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Proximity-based labelling of the HDA14 interactome

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Histone deacetylases (HDACs) are a pivotal enzyme in the removing of lysine acetylation on various proteins. While most work has focused on the role of Arabidopsis HDACs on histone acetylation, their role in the deacetylation of non-histone proteins is much less known, although proteins of many different organelles have been found to be lysine-acetylated. From the 18 HDACs found in Arabidopsis, only HDA14 has been found to be dual-localized in plastids and mitochondria. Considering the dynamic nature of these post-translational modifications across various cell types, growth conditions, and time points, our objective is to identify the interplay of protein modifications and regulatory proteins interacting with HDA14. For this, we employ pull-down methods and proximity labeling utilizing the biotin ligase Turbo-ID, fused to the open reading frame of HDA14 and stably integrated into Arabidopsis. Here, we will present our experimental approach and initial findings.

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