Mikhail M Savitski

List of Publications by Citations

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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	Mass-spectrometry-based draft of the human proteome. *Nature*, **2014**, 509, 582-7	50.4	1332
96	Inhibition of BET recruitment to chromatin as an effective treatment for MLL-fusion leukaemia. *Nature*, **2011**, 478, 529-33	50.4	1144
95	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. *Analytical and Bioanalytical Chemistry*, **2012**, 404, 939-65	4.4	585
94	Tracking cancer drugs in living cells by thermal profiling of the proteome. *Science*, **2014**, 346, 1255784	33.3	526
93	Chemoproteomics profiling of HDAC inhibitors reveals selective targeting of HDAC complexes. *Nature Biotechnology*, **2011**, 29, 255-65	44.5	505
92	Thermal proteome profiling for unbiased identification of direct and indirect drug targets using multiplexed quantitative mass spectrometry. *Nature Protocols*, **2015**, 10, 1567-93	18.8	293
91	A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. *Molecular and Cellular Proteomics*, **2015**, 14, 2394-404	7.6	210
90	A new antibiotic selectively kills Gram-negative pathogens. *Nature*, **2019**, 576, 459-464	50.4	202
89	Measuring and managing ratio compression for accurate iTRAQ/TMT quantification. *Journal of Proteome Research*, **2013**, 12, 3586-98	5.6	177
88	Ion coalescence of neutron encoded TMT 10-plex reporter ions. *Analytical Chemistry*, **2014**, 86, 3594-601	7.8	174
87	Thermal proteome profiling monitors ligand interactions with cellular membrane proteins. *Nature Methods*, **2015**, 12, 1129-31	21.6	173
86	De novo peptide sequencing and identification with precision mass spectrometry. *Journal of Proteome Research*, **2007**, 6, 114-23	5.6	173
85	ModifiComb, a new proteomic tool for mapping substoichiometric post-translational modifications, finding novel types of modifications, and fingerprinting complex protein mixtures. *Molecular and Cellular Proteomics*, **2006**, 5, 935-48	7.6	160
84	High-resolution enabled TMT 8-plexing. *Analytical Chemistry*, **2012**, 84, 7188-94	7.8	150
83	Systematic analysis of protein turnover in primary cells. *Nature Communications*, **2018**, 9, 689	17.4	145
82	Proteomics-grade de novo sequencing approach. *Journal of Proteome Research*, **2005**, 4, 2348-54	5.6	142
81	Species-specific activity of antibacterial drug combinations. *Nature*, **2018**, 559, 259-263	50.4	137

80	Multiplexed Proteome Dynamics Profiling Reveals Mechanisms Controlling Protein Homeostasis. *Cell*, **2018**, 173, 260-274.e25	56.2	125
79	Improving protein identification using complementary fragmentation techniques in fourier transform mass spectrometry. *Molecular and Cellular Proteomics*, **2005**, 4, 835-45	7.6	123
78	Thermal profiling reveals phenylalanine hydroxylase as an off-target of panobinostat. *Nature Chemical Biology*, **2016**, 12, 908-910	11.7	120
77	A selective inhibitor reveals PI3K□dependence of T(H)17 cell differentiation. *Nature Chemical Biology*, **2012**, 8, 576-82	11.7	117
76	Hydrogen rearrangement to and from radical z fragments in electron capture dissociation of peptides. *Journal of the American Society for Mass Spectrometry*, **2007**, 18, 113-20	3.5	113
75	Pervasive Protein Thermal Stability Variation during the Cell Cycle. *Cell*, **2018**, 173, 1495-1507.e18	56.2	109
74	The functional landscape of the human phosphoproteome. *Nature Biotechnology*, **2020**, 38, 365-373	44.5	106
73	Proteome-wide solubility and thermal stability profiling reveals distinct regulatory roles for ATP. *Nature Communications*, **2019**, 10, 1155	17.4	88
72	A Dual-Mechanism Antibiotic Kills Gram-Negative Bacteria and Avoids Drug Resistance. *Cell*, **2020**, 181, 1518-1532.e14	56.2	88
71	The commonly used PI3-kinase probe LY294002 is an inhibitor of BET bromodomains. *ACS Chemical Biology*, **2014**, 9, 495-502	4.9	85
70	Mitochondrial protein-induced stress triggers a global adaptive transcriptional programme. *Nature Cell Biology*, **2019**, 21, 442-451	23.4	84
69	Extent of modifications in human proteome samples and their effect on dynamic range of analysis in shotgun proteomics. *Molecular and Cellular Proteomics*, **2006**, 5, 2384-91	7.6	83
68	Thermal proteome profiling in bacteria: probing protein state. *Molecular Systems Biology*, **2018**, 14, e8242	12.2	82
67	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. *Molecular and Cellular Proteomics*, **2005**, 4, 1180-8	7.6	81
66	Delayed fragmentation and optimized isolation width settings for improvement of protein identification and accuracy of isobaric mass tag quantification on Orbitrap-type mass spectrometers. *Analytical Chemistry*, **2011**, 83, 8959-67	7.8	79
65	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. *Nature Microbiology*, **2017**, 2, 17047	26.6	74
64	Targeted data acquisition for improved reproducibility and robustness of proteomic mass spectrometry assays. *Journal of the American Society for Mass Spectrometry*, **2010**, 21, 1668-79	3.5	74
63	Liquid chromatography at critical conditions: comprehensive approach to sequence-dependent retention time prediction. *Analytical Chemistry*, **2006**, 78, 7770-7	7.8	68

