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Makraki, Eleni, Carneiro, Marta G., Heyam, Alex et al. (3 more authors) (2020) Correction to :  $^1\text{H}$ ,  $^{13}\text{C}$ ,  $^{15}\text{N}$  backbone and IVL methyl group resonance assignment of the fungal  $\beta$ -glucosidase from *Trichoderma reesei* (Biomolecular NMR Assignments, (2020), 10.1007/s12104-020-09959-2). Biomolecular NMR assignments. ISSN 1874-270X

<https://doi.org/10.1007/s12104-020-09967-2>

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# $^1\text{H}$ , $^{13}\text{C}$ , $^{15}\text{N}$ backbone and IVL methyl group resonance assignment of the fungal $\beta$ -glucosidase from *Trichoderma reesei*

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Received: 10 March 2020 / Accepted: 16 May 2020  
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## Abstract

$\beta$ -glucosidases have received considerable attention due to their essential role in bioethanol production from lignocellulosic biomass.  $\beta$ -glucosidase can hydrolyse cellobiose in cellulose degradation and its low activity has been considered as one of the main limiting steps in the process. Large-scale conversions of cellulose therefore require high enzyme concentration which increases the cost.  $\beta$ -glucosidases with improved activity and thermostability are therefore of great commercial interest. The fungus *Trichoderma reesei* expresses thermostable cellulolytic enzymes which have been widely studied as attractive targets for industrial applications. Genetically modified  $\beta$ -glucosidases from *Trichoderma reesei* have been recently commercialised. We have developed an approach in which screening of low molecular weight molecules (fragments) identifies compounds that increase enzyme activity and are currently characterizing fragment-based activators of *TrBgl2*. A structural analysis of the 55 kDa apo form of *TrBgl2* revealed a classical  $(\alpha/\beta)_8$ -TIM barrel fold. In the present study we present a partial assignment of backbone chemical shifts, along with those of the Ile (I)-Val (V)-Leu (L) methyl groups of *TrBgl2*. These data will be used to characterize the interaction of *TrBgl2* with the small molecule activators.

**Keywords** *TrBgl2* ·  $\beta$ -glucosidase · Resonance assignment · Enzyme activators

## Biological context

The depletion of fossil fuel in combination with the increasing demand for energy worldwide has instigated research on alternative and sustainable energy sources such as biofuels. Lignocellulosic (LC) biomass such as wood, agricultural residues and dedicated energy crops are abundant and available at low cost and have received considerable global attention as the most promising alternative, renewable source for

biofuel production. LC biomass, the structural backbone of all plant cell walls, is composed mainly of cellulose, in combination with hemicellulose and lignin (Service 2007). A mixture of enzymes that together are known as cellulase, catalyze cellulose degradation and comprise three categories of enzymes; endoglucanases (EC 3.2.1.4), exoglucanases or cellobiohydrolases (EC 3.2.1.91) and  $\beta$ -glucosidases (EC 3.2.1.21) (Sticklen 2008) (Brethauer and Studer 2015). Endoglucanases cleave the internal  $\beta$ -1,4-glycosidic bonds of cellulose microfibrils releasing small fragments. Subsequently, exoglucanases or cellobiohydrolases (CBH) act on the reducing and non-reducing ends resulting in short chain cello-oligosaccharides such as cellobiose, which are hydrolysed into glucose by the action of  $\beta$ -glucosidases (Sticklen 2008). However, the activity of  $\beta$ -glucosidase is a rate limiting step which results in accumulation of cellobiose and subsequent inhibition of other cellulases (Lynd et al. 2002; Bommarius et al. 2008; Resa and Buckin 2011; Brethauer and Studer 2015). Currently, this is overcome by using high concentrations of  $\beta$ -glucosidases increasing the cost of large-scale conversions. Many efforts have therefore been directed towards the improvement of catalytic activity

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and thermostability of the enzyme using mainly traditional genetic approaches (Lee et al. 2012).

*Trichoderma reesei* produces large amounts of thermostable cellulolytic enzymes, which make them attractive targets for industrial applications (Gao et al. 2017). Genetically modified  $\beta$ -glucosidases from *Trichoderma reesei* have been commercialized and are included in cellulolytic enzyme cocktails that have been developed by companies. Recently, Jeng et al. (2011) solved the crystal structure of the 55 kDa  $\beta$ -glucosidase from *Trichoderma reesei* (TrBgl2) at 1.63 Å resolution, which was found to adopt a classical  $(\alpha/\beta)_8$ -TIM barrel fold and be in tight association with a TRIS molecule at the active site (Jeng et al. 2011).

