

1. Sidoli S, et al. Complete Workflow for Analysis of Histone Post-translational Modifications Using Bottom-up Mass Spectrometry: From Histone Extraction to Data Analysis. *J Vis Exp*. 2016 May 17;(111).
2. Karch KR, et al. Identification and Quantification of Histone PTMs Using High-Resolution Mass Spectrometry. *Methods Enzymol*. 2016;574:3-29.
3. Yuan ZF, et al. EpiProfile Quantifies Histone Peptides With Modifications by Extracting Retention Time and Intensity in High-resolution Mass Spectra. *Mol Cell Proteomics*. 2015 Jun;14(6):1696-707.
4. Yuan ZF, et al. EpiProfile 2.0: A Computational Platform for Processing Epi-Proteomics Mass Spectrometry Data. *J Proteome Res*. 2018 Jul 6;17(7):2533-2541.