

Erratum

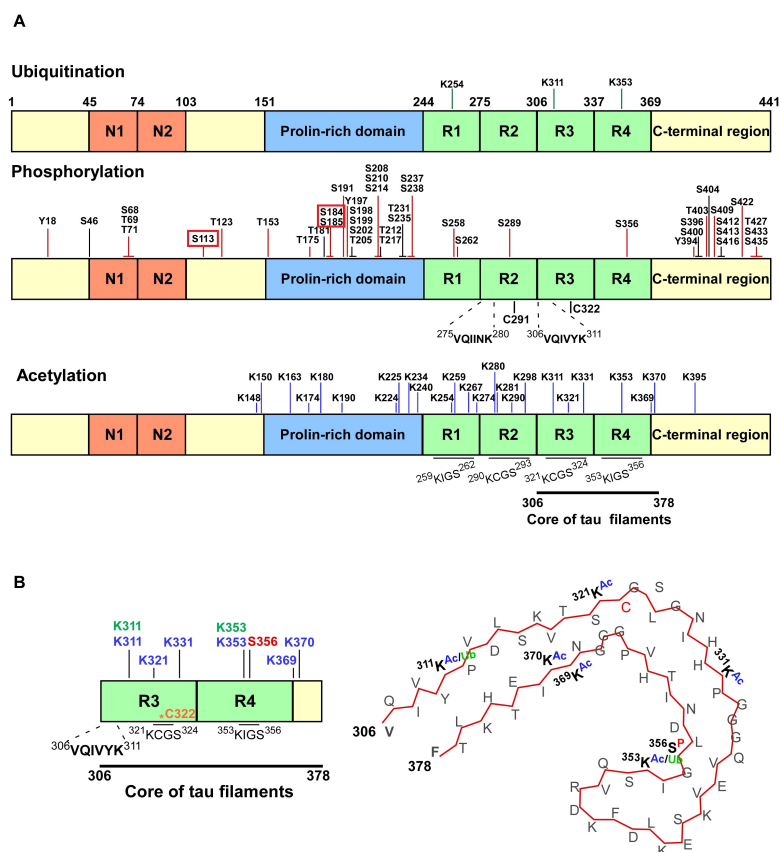
# Erratum to: Degradation or aggregation: the ramifications of post-translational modifications on tau

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The BMB Reports would like to correct in the Figure 2 of BMB Rep. 51(6): 265-273 titled “Degradation or aggregation: the ramifications of post-translational modifications on tau.” The original version of this article unfortunately contained typographical errors in the Figure 2. This article has been updated to correct these errors (red squares) in Figure 2.



**Fig. 2.** Post-translational modification (PTM) sites of human tau. (A) Representative PTMs on the 4R/2N isoform of tau. Three confirmed ubiquitination sites (all in the MBD) are labeled with green bars. Phosphorylation sites are indicated with red (found in AD brain only) or black bars (found both in normal and AD brain). Sites that are acetylated by p300 and/or CPB are depicted with blue bars. Two hexapeptide motifs (275VQIINK<sup>280</sup> and 306VQIVYK<sup>311</sup>) and two Cys residues (Cys291 and Cys322) in tau are located within R2 and R3. (B) The PTMs on the tau protofilament core, which spans residues 306 to 378 with R3, R4, and a portion of the C-terminal region, and its structure identified from human AD brain. The tau core contains one hexapeptide motif (306VQIVYK<sup>311</sup>), one Cys residue (Cys322), two KXGS motifs, six acetylation, two ubiquitination, and one phosphorylation sites. Same color schemes as described above are used to depict the PTMs.