

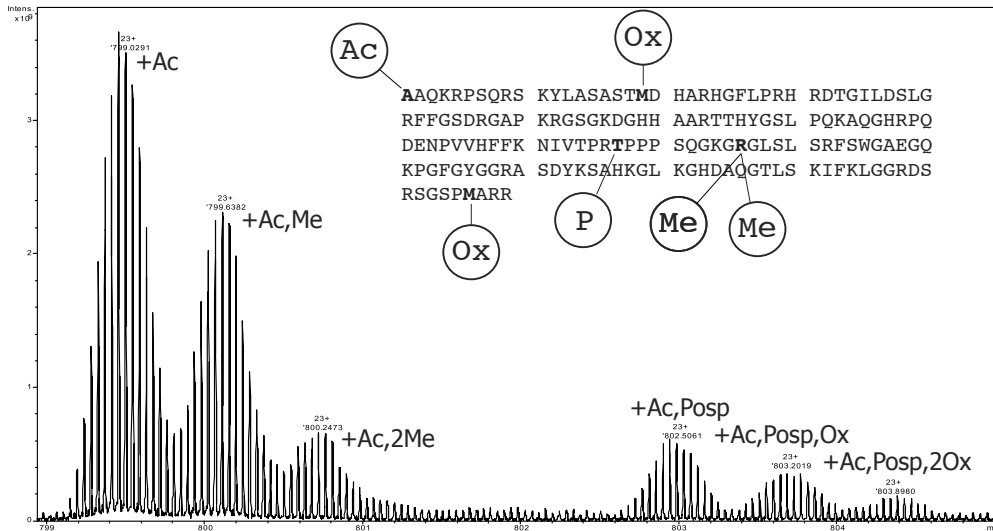
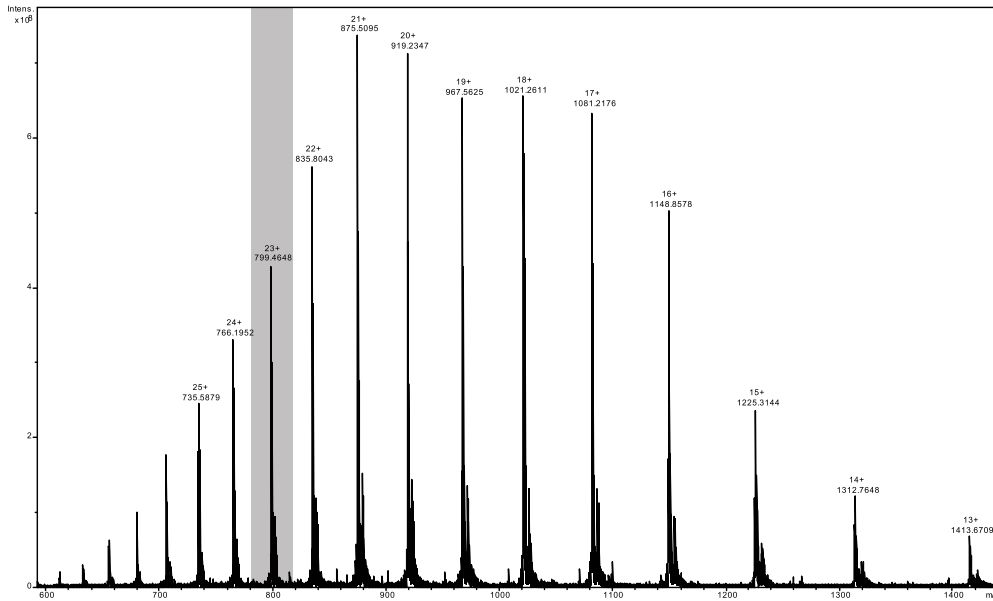
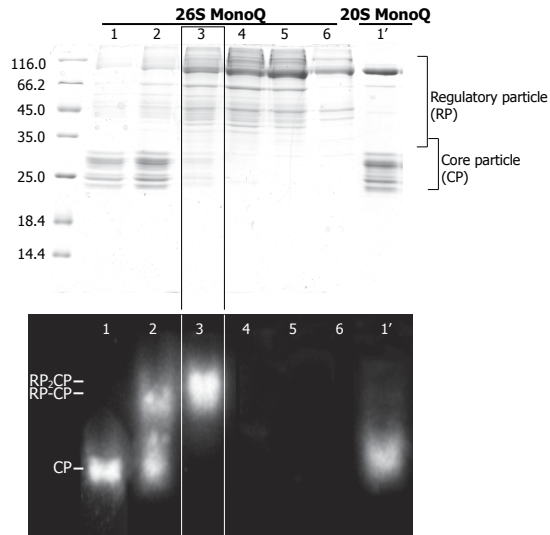
A**B**

Figure S1 | (A) Representative mass spectrogram shows the multiple-charged highly purified MBP (top) and a stretched out peak with charge +23 as an example (bottom). Isotope masses were calculated in automatic mode using Bruker Data Analysis software and the SNAP algorithm. The inset shows the sequence of bovine MBP in single-letter code (<http://www.ncbi.nlm.nih.gov/protein/P02687.1>) with corresponding modifications, which are indicated on the mass spectrogram. The N-terminus of myelin basic protein is completely acetylated (Ac), R106 is partly mono- or dimethylated (Me), T97 is phosphorylated (P), and M19 and M166 may be oxidized (Ox), as determined by tandem mass spectrometric sequence of the fragmented peptides. (B) Denaturing (upper part) and nondenaturing (bottom part) PAGE of 20S and 26S proteasome fractions (2.5 μ g per lane) from a MonoQ column.