

# 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	Drug Target Identification in Tissues by Thermal Proteome Profiling. <i>Annual Review of Pharmacology and Toxicology</i> , 2022, 62, 465-482.	4.2	31
2	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , 2022, 40, 382-390.	9.4	24
3	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
4	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
5	Bacterial retrons encode phage-defending tripartite toxin-antitoxin systems. <i>Nature</i> , 2022, 609, 144-150.	13.7	52
6	Rtpca: an R package for differential thermal proximity coaggregation analysis. <i>Bioinformatics</i> , 2021, 37, 431-433.	1.8	14
7	Isocotoin suppresses hepatitis E virus replication through inhibition of heat shock protein 90. <i>Antiviral Research</i> , 2021, 185, 104997.	1.9	15
8	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
9	SARS-CoV-2 infection remodels the host protein thermal stability landscape. <i>Molecular Systems Biology</i> , 2021, 17, e10188.	3.2	17
10	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. <i>Science Advances</i> , 2021, 7, .	4.7	45
11	Impact of phosphorylation on thermal stability of proteins. <i>Nature Methods</i> , 2021, 18, 757-759.	9.0	58
12	The rise of proteome-wide biophysics. <i>Molecular Systems Biology</i> , 2021, 17, e10442.	3.2	9
13	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
14	Transcriptional and Post-Transcriptional Polar Effects in Bacterial Gene Deletion Libraries. <i>MSystems</i> , 2021, 6, e0081321.	1.7	9
15	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021, 597, 533-538.	13.7	159
16	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020, 38, 365-373.	9.4	273
17	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PP1 and PP2A. <i>Nature Communications</i> , 2020, 11, 3583.	5.8	38
18	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

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19	The functional proteome landscape of Escherichia coli. Nature, 2020, 588, 473-478.	13.7	58
20	Systematic Localization of Escherichia coli Membrane Proteins. MSystems, 2020, 5, .	1.7	24
21	A Dual-Mechanism Antibiotic Kills Gram-Negative Bacteria and Avoids Drug Resistance. Cell, 2020, 181, 1518-1532.e14.	13.5	202
22	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. Nature Microbiology, 2020, 5, 1119-1133.	5.9	30
23	A genetic analysis reveals novel histone residues required for transcriptional reprogramming upon stress. Nucleic Acids Research, 2020, 48, 3455-3475.	6.5	14
24	A misprocessed form of Apolipoprotein A-I is specifically associated with recurrent Focal Segmental Glomerulosclerosis. Scientific Reports, 2020, 10, 1159.	1.6	10
25	Identifying drug targets in tissues and whole blood with thermal-shift profiling. Nature Biotechnology, 2020, 38, 303-308.	9.4	111
26	Thermal proteome profiling for interrogating protein interactions. Molecular Systems Biology, 2020, 16, e9232.	3.2	150
27	Meltome atlas—thermal proteome stability across the tree of life. Nature Methods, 2020, 17, 495-503.	9.0	152
28	Outer membrane lipoprotein Nlpl scaffolds peptidoglycan hydrolases within multi-enzyme complexes in Escherichia coli. EMBO Journal, 2020, 39, e102246.	3.5	69
29	Aggregation and disaggregation features of the human proteome. Molecular Systems Biology, 2020, 16, e9500.	3.2	25
30	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins*. Molecular and Cellular Proteomics, 2019, 18, 2506-2515.	2.5	75
31	Effect of Sec61 interaction with Mpd1 on endoplasmic reticulum-associated degradation. PLoS ONE, 2019, 14, e0211180.	1.1	10
32	Mitochondrial protein-induced stress triggers a global adaptive transcriptional programme. Nature Cell Biology, 2019, 21, 442-451.	4.6	146
33	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. Nature Communications, 2019, 10, 1155.	5.8	181
34	A new antibiotic selectively kills Gram-negative pathogens. Nature, 2019, 576, 459-464.	13.7	456
35	TRRAP is essential for regulating the accumulation of mutant and wild-type p53 in lymphoma. Blood, 2018, 131, 2789-2802.	0.6	25
36	Systematic analysis of protein turnover in primary cells. Nature Communications, 2018, 9, 689.	5.8	280

