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from genes to function

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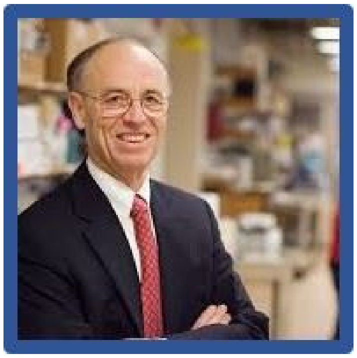

Donald F. Hunt, PhD (Bio)

Donald F. Hunt Distinguished Contribution in Proteomics Award

This award is fully funded by:

The Donald F. Hunt Distinguished Contribution in Proteomics Award recognizes a focused or singular achievement in the field of proteomics. Awardees will be recognized for outstanding contributions to the field of proteomics based upon scientific achievement as well as their contribution to mentorship, improving equity and inclusion within the field. This award was established to recognize Prof. Hunt's significant contributions to the field of proteomics. Prof. Hunt was honored as the first recipient of this award which now bears his name. Nominations will be held for 3 years.

Eligibility

- Current US HUPO membership.
- The awardee must be available to present at the annual conference (February 21 - 25, 2026) in St. Louis, MO to receive the award and present the lecture.
- A three-year waiting period after receipt of one of the US HUPO career awards is required prior to receiving another award, nominations made for a candidate during the period of ineligibility will not be considered until eligibility reopens.

Award nominations are closed for 2026 and will open for 2027 on March 1, 2026.

2026 Recipient: Michael MacCoss, University of Washington

Michael MacCoss has been working with mass spectrometry instrumentation since 1994 when he was an undergraduate in a stable isotope geochemistry lab at the University of Vermont. He became interested in biomedical applications working in Dr. Patrick Griffin’s protein mass spectrometry lab at Merck Research Laboratories during two summer internships in 1995 and 1996. In 2001, he completed a Ph.D. in Analytical Chemistry with Professor Dwight Matthews in the development of stable isotope and mass spectrometry methodologies for the measurement of human amino acid and protein metabolism. After completing his degree, Dr. MacCoss moved to The Scripps Research Institute to work with the proteomics pioneer John R. Yates III as a postdoctoral fellow. During his postdoctoral training, Dr. MacCoss worked on methodology and software for many areas of proteomics, ranging from the improved characterization of post-translational modifications and the quantitative analysis of complex protein mixtures. Dr. MacCoss moved to the University of Washington in 2004 as an Assistant Professor of Genome Sciences and was promoted to Professor in 2014. At the University of Washington, his lab has focused on the development and application of mass spectrometry-based technologies for the high throughput characterization of complex protein mixtures. Realizing that software was a major limitation in proteomics, Dr. MacCoss has established a major software engineering effort within his group at the University of Washington. Their laboratory’s software is noted for its robustness, versatility, support, and user friendliness. Dr. MacCoss and his team continually work to improve their tools, provide documentation, and a community around their software. In 2007 he was the recipient of a Presidential Award for Scientists and Engineers (PECASE). He was selected to receive the Biemann Medal from the American

Society for Mass Spectrometry and the 2016 HUPO Award for Discovery in Proteomics Sciences. The MacCoss lab's research has been at the intersection of biochemistry, instrumentation, engineering, computer science, and statistics.

Past Recipients of the Donald F. Hunt Distinguished Contribution in Proteomics Award

Year	Recipient	Contribution
2025	Josh Coon, University of Wisconsin- Madison	Co-invented electron transfer dissociation (ETD) for peptide sequencing by mass spectrometry.
2024	Neil Kelleher, Northwestern University	Driven the field of top-down proteomics including whole protein fractionation methods, automating new MS instrumentation, and development of software specialized for intact protein analysis.
2023	David Muddiman, North Carolina State University	Developing, understanding, and applying novel approaches to measuring amino acids, peptides, and proteins.
2022	Jonathan Sweedler, Univerity of Illinois at Urbana-Champaign	Single cell proteomics.
2021	Peipei Ping, University of California, Los Angeles	Utilization of basic and translational work in applying cardiovascular proteomics to understand ischemic heart injuries and heart failure.
2020	Steven Gygi, Harvard Medical School	Quantification methods for proteomics, analysis of post-translational modifications, and protein-protein interactions.
2019	Jennifer Van Eyk (Cedars-Sinai Medical Center)	Discovery of disease-induced modifications of cardiac troponin I (cTnI) that revolutionized our understanding of heart disease.
2018	Donald F. Hunt (University of Virginia)	

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