

Mikhail M Savitski

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

13,299
citations

43973

48
h-index

46693

89
g-index

108
all docs

108
docs citations

108
times ranked

17806
citing authors

#	ARTICLE	IF	CITATIONS
1	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014, 509, 582-587.	13.7	1,697
2	Inhibition of BET recruitment to chromatin as an effective treatment for MLL-fusion leukaemia. <i>Nature</i> , 2011, 478, 529-533.	13.7	1,354
3	Tracking cancer drugs in living cells by thermal profiling of the proteome. <i>Science</i> , 2014, 346, 1255784.	6.0	812
4	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 939-965.	1.9	695
5	Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes. <i>Nature Biotechnology</i> , 2011, 29, 255-265.	9.4	597
6	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. <i>Nature Protocols</i> , 2015, 10, 1567-1593.	5.5	481
7	A new antibiotic selectively kills Gram-negative pathogens. <i>Nature</i> , 2019, 576, 459-464.	13.7	456
8	A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2394-2404.	2.5	350
9	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , 2018, 9, 689.	5.8	280
10	Species-specific activity of antibacterial drug combinations. <i>Nature</i> , 2018, 559, 259-263.	13.7	276
11	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	9.4	273
12	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , 2015, 12, 1129-1131.	9.0	244
13	Measuring and Managing Ratio Compression for Accurate iTRAQ/TMT Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 3586-3598.	1.8	238
14	Ion Coalescence of Neutron Encoded TMT 10-Plex Reporter Ions. <i>Analytical Chemistry</i> , 2014, 86, 3594-3601.	3.2	235
15	A Dual-Mechanism Antibiotic Kills Gram-Negative Bacteria and Avoids Drug Resistance. <i>Cell</i> , 2020, 181, 1518-1532.e14.	13.5	202
16	Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. <i>Nature Chemical Biology</i> , 2016, 12, 908-910.	3.9	189
17	Multiplexed Proteome Dynamics Profiling Reveals Mechanisms Controlling Protein Homeostasis. <i>Cell</i> , 2018, 173, 260-274.e25.	13.5	186
18	De Novo Peptide Sequencing and Identification with Precision Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 114-123.	1.8	185

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19	Pervasive Protein Thermal Stability Variation during the Cell Cycle. <i>Cell</i> , 2018, 173, 1495-1507.e18.	13.5	183
20	High-Resolution Enabled TMT 8-plexing. <i>Analytical Chemistry</i> , 2012, 84, 7188-7194.	3.2	181
21	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <i>Nature Communications</i> , 2019, 10, 1155.	5.8	181
22	ModifiComb, a New Proteomic Tool for Mapping Substoichiometric Post-translational Modifications, Finding Novel Types of Modifications, and Fingerprinting Complex Protein Mixtures. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 935-948.	2.5	178
23	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021, 597, 533-538.	13.7	159
24	Meltome atlas thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	9.0	152
25	Thermal proteome profiling for interrogating protein interactions. <i>Molecular Systems Biology</i> , 2020, 16, e9232.	3.2	150
26	Proteomics-Grade de Novo Sequencing Approach. <i>Journal of Proteome Research</i> , 2005, 4, 2348-2354.	1.8	147
27	Mitochondrial protein-induced stress triggers a global adaptive transcriptional programme. <i>Nature Cell Biology</i> , 2019, 21, 442-451.	4.6	146
28	A selective inhibitor reveals PI3K β dependence of TH17 cell differentiation. <i>Nature Chemical Biology</i> , 2012, 8, 576-582.	3.9	136
29	Thermal proteome profiling in bacteria: probing protein state <i>in vivo</i> . <i>Molecular Systems Biology</i> , 2018, 14, e8242.	3.2	130
30	Improving Protein Identification Using Complementary Fragmentation Techniques in Fourier Transform Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 835-845.	2.5	128
31	Hydrogen rearrangement to and from radical z fragments in electron capture dissociation of peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 113-120.	1.2	120
32	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , 2020, 38, 303-308.	9.4	111
33	Delayed Fragmentation and Optimized Isolation Width Settings for Improvement of Protein Identification and Accuracy of Isobaric Mass Tag Quantification on Orbitrap-Type Mass Spectrometers. <i>Analytical Chemistry</i> , 2011, 83, 8959-8967.	3.2	102
34	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , 2017, 2, 17047.	5.9	102
35	Thermal proteome profiling: unbiased assessment of protein state through heat-induced stability changes. <i>Proteome Science</i> , 2016, 15, 13.	0.7	101
36	The Commonly Used PI3-Kinase Probe LY294002 Is an Inhibitor of BET Bromodomains. <i>ACS Chemical Biology</i> , 2014, 9, 495-502.	1.6	97

