaomicron |
| 101 | c3d1nK_ | Alignment | not modelled | 20.2 | 26 | **PDB header:**transcription regulator/dna<br>**Chain:** K: **PDB Molecule:**pou domain, class 6, transcription factor 1;<br>**PDBTitle:** structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter |
| 102 | d1xyza_ | Alignment | not modelled | 20.0 | 11 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-glycanases |
| 103 | c1xyzA_ | Alignment | not modelled | 20.0 | 11 | **PDB header:**glycosyltransferase<br>**Chain:** A: **PDB Molecule:**1,4-beta-d-xylan-xylanohydrolase;<br>**PDBTitle:** a common protein fold and similar active site in two2 distinct families of beta-glycanases |