



TECHNICAL DATASHEET

PROTIFI™

Bringing precision omics to life!™

info@protifi.com | https://protifi.com

S-Trap™ Multi-Attribute Method (MAM) Kit



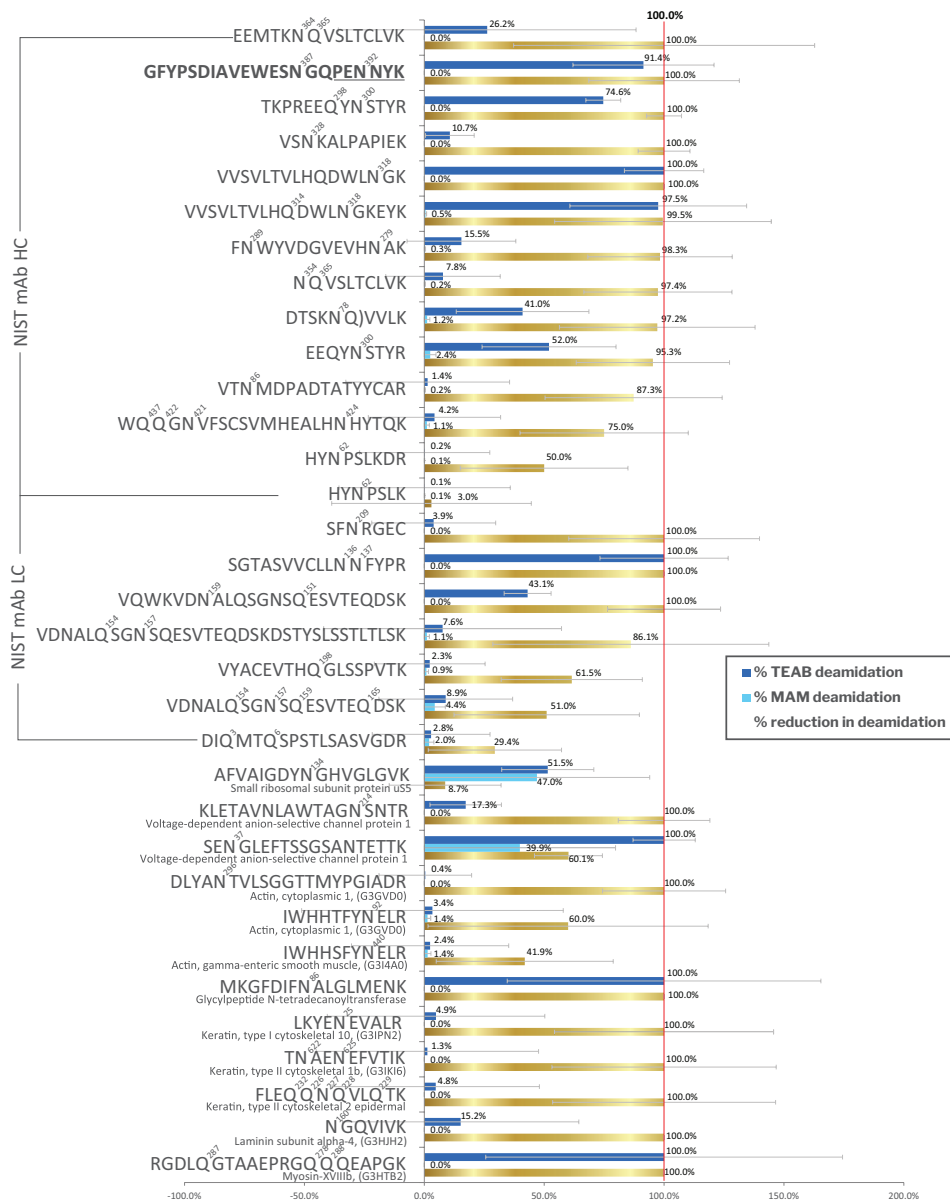
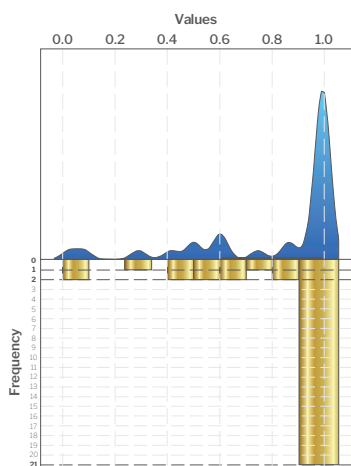
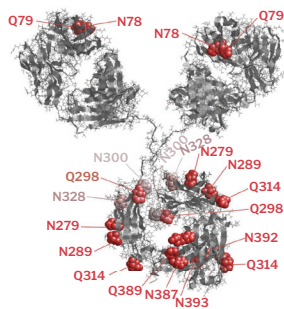
ProtiFi's™ Multi-Attribute Method (MAM) Kit offers a comprehensive, robust solution to ensure reproducible sample preparation, prevent artifacts like deamidation, and enable efficient PTM analyses of biological medicines.

