# Protein Metrics

# Case study of inter-laboratory multi-attribute method (MAM) data comparison in Japan using NIST mAb

## Summary

For Multi-attribute method (MAM) round robin study in Japan, both purchased and in-house digested NISTmAb were analyzed with individual LC and MS

Sample 1 NIST mAb (NIST, RM 8671)

Time (min)	Buffer A (%)	Buffer B (%)
0	99	1
5	99	1
70	60	40
75	10	90
85	10	90
85.1	99	1
100	99	1





systems, acquired in MS1 only and in MS/MS modes. We compared the relative abundance of several predefined reference NIST mAb CQAs (deamidation,

ammonia-loss, oxidation, terminal Lys-loss and pyroQ) using Byosphere.



### Fig.4 Retention time variation for each reference peptide



The sum of the percent mod for the oxidation of peptide DTLMISR had some outliers in two labs data. For the deamidated peptide a PENNY peptide, the sum of the percent mod didn't show any outliers.



## Birds-eye view allows researchers to quickly find outliers and improve sample preparation, MS parameters, and separation conditions.

One lab data for purchased digested sample showed outliers, however, the reproducibility of retention times were similar among other participants data. This indicates that the data are sufficient for comparison in this study.

## Conclusion

Byosphere dashboard feature allows users to see peptide modification ratio and system suitability across samples and labs and enabled to gain insight from a large amount of data.

## **Acknowledgements and Conflict of Interest** Statement

The authors wish to thank to Dr. Kohsaku Kawakami from National Institute for Materials Science (NIMS) and the pharmaceutical companies participating in Materials Open Platform (MOP) for Pharmaceutical Science.

Authors are employees of Protein Metrics, LLC, which has commercialized the software described here.