

Establishment of a Bioinformatic Pipeline to Characterize the Phase Separation of Proteins in Plant Cells

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Formation of biomolecular condensates by liquid-liquid phase separation is a dynamic process that is triggered by variations in environmental conditions such as temperature, pH or ionic strength. Characterising the phase separation behaviour of individual proteins is crucial to understand the mechanism and function of condensate assembly. By using the two paralogs of the eukaryotic Elongation Factor EF1B β , named eEF1BB β 1 and eEF1BB β 2, of *Arabidopsis thaliana* that exhibit a differential temperature-dependent condensation behaviour, two different bioinformatic tools for assessing condensation behaviour in a quantitative and qualitative manner are presented: The first is a pipeline implementing the CellProfiler granularity measurement, an open-source analytical tool (Carpenter et al., 2006; McQuin et al., 2018) and the second is based on the artificial intelligence object segmentation of the Nikon NIS Elements software (RRID:SCR_014329).

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