BIOGRAPHICAL SKETCH

NAME: Michael J MacCoss

eRA COMMONS USER NAME (credential, e.g., agency login): MACCOSS

POSITION TITLE: Professor

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE(if applicable) | Completion DateMM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| University of Vermont, Burlington, VT | BA | 05/1996 | Chemistry |
| University of Vermont, Burlington, VT | Ph.D | 01/2001 | Chemistry |
| The Scripps Research Institute, La Jolla, CA | Post-Doc | 01/2004 | Proteomics |

1. **Personal Statement**

The focus of the MacCoss laboratory is in the development and application of cutting-edge mass spectrometry-based technologies for the analysis of complex protein mixtures. Dr. MacCoss’ primary area of expertise is in protein biochemistry, nanoflow liquid chromatography, mass spectrometry instrumentation, and computational analysis of mass spectrometry data. He has ~30 years of mass spectrometry experience that bridges the fields of protein mass spectrometry, isotope ratio mass spectrometry, and quantitative mass spectrometry. The MacCoss laboratory has been actively applying these tools to important areas of biology including but not limited to, the basic biology of aging, neurodegenerative disease, protein-protein interactions, insulin signaling, cancer, measurement of protein half-life, transcriptional regulation, characterization of post-translational modifications, proteogenomics, and clinical diagnostics. The MacCoss laboratory is widely known for its expertise in the development and support of proteomics software tools. This expertise in mass spectrometry and the support of open-source software tools will be critical to the success of this project. Dr. MacCoss has been actively involved in the scientific direction and management of NIH centers, program projects, consortia, and large quantitative proteomics data production efforts since he arrived at UW in 2004.

The MacCoss lab has trained 15 Ph.D. students and 15 postdoctoral fellows. There have been 1000s of individuals who have attended the Quantitative Proteomics Courses co-taught by Dr. MacCoss and lab personnel.

Ongoing projects that I would like to highlight include:

R24 GM141156 (MacCoss) 5/1/2021 – 4/30/2026

NIH / NIGMS

**Seattle Quant: A Resource for the Skyline Software Ecosystem**

The Skyline software ecosystem is one of the most widely used software platforms in all of mass spectrometry. The Skyline project has grown beyond the bounds of a single tool. In this grant, we propose creating a resource that will enable the continued development and maintenance of these community tools and their dissemination within the community.

Role: Principal Investigator

U01 DK137097 (MPI: Hoofnagle, MacCoss) 7/01/24-6/30/27

NIH/NIA

**Quantifying proteins in plasma to democratize personalized medicine for patients with type 1 diabetes** This project aims to make new blood tests that researchers and clinical laboratories can easily recreate at their own institutions, which will make research findings more reproducible and will help facilitate their translation into patient care.

Role: Multiple Principal Investigator

P30 AG013280-26 (Marcinek and Young) 9/15/2010 – 5/31/2030

NIH / NIA

**Nathan Shock Center of Excellence in Basic Biology of Aging**

**Core C: Protein Phenotypes of Aging**

This center provides resources in support of Seattle based investigators interested in the basic biology of aging. Dr. MacCoss is the director of the Functional Genomics Core and provides support to investigators through proteomics collaborations and consultation.

Role: Core Director

**B. Positions, Scientific Appointments, and Honors**

**Positions**

2014-present Professor, University of Washington, Department of Genome Sciences

2009-2014 Associate Professor, University of Washington, Department of Genome Sciences

2004-2009 Assistant Professor, University of Washington, Department of Genome Sciences

2001-2003 Post-Doctoral Fellow, The Scripps Research Institute, Department of Cell Biology

