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## **KaPPA-View for integrating quantitative transcriptomic and metabolomic data on plant metabolic pathway maps**

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### **Abstract:**

With advanced technologies in DNA array, vast amounts of transcriptome data have been produced and state-of-the-art mass spectrometers have contributed to the massive production of metabolome data. Interpretation of the metabolome data in conjunction with the transcriptome data is one of the major concerns associated with research into identifying metabolism-related gene function. The web-based tool KaPPA-View was developed for representing quantitative data for individual transcripts and/or metabolites on plant metabolic pathway maps. The presentation of data in this manner facilitates a good grasp of the transcripts and metabolites, leading to hypotheses of gene function in the metabolic pathway being examined. Here, we comment on a practical use of this omics tool.

### **Keywords:**

metabolome, metabolomics, transcriptome, transcriptomics, omics, Arabidopsis



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