

## **MASCP Gator and ModHunter, bioinformatics tools for identifying post translational modifications in Arabidopsis**

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### **Project Goal:**

**To develop a technique that can be used to support experimental approaches in identifying protein modifications involved in cell wall biosynthesis**

The understanding of the mechanisms of post-translational modification (PTM) is vital to elucidating the role of proteins within living organisms. To date, over 600 different types of post-translational modification have been catalogued. However, unlike the proteome, it is currently unfeasible to compute the protein modification repertoire for any system purely from the genome. Modern mass spectrometry is incredibly sensitive and results in a wealth of mass data points on the mass composition of the sample. This high accuracy technique enables the rapid identification of PTMs through delta mass calculations (comparing to an unmodified peptide mass). Phosphorylation has been fairly amenable to characterization using these techniques, and much data exists covering this. However, even with the ability to characterize some PTMs well, only about 25% of mass data from spectrometers match to unmodified peptides. This leaves a large search space in which information about PTMs could be found. However, the analysis of this data is non-trivial, and sophisticated computational techniques are needed to overcome the complex nature of calculations.