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iTRAQ Protein Profile Analysis of Developmental Dynamics in Soybean [*Glycine max* (L.) Merr.] Leaves

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Zao5241 is an elite soybean [*Glycine max* (L.) Merr.] line and backbone parent. In this study, we employed iTRAQ to analyze the proteomes and protein expression profiles of Zao5241 during leaf development. We identified 1,245 proteins in all experiments, of which, only 45 had been previously annotated. Among overlapping proteins between three biological replicates, 598 proteins with 2 unique peptides identified were reliably quantified. The protein datasets were classified into 36 GO functional terms, and the photosynthesis term was most significantly enriched. A total of 113 proteins were defined as being differentially expressed during leaf development; 41 proteins were found to be differently expressed between two and four week old leaves, and 84 proteins were found to be differently expressed between two and six week old leaves, respectively. Cluster analysis of the data revealed dynamic proteomes. Proteins annotated as electron carrier activity were greatly enriched in the peak expression profiles, and photosynthesis proteins were negatively modulated along the whole time course. This dataset will serve as the foundation for a systems biology approach to understanding photosynthetic development.