1998-2000 Visiting Scientist, Merck Research Laboratories, Rahway, NJ

1996-2001 Graduate Student, University of Vermont, Department of Chemistry

1995, 1996 Intern, Merck Research Laboratories, Rahway, NJ

**Honors**

2024 University of Washington Science in Medicine Collaborative Lecture (with Andy Hoofnagle)

2016 HUPO Award for Discovery in Proteomics Sciences

2015 American Association for Clinical Chemistry Outstanding Speaker Award

2015 Biemann Medal, American Society for Mass Spectrometry

2007 Presidential Early Career Award for Scientists and Engineers (PECASE)

2006 Genome Technology, Rising Young Investigator

2004 American Society for Mass Spectrometry Research Award

2001-2003 National Institutes of Health, National Research Service Award

2000 American Society for Clinical Nutrition, Young Investigator Award

2000 Endocrinology and Metabolism Section of the American Physiological Society, Research Award

1. **Contributions to Science**
2. **Our laboratory has been leaders in the development and application of quantitative methods for the measurement of proteins in complex matrixes. These methods are based on the use of mass spectrometry, and we were some of the early leaders in the use of targeted proteomics.**
	1. **Wu CC, Tsantilas KA, Park J, Plubell D, Sanders JA, Naicker P, Govender I, Buthelezi S, Stoychev S, Jordaan J, Merrihew G, Huang E, Parker ED, Riffle M, Hoofnagle AN, Noble WS, Poston KL, Montine TJ, MacCoss MJ. Enrichment of extracellular vesicles using Mag-Net for the analysis of the plasma proteome. Nat Commun. 2025 Jul 1;16(1):5447. doi: 10.1038/s41467-025-60595-7. PMID: 40595564; PMCID: PMC12219689.**
	2. **Tsantilas KA, Merrihew GE, Robbins JE, Johnson RS, Park J, Plubell DL, Huang E, Riffle M, Sharma V, MacLean BX, Eckels J, Wu CC, Bereman MS, Spencer SE, Hoofnagle AN, MacCoss MJ. A framework for quality control in quantitative proteomics. bioRxiv [Preprint]. 2024 Apr 25:2024.04.12.589318. doi:10.1101/2024.04.12.589318. PMID: 38645098; PMCID: PMC11030400.**
	3. **Merrihew GE, Park J, Plubell D, Searle BC, Keene CD, Larson EB, Bateman R, Perrin RJ, Chhatwal JP, Farlow MR, McLean CA, Ghetti B, Newell KL, Frosch MP, Montine TJ, MacCoss MJ. A peptide-centric quantitative proteomics dataset for the phenotypic assessment of Alzheimer's disease. Sci Data. 2023 Apr 14;10(1):206. doi: 10.1038/s41597-023-02057-7. PMID: 37059743; PMCID:PMC10104800.**
	4. **MacCoss MJ, Alfaro JA, Faivre DA, Wu CC, Wanunu M, Slavov N. Sampling the proteome by emerging single-molecule and mass spectrometry methods. Nat Methods. 2023 Mar;20(3):339-346. doi: 10.1038/s41592-023-01802-5. PMID: 36899164; PMCID:PMC10044470.**
3. **Our laboratory at the University of Washington has focused on improving mass spectrometry technology and workflows. To accomplish this, we have worked on the development of mass spectrometry hardware and instrument control. This work has enabled new experiments, improved robustness, and simplified complicated hardware.**
	1. **Hsu C, Shulman N, Stewart H, Petzoldt J, Pashkova A, Plubell DL, Denisov E, Hagedorn B, Damoc E, MacLean BX, Remes P, Canterbury JD, Makarov A, Hock C, Zabrouskov V, Wu CC, MacCoss MJ. Evaluation of a prototype Orbitrap Astral Zoom mass spectrometer for quantitative proteomics - Beyond identification lists. bioRxiv [Preprint]. 2025 PMID: 40501761; PMCID: PMC12154736.**
	2. **Plubell DL, Huang E, Spencer SE, Poston KL, Montine TJ, MacCoss MJ. Data Independent Acquisition to Inform the Development of Targeted Proteomics Assays Using a Triple Quadrupole Mass Spectrometer. J Proteome Res. 2025 May 6. doi: 10.1021/acs.jproteome.5c00016. Epub ahead of print. PMID: 40328514.**
	3. **Remes PM, Jacob CC, Heil LR, Shulman N, MacLean BX, MacCoss MJ. Hybrid Quadrupole Mass Filter-Radial Ejection Linear Ion Trap and Intelligent Data Acquisition Enable Highly Multiplex Targeted Proteomics. J Proteome Res. 2024 Oct 30. doi: 10.1021/acs.jproteome.4c00599. Epub ahead of print. PMID: 39475161.**
