

CORRECTION

Correction: The Effects of Threonine Phosphorylation on the Stability and Dynamics of the Central Molecular Switch Region of 18.5-kDa Myelin Basic Protein

The *PLOS ONE* Staff

[Fig 2](#) is missing from the PDF version of this paper. The publisher apologizes for the error. Please see [Fig 2](#) in the online version of the article or below.



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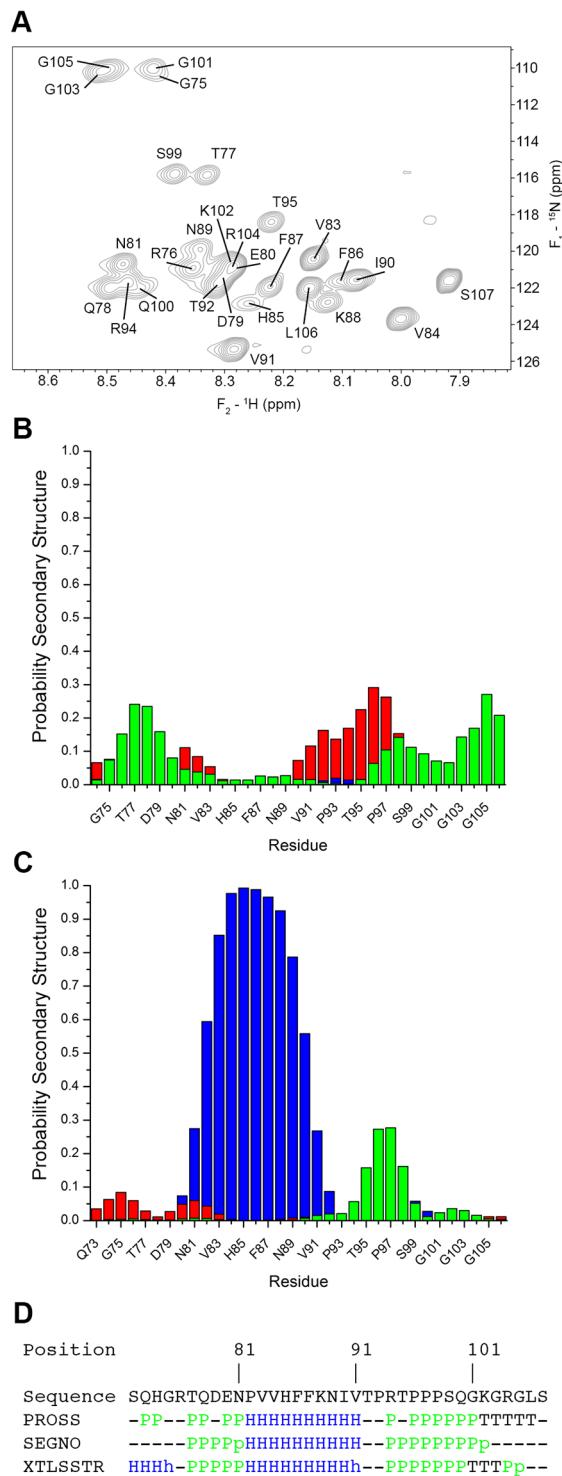


Fig 2. Nitrogen-HSQC spectra and secondary structure analysis of the MBP α_2 -peptide. (A) The ${}^1\text{H}-{}^{15}\text{N}$ HSQC spectrum of uniformly ${}^{13}\text{C}-{}^{15}\text{N}$ -labelled α_2 -peptide (S72-S107) dissolved in 20 mM HEPES-NaOH, 100 mM NaCl, and 10% D_2O at a concentration of 1.47 mM, and recorded at 295 K. A total of 29 of 31 expected backbone peaks were assigned (there are 5 prolyl residues). The HSQC spectrum was processed by applying a 90° -shifted squared-sine bell function, and zero-filled up to 256 and 2048 complex points along F_1 and F_2 , respectively, prior to Fourier transformation using NMRPipe. (B) Prediction of secondary structure probabilities for each residue (populations per residue) in the α_2 -peptide in aqueous solution, using a method designed for disordered proteins [68]. The method differentiates between α -helix

(blue), β -sheet (red), PPII (green), and random coil (not shown). The probabilities were calculated using the H_{α} , H_N , C_{α} , C_{β} , C' , and N chemical shift assignments for the α_2 -peptide. (C) Prediction of secondary structure probabilities for each residue in the α_2 -peptide in the presence of DPC, using a method designed for disordered proteins [49,68]. The H_{α} , H_N , C_{α} , C_{β} , C' , and N chemical shift assignments deposited in BMRB 6100 were used to calculate the secondary structure probabilities. (D) Secondary structure assignment methods used on the α_2 -peptide in the presence of DPC (PDB ID 2LUG). The XTLSSTR [91], PROSS [92], and SEGNO [93] methods all take into consideration PPII conformations, and differentiate them from coil, α , and β structures. The PROSS and SEGNO results were calculated using the “Polyproline” server created by the DSIMB bioinformatics team. The XTLSSTR results were obtained via the 2struc server created by the Wallace Laboratory [109]. The assignment indicates that the proline-rich region has a PPII conformation.

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Reference

1. Vassall KA, Bessonov K, De Avila M, Polverini E, Harauz G (2013) The Effects of Threonine Phosphorylation on the Stability and Dynamics of the Central Molecular Switch Region of 18.5-kDa Myelin Basic Protein. PLoS ONE 8(7): e68175. doi: [10.1371/journal.pone.0068175](https://doi.org/10.1371/journal.pone.0068175) PMID: [23861868](https://pubmed.ncbi.nlm.nih.gov/23861868/)