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Title: Towards complete proteomes: Technology and applications

Biography: Matthias Mann studied physics and mathematics at Göttingen University in Germany and obtained his Ph.D. in chemical engineering at Yale University. Here he was decisively involved in the development of electrospray ionization, which has become a key technology of the life sciences. As a post-doctoral fellow and later as a professor for bioinformatics at the University of Southern Denmark in Odense, he developed, amongst others techniques, the first bioinformatic search algorithms for peptide fragmentation data and SILAC, a new method of quantitative proteomics and a breakthrough in the mapping of protein interactions.

In 2005, Matthias Mann took up a director position at the Max-Planck Institute of Biochemistry in Munich. Here his group continues to address a wide range of biological questions using proteomic technology, as well as to develop this technology. The group is also heavily involved in providing proteomic methods and tools to the community. Most importantly in this regard, they have provided the MaxQuant suite of computational proteomics algorithms; this software promises to significantly advance the state of the field. More recently his group used the SILAC technology in conjunction with MaxQuant to described the first comprehensive identification and quantification of a proteome. (<http://www.biochem.mpg.de/en/rd/mann>)

In 2009 Dr. Mann was additionally appointed director of the proteomics department of the Novo Nordisk Foundation Center for Protein Research in Copenhagen.

Matthias Mann has authored and co-authored more than 500 publications with a total citation count of more than 50,000, making him one of the most highly cited researchers worldwide, has been elected to membership of the European Molecular Biology Organization, Royal Danish Academy of Arts and Sciences and the Leopoldina German National Academy of Sciences as well as to a visiting professorship at Harvard Medical

School. He has received two honorary degrees from Utrecht University and the University of Dundee, respectively.

In 2012 he was awarded the Leibniz Prize from the German Research Foundation, the Ernst Schering Prize, the Louis-Jeantet Foundation Prize for Medicine and the Körber European Science Prize.

Ten most important publications to date:

- 1) Wilm, M., Shevchenko, A., Houthaeve, T., Breit, S., Schweigerer, L., Fotsis, T., and Mann, M. (1996). Femtomole Sequencing of Proteins from Polyacrylamide Gels by Nano Electrospray Mass Spectrometry. *Nature* 379, 466 - 469.
- 2) Mann, M., and Wilm, M.S. (1994). Error Tolerant Identification of Peptides in Sequence Databases by Peptide Sequence Tags. *Analytical Chemistry* 66, 4390-4399.
- 3) Neubauer, G., King, A., Rappsilber, J., Calvio, C., Watson, M., Ajuh, P., Sleeman, J., Lamond, A.I., and Mann, M. (1998). Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. *Nat Genet* 20, 46-50.
- 4) Ong, S.E., Blagoev, B., Kratchmarova, I., Kristensen, D.B., Steen, H., Pandey, A., and Mann, M. (2002). Stable Isotope Labeling by Amino Acids in Cell Culture, SILAC, as a Simple and Accurate Approach to Expression Proteomics. *Mol Cell Proteomics* 1, 376-386.
- 5) Olsen, J.V., Blagoev, B., Gnäd, F., Macek, B., Kumar, C., Mortensen, P., and Mann, M. (2006). Global, In Vivo, and Site-Specific Phosphorylation Dynamics in Signaling Networks. *Cell* 127, 635-648.
- 6) de Godoy, L.M., Olsen, J.V., Cox, J., Nielsen, M.L., Hubner, N.C., Frohlich, F., Walther, T.C., and Mann, M. (2008). Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. *Nature* 455, 1251-1254.
- 7) Choudhary, C., Kumar, C., Gnäd, F., Nielsen, M.L., Rehman, M., Walther, T.C., Olsen, J.V., and Mann, M. (2009). Lysine acetylation targets protein complexes and co-regulates major cellular functions. *Science* 325, 834-840.
- 8) Zielinska DF, Gnäd F, Wiśniewski JR, Mann M. Precision mapping of an in vivo N-glycoproteome reveals rigid topological and sequence constraints. *Cell*. 2010 May 28;141(5):897-907.
- 9) Vermeulen M, Eberl HC, Matarese F, Marks H, Denissov S, Butter F, Lee KK, Olsen JV, Hyman AA, Stunnenberg HG, Mann M. Quantitative interaction proteomics and genome-wide profiling of epigenetic histone marks and their readers. *Cell*. 2010 Sep 17;142(6):967-80.
- 10) Nagaraj N, Kulak NA, Cox J, Neuhauser N, Mayr K, Hoerning O, Vorm O, Mann M. System-wide perturbation analysis with nearly complete coverage of the yeast proteome by single-shot ultra HPLC runs on a bench top Orbitrap. *Mol Cell Proteomics*. 2012 Mar;11(3)