In previous studies, we have identified fragment-based activators of enzyme activity (Darby et al. 2014). We are currently characterizing fragment-based activators of TrBgl2. The work reported here is a partial assignment of backbone chemical shifts, along with those of the Ile (I)-Val (V)-Leu (L) methyl groups of TrBgl2. These assignments will provide the basis for a study of the interaction of TrBgl2 with the small molecule activators.

## Methods and experiments

### Sample preparation

The codon-optimized DNA sequence for TrBgl2 was inserted into the pET-YSBLIC3C plasmid with an N-terminal His<sub>6</sub> cleavable tag (Fogg and Wilkinson 2008). The plasmid was transformed into the E. coli BL21 (DE3) bacterial strain. Expression was performed using the method from Gans et al. (2010) with some modifications. Labelled samples were grown in M9/D<sub>2</sub>O minimal media containing <sup>15</sup>NH<sub>4</sub>Cl (1.0 g/L) and <sup>13</sup>C<sub>6</sub>-glucose (1.5 g/L). The cells were incubated at 37 °C until reaching an OD<sub>600</sub> of 0.4 when 2-Keto-3-(methyl-d3)-butyric acid-1,2,3,4-<sup>13</sup>C<sub>4</sub>, 3-d sodium salt (SIGMA, Cat. 637858) and 2-Ketobutyric acid-<sup>13</sup>C<sub>4</sub>,3,3-d<sub>2</sub> sodium salt hydrate (SIGMA, Cat. 607541) were added (Gans et al. 2010; Tugarinov and Kay 2003). The cells were further incubated at 37 °C until reaching an OD<sub>600</sub> of 0.7–0.8. The temperature was then decreased to 16 °C and the protein expression was induced with 0.5 mM IPTG and cells were harvested after overnight incubation at 16 °C. The cells were resuspended in a buffer containing 20 mM TRIS–HCl pH 7.5, 400 mM NaCl, 10 mM Imidazole and then disrupted by using the Cell Disruption System (Benttop, Constant Systems Ltd). After centrifugation, the soluble TrBgl2 was initially purified by Ni<sup>2+</sup>-NTA chromatography as described previously (Jeng et al. 2011). The sample was then loaded onto a size exclusion column (16/600 Superdex 200, GE Healthcare), and eluted with a buffer containing 50 mM TRIS–HCl pH 8, 100 mM NaCl, 3 mM DTT. The

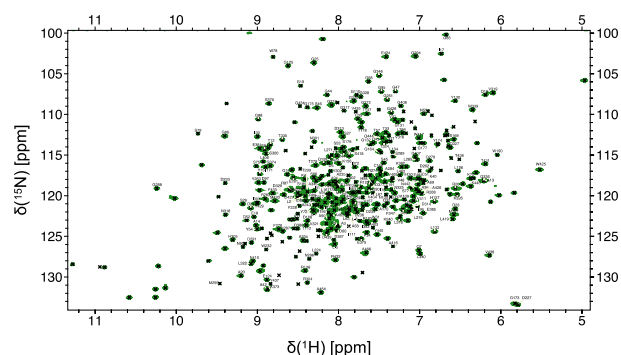
purified protein was concentrated by ultrafiltration with 10 kDa cut-off filter and analyzed by SDS-PAGE. Samples were prepared with 10% D<sub>2</sub>O (v/v) yielding concentration of 0.25 mM.

### NMR experiments

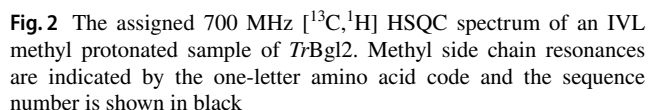
All NMR data were collected at 298 K on a Bruker Avance Neo 700 MHz and a Bruker Avance III 850 MHz spectrometers equipped with triple-resonance cryogenic probes. Sequential backbone assignments were obtained using Transverse relaxation-optimized spectroscopy (TROSY) versions (Pervushin et al. 1997) of conventional three-dimensional experiments (HNCO, HN(CA)CO, HNCA, HN(CO)CA, HN(CO)CACB, HNCACB and HN(CA)CB) (Sattler et al. 1999). IVL methyl group assignments were obtained using a two-dimensional constant time (CT) <sup>1</sup>H-<sup>13</sup>C<sub>methyl</sub> HMQC (Tugarinov and Kay 2003) and three-dimensional HMMCM, HMCM(C)CB, HMCM(CC)CA and HMCM(CCC)CO (Sinha et al. 2013). Additionally, a 3D <sup>13</sup>Ch-<sup>13</sup>CH<sub>3</sub> SOFAST-HMQC-NOESY-HMQC with a mixing time of 200 ms (Rossi et al. 2016), a 3D <sup>15</sup>N-resolved NOESY with a mixing time of 400 ms, and a 3D <sup>13</sup>C-resolved NOESY with a mixing time of 400 ms were used. All methyl assignment experiments were recorded with non-uniform sampling (NUS). NMR data were processed with Topspin 3.2 (Bruker), or with NMRPipe (Delaglio et al. 1995) and SMILE (Ying et al. 2017) and analyzed with Sparky (Lee et al. 2015).

