

## Review

- 1 **Popular Computational Methods to Assess Multiprotein Complexes Derived From Label-Free Affinity Purification and Mass Spectrometry (AP-MS) Experiments**  
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On the cover: High-performance mass spectrometry-based proteomics enabled the construction of a detailed proteome atlas for *Populus*, a woody plant model organism. For a network-wide perspective of *Populus* metabolism, we employed the use of iPath2.0 to navigate and explore the predicted KEGG metabolic pathways. Mapping protein expression to pathways revealed a holistic view of plant-wide protein expression and captured catalytic and regulatory pathways spanning the entire tree. For details, see the article by Robert L. Hettich, et al., pages 106 -119.

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