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37	Extent of Modifications in Human Proteome Samples and Their Effect on Dynamic Range of Analysis in Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2384-2391.	2.5	93
38	New Data Base-independent, Sequence Tag-based Scoring of Peptide MS/MS Data Validates Mowse Scores, Recovers Below Threshold Data, Singles Out Modified Peptides, and Assesses the Quality of MS/MS Techniques. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1180-1188.	2.5	88
39	Targeted data acquisition for improved reproducibility and robustness of proteomic mass spectrometry assays. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1668-1679.	1.2	83
40	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2016, 11, 1245-1254.	1.6	82
41	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2506-2515.	2.5	75
42	Liquid Chromatography at Critical Conditions: A Comprehensive Approach to Sequence-Dependent Retention Time Prediction. <i>Analytical Chemistry</i> , 2006, 78, 7770-7777.	3.2	73
43	Affinity Profiling of the Cellular Kinome for the Nucleotide Cofactors ATP, ADP, and GTP. <i>ACS Chemical Biology</i> , 2013, 8, 599-607.	1.6	73
44	Outer membrane lipoprotein Nlpl scaffolds peptidoglycan hydrolases within multi-enzyme complexes in <i>Escherichia coli</i> . <i>EMBO Journal</i> , 2020, 39, e102246.	3.5	69
45	Side-Chain Losses in Electron Capture Dissociation To Improve Peptide Identification. <i>Analytical Chemistry</i> , 2007, 79, 2296-2302.	3.2	68
46	The functional proteome landscape of <i>Escherichia coli</i> . <i>Nature</i> , 2020, 588, 473-478.	13.7	58
47	Impact of phosphorylation on thermal stability of proteins. <i>Nature Methods</i> , 2021, 18, 757-759.	9.0	58
48	Bifurcating Fragmentation Behavior of Gas-Phase Tryptic Peptide Dications in Collisional Activation. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1755-1763.	1.2	55
49	Immunoaffinity Enrichments Followed by Mass Spectrometric Detection for Studying Global Protein Tyrosine Phosphorylation. <i>Journal of Proteome Research</i> , 2008, 7, 2897-2910.	1.8	52
50	Chemoproteomics Reveals Time-Dependent Binding of Histone Deacetylase Inhibitors to Endogenous Repressor Complexes. <i>ACS Chemical Biology</i> , 2014, 9, 1736-1746.	1.6	52
51	Bacterial retrons encode phage-defending tripartite toxin-antitoxin systems. <i>Nature</i> , 2022, 609, 144-150.	13.7	52
52	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. <i>Nature Methods</i> , 2021, 18, 84-91.	9.0	49
53	Leaderless secreted peptide signaling molecule alters global gene expression and increases virulence of a human bacterial pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8498-E8507.	3.3	46
54	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. <i>Science Advances</i> , 2021, 7,	4.7	45

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55	Analytical Utility of Small Neutral Losses from Reduced Species in Electron Capture Dissociation Studied Using SwedECD Database. <i>Analytical Chemistry</i> , 2008, 80, 8089-8094.	3.2	42
56	Dendritic autophagy degrades postsynaptic proteins and is required for long-term synaptic depression in mice. <i>Nature Communications</i> , 2022, 13, 680.	5.8	41
57	PhosTShunter: A Fast and Reliable Tool to Detect Phosphorylated Peptides in Liquid Chromatography Fourier Transform Tandem Mass Spectrometry Data Sets. <i>Journal of Proteome Research</i> , 2006, 5, 659-668.	1.8	39
58	Global mapping of <i>Salmonella enterica</i> -host protein-protein interactions during infection. <i>Cell Host and Microbe</i> , 2021, 29, 1316-1332.e12.	5.1	39
59	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PPI and PP2A. <i>Nature Communications</i> , 2020, 11, 3583.	5.8	38
60	Determination of the location of positive charges in gas-phase polypeptide polycations by tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2006, 252, 204-212.	0.7	34
61	H-Score, a Mass Accuracy Driven Rescoring Approach for Improved Peptide Identification in Modification Rich Samples. <i>Journal of Proteome Research</i> , 2010, 9, 5511-5516.	1.8	34
62	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , 2020, 11, 5783.	5.8	34
63	On studying protein phosphorylation patterns using bottom-up LC-MS/MS: the case of human κ -casein. <i>Analyst</i> , 2007, 132, 768-776.	1.7	33
64	Drug Target Identification in Tissues by Thermal Proteome Profiling. <i>Annual Review of Pharmacology and Toxicology</i> , 2022, 62, 465-482.	4.2	31
65	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during <i>Salmonella</i> infection. <i>Nature Microbiology</i> , 2020, 5, 1119-1133.	5.9	30
66	SwedCAD, a Database of Annotated High-Mass Accuracy MS/MS Spectra of Tryptic Peptides. <i>Journal of Proteome Research</i> , 2007, 6, 4063-4067.	1.8	28
67	Two Dimensional Mass Mapping as a General Method of Data Representation in Comprehensive Analysis of Complex Molecular Mixtures. <i>Analytical Chemistry</i> , 2009, 81, 3738-3745.	3.2	26
68	<i>In Vitro</i> Neurotoxicity of PBDE-99: Immediate and Concentration-Dependent Effects on Protein Expression in Cerebral Cortex Cells. <i>Journal of Proteome Research</i> , 2010, 9, 1226-1235.	1.8	26
69	TRRAP is essential for regulating the accumulation of mutant and wild-type p53 in lymphoma. <i>Blood</i> , 2018, 131, 2789-2802.	0.6	25
70	Aggregation and disaggregation features of the human proteome. <i>Molecular Systems Biology</i> , 2020, 16, e9500.	3.2	25
71	Systematic Localization of <i>Escherichia coli</i> Membrane Proteins. <i>MSystems</i> , 2020, 5, .	1.7	24
72	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , 2022, 40, 382-390.	9.4	24

