

# Michael J Sweredoski

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

2,625  
citations

257450

24  
h-index

377865

34  
g-index

42  
all docs

42  
docs citations

42  
times ranked

4613  
citing authors

#	ARTICLE	IF	CITATIONS
1	Human Gut Microbiota from Autism Spectrum Disorder Promote Behavioral Symptoms in Mice. <i>Cell</i> , 2019, 177, 1600-1618.e17.	28.9	701
2	Cand1 Promotes Assembly of New SCF Complexes through Dynamic Exchange of F Box Proteins. <i>Cell</i> , 2013, 153, 206-215.	28.9	228
3	Evaluation and Optimization of Mass Spectrometric Settings during Data-dependent Acquisition Mode: Focus on LTQ-Orbitrap Mass Analyzers. <i>Journal of Proteome Research</i> , 2013, 12, 3071-3086.	3.7	148
4	A conserved quality-control pathway that mediates degradation of unassembled ribosomal proteins. <i>ELife</i> , 2016, 5, .	6.0	147
5	Glutamine Triggers Acetylation-Dependent Degradation of Glutamine Synthetase via the Thalidomide Receptor Cereblon. <i>Molecular Cell</i> , 2016, 61, 809-820.	9.7	132
6	Composition and Regulation of the Cellular Repertoire of SCF Ubiquitin Ligases. <i>Cell</i> , 2017, 171, 1326-1339.e14.	28.9	118
7	Ribosomal proteins produced in excess are degraded by the ubiquitin-proteasome system. <i>Molecular Biology of the Cell</i> , 2016, 27, 2642-2652.	2.1	105
8	Cell-specific proteomic analysis in <i>Caenorhabditis elegans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2705-2710.	7.1	99
9	Quantitative, Time-Resolved Proteomic Analysis by Combining Bioorthogonal Noncanonical Amino Acid Tagging and Pulsed Stable Isotope Labeling by Amino Acids in Cell Culture. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1352-1358.	3.8	83
10	Systematic approach for dissecting the molecular mechanisms of transcriptional regulation in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4796-E4805.	7.1	81
11	Identification of Mechanism-Based Inactivation in P450-Catalyzed Cyclopropanation Facilitates Engineering of Improved Enzymes. <i>Journal of the American Chemical Society</i> , 2016, 138, 12527-12533.	13.7	58
12	PYCR1 and PYCR2 Interact and Collaborate with RRM2B to Protect Cells from Overt Oxidative Stress. <i>Scientific Reports</i> , 2016, 6, 18846.	3.3	58
13	LONP1 and mtHSP70 cooperate to promote mitochondrial protein folding. <i>Nature Communications</i> , 2021, 12, 265.	12.8	58
14	Mitochondrial fusion is required for spermatogonial differentiation and meiosis. <i>ELife</i> , 2019, 8, .	6.0	58
15	PIKES Analysis Reveals Response to Degradation and Key Regulatory Mechanisms of the CRL4 Network. <i>Molecular Cell</i> , 2020, 77, 1092-1106.e9.	9.7	56
16	A <i>Trichomonas vaginalis</i> Rhomboid Protease and Its Substrate Modulate Parasite Attachment and Cytolysis of Host Cells. <i>PLoS Pathogens</i> , 2015, 11, e1005294.	4.7	43
17	Bioorthogonal Noncanonical Amino Acid Tagging (BONCAT) Enables Time-Resolved Analysis of Protein Synthesis in Native Plant Tissue. <i>Plant Physiology</i> , 2017, 173, 1543-1553.	4.8	43
18	BUD13 Promotes a Type I Interferon Response by Countering Intron Retention in <i>Irf7</i> . <i>Molecular Cell</i> , 2019, 73, 803-814.e6.	9.7	39

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19	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. <i>ELife</i> , 2019, 8, .	6.0	36
20	Data-Independent Acquisition for the Orbitrap Q Exactive HF: A Tutorial. <i>Journal of Proteome Research</i> , 2019, 18, 803-813.	3.7	35
21	Tyramide signal amplification mass spectrometry (TSA-MS) ratio identifies nuclear speckle proteins. <i>Journal of Cell Biology</i> , 2020, 219, .	5.2	33
22	Deciphering the regulatory genome of <i>Escherichia coli</i> , one hundred promoters at a time. <i>ELife</i> , 2020, 9, .	6.0	31
23	Stable Isotope Analysis of Intact Oxyanions Using Electrospray Quadrupole-Orbitrap Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 3077-3085.	6.5	30
24	WNK1 is an assembly factor for the human ER membrane protein complex. <i>Molecular Cell</i> , 2021, 81, 2693-2704.e12.	9.7	29
25	Scanning the isotopic structure of molecules by tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2018, 434, 276-286.	1.5	28
26	Degradation of the Deubiquitinating Enzyme USP33 Is Mediated by p97 and the Ubiquitin Ligase HERC2. <i>Journal of Biological Chemistry</i> , 2014, 289, 19789-19798.	3.4	26
27	High Resolution Parallel Reaction Monitoring with Electron Transfer Dissociation for Middle-Down Proteomics. <i>Analytical Chemistry</i> , 2015, 87, 8360-8366.	6.5	26
28	Improved 6-Plex Tandem Mass Tags Quantification Throughput Using a Linear Ion Trapâ€“High-Energy Collision Induced Dissociation MS <sup>3</sup> Scan. <i>Analytical Chemistry</i> , 2016, 88, 7471-7475.	6.5	24
29	Bacterial flagellar motor PL-ring disassembly subcomplexes are widespread and ancient. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8941-8947.	7.1	23
30	Co-evolution of Two GTPases Enables Efficient Protein Targeting in an RNA-less Chloroplast Signal Recognition Particle Pathway. <i>Journal of Biological Chemistry</i> , 2017, 292, 386-396.	3.4	9
31	A Novel <i>Trichomonas vaginalis</i> Surface Protein Modulates Parasite Attachment via Protein:Host Cell Proteoglycan Interaction. <i>MBio</i> , 2021, 12, .	4.1	9
32	Amino Acid Analog Induces Stress Response in Marine <i>Synechococcus</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0020021.	3.1	5
33	A Targeted MRM Approach for Tempo-Spatial Proteomics Analyses. <i>Methods in Molecular Biology</i> , 2016, 1394, 75-85.	0.9	4
34	Nano volume fractionation strategy for dilute-and-shoot injections in off-line loss-less proteomic workflows for extensive protein identifications of ultra-low sample amounts. <i>Journal of Chromatography A</i> , 2020, 1609, 460507.	3.7	4