	4. **Heil LR, Damoc E, Arrey TN, Pashkova A, Denisov E, Petzoldt J, Peterson AC, Hsu C, Searle BC, Shulman N, Riffle M, Connolly B, MacLean BX, Remes PM, Senko MW, Stewart HI, Hock C, Makarov AA, Hermanson D, Zabrouskov V, Wu CC, MacCoss MJ. Evaluating the Performance of the Astral Mass Analyzer for Quantitative Proteomics Using Data-Independent Acquisition. J Proteome Res. 2023 Oct 6;22(10):3290-3300. doi: 10.1021/acs.jproteome.3c00357. Epub 2023 Sep 8. PMID:37683181; PMCID: PMC10563156.**
4. **We have become one of the leaders in the development of new software tools for proteomics. We have developed tools for feature finding, quantitative analysis, targeted proteomics method development, storage and sharing of mass spectrometry data, and machine learning. These tools are widely distributed, are actively supported, and have extensive documentation.**
	1. **Riffle M, Zelter A, Jaschob D, Hoopmann MR, Faivre DA, Moritz RL, Davis TN, MacCoss MJ, Isoherranen N. Limelight: An Open, Web-Based Tool for Visualizing, Sharing, and Analyzing Mass Spectrometry Data from DDA Pipelines. J Proteome Res. 2025 Apr 4;24(4):1895-1906. doi: 10.1021/acs.jproteome.4c00968. Epub 2025 Mar 4. PMID: 40036265; PMCID: PMC11977539.**
	2. **Deutsch EW, Bandeira N, Perez-Riverol Y, Sharma V, Carver JJ, Mendoza L, Kundu DJ, Wang S, Bandla C, Kamatchinathan S, Hewapathirana S, Pullman BS, Wertz J, Sun Z, Kawano S, Okuda S, Watanabe Y, MacLean B, MacCoss MJ, Zhu Y, Ishihama Y, Vizcaíno JA. The ProteomeXchange consortium at 10 years: 2023 update. Nucleic Acids Res. 2023 Jan 6;51(D1):D1539-D1548. doi: 10.1093/nar/gkac1040. PMID: 36370099; PMCID: PMC9825490.**
	3. **Marsh AN, Sharma V, Mani SK, Vitek O, MacCoss MJ, MacLean BX. Skyline Batch: An Intuitive User Interface for Batch Processing with Skyline. J Proteome Res. 2022 Jan 7;21(1):289-294. doi: 10.1021/acs.jproteome.1c00749. Epub 2021 Dec 17. PMID: 34919405; PMCID: PMC8749956.**
	4. **Searle BC, Lawrence RT, MacCoss MJ, Villén J. Thesaurus: quantifying phosphopeptide positional isomers. Nat Methods. 2019 Aug;16(8):703-706. doi:10.1038/s41592-019-0498-4. Epub 2019 Jul 29. PMID: 31363206; PMCID: PMC7012383.**
5. **I have worked on applications of and technologies for the analysis of stable isotope enriched molecules since 1995. Our work has looked at the fundamental limits of stable isotope tracer measurement, use of stable isotope labeled amino acids to measure flux, and the use of isotopomer distribution analysis for the measurement of precursor corrected protein turnover measurements in invertebrates and vertebrates. This work has enabled us to develop new methods and tools for quantitative analysis by mass spectrometry.**
	1. **Basisty N, Shulman N, Wehrfritz C, Marsh AN, Shah S, Rose J, Ebert S, Miller M, Dai DF, Rabinovitch PS, Adams CM, MacCoss MJ, MacLean B, Schilling B. TurnoveR: A Skyline External Tool for Analysis of Protein Turnover in Metabolic Labeling Studies. J Proteome Res. 2023 Feb 3;22(2):311-322. doi: 10.1021/acs.jproteome.2c00173. Epub 2022 Sep 27. PMID: 36165806; PMCID: PMC10066879.**
	2. **Vincow ES, Merrihew G, Thomas RE, Shulman NJ, Beyer RP, MacCoss MJ, Pallanck LJ. The PINK1-Parkin pathway promotes both mitophagy and selective respiratory chain turnover in vivo. Proc Natl Acad Sci U S A. 2013 Apr 16;110(16):6400-5. doi: 10.1073/pnas.1221132110. Epub 2013 Mar 18. PubMed PMID: 23509287; PubMed Central PMCID: PMC3631677.**
	3. **Hsieh EJ, Shulman NJ, Dai DF, Vincow ES, Karunadharma PP, Pallanck L, Rabinovitch PS, MacCoss MJ. Topograph, a software platform for precursor enrichment corrected global protein turnover measurements. Mol Cell Proteomics. 2012 Nov;11(11):1468-74. doi: 10.1074/mcp.O112.017699. Epub 2012 Aug 3. PubMedPMID: 22865922; PubMed Central PMCID: PMC3494182.**
	4. **Tomazela DM, Patterson BW, Hanson E, Spence KL, Kanion TB, Salinger DH, Vicini P, Barret H, Heins HB, Cole FS, Hamvas A, MacCoss MJ. Measurement of human surfactant protein-B turnover in vivo from tracheal aspirates using targeted proteomics. Anal Chem. 2010 Mar 15;82(6):2561-7. doi: 10.1021/ac1001433. PubMed PMID: 20178338; PubMed Central PMCID: PMC2843406.**

**Complete list of published work in MyBibliography:**

<http://www.ncbi.nlm.nih.gov/myncbi/browse/collection/41150153/?sort=date>