

What is claimed is:

1. A method of quantifying multiple quality attributes of multiple samples in a single mass spectrometry (MS) run, comprising:
 - contacting two or more samples with a digesting solution under conditions sufficient to digest the two or more samples, wherein each sample is digested separately and the digesting solution is a Tris-free buffer solution;
 - contacting each of the two or more digested samples with a specific Tandem Mass Tag (TMT) labeling reagent under conditions sufficient to label peptides within each of the two or more digested samples with the specific TMT labeling reagent;
 - quenching labeling of peptides within each of the two or more digested samples;
 - combining equal volumes of the two or more labeled, digested samples into a single combined sample solution; and
 - analyzing the single combined sample solution by targeted mass spectral analysis, thereby allowing multiple quality attributes of the two or more samples to be quantified in a single MS run.
2. The method of claim 1, wherein multiple quality attributes comprise a post translational modification (PTM).
3. The method of claim 2, wherein the PTM comprises one or more of deamidation, oxidation, glycation, disulfide formation, N-terminal pyroglutamate formation, C-terminal lysine removal, and glycosylation.
4. The method of claim 3, wherein the PTM comprises glycosylation.
5. The method of any one of claims 2 to 4, wherein quantifying multiple quality attributes in a single MS run, comprises quantifying the PTM by quantifying relative abundance of PTM from extracted peak areas of a resultant report ion generated in targeted mass spectra.
6. The method of any one of claims 1 to 5, further comprising contacting each of the two or more digested samples with a small molecule additive prior to contacting each of the two or more digested samples with a specific TMT labeling reagent.

7. The method of claim 5, wherein the small molecule additive is selected from the group consisting of BOC-Y-OH, p-Cresol, Hydroxy-phenyl acetic acid (HPAA), hydroxy benzoic acid (HBA), acetaminophen, and p-Amino Benzoic acid (PABA).
8. The method of claim 6, wherein the small molecule additive is PABA.
9. The method of any one of claims 1 to 8, wherein the peptides are glycopeptides.
10. The method of claim 9, wherein the glycopeptides are obtained from a monoclonal antibody.
11. The method of claim 10, wherein the monoclonal antibody is of isotype IgG1, IgG2, IgG3, IgG4, or mixed isotype.
12. The method of any one of claims 1 to 11, wherein two or more samples are between 2 and 11 samples.
13. The method of any one of claims 1 to 12, further comprising obtaining two or samples to be analyzed.
14. The method of any one of claims 1 to 13, further comprising preparing the two or more samples for digestion prior to contacting the two or more samples with a digesting solution under conditions sufficient to digest the two or more samples.
15. The method of claim 14, wherein preparing the two or more samples prior to digestion comprises contacting each of the two or more samples with a denaturing and reducing solution under conditions that permit sample denaturation and reduction; and contacting each of the two or more denatured and reduced samples with an alkylating solution under conditions that permit sample alkylation.
16. The method of any one of claims 1 to 15, wherein analyzing the single combined sample solution by targeted mass spectral analysis comprises applying the single combined sample to a separation column and performing targeted mass spectral analysis on eluted sample components.

17. The method of claim 16, wherein the separation column is a liquid chromatography column.
18. The method of claim 16 or 17, wherein performing targeted mass spectral analysis on eluted sample components comprises applying electrospray ionization to generate charged ions from the eluted sample components and measuring the generated charge ions.
19. A method of quantifying post translational modifications (PTMs) of multiple samples in a single mass spectrometry (MS) run, comprising:
contacting two or more samples with a digesting solution under conditions sufficient to digest the two or more samples, wherein each sample is digested separately and the digesting solution is a Tris-free buffer solution;
contacting each of the two or more digested samples with a small molecule additive;
contacting each of the two or more digested samples with a specific Tandem Mass Tag (TMT) labeling reagent under conditions sufficient to label peptides within each of the two or more digested samples with the specific TMT labeling reagent;
quenching labeling of peptides within each of the two or more digested samples;
combining equal volumes of the two or more labeled, digested samples into a single combined sample solution; and
analyzing the single combined sample solution by targeted mass spectral analysis, thereby allowing PTMs of the two or more samples to be quantified in a single MS run.
20. The method of claim 21, wherein the PTMs comprise one or more of deamidation, oxidation, glycation, disulfide formation, N-terminal pyroglutamate formation, C-terminal lysine removal, and glycosylation.
21. The method of claim 20, wherein PTMs comprise glycosylation.
22. The method of any one of claims 19 to 21, wherein quantifying PTMs comprises quantifying relative abundance of PTM from extracted peak areas of a resultant report ion generated in targeted mass spectra.
23. The method of any one of claims 19 to 22, wherein the small molecule additive is selected from the group consisting of BOC-Y-OH, p-Cresol, Hydroxy-phenyl acetic acid (HPAA), hydroxy benzoic acid (HBA), acetaminophen, and p-Amino Benzoic acid (PABA).

24. The method of claim 23, wherein the small molecule additive is PABA.
25. The method of any one of claims 19 to 24, wherein the peptides are glycopeptides.
26. The method of claim 25, wherein the glycopeptides are obtained from a monoclonal antibody.
27. The method of claim 26, wherein the monoclonal antibody is of isotype IgG1, IgG2, IgG3, IgG4, or mixed isotype.
28. The method of any one of claims 19 to 27, wherein two or more samples are between 2 and 16 samples.
29. The method of any one of claims 19 to 28, further comprising obtaining two or samples to be analyzed.
30. The method of any one of claims 19 to 29, further comprising preparing the two or more samples for digestion prior to contacting the two or more samples with a digesting solution under conditions sufficient to digest the two or more samples.
31. The method of claim 30, wherein preparing the two or more samples prior to digestion comprises contacting each of the two or more samples with a denaturing and reducing solution under conditions that permit sample denaturation and reduction; and contacting each of the two or more denatured and reduced samples with an alkylating solution under conditions that permit sample alkylation.
32. The method of any one of claims 19 to 31, wherein analyzing the single combined sample solution by targeted mass spectral analysis comprises applying the single combined sample to a separation column and performing targeted mass spectral analysis on eluted sample components.
33. The method of claim 32, wherein the separation column is a liquid chromatography column.

34. The method of claim 32 or 33, wherein performing targeted mass spectral analysis on eluted sample components comprises applying electrospray ionization to generate charged ions from the eluted sample components and measuring the generated charge ions.