

# Mikhail M Savitski

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97  
papers

9,145  
citations

44  
h-index

95  
g-index

108  
ext. papers

11,543  
ext. citations

16.5  
avg, IF

5.85  
L-index

#	Paper	IF	Citations
97	Dendritic autophagy degrades postsynaptic proteins and is required for long-term synaptic depression in mice.. <i>Nature Communications</i> , <b>2022</b> , 13, 680	17.4	3
96	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> , <b>2022</b> , 43-64	1.4	0
95	High-throughput functional characterization of protein phosphorylation sites in yeast. <i>Nature Biotechnology</i> , <b>2021</b> ,	44.5	3
94	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	7
93	Impact of phosphorylation on thermal stability of proteins. <i>Nature Methods</i> , <b>2021</b> , 18, 757-759	21.6	15
92	Rtpca: an R package for differential thermal proximity coaggregation analysis. <i>Bioinformatics</i> , <b>2021</b> , 37, 431-433	7.2	3
91	Isocotoin suppresses hepatitis E virus replication through inhibition of heat shock protein 90. <i>Antiviral Research</i> , <b>2021</b> , 185, 104997	10.8	4
90	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. <i>Nature Methods</i> , <b>2021</b> , 18, 84-91	21.6	12
89	SARS-CoV-2 infection remodels the host protein thermal stability landscape. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e10188	12.2	5
88	The rise of proteome-wide biophysics. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e10442	12.2	1
87	Global mapping of Salmonella enterica-host protein-protein interactions during infection. <i>Cell Host and Microbe</i> , <b>2021</b> , 29, 1316-1332.e12	23.4	13
86	Transcriptional and Post-Transcriptional Polar Effects in Bacterial Gene Deletion Libraries. <i>MSystems</i> , <b>2021</b> , 6, e0081321	7.6	1
85	Drug Target Identification in Tissues by Thermal Proteome Profiling. <i>Annual Review of Pharmacology and Toxicology</i> , <b>2021</b> ,	17.9	2
84	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , <b>2021</b> , 597, 533-538	50.4	29
83	The functional proteome landscape of Escherichia coli. <i>Nature</i> , <b>2020</b> , 588, 473-478	50.4	14
82	Systematic Localization of Escherichia coli Membrane Proteins. <i>MSystems</i> , <b>2020</b> , 5,	7.6	8
81	A Dual-Mechanism Antibiotic Kills Gram-Negative Bacteria and Avoids Drug Resistance. <i>Cell</i> , <b>2020</b> , 181, 1518-1532.e14	56.2	88

80	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. <i>Nature Microbiology</i> , <b>2020</b> , 5, 1119-1133	26.6	17
79	A genetic analysis reveals novel histone residues required for transcriptional reprogramming upon stress. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 3455-3475	20.1	7
78	A misprocessed form of Apolipoprotein A-I is specifically associated with recurrent Focal Segmental Glomerulosclerosis. <i>Scientific Reports</i> , <b>2020</b> , 10, 1159	4.9	7
77	Identifying drug targets in tissues and whole blood with thermal-shift profiling. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 303-308	44.5	46
76	Thermal proteome profiling for interrogating protein interactions. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9232	12.2	53
75	Meltome atlas-thermal proteome stability across the tree of life. <i>Nature Methods</i> , <b>2020</b> , 17, 495-503	21.6	53
74	Outer membrane lipoprotein Nlpl scaffolds peptidoglycan hydrolases within multi-enzyme complexes in Escherichia coli. <i>EMBO Journal</i> , <b>2020</b> , 39, e102246	13	36
73	Aggregation and disaggregation features of the human proteome. <i>Molecular Systems Biology</i> , <b>2020</b> , 16, e9500	12.2	9
72	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 365-373	44.5	106
71	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PP1 and PP2A. <i>Nature Communications</i> , <b>2020</b> , 11, 3583	17.4	7
70	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. <i>Nature Communications</i> , <b>2020</b> , 11, 5783	17.4	8
69	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 2506-2515	7.6	34
68	Effect of Sec61 interaction with Mpd1 on endoplasmic reticulum-associated degradation. <i>PLoS ONE</i> , <b>2019</b> , 14, e0211180	3.7	4
67	Mitochondrial protein-induced stress triggers a global adaptive transcriptional programme. <i>Nature Cell Biology</i> , <b>2019</b> , 21, 442-451	23.4	84
66	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. <i>Nature Communications</i> , <b>2019</b> , 10, 1155	17.4	88
65	Target Discovery Using Thermal Proteome Profiling <b>2019</b> , 267-291		3
64	A new antibiotic selectively kills Gram-negative pathogens. <i>Nature</i> , <b>2019</b> , 576, 459-464	50.4	202
63	TRRAP is essential for regulating the accumulation of mutant and wild-type p53 in lymphoma. <i>Blood</i> , <b>2018</b> , 131, 2789-2802	2.2	17

