

MeCAT labeling for absolute quantification of intact proteins using label-specific isotope dilution ICP-MS

D. Esteban-Fernández¹, F. S. Bierkandt², M. W. Linscheid^{*1}

Keywords: ICP-MS, MeCAT labeling, absolute quantification, laser ablation, intact proteins

¹ Department of Chemistry, Humboldt-Universität zu Berlin, Brook-Taylor Str. 2, 12489 Berlin, Germany

² BAM Federal Institute for Materials Research & Testing, Richard-Willstätter Str. 11, 12489, Berlin, Germany

*Corresponding author: M. W. Linscheid. E-mail: m.linscheid@chemie.hu-berlin.de
Fax: +49 (0)30 2093 6985; Tel: +49 (0)30 2093 7575

Supporting information

The present document provides further information on the paper mentioned above.

Contents:

- Figures S-1 to S-3

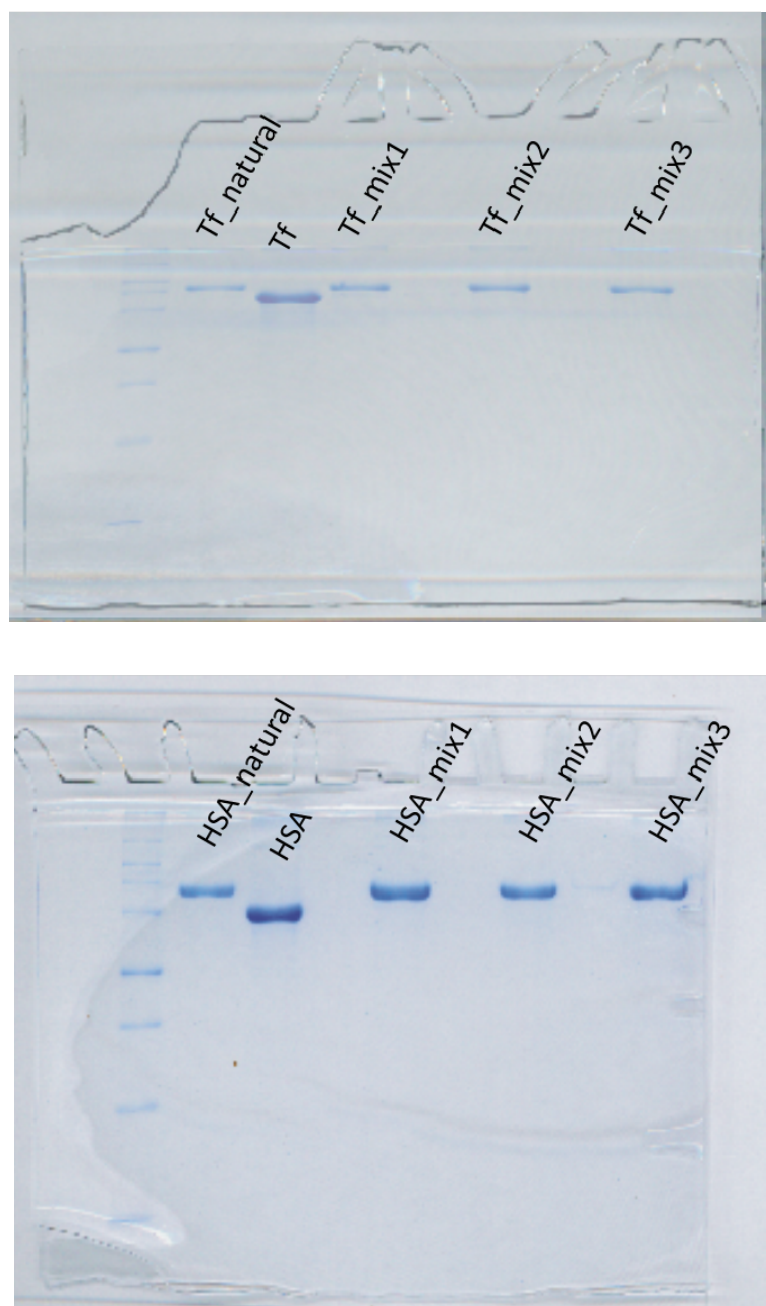


Figure S-1. Gel electrophoresis analysis of labeled and unlabeled standard HSA and Tf. The samples were loaded in the following order: Proteins labeled with MeCAT(Yb)-IA, unlabeled proteins and three replicates of MeCAT(Yb)-IA labeled proteins spiked with a known amount of the proteins labeled with isotopically-enriched MeCAT(^{171}Yb)-IA.

