

Mikhail V Gorshkov

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.

119
papers

2,242
citations

27
h-index

42
g-index

130
ext. papers

2,678
ext. citations

3.7
avg, IF

4.82
L-index

#	Paper	IF	Citations
119	Proteomics of Cellular Response to Stress: Taking Control of False Positive Results. <i>Biochemistry (Moscow)</i> , 2021 , 86, 338-349	2.9	1
118	Boosting MS1-only Proteomics with Machine Learning Allows 2000 Protein Identifications in Single-Shot Human Proteome Analysis Using 5 min HPLC Gradient. <i>Journal of Proteome Research</i> , 2021 , 20, 1864-1873	5.6	5
117	Improving the Protein Inference from Bottom-Up Proteomic Data Using Identifications from MS1 Spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1258-1262	3.5	
116	Identification-Free Control over the Precursor Isotopic Mass Misassignment in Orbitrap-Based Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 218-224	3.5	1
115	Cysteine alkylation methods in shotgun proteomics and their possible effects on methionine residues. <i>Journal of Proteomics</i> , 2021 , 231, 104022	3.9	7
114	Accelerating photofragmentation UV Spectroscopy-Mass spectrometry fingerprinting for quantification of isomeric peptides. <i>Talanta</i> , 2021 , 232, 122412	6.2	1
113	AA_stat: Intelligent profiling of in vivo and in vitro modifications from open search results. <i>Journal of Proteomics</i> , 2021 , 248, 104350	3.9	0
112	Towards increasing the performance of FTICR-MS with signal detection at frequency multiples: Signal theory and numerical study. <i>International Journal of Mass Spectrometry</i> , 2021 , 469, 116669	1.9	1
111	Biosaur: An open-source Python software for liquid chromatography-mass spectrometry peptide feature detection with ion mobility support. <i>Rapid Communications in Mass Spectrometry</i> , 2021 , e9045	2.2	3
110	Is It Possible to Find Needles in a Haystack? Meta-Analysis of 1000+ MS/MS Files Provided by the Russian Proteomic Consortium for Mining Missing Proteins. <i>Proteomes</i> , 2020 , 8,	4.6	2
109	Rpn4 and proteasome-mediated yeast resistance to ethanol includes regulation of autophagy. <i>Applied Microbiology and Biotechnology</i> , 2020 , 104, 4027-4041	5.7	8
108	DirectMS1: MS/MS-Free Identification of 1000 Proteins of Cellular Proteomes in 5 Minutes. <i>Analytical Chemistry</i> , 2020 , 92, 4326-4333	7.8	14
107	Single Cell Proteogenomics - Immediate Prospects. <i>Biochemistry (Moscow)</i> , 2020 , 85, 140-146	2.9	5
106	Proteome-Wide Analysis of ADAR-Mediated Messenger RNA Editing during Fruit Fly Ontogeny. <i>Journal of Proteome Research</i> , 2020 , 19, 4046-4060	5.6	0
105	PhosphoShield: Improving Trypsin Digestion of Phosphoproteins by Shielding the Negatively Charged Phosphate Moiety. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 2053-2060	3.5	2
104	Method for Identification of Threonine Isoforms in Peptides by Ultraviolet Photofragmentation of Cold Ions. <i>Analytical Chemistry</i> , 2019 , 91, 6709-6715	7.8	4
103	Brain Proteome of <i>Drosophila melanogaster</i> Is Enriched with Nuclear Proteins. <i>Biochemistry (Moscow)</i> , 2019 , 84, 71-78	2.9	2

