## Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases

Marija Buljan<sup>1</sup>, Rodolfo Ciuffa<sup>1</sup>, Audrey van Drogen<sup>1</sup>, Ruedi Aebersold<sup>1</sup>, Matthias Gstaiger<sup>1</sup>,

Empa, Materials Science and Technology, Zurich, CH<sup>1</sup>

Protein kinases are essential for signal transduction and control of most cellular processes, including metabolism, membrane transport, motility, and cell cycle. Despite the critical role of kinases in cells and their strong association with diseases, good coverage of their interactions is available for only a fraction of the 535 human kinases. In this study, we present a comprehensive mass-spectrometry-based analysis of a human kinase interaction network covering more than 300 kinases. The interaction dataset is a high-quality resource with more than 5,000 previously unreported interactions. We extensively characterized the obtained network and were able to identify previously described, as well as predict new, kinase functional associations, including those of the less well-studied kinases PIM3 and protein Omannose kinase (POMK). Importantly, the presented interaction map is a valuable resource for assisting biomedical studies. We uncover dozens of kinase-disease associations spanning from genetic disorders to complex diseases, including cancer.