Without method development, it enables reliable, scalable quality control throughout the entire product lifecycle regardless of product form or contaminant, all within a single, harmonized kit.

REDUCTION OF ARTIFICIAL DEAMIDATION

The S-Trap™ MAM Kit minimizes deamidation in NIST mAb peptides. Of 33 deamidated peptides detected, 16 showed complete prevention and 5 were >95% protected. The rest likely reflect pre-existing deamidation.

Note: Large error bars are due to high variability in TEAB digestion (~30% CV), not the MAM Kit, which delivers consistent results with an average CV of just 3.7%.





TECHNICAL DATASHEET

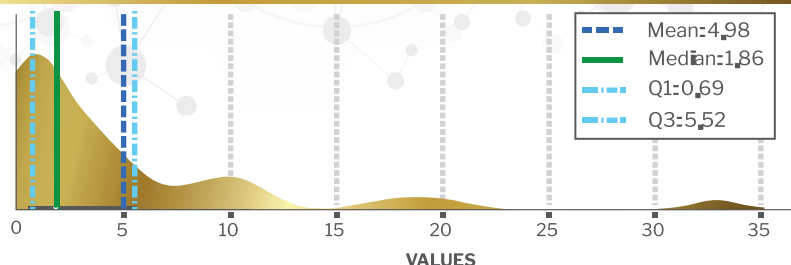
PROTIFI™

Bringing precision omics to life!™

info@protifi.com | https://protifi.com

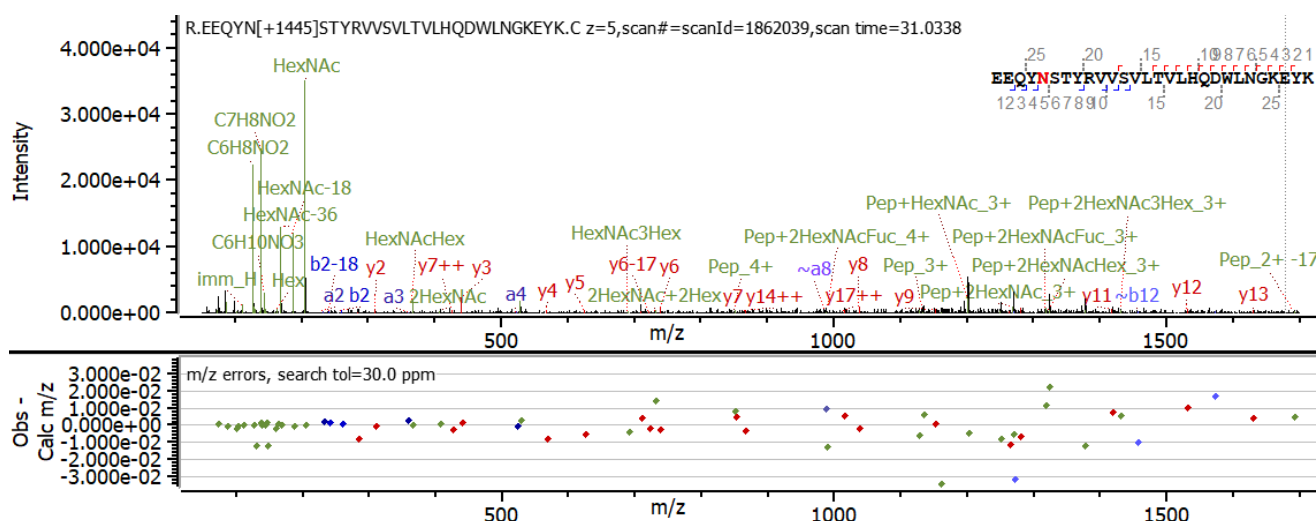
RATIO OF SIGNAL INCREASE

Processing on three separate days of NIST mAb samples afforded significantly greater signal strength than a standard TEAB overnight digestion; mean and median increases: 5.0 and 1.9 respectively.



PROTEIN CHARACTERIZATION

The MAM kit reproducibly yields PTM-containing peptides including those with glycosylations, oxidation, and deamidation.



CONTAMINANT REMOVAL

1% tween-20 was removed to undetectable levels. 100 μ L of 1% tween-20 containing 100 μ g mAb was processed by S-Trap™. 2% of the sample was then injected. The lower panel is a 1 μ L injection of a 1:10,000 dilution of 1% tween-20 representing a 20,000 fold dilution compared to the upper panel.

Assuming a linear response with increasing concentration the equivalent detergent signal would be in the range of 4E12.