62	Systematic analysis of protein turnover in primary cells. <i>Nature Communications</i> , <b>2018</b> , 9, 689	17.4	145
61	Pervasive Protein Thermal Stability Variation during the Cell Cycle. <i>Cell</i> , <b>2018</b> , 173, 1495-1507.e18	56.2	109
60	Multiplexed Proteome Dynamics Profiling Reveals Mechanisms Controlling Protein Homeostasis. <i>Cell</i> , <b>2018</b> , 173, 260-274.e25	56.2	125
59	Thermal proteome profiling in bacteria: probing protein state. <i>Molecular Systems Biology</i> , <b>2018</b> , 14, e82422.2	42.2	82
58	Species-specific activity of antibacterial drug combinations. <i>Nature</i> , <b>2018</b> , 559, 259-263	50.4	137
57	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17047	26.6	74
56	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> , <b>2017</b> , 114, E8498-E8507	11.5	27
55	Wilhelm et al. reply. <i>Nature</i> , <b>2017</b> , 547, E23	50.4	4
54	Thermal proteome profiling: unbiased assessment of protein state through heat-induced stability changes. <i>Proteome Science</i> , <b>2016</b> , 15, 13	2.6	62
53	Mutational Analysis of Glycogen Synthase Kinase 3 $\beta$ 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> , <b>2016</b> , 36, 1007-18	4.8	8
52	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. <i>ACS Chemical Biology</i> , <b>2016</b> , 11, 1245-54	4.9	58
51	Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. <i>Nature Chemical Biology</i> , <b>2016</b> , 12, 908-910	11.7	120
50	A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. <i>Molecular and Cellular Proteomics</i> , <b>2015</b> , 14, 2394-404	7.6	210
49	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. <i>Nature Methods</i> , <b>2015</b> , 12, 1129-31	21.6	173
48	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. <i>Nature Protocols</i> , <b>2015</b> , 10, 1567-93	18.8	293
47	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , <b>2014</b> , 509, 582-7	50.4	1332
46	The commonly used PI3-kinase probe LY294002 is an inhibitor of BET bromodomains. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 495-502	4.9	85
45	Ion coalescence of neutron encoded TMT 10-plex reporter ions. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 3594-6017.8	17.8	174

44	Chemoproteomics reveals time-dependent binding of histone deacetylase inhibitors to endogenous repressor complexes. <i>ACS Chemical Biology</i> , <b>2014</b> , 9, 1736-46	4.9	43
43	Tracking cancer drugs in living cells by thermal profiling of the proteome. <i>Science</i> , <b>2014</b> , 346, 1255784	33.3	526
42	Affinity profiling of the cellular kinome for the nucleotide cofactors ATP, ADP, and GTP. <i>ACS Chemical Biology</i> , <b>2013</b> , 8, 599-607	4.9	58
41	Measuring and managing ratio compression for accurate iTRAQ/TMT quantification. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 3586-98	5.6	177
40	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. <i>Analytical and Bioanalytical Chemistry</i> , <b>2012</b> , 404, 939-65	4.4	585
39	High-resolution enabled TMT 8-plexing. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 7188-94	7.8	150
38	A selective inhibitor reveals PI3K dependence of T(H)17 cell differentiation. <i>Nature Chemical Biology</i> , <b>2012</b> , 8, 576-82	11.7	117
37	Inhibition of BET recruitment to chromatin as an effective treatment for MLL-fusion leukaemia. <i>Nature</i> , <b>2011</b> , 478, 529-33	50.4	1144
36	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> , <b>2011</b> , 83, 8959-67	7.8	79
35	Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 255-65	44.5	505
34	ATP enhances neuronal differentiation of PC12 cells by activating PKC interactions with cytoskeletal proteins. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 529-40	5.6	8
33	In vitro neurotoxicity of PBDE-99: immediate and concentration-dependent effects on protein expression in cerebral cortex cells. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 1226-35	5.6	22
32	H-score, a mass accuracy driven rescoring approach for improved peptide identification in modification rich samples. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 5511-6	5.6	33
31	Evaluation of data analysis strategies for improved mass spectrometry-based phosphoproteomics. <i>Analytical Chemistry</i> , <b>2010</b> , 82, 9843-9	7.8	7
30	Targeted data acquisition for improved reproducibility and robustness of proteomic mass spectrometry assays. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2010</b> , 21, 1668-79	3.5	74
29	Two dimensional mass mapping as a general method of data representation in comprehensive analysis of complex molecular mixtures. <i>Analytical Chemistry</i> , <b>2009</b> , 81, 3738-45	7.8	23
28	Analytical utility of small neutral losses from reduced species in electron capture dissociation studied using SwedECD database. <i>Analytical Chemistry</i> , <b>2008</b> , 80, 8089-94	7.8	40
27	Immunoaffinity enrichments followed by mass spectrometric detection for studying global protein tyrosine phosphorylation. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 2897-910	5.6	44