102	Protein corona formed on silver nanoparticles in blood plasma is highly selective and resistant to physicochemical changes of the solution. <i>Environmental Science: Nano</i> , 2019 , 6, 1089-1098	7.1	36
101	Profiling modifications for glioblastoma proteome using ultra-tolerant database search: Are the peptide mass shifts biologically relevant or chemically induced?. <i>Journal of Proteomics</i> , 2019 , 191, 16-21	3.9	6
100	Adenosine-to-Inosine RNA Editing in Mouse and Human Brain Proteomes. <i>Proteomics</i> , 2019 , 19, e190019	4.8	6
99	viQC: Visual and Intuitive Quality Control for Mass Spectrometry-Based Proteome Analysis. <i>Journal of Analytical Chemistry</i> , 2019 , 74, 1363-1370	1.1	1
98	Pyteomics 4.0: Five Years of Development of a Python Proteomics Framework. <i>Journal of Proteome Research</i> , 2019 , 18, 709-714	5.6	57
97	Scavager: A Versatile Postsearch Validation Algorithm for Shotgun Proteomics Based on Gradient Boosting. <i>Proteomics</i> , 2019 , 19, e1800280	4.8	23
96	IdentiPy: An Extensible Search Engine for Protein Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 2249-2255	5.6	26
95	FractionOptimizer: a method for optimal peptide fractionation in bottom-up proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2018 , 410, 3827-3833	4.4	6
94	High Speed Intact Protein Characterization Using 4X Frequency Multiplication, Ion Trap Harmonization, and 21 Tesla FTICR-MS. <i>Analytical Chemistry</i> , 2018 , 90, 5557-5562	7.8	17
93	Proteogenomics of Malignant Melanoma Cell Lines: The Effect of Stringency of Exome Data Filtering on Variant Peptide Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 1801-1811	5.6	10
92	Identification of isoforms of aspartic acid residues in peptides by 2D UV-MS fingerprinting of cold ions. <i>Analyst, The</i> , 2018 , 143, 833-836	5	7
91	Brute-Force Approach for Mass Spectrometry-Based Variant Peptide Identification in Proteogenomics without Personalized Genomic Data. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 435-438	3.5	2
90	Chemical-Mediated Digestion: An Alternative Realm for Middle-down Proteomics?. <i>Journal of Proteome Research</i> , 2018 , 17, 2005-2016	5.6	8
89	Identification of Single Amino Acid Substitutions in Proteogenomics. <i>Biochemistry (Moscow)</i> , 2018 , 83, 250-258	2.9	4
88	Semi-supervised quality control method for proteome analyses based on tandem mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2018 , 427, 59-64	1.9	3
87	Comparative proteomics as a tool for identifying specific alterations within interferon response pathways in human glioblastoma multiforme cells. <i>Oncotarget</i> , 2018 , 9, 1785-1802	3.3	7
86	Multiplexed Middle-Down Mass Spectrometry as a Method for Revealing Light and Heavy Chain Connectivity in a Monoclonal Antibody. <i>Analytical Chemistry</i> , 2018 , 90, 12527-12535	7.8	27
85	Proteogenomics of Adenosine-to-Inosine RNA Editing in the Fruit Fly. <i>Journal of Proteome Research</i> , 2018 , 17, 3889-3903	5.6	5