### Assignment and data deposition

Spectra of TrBgl2 were initially assessed in a phosphate-based buffer at pH 6.0 and a TRIS-based buffer at pH 8.0. Spectral quality was markedly improved in TRIS buffer at pH 8.0, with several additional peaks becoming visible (data not shown). This observation, together the fact that a TRIS

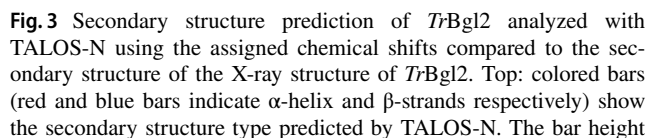


**Fig. 1** The assigned 700 MHz [<sup>15</sup>N,<sup>1</sup>H] TROSY NMR spectrum of TrBgl2. Assigned backbone N–H cross peaks are labelled with the corresponding residue number



The chemical shift assignment of *TrbG12* was performed in semi-automatic mode using the FLYA algorithm (Schmidt and Guntert 2012). The FLYA assignments were manually inspected and extended. Recombinant *TrbG12* consists of 488 amino acids (including an N-terminal His<sub>6</sub> cleavable tag) and has a molecular weight of 55 kDa. In total, we were able to assign 265 backbone amide resonances and 55% of the methyl group resonances of the IVL residues, from 459 non-proline residues (Figs. 1 and 2). Assignment completeness is limited possibly due to incomplete back-exchange of perdeuterated amide groups, with only ~75% of the expected resonances being observed in the [<sup>15</sup>N, <sup>1</sup>H] TROSY spectrum of perdeuterated *TrbG12*. Nonetheless, the assignments here reported provide a useful NMR basis for studies of the interaction of *TrbG12* with small molecules. The assignment of chemical shifts of *TrbG12* has been deposited into BMRB (<https://www.bmrblib.org/>) with accession number 50158.

*Tr*Bgl2 secondary structure motifs were predicted by the TALOS-N software (Shen and Bax 2013) using the assigned backbone resonances as input data. The software indicated that the overall secondary structures are in agreement with the X-ray structure of *Tr*Bgl2 (PDB ID 3AHY) (Jeng et al. 2011) (Fig. 3).



represents the prediction confidence. The black line shows the predicted S<sup>2</sup> order parameter, a measure of flexibility. Bottom: the secondary structure of TrBgl2 as determined by X-ray crystallography (PDB ID 3AHY) (Jeng et al. 2011)

**Acknowledgements** EM is very grateful to Michael Plevin (University of York) for his help and support in sample preparation. This work was supported by the European Union's Horizon2020 MSCA Programme under grant agreement 675899 (FRAGNET); research in the group of R.E.H. was additionally supported by research Grants from the BBSRC (BB/N008332/1) and institutional infrastructure support from funds provided by the Wellcome Trust and EPSRC.

**Funding** This work was supported by the European Union's Horizon2020 MSCA Programme under Grant agreement 675899 (FRAGNET); research in the group of R.E.H. was additionally supported by Research Grants from the BBSRC (BB/N008332/1) and institutional infrastructure support from funds provided by the Wellcome Trust and EPSRC.

**Data availability** The data that support the findings of this work are available on BMRB with the following entry assigned accession number: 50158.

