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CORRECTION

Correction to: NMR resonance assignments of 18.5 kDa complex of *Arabidopsis thaliana* DRB7.2:DRB4 interaction domains

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Correction to: Biomolecular NMR Assignments
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In the original article, Figs. 1B and 2B were incorrectly published. The chemical shift deviation in Cα residues for DRB7.2M and DRB4D3, adjusted for ^{2}H isotope effect in corresponding random coil chemical shift values, are replotted, replacing Figs. 1B and 2B.

Additionally, the authors state that they have used the TALOS-N web server {Ref: Shen, Y., Bax, A. Protein backbone and side chain torsion angles predicted from NMR chemical shifts using artificial neural networks. J Biomol NMR 56, 227–241 (2013). doi:https://doi.org/10.1007/s10858-013-9741-y} to calculate Δ(Cα) represented in Figs. 1B and 2B. The correction does not alter any assigned chemical shifts DRB7.2M and DRB4D3, and the secondary structure prediction derived from the revised Figs. 1B and 2B is identical to the uncorrected figure. The corrected Figs. 1B and 2B should have appeared as shown below. The original article has been corrected.

The original article can be found online at https://doi.org/10.1007/s12104-023-10137-3.

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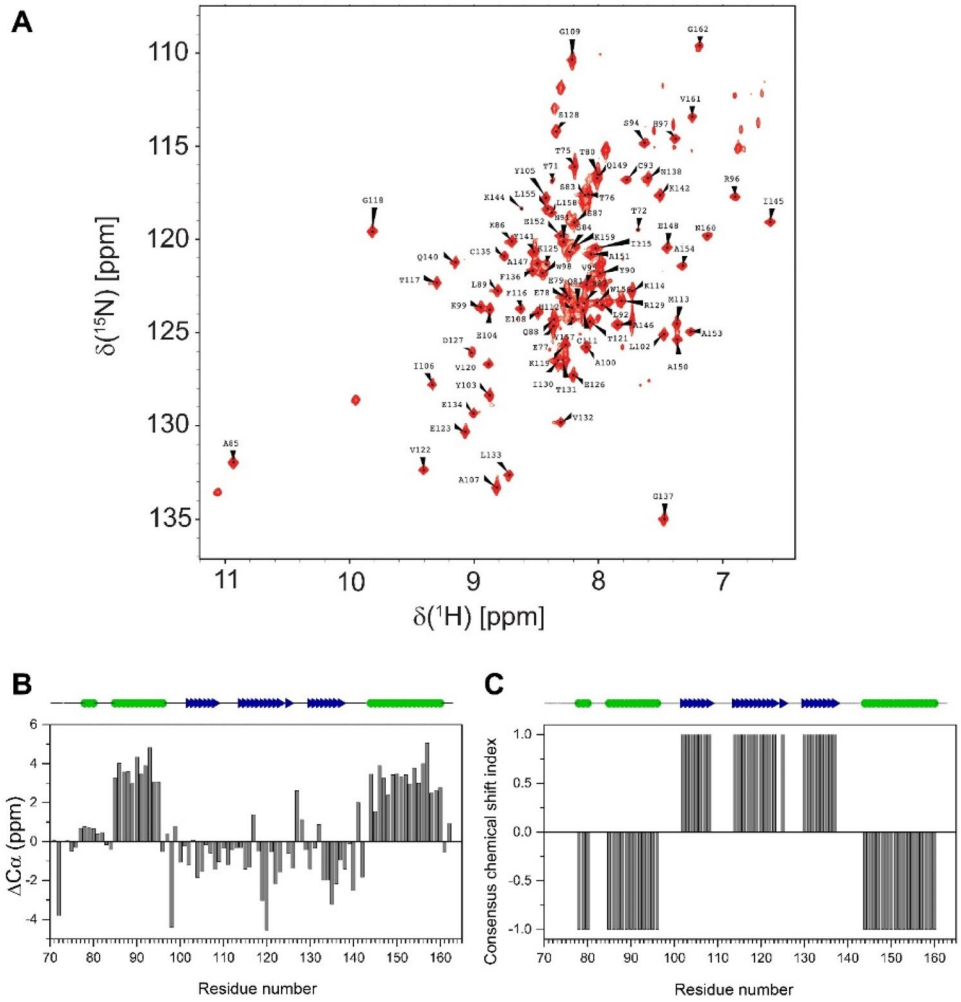

