

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.

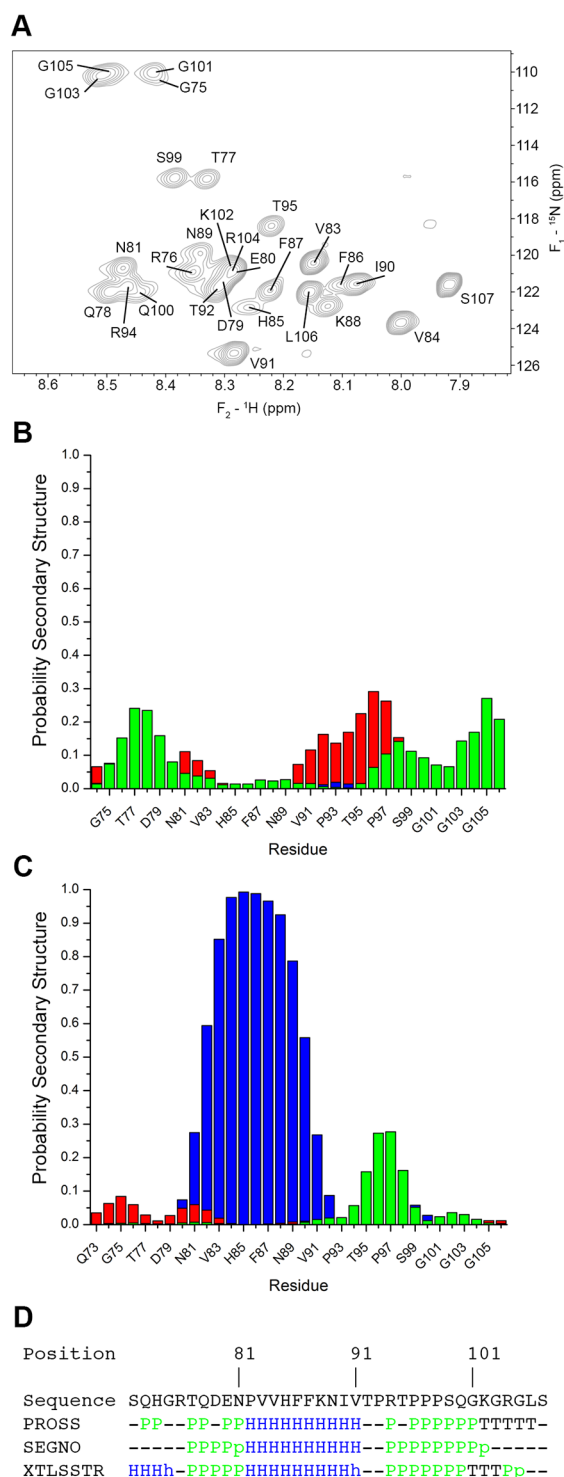


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**Fig 2. Nitrogen-HSQC NMR spectra and secondary structure analysis of the MBP  $\alpha_2$ -peptide.** (A) The  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectrum of uniformly  $^{13}\text{C}$ - $^{15}\text{N}$ -labelled  $\alpha_2$ -peptide (S72-S107) dissolved in 20 mM HEPES-NaOH, 100 mM NaCl, and 10%  $\text{D}_2\text{O}$  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  $90^\circ$ -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  $\alpha_2$ -peptide in aqueous solution, using a method designed for disordered proteins [68]. The method differentiates between  $\alpha$ -helix

(blue),  $\beta$ -sheet (red), PPII (green), and random coil (not shown). The probabilities were calculated using the  $H_{\alpha}$ ,  $H_N$ ,  $C_{\alpha}$ ,  $C_{\beta}$ ,  $C'$ , and N chemical shift assignments for the  $\alpha_2$ -peptide. (C) Prediction of secondary structure probabilities for each residue in the  $\alpha_2$ -peptide in the presence of DPC, using a method designed for disordered proteins [49,68]. The  $H_{\alpha}$ ,  $H_N$ ,  $C_{\alpha}$ ,  $C_{\beta}$ ,  $C'$ , 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  $\alpha_2$ -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,  $\alpha$ , and  $\beta$  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/)