

# Data Integration and Analysis of SILAC Phosphoproteomics Applied to Mammalian Cells

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Quantitative data generated by stable isotope labeling by amino acids in cell culture (SILAC) phospho-proteomics experiments provide detailed information on the overall phosphorylation state change under two different conditions. Integration of such data can be used to unveil kinase cascade pathways as well as unravel the regulatory axis of the kinome regulatory network. By computing the overlap of newly discovered sets of phosphorylation sites (phospho-sites) with sets from prior SILAC experiments, the prior studies can be ranked based on similarity to the new studies. Such comparison can assist in generating new hypotheses about the phospho-sites involvement in particular cellular responses. For this project we compiled an initial database with data from thirteen previously published SILAC phospho-proteomics experiments applied to mammalian cells. We examine the overlap between the experiments and assess the dimensionality of the data. The database is delivered as a web-based software application that enables users to compare their lists of proteins and phospho-sites with those from prior SILAC phospho-proteomics experiments. The application returns p-values of the overlap between the user-provided list and the data from individual SILAC experiments.