

**From Interaction to Function, What Can We Learn About
Metabolites from Knowing Their Protein Partners?**

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Functional diversity reflects the immense chemical diversity of living organisms that produce hundreds of thousands of small molecule compounds, most of which remain to be chemically and functionally characterized. Because small molecules rarely work on their own but rather via interactions with proteins, following the proverbial "tell me who your friends are, and I will tell you who you are," identification of protein interactors can be used to unravel the function of a metabolite. The complex and dynamic protein-metabolite interactions (PMIs) network underlies all biological processes but remains under-characterized. In my group, we adapted co-fractionation mass-spectrometry (CF-MS), a well-established approach to map protein assemblies, for proteome and metabolome-wide identification of the protein-metabolite complexes. CF-MS experiments combine the separation of native complexes with MS analysis of the obtained fractions and use the similarity of elution profiles, referred to as co-elution or co-fractionation, to delineate interactors. CF-MS enables the untargeted identification of complexes without needing a protein or a metabolite bait. The PMI networks generated in the group comprise tens of annotated metabolites and hundreds of unknown metabolic features. During my seminar, I will discuss how we use the obtained interaction data to uncover novel regulatory functions of compounds, focusing on dipeptides and cyclic dipeptides and their role in regulating central carbon metabolism and organismal health in plants and animals.

If you would like to visit with Dr. Aleksandra Skirycz, please contact Dr. Kathrin Schrick at kschrick@ksu.edu.

Coffee & snacks served preceding the seminar in Ackert Hall, Room 225