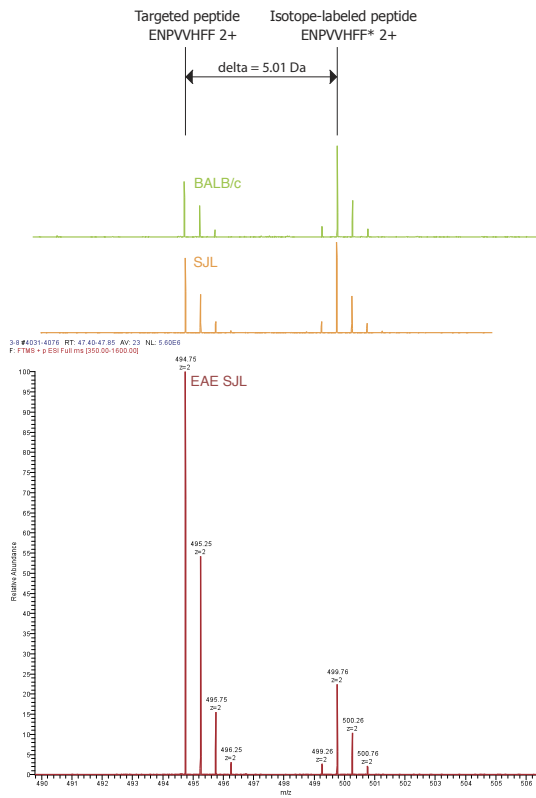
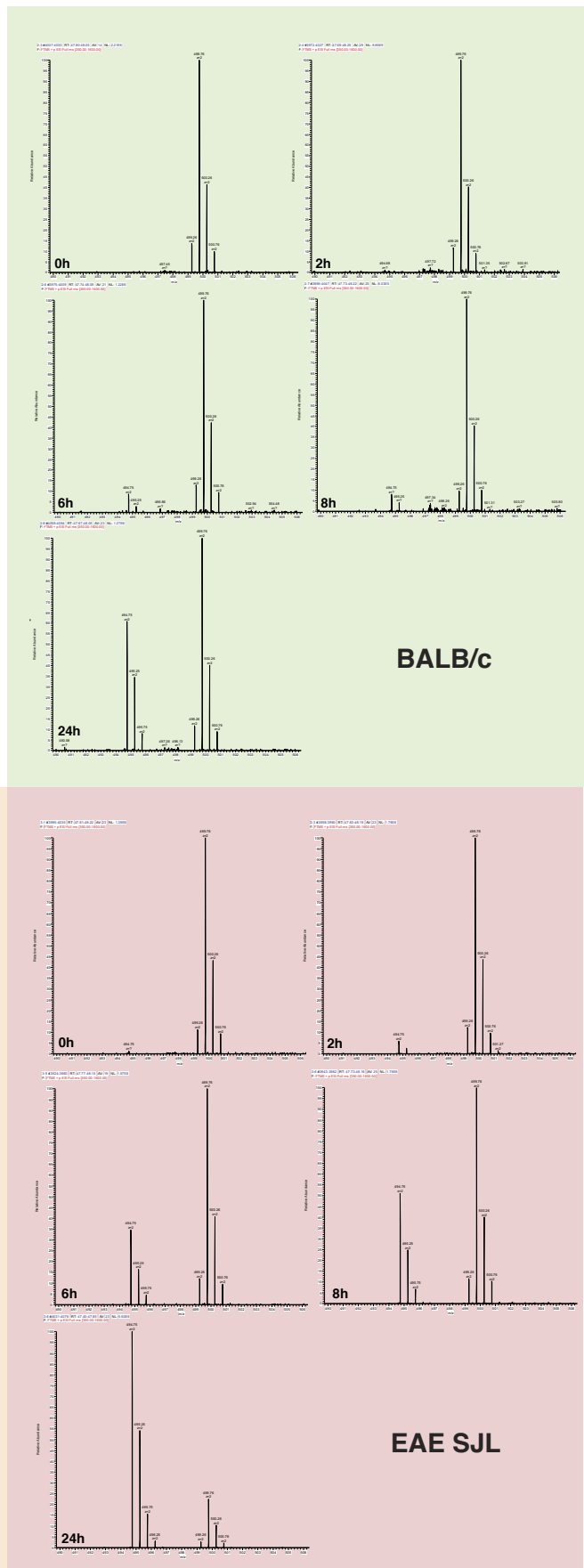


**A****B**

**Figure S3 |** (A) Representative LC-ESI-MS analysis of MBP proteolysis by proteasomes isolated from EAE SJL, SJL and BALB/c mice. For quantitative analysis, the isotopically labeled peptide ENPVVHFF\* ( $F^* = {}^{13}\text{C}_9\text{H}_9{}^{15}\text{NO}$ ) was mixed with all samples at the same ratio. The amount of the peptide was determined as the ratio of the relative peak intensities of labeled and non-labeled peptide in the mass spectrum. The relative peak intensities were determined from the extracted MS ion chromatograms using Xcalibur software. (B) Time-course of release of ENPVVHFF peptide during MBP hydrolysis by proteasomes isolated from BALB/c, SJL and EAE SJL mice, monitored by quantitative mass spectrometry using isotopically labeled peptides.