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37	Pervasive Protein Thermal Stability Variation during the Cell Cycle. <i>Cell</i> , 2018, 173, 1495-1507.e18.	13.5	183
38	Multiplexed Proteome Dynamics Profiling Reveals Mechanisms Controlling Protein Homeostasis. <i>Cell</i> , 2018, 173, 260-274.e25.	13.5	186
39	Species-specific activity of antibacterial drug combinations. <i>Nature</i> , 2018, 559, 259-263.	13.7	276
40	Thermal proteome profiling in bacteria: probing protein state <i>in vivo</i> . <i>Molecular Systems Biology</i> , 2018, 14, e8242.	3.2	130
41	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
42	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
43	Wilhelm et al. reply. <i>Nature</i> , 2017, 547, E23-E23.	13.7	7
44	Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. <i>Nature Chemical Biology</i> , 2016, 12, 908-910.	3.9	189
45	Thermal proteome profiling: unbiased assessment of protein state through heat-induced stability changes. <i>Proteome Science</i> , 2016, 15, 13.	0.7	101
46	Mutational Analysis of Glycogen Synthase Kinase 3 <sup>β</sup> 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
47	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2016, 11, 1245-1254.	1.6	82
48	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
49	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , 2015, 12, 1129-1131.	9.0	244
50	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
51	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014, 509, 582-587.	13.7	1,697
52	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
53	Ion Coalescence of Neutron Encoded TMT 10-Plex Reporter Ions. <i>Analytical Chemistry</i> , 2014, 86, 3594-3601.	3.2	235
54	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

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55	Tracking cancer drugs in living cells by thermal profiling of the proteome. <i>Science</i> , 2014, 346, 1255784.	6.0	812
56	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
57	Measuring and Managing Ratio Compression for Accurate iTRAQ/TMT Quantification. <i>Journal of Proteome Research</i> , 2013, 12, 3586-3598.	1.8	238
58	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
59	High-Resolution Enabled TMT 8-plexing. <i>Analytical Chemistry</i> , 2012, 84, 7188-7194.	3.2	181
60	A selective inhibitor reveals PI3K <sup>Î³</sup> dependence of TH17 cell differentiation. <i>Nature Chemical Biology</i> , 2012, 8, 576-582.	3.9	136
61	ATP Enhances Neuronal Differentiation of PC12 Cells by Activating PKC <sup>Î±</sup> Interactions with Cytoskeletal Proteins. <i>Journal of Proteome Research</i> , 2011, 10, 529-540.	1.8	11
62	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
63	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
64	Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes. <i>Nature Biotechnology</i> , 2011, 29, 255-265.	9.4	597
65	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
66	<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
67	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
68	Evaluation of Data Analysis Strategies for Improved Mass Spectrometry-Based Phosphoproteomics. <i>Analytical Chemistry</i> , 2010, 82, 9843-9849.	3.2	8
69	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
70	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
71	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
72	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

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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	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
75	On studying protein phosphorylation patterns using bottom-up LC-MS/MS: the case of human $\beta$ -casein. <i>Analyst</i> , 2007, 132, 768-776.	1.7	33
76	Side-Chain Losses in Electron Capture Dissociation To Improve Peptide Identification. <i>Analytical Chemistry</i> , 2007, 79, 2296-2302.	3.2	68
77	De Novo Peptide Sequencing and Identification with Precision Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 114-123.	1.8	185
78	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
79	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
80	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
81	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
82	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
83	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
84	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
85	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
86	Proteomics-Grade de Novo Sequencing Approach. <i>Journal of Proteome Research</i> , 2005, 4, 2348-2354.	1.8	147
87	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
88	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