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73	Relative Specificities of Water and Ammonia Losses from Backbone Fragments in Collision-Activated Dissociation. <i>Journal of Proteome Research</i> , 2007, 6, 2669-2673.	1.8	23
74	Physicochemical Properties Determining the Detection Probability of Tryptic Peptides in Fourier Transform Mass Spectrometry. A Correlation Study. <i>Analytical Chemistry</i> , 2004, 76, 5872-5877.	3.2	21
75	SARS-CoV-2 infection remodels the host protein thermal stability landscape. <i>Molecular Systems Biology</i> , 2021, 17, e10188.	3.2	17
76	Isocotoin suppresses hepatitis E virus replication through inhibition of heat shock protein 90. <i>Antiviral Research</i> , 2021, 185, 104997.	1.9	15
77	Shifted-basis technique improves accuracy of peak position determination in Fourier transform mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 457-461.	1.2	14
78	A genetic analysis reveals novel histone residues required for transcriptional reprogramming upon stress. <i>Nucleic Acids Research</i> , 2020, 48, 3455-3475.	6.5	14
79	Rtpca: an R package for differential thermal proximity coaggregation analysis. <i>Bioinformatics</i> , 2021, 37, 431-433.	1.8	14
80	ATP Enhances Neuronal Differentiation of PC12 Cells by Activating PKC \pm Interactions with Cytoskeletal Proteins. <i>Journal of Proteome Research</i> , 2011, 10, 529-540.	1.8	11
81	Effect of Sec61 interaction with Mpd1 on endoplasmic reticulum-associated degradation. <i>PLoS ONE</i> , 2019, 14, e0211180.	1.1	10
82	A misprocessed form of Apolipoprotein A-I is specifically associated with recurrent Focal Segmental Glomerulosclerosis. <i>Scientific Reports</i> , 2020, 10, 1159.	1.6	10
83	Mutational Analysis of Glycogen Synthase Kinase 3 β Protein Kinase Together with Kinome-Wide Binding and Stability Studies Suggests Context-Dependent Recognition of Kinases by the Chaperone Heat Shock Protein 90. <i>Molecular and Cellular Biology</i> , 2016, 36, 1007-1018.	1.1	9
84	The rise of proteome-wide biophysics. <i>Molecular Systems Biology</i> , 2021, 17, e10442.	3.2	9
85	Transcriptional and Post-Transcriptional Polar Effects in Bacterial Gene Deletion Libraries. <i>MSystems</i> , 2021, 6, e0081321.	1.7	9
86	Evaluation of Data Analysis Strategies for Improved Mass Spectrometry-Based Phosphoproteomics. <i>Analytical Chemistry</i> , 2010, 82, 9843-9849.	3.2	8
87	Wilhelm et al. reply. <i>Nature</i> , 2017, 547, E23-E23.	13.7	7
88	PLDMS: Phosphopeptide Library Dephosphorylation Followed by Mass Spectrometry Analysis to Determine the Specificity of Phosphatases for Dephosphorylation Site Sequences. <i>Methods in Molecular Biology</i> , 2022, , 43-64.	0.4	1