62	Side-chain losses in electron capture dissociation to improve peptide identification. *Analytical Chemistry*, **2007**, 79, 2296-302	7.8	65
61	Thermal proteome profiling: unbiased assessment of protein state through heat-induced stability changes. *Proteome Science*, **2016**, 15, 13	2.6	62
60	Chemical Proteomics Reveals Ferrochelatase as a Common Off-target of Kinase Inhibitors. *ACS Chemical Biology*, **2016**, 11, 1245-54	4.9	58
59	Affinity profiling of the cellular kinome for the nucleotide cofactors ATP, ADP, and GTP. *ACS Chemical Biology*, **2013**, 8, 599-607	4.9	58
58	Bifurcating fragmentation behavior of gas-phase tryptic peptide dications in collisional activation. *Journal of the American Society for Mass Spectrometry*, **2008**, 19, 1755-63	3.5	54
57	Thermal proteome profiling for interrogating protein interactions. *Molecular Systems Biology*, **2020**, 16, e9232	12.2	53
56	Meltome atlas-thermal proteome stability across the tree of life. *Nature Methods*, **2020**, 17, 495-503	21.6	53
55	Identifying drug targets in tissues and whole blood with thermal-shift profiling. *Nature Biotechnology*, **2020**, 38, 303-308	44.5	46
54	Immunoaffinity enrichments followed by mass spectrometric detection for studying global protein tyrosine phosphorylation. *Journal of Proteome Research*, **2008**, 7, 2897-910	5.6	44
53	Chemoproteomics reveals time-dependent binding of histone deacetylase inhibitors to endogenous repressor complexes. *ACS Chemical Biology*, **2014**, 9, 1736-46	4.9	43
52	Analytical utility of small neutral losses from reduced species in electron capture dissociation studied using SwedECD database. *Analytical Chemistry*, **2008**, 80, 8089-94	7.8	40
51	PhosTShunter: a fast and reliable tool to detect phosphorylated peptides in liquid chromatography Fourier transform tandem mass spectrometry data sets. *Journal of Proteome Research*, **2006**, 5, 659-68	5.6	37
50	Outer membrane lipoprotein NlpI scaffolds peptidoglycan hydrolases within multi-enzyme complexes in Escherichia coli. *EMBO Journal*, **2020**, 39, e102246	13	36
49	Nonparametric Analysis of Thermal Proteome Profiles Reveals Novel Drug-binding Proteins. *Molecular and Cellular Proteomics*, **2019**, 18, 2506-2515	7.6	34
48	H-score, a mass accuracy driven rescoring approach for improved peptide identification in modification rich samples. *Journal of Proteome Research*, **2010**, 9, 5511-6	5.6	33
47	On studying protein phosphorylation patterns using bottom-up LC-MS/MS: the case of human alpha-casein. *Analyst, The*, **2007**, 132, 768-76	5	32
46	Determination of the location of positive charges in gas-phase polypeptide polycations by tandem mass spectrometry. *International Journal of Mass Spectrometry*, **2006**, 252, 204-212	1.9	30
45	Bioaccumulation of therapeutic drugs by human gut bacteria. *Nature*, **2021**, 597, 533-538	50.4	29