Fig. 1 Chemical shift assignments and secondary structure predic tion of DRB7.2M. **A** ^{1}H-^{15}N TROSY-HSQC spectrum of labeled DRB7.2M (complex with deuterated (~98%) DRB4D3) with each resonance annotated with a one-letter code and the sequence number. **B** Residue-specific chemical shift deviation in Cα resonances from its random coil values as a function of residue number. The derived secondary structures are represented in the upper panel as green circles for α-helices, blue arrows for β-strands, and black lines for loops. **C** The consensus chemical shift index plotted based on the Cα, Cβ, and CO chemical shifts from random coil values where α-helix, β-sheet, and random coil/loops are given values of − 1, + 1, and 0, respectively. The derived secondary structures are represented in the upper panel as green circles for α-helices, blue arrows for β-strands, and black lines for loops

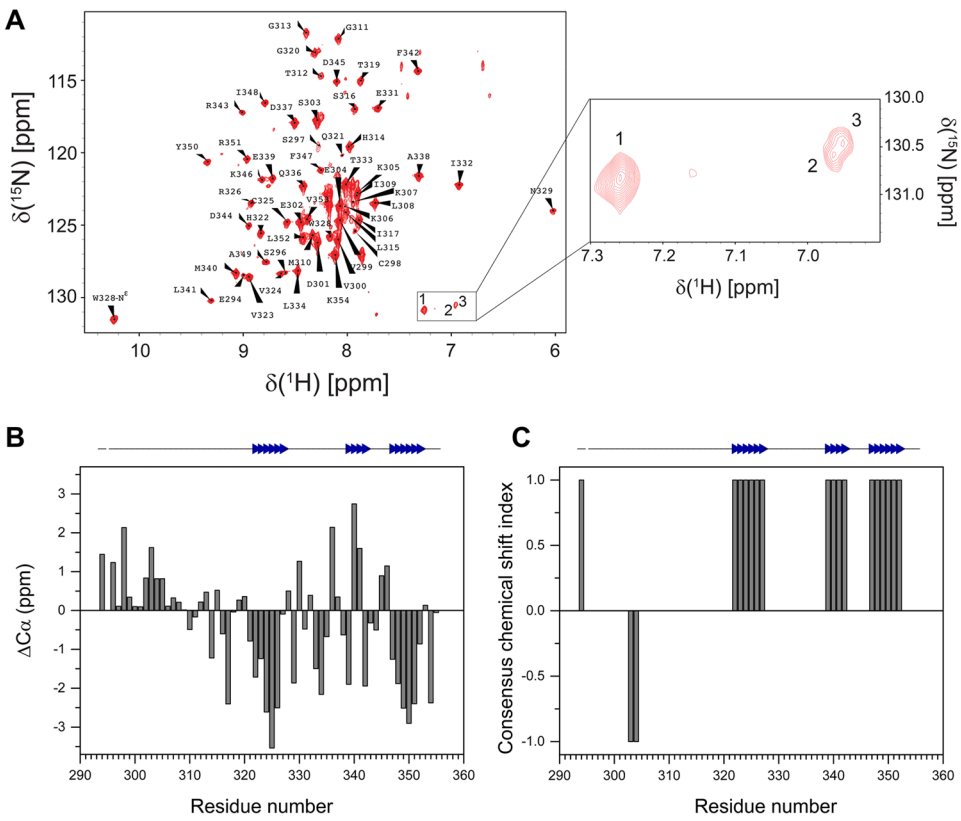

Fig. 2 Chemical shift assignment and secondary structure prediction of DRB4D3. **A** Assigned ^{1}H-^{15}N TROSY-HSQC spectrum of labeled DRB4D3 (complex with deuterated (~98%) DRB7.2M) displaying each resonance with a corresponding one-letter code and the sequence number. Inset highlights three folded resonances that correspond to the three salt bridges formed by DRB4D3 in a complex with DRB7.2M. **B** Residue-specific chemical shift deviation in Cα resonances from its random coil values as a function of residue number. The derived secondary structures are represented in the upper panel as blue arrows for β-strands and black lines for loops. **C** The consensus chemical shift index plotted based on the Cα, Cβ, and CO chemical shifts from random coil values where α-helix, β-sheet and random coil/loops are given values of − 1, + 1, and 0, respectively