

## Hannes Rost

We use computational approaches to understand clinical phenomena on a personalized level and study biological phenomena from a systems perspective. We specifically focus on next-generation mass spectrometry approaches using a combination of high mass resolution and fast scan speeds MS to comprehensively acquire information about a biological specimen. In particular, we have developed methods and software for data-independent acquisition (DIA) mass spectrometry, most notably the OpenSWATH and TRIC software which allow automated analysis of SWATH mass spectrometry data. Our software is developed as open source and our lab is one of the core developers of the OpenMS C++ framework. We combine robust software engineering with advanced signal processing and machine learning methods to extract information from highly multiplexed MS data (specifically DIA data). We apply these methods to acquire comprehensive data about protein or small molecule analytes in complex biological samples such as whole cell lysates or tissue samples.



### *Most Significant Publications*

1. Röst HL\*, Sachsenberg T\*, Aiche S\*, Bielow C\*, Weisser H\*, Aicheler F, Andreotti S, Ehrlich HC, Gutenbrunner P, Kenar E, Liang X, Nahnsen S, Nilse L, Pfeuffer J, Rosenberger G, Rurik M, Schmitt U, Veit J, Walzer M, Wojnar D, Wolski WE, Schilling O, Choudhary JS, Malmström L, Aebersold R, Reinert K, Kohlbacher O. "OpenMS: a flexible open-source software platform for mass spectrometry data analysis." *Nat Methods*. 2016 Aug 30;13(9):741-8.
2. Röst HL, Liu Y, D'Agostino G, Zanella M, Navarro P, Rosenberger G, Collins BC, Gillet L, Testa G, Malmström L, Aebersold R. "TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics." *Nat Methods*. 2016 Sep;13(9):777-83.
3. Röst HL\*, Rosenberger G\*, Navarro P, Gillet L, Miladinović SM, Schubert OT, Wolski W, Collins BC, Malmström J, Malmström L, Aebersold R. "OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data." *Nat Biotechnol*. 2014 Mar;32(3):219-23.
4. Röst H, Malmström L, Aebersold R. "A computational tool to detect and avoid redundancy in selected reaction monitoring." *Mol Cell Proteomics*. 2012 Aug;11(8):540-9.
5. Gillet LC, Navarro P, Tate S, Röst H, Selevsek N, Reiter L, Bonner R, Aebersold R. "Targeted data extraction of the MS/MS spectra generated by data-independent acquisition: a new concept for consistent and accurate proteome analysis." *Mol Cell Proteomics*. 2012 Jun;11(6):O111.016717.

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