44	Leaderless secreted peptide signaling molecule alters global gene expression and increases virulence of a human bacterial pathogen. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E8498-E8507	11.5	27
43	SwedCAD, a database of annotated high-mass accuracy MS/MS spectra of tryptic peptides. *Journal of Proteome Research*, **2007**, 6, 4063-7	5.6	27
42	Two dimensional mass mapping as a general method of data representation in comprehensive analysis of complex molecular mixtures. *Analytical Chemistry*, **2009**, 81, 3738-45	7.8	23
41	In vitro neurotoxicity of PBDE-99: immediate and concentration-dependent effects on protein expression in cerebral cortex cells. *Journal of Proteome Research*, **2010**, 9, 1226-35	5.6	22
40	Relative specificities of water and ammonia losses from backbone fragments in collision-activated dissociation. *Journal of Proteome Research*, **2007**, 6, 2669-73	5.6	20
39	Physicochemical properties determining the detection probability of tryptic peptides in Fourier transform mass spectrometry. A correlation study. *Analytical Chemistry*, **2004**, 76, 5872-7	7.8	20
38	Spatiotemporal proteomics uncovers cathepsin-dependent macrophage cell death during Salmonella infection. *Nature Microbiology*, **2020**, 5, 1119-1133	26.6	17
37	TRRAP is essential for regulating the accumulation of mutant and wild-type p53 in lymphoma. *Blood*, **2018**, 131, 2789-2802	2.2	17
36	Bacterial retrons encode tripartite toxin/antitoxin systems		15
35	Phage proteins block and trigger retron toxin/antitoxin systems		15
34	Impact of phosphorylation on thermal stability of proteins. *Nature Methods*, **2021**, 18, 757-759	21.6	15
33	The functional proteome landscape of Escherichia coli. *Nature*, **2020**, 588, 473-478	50.4	14
32	Global mapping of Salmonella enterica-host protein-protein interactions during infection. *Cell Host and Microbe*, **2021**, 29, 1316-1332.e12	23.4	13
31	Cell surface thermal proteome profiling tracks perturbations and drug targets on the plasma membrane. *Nature Methods*, **2021**, 18, 84-91	21.6	12
30	Shifted-basis technique improves accuracy of peak position determination in Fourier transform mass spectrometry. *Journal of the American Society for Mass Spectrometry*, **2004**, 15, 457-61	3.5	11
29	Aggregation and disaggregation features of the human proteome. *Molecular Systems Biology*, **2020**, 16, e9500	12.2	9
28	Systematic Localization of Escherichia coli Membrane Proteins. *MSystems*, **2020**, 5,	7.6	8
27	Mutational Analysis of Glycogen Synthase Kinase 3β Protein Kinase Together with Kinome-Wide Binding and Stability Studies Suggests Context-Dependent Recognition of Kinases by the Chaperone Heat Shock Protein 90. *Molecular and Cellular Biology*, **2016**, 36, 1007-18	4.8	8

26	ATP enhances neuronal differentiation of PC12 cells by activating PKC interactions with cytoskeletal proteins. *Journal of Proteome Research*, **2011**, 10, 529-40	5.6	8
25	A computational method for detection of ligand-binding proteins from dose range thermal proteome profiles. *Nature Communications*, **2020**, 11, 5783	17.4	8
24	A genetic analysis reveals novel histone residues required for transcriptional reprogramming upon stress. *Nucleic Acids Research*, **2020**, 48, 3455-3475	20.1	7
23	A misprocessed form of Apolipoprotein A-I is specifically associated with recurrent Focal Segmental Glomerulosclerosis. *Scientific Reports*, **2020**, 10, 1159	4.9	7
22	Evaluation of data analysis strategies for improved mass spectrometry-based phosphoproteomics. *Analytical Chemistry*, **2010**, 82, 9843-9	7.8	7
21	Impact of phosphorylation on thermal stability of proteins		7
20	Dissecting the sequence determinants for dephosphorylation by the catalytic subunits of phosphatases PP1 and PP2A. *Nature Communications*, **2020**, 11, 3583	17.4	7
19	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. *Science Advances*, **2021**, 7,	14.3	7
18	Global mapping ofSalmonella enterica-host protein-protein interactions during infection		6
17	Towards a systematic map of the functional role of protein phosphorylation		6
16	The outer membrane lipoprotein NlpI nucleates hydrolases within peptidoglycan multi-enzyme complexes inEscherichia coli		5
15	SARS-CoV-2 infection remodels the host protein thermal stability landscape. *Molecular Systems Biology*, **2021**, 17, e10188	12.2	5
14	Effect of Sec61 interaction with Mpd1 on endoplasmic reticulum-associated degradation. *PLoS ONE* , **2019**, 14, e0211180	3.7	4
13	Wilhelm et al. reply. *Nature*, **2017**, 547, E23	50.4	4
12	Isocotoin suppresses hepatitis E virus replication through inhibition of heat shock protein 90. *Antiviral Research*, **2021**, 185, 104997	10.8	4
11	Target Discovery Using Thermal Proteome Profiling **2019**, 267-291		3
10	Dendritic autophagy degrades postsynaptic proteins and is required for long-term synaptic depression in mice.. *Nature Communications*, **2022**, 13, 680	17.4	3
9	High-throughput functional characterization of protein phosphorylation sites in yeast. *Nature Biotechnology*, **2021**,	44.5	3

8	Rtpca: an R package for differential thermal proximity coaggregation analysis. *Bioinformatics*, **2021**, 37, 431-433	7.2	3
7	Drug Target Identification in Tissues by Thermal Proteome Profiling. *Annual Review of Pharmacology and Toxicology*, **2021**,	17.9	2
6	Aggregation and Disaggregation Features of the Human Proteome		1
5	A dual-mechanism antibiotic targets Gram-negative bacteria and avoids drug resistance		1
4	Computational analysis of ligand dose range thermal proteome profiles		1
3	The rise of proteome-wide biophysics. *Molecular Systems Biology*, **2021**, 17, e10442	12.2	1
2	Transcriptional and Post-Transcriptional Polar Effects in Bacterial Gene Deletion Libraries. *MSystems*, **2021**, 6, e0081321	7.6	1
1	PLDMS: Phosphopeptide Library Dephosphorylation Followed by Mass Spectrometry Analysis to Determine the Specificity of Phosphatases for Dephosphorylation Site Sequences. *Methods in Molecular Biology*, **2022**, 43-64	1.4	0