

QUAIL TAGS: PRECISION PROTEOMICS REDEFINED

QUAIL Tags ensure identification of miniscule quantities of proteins in mass spectrometry (MS)-based proteomics. These chemical tags enhance the ionization and fragmentation of peptides. This enables precise detection and quantification of post-translational modifications (PTMs). Designed with a unique ionizable head, cleavable linker, and reporter group, QUAIL Tags address limitations of traditional isobaric labeling techniques such as Tandem Mass Tags (TMT) and Isobaric Tags for Relative and Absolute Quantification (iTRAQ).

- **Enhanced Sensitivity:** Improved ionization and efficient cleavage of reporter ions significantly boost MS detection capabilities, especially for poorly ionizable peptides
- **High Multiplexing Capacity:** Supports multiplex sample analysis in a single run, increasing throughput for large-scale proteomics applications
- **Cost-Effective Synthesis:** Simple, one-step click chemistry ensures high-yield, scalable production at reduced costs
- **Improved Quantification Accuracy:** Minimizes interference from co-eluting peptides, enhancing reliability in complex samples
- **Customizable Design:** Adjustable polyethylene glycol (PEG) linkers optimize solubility and stability, catering to specific needs
- **Broad Applicability:** Ideal for detecting clinically relevant biomarkers, such as PTMs in cancer, cardiovascular diseases, diabetes, and neurodegenerative disorders



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