## Compliance with ethical standards

**Conflict of interest** I confirm that all authors of the manuscript have no conflict of interest to declare.

**Informed consent** I confirm that all authors of the manuscript have given consent to participate to this work.

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## References

- Bommarius AS et al (2008) Cellulase kinetics as a function of cellulose pretreatment. *Metab Eng* 10(6):370–381. <https://doi.org/10.1016/j.ymben.2008.06.008>
- Brethauer S, Studer MH (2015) Biochemical conversion processes of lignocellulosic biomass to fuels and chemicals—a review. <https://www.ingentaconnect.com/content/scs/chimia/2015/00000069/00000010/art00002>
- Darby JF et al (2014) Discovery of selective small-molecule activators of a bacterial glycoside hydrolase. *Angew Chem Int Ed Engl* 53(49):13419–13423. <https://doi.org/10.1002/anie.201407081>
- Delaglio F et al (1995) NMRPipe: a multidimensional spectral processing system based on UNIX pipes. *J Biomol NMR* 6(3):277–293. <https://doi.org/10.1007/bf00197809>
- Fogg MJ, Wilkinson AJ (2008) Higher-throughput approaches to crystallization and crystal structure determination. *Biochem Soc Trans* 36(4):771–775. <https://doi.org/10.1042/bst0360771>
- Gans P et al (2010) Stereospecific isotopic labeling of methyl groups for NMR spectroscopic studies of high-molecular-weight proteins. *Angew Chem Int Ed Engl* 49(11):1958–1962. <https://doi.org/10.1002/anie.200905660>
- Gao J et al (2017) Production of the versatile cellulase for cellulose bioconversion and cellulase inducer synthesis by genetic improvement of *Trichoderma reesei*. *Biotechnol Biofuels* 10:272. <https://doi.org/10.1186/s13068-017-0963-1>
- Jeng WY et al (2011) Structural and functional analysis of three beta-glucosidases from bacterium *Clostridium cellulovorans*, fungus *Trichoderma reesei* and termite *Neotermes koshunensis*. *J Struct Biol* 173(1):46–56. <https://doi.org/10.1016/j.jsb.2010.07.008>
- Lee HL et al (2012) Mutations in the substrate entrance region of beta-glucosidase from *Trichoderma reesei* improve enzyme activity and thermostability. *Protein Eng Des Sel* 25(11):733–740. <https://doi.org/10.1093/protein/gz073>
- Lee W, Tonelli M, Markley JL (2015) NMRFAM-SPARKY: enhanced software for biomolecular NMR spectroscopy. *Bioinformatics* 31(8):1325–1327. <https://doi.org/10.1093/bioinformatics/btu830>
- Lynd LR et al (2002) Microbial cellulose utilization: fundamentals and biotechnology. *Microbiol Mol Biol Rev* 66(3):506–577. <https://doi.org/10.1128/mmb.66.3.506-577.2002>
- Pervushin K et al (1997) Attenuated T2 relaxation by mutual cancellation of dipole-dipole coupling and chemical shift anisotropy indicates an avenue to NMR structures of very large biological macromolecules in solution. *Proc Natl Acad Sci USA* 94(23):12366–12371. <https://doi.org/10.1073/pnas.94.23.12366>
- Resa P, Buckin V (2011) Ultrasonic analysis of kinetic mechanism of hydrolysis of cellobiose by beta-glucosidase. *Anal Biochem* 415(1):1–11. <https://doi.org/10.1016/j.ab.2011.03.003>
- Rossi P et al (2016) 15N and 13C-SOFAST-HMQC editing enhances 3D-NOESY sensitivity in highly deuterated, selectively [1H,13C]-labeled proteins. *J Biomol NMR* 66(4):259–271. <https://doi.org/10.1007/s10858-016-0074-5>
- Sattler M, Schleucher J, Griesinger C (1999) NMR experiments for the structure determination of proteins in solution employing pulsed field gradients. *Progress Nucl Magnet Resonance Spectrosc* 34:93–158. [https://doi.org/10.1016/S0079-6565\(98\)00025-9](https://doi.org/10.1016/S0079-6565(98)00025-9)
- Schmidt E, Guntert P (2012) A new algorithm for reliable and general NMR resonance assignment. *J Am Chem Soc* 134(30):12817–12829. <https://doi.org/10.1021/ja305091n>
- Service RF (2007) Cellulosic ethanol: biofuel researchers prepare to reap a new harvest. *Science* 315:1488–1491
- Shen Y, Bax A (2013) Protein backbone and sidechain torsion angles predicted from NMR chemical shifts using artificial neural networks. *J Biomol NMR* 56(3):227–241. <https://doi.org/10.1007/s10858-013-9741-y>
- Sinha K, Jen-Jacobson L, Rule GS (2013) Divide and conquer is always best: sensitivity of methyl correlation experiments. *J Biomol NMR* 56(4):331–335. <https://doi.org/10.1007/s10858-013-9751-9>
- Sticklen MB (2008) Plant genetic engineering for biofuel production: towards affordable cellulosic ethanol. *Nat Rev Genet* 9(6):433–443. <https://doi.org/10.1038/nrg2336>
- Tugarinov V, Kay LE (2003) Ile, Leu, and Val methyl assignments of the 723-residue malate synthase G using a new labeling strategy and novel NMR methods. *J Am Chem Soc* 125(45):13868–13878. <https://doi.org/10.1021/ja030345s>
- Ying J et al (2017) Sparse multidimensional iterative lineshape-enhanced (SMILE) reconstruction of both non-uniformly sampled and conventional NMR data. *J Biomol NMR* 68(2):101–118. <https://doi.org/10.1007/s10858-016-0072-7>

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