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Detecting TOR regulated phosphorylations in Saccharomyces cerevisiae using affinity chromatography and quantitative proteomics

The TOR (Target of Rapamycin) kinases are vital in all eukaryotes for the regulation of cell growth and development. TOR kinases regulates downstream biological pathways through post translational phosphorylation. Identifying these targets of phosphorylation will help us better understand how TOR regulates growth and development. Here we apply ProQ Diamond enrichment and detection with iTRAQ labeling and mass spectrometry analysis to identify possible phosphorylation targets of TOR in *Saccharomyces cerevisiae*. Using rapamycin, a known inhibitor of TOR, we collected protein samples with different time treatments. Each sample was enriched for phosphoproteins with ProQ Diamond then digested with trypsin and labeled with iTRAQ tags. Samples were pooled then fractionated via SCX then loaded onto an LTQ mass spectrometer. Data analysis will identify protein phosphorylations that changes in abundance upon TOR inhibition. This experiment will show for the first time phosphorylation events regulated by TOR in *S. cerevisiae* and may also identify new TOR substrates.



Poster Number: Session: