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Selected Publication

Hatimy AA, Browne MJG, Flaus A, Sweet SMM (2015). Histone H2AX Y142 phosphorylation is a low abundance modification. *Int J Mass Spec*, online pre-publication.

Research Aims and Interests

The Sweet lab uses quantitative, targeted mass spectrometry to track changes in histone variants and modifications after DNA damage, specifically double-strand breaks (DSB). We are developing methods to enrich chromatin close to the DSB, in order to detect changes in histone acetylation, methylation and ubiquitination. We employ SILAC (stable-isotope labelling by amino acids in cell culture) to distinguish between pre-existing and damage-induced modifications. We will also employ cross-linking to identify repair proteins associated with DSB at different times after the damage.