PROTEOME DYNAMICS

Quantitative Ubiquitination Profiling

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Protein ubiquitination is an essential regulatory modification that controls protein turnover. LC-MS is a powerful tool for specific identification of ubiquitination sites via the diGly remnant produced following trypsinolysis of ubiquitinated lysines. IQ Proteomics offers unbiased, multiplexed proteome-wide quantification of ubiquitination dynamics.

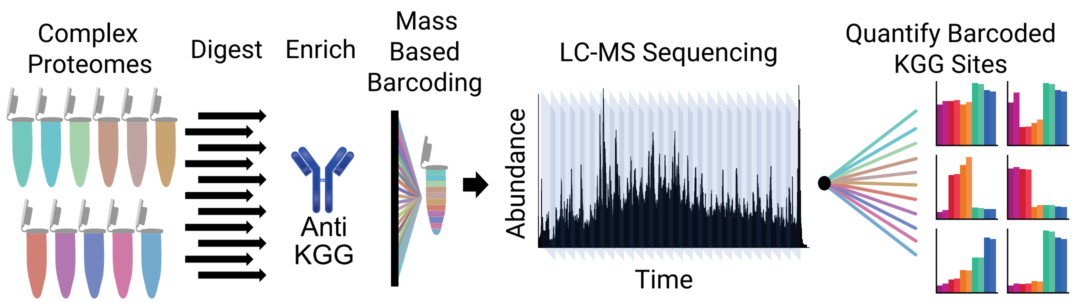
Features

- Thousands of Ub Sites Quantified
- High Affinity Enrichment:
  PTMScan® Technology
- High Throughput Proteomics:
  TMT™ 18-Plex Technology
  Orbitrap Eclipse (RTS-MS3)

Applications

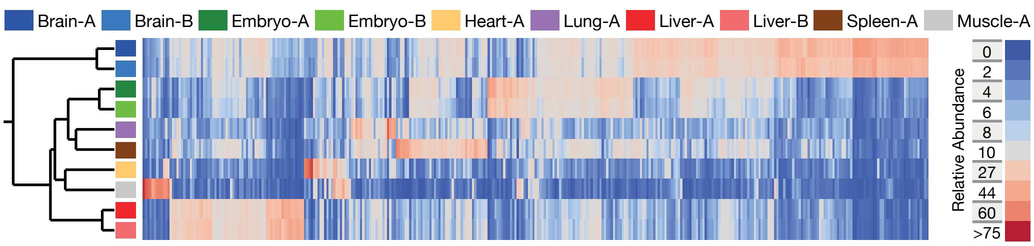
- Protein Turnover
- PROTAC Specificity Screening
- Cell Lines/Tissues

ASSAY OVERVIEW



Protein extracts from up to 18 samples are digested with trypsin. Ubiquitinated peptides are immunoenriched through the characteristic diGly remnant on modified lysines following trypsinolysis. Enriched peptides are barcoded with isobaric labeling reagents for multiplexing (up to 18 samples), mixed, and analyzed by LC-MS. Quantification via RTS-MS3 on Orbitrap Eclipse instruments ensures sensitive and reliable measurements across thousands of diGly sites with no missing values.

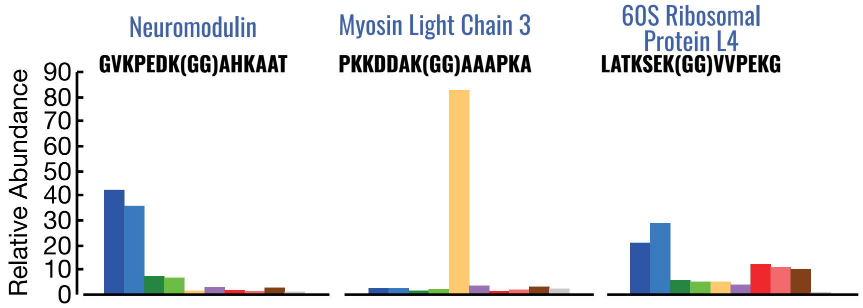
DATA OVERVIEW



4730 Unique Ubiquitination Sites Quantified Across 1984 Proteins

10 mouse tissues were prepared for comprehensive quantitative profiling of Ubiquitination signalling in a single 10-plex multiplexed LC-MS experiment. Distinct ubiquitination signatures for each tissue type are readily apparent, with excellent reproducibility of these signatures across biological replicates. A single experiment provided excellent coverage of steady state ubiquitination (4730 distinct ubiquitination sites quantified across 1984 proteins).

DATA SPOTLIGHT



-Excellent diGly quantitative reproducibility across biological replicates (Neuromodulin, blue bars)

-Tissue-specific ubiquitination quantified with excellent dynamic range (Myosin Light Chain 3, yellow bar)

-IQ Proteomics' sensitive workflow for proteome-wide ubiquitin characterization permits reproducible quantification of subtle differences between samples (60S Ribosomal Protein)

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