26	Bifurcating fragmentation behavior of gas-phase tryptic peptide dications in collisional activation. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2008</b> , 19, 1755-63	3.5	54
25	Relative specificities of water and ammonia losses from backbone fragments in collision-activated dissociation. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 2669-73	5.6	20
24	SwedCAD, a database of annotated high-mass accuracy MS/MS spectra of tryptic peptides. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 4063-7	5.6	27
23	On studying protein phosphorylation patterns using bottom-up LC-MS/MS: the case of human alpha-casein. <i>Analyst, The</i> , <b>2007</b> , 132, 768-76	5	32
22	Side-chain losses in electron capture dissociation to improve peptide identification. <i>Analytical Chemistry</i> , <b>2007</b> , 79, 2296-302	7.8	65
21	De novo peptide sequencing and identification with precision mass spectrometry. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 114-23	5.6	173
20	Hydrogen rearrangement to and from radical z fragments in electron capture dissociation of peptides. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2007</b> , 18, 113-20	3.5	113
19	Extent of modifications in human proteome samples and their effect on dynamic range of analysis in shotgun proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2006</b> , 5, 2384-91	7.6	83
18	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> , <b>2006</b> , 5, 935-48	7.6	160
17	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> , <b>2006</b> , 5, 659-68	5.6	37
16	Determination of the location of positive charges in gas-phase polypeptide polycations by tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , <b>2006</b> , 252, 204-212	1.9	30
15	Liquid chromatography at critical conditions: comprehensive approach to sequence-dependent retention time prediction. <i>Analytical Chemistry</i> , <b>2006</b> , 78, 7770-7	7.8	68
14	Proteomics-grade de novo sequencing approach. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 2348-54	5.6	142
13	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> , <b>2005</b> , 4, 1180-8	7.6	81
12	Improving protein identification using complementary fragmentation techniques in fourier transform mass spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2005</b> , 4, 835-45	7.6	123
11	Shifted-basis technique improves accuracy of peak position determination in Fourier transform mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2004</b> , 15, 457-61	3.5	11
10	Physicochemical properties determining the detection probability of tryptic peptides in Fourier transform mass spectrometry. A correlation study. <i>Analytical Chemistry</i> , <b>2004</b> , 76, 5872-7	7.8	20
9	Aggregation and Disaggregation Features of the Human Proteome		1

8	A dual-mechanism antibiotic targets Gram-negative bacteria and avoids drug resistance	1
7	Impact of phosphorylation on thermal stability of proteins	7
6	Global mapping of <i>Salmonella enterica</i> -host protein-protein interactions during infection	6
5	Computational analysis of ligand dose range thermal proteome profiles	1
4	Bacterial retrons encode tripartite toxin/antitoxin systems	15
3	Phage proteins block and trigger retron toxin/antitoxin systems	15
2	The outer membrane lipoprotein Nlpl nucleates hydrolases within peptidoglycan multi-enzyme complexes in <i>Escherichia coli</i>	5
1	Towards a systematic map of the functional role of protein phosphorylation	6