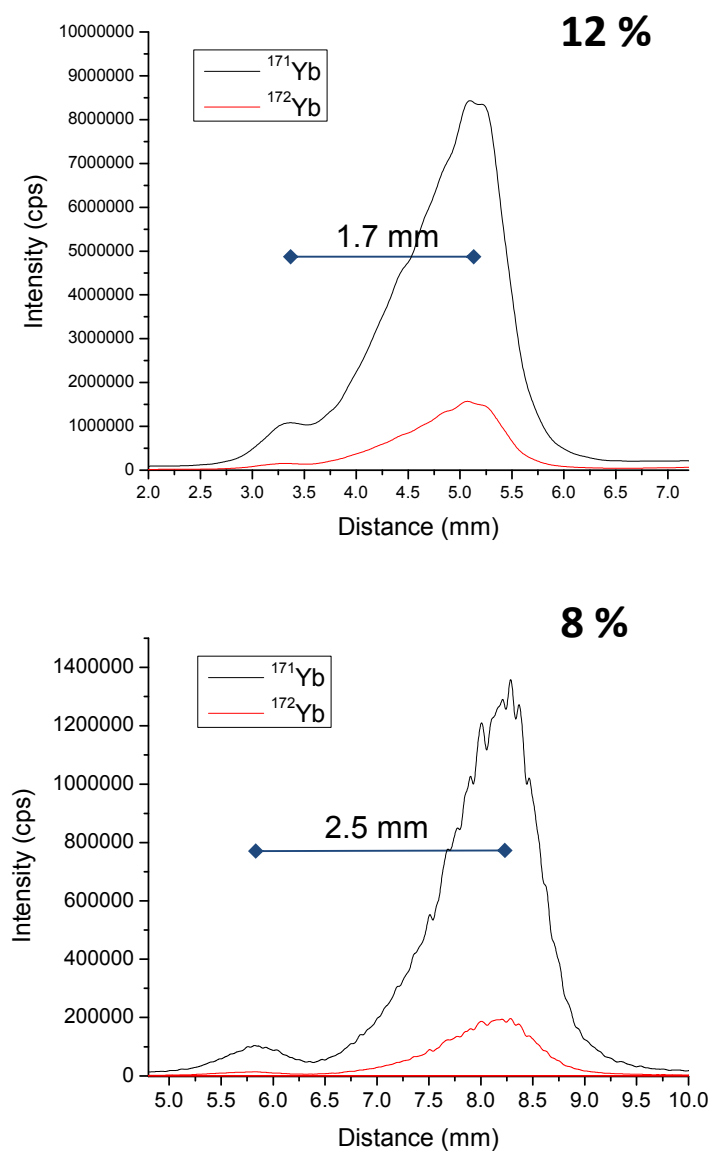


Figure S-2. Comparison of the resolution achieved for spiked serum samples with gels containing 8 and 12% acrylamide. Single lane monitoring of isotopes ^{171}Yb and ^{172}Yb by LA-ICP-MS in the migration direction. Spot size $100\text{ }\mu\text{m}$, scan rate $100\text{ }\mu\text{m s}^{-1}$.

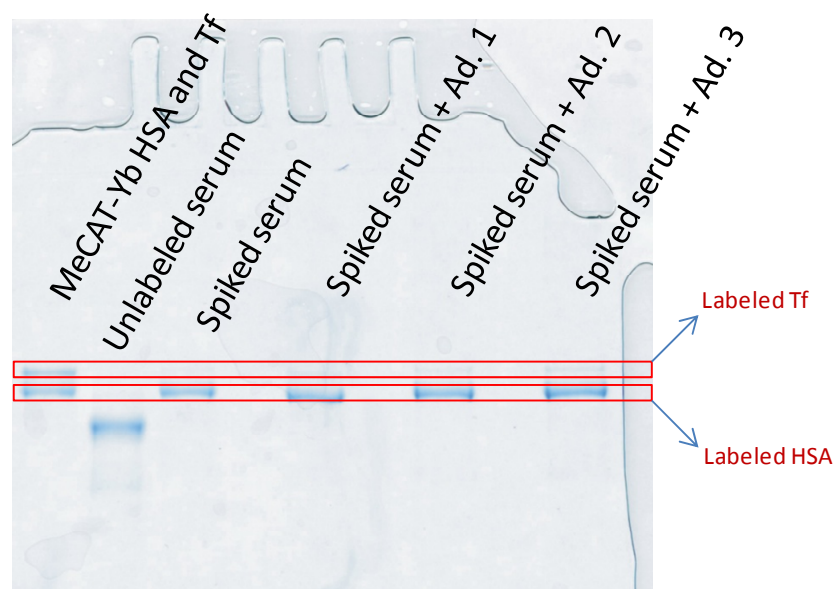


Figure S-3. Coomassie Blue stained gel containing spiked serum and three different standard additions. Standard HSA and Tf labeled with MeCAT(Yb)-IA (ca. 0.5 μg per protein) were separated in the first lane to calibrate migration distances.