84	Validation of Peptide Identification Results in Proteomics Using Amino Acid Counting. <i>Proteomics</i> , 2018 , 18, e1800117	4.8	5
83	Comparative evaluation of label-free quantification methods for shotgun proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2017 , 31, 606-612	2.2	32
82	Unbiased False Discovery Rate Estimation for Shotgun Proteomics Based on the Target-Decoy Approach. <i>Journal of Proteome Research</i> , 2017 , 16, 393-397	5.6	33
81	Reply to 'Comparison of peptide retention prediction algorithm in reversed-phase chromatography. Comment on "Predictive chromatography of peptides and proteins as a complementary tool for proteomics"', by O. V. Krokhin, <i>Analyst</i> , 2017 , 142, DOI: 10.1039/c6an02510b. <i>Analyst The</i> , 2017 , 142, 2052-2053	5	
80	Comparison of False Discovery Rate Control Strategies for Variant Peptide Identifications in Shotgun Proteogenomics. <i>Journal of Proteome Research</i> , 2017 , 16, 1936-1943	5.6	11
79	MS/MS-Free Protein Identification in Complex Mixtures Using Multiple Enzymes with Complementary Specificity. <i>Journal of Proteome Research</i> , 2017 , 16, 3989-3999	5.6	6
78	Applicability of the critical-chromatography concept to proteomics problems: Separation of peptides modeled by a heterogeneous rod. <i>Polymer Science - Series A</i> , 2017 , 59, 451-464	1.2	1
77	Enhancing the Cytotoxic Activity of Anticancer PtIV Complexes by Introduction of Lonidamine as an Axial Ligand. <i>European Journal of Inorganic Chemistry</i> , 2017 , 2017, 1785-1791	2.3	18
76	Correction: Predictive chromatography of peptides and proteins as a complementary tool for proteomics. <i>Analyst The</i> , 2017 , 142, 2054	5	
75	Predictive Liquid Chromatography of Peptides Based on Hydrophilic Interactions for Mass Spectrometry-Based Proteomics. <i>Journal of Analytical Chemistry</i> , 2017 , 72, 1375-1382	1.1	1
74	Influence of the Number of Axial Bexarotene Ligands on the Cytotoxicity of Pt(IV) Analogs of Oxaliplatin. <i>Bioinorganic Chemistry and Applications</i> , 2017 , 2017, 4736321	4.2	2
73	Advanced Precursor Ion Selection Algorithms for Increased Depth of Bottom-Up Proteomic Profiling. <i>Journal of Proteome Research</i> , 2016 , 15, 3563-3573	5.6	9
72	Predictive chromatography of peptides and proteins as a complementary tool for proteomics. <i>Analyst The</i> , 2016 , 141, 4816-4832	5	24
71	Adaptation of Decoy Fusion Strategy for Existing Multi-Stage Search Workflows. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 1579-82	3.5	3
70	Applicability of the critical chromatography concept to proteomics problems: I. Effect of the stationary phase and the size of the chromatographic column on the dependence of the retention time of peptides and proteins on the amino acid sequence. <i>Journal of Analytical Chemistry</i> , 2016 , 71, 110-125	1.1	3
69	Exome-based proteogenomics of HEK-293 human cell line: Coding genomic variants identified at the level of shotgun proteome. <i>Proteomics</i> , 2016 , 16, 1980-91	4.8	18
68	Threonine versus isothreonine in synthetic peptides analyzed by high-resolution liquid chromatography/tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2016 , 30, 1323-31	2.2	3
67	Depletion of human serum albumin in embryo culture media for in vitro fertilization using monolithic columns with immobilized antibodies. <i>Electrophoresis</i> , 2016 , 37, 2322-7	3.6	8

66	GroupFilter: A software tool for efficient filtering of Morpheus search engine results. <i>Journal of Analytical Chemistry</i> , 2016 , 71, 1275-1279	1.1	1
65	Applicability of the critical chromatography concept to proteomic problems. II. Effect of mobile phase on the separation of peptides and proteins taking into account the amino acid sequence. <i>Journal of Analytical Chemistry</i> , 2016 , 71, 1188-1197	1.1	
64	Methionine to isothreonine conversion as a source of false discovery identifications of genetically encoded variants in proteogenomics. <i>Journal of Proteomics</i> , 2015 , 120, 169-78	3.9	19
63	Ion coalescence in Fourier transform mass spectrometry: should we worry about this in shotgun proteomics?. <i>European Journal of Mass Spectrometry</i> , 2015 , 21, 459-70	1.1	9
62	Application of Statistical Thermodynamics To Predict the Adsorption Properties of Polypeptides in Reversed-Phase HPLC. <i>Analytical Chemistry</i> , 2015 , 87, 6562-9	7.8	8
61	Pepxmltk $\bar{\bar{}}$ format converter for peptide identification results obtained from tandem mass spectrometry data using X!Tandem search engine. <i>Journal of Analytical Chemistry</i> , 2015 , 70, 1598-1599	1.1	8
60	Peptide identification in $\bar{\bar{}}$ shotgun $\bar{\bar{}}$ proteomics using tandem mass spectrometry: Comparison of search engine algorithms. <i>Journal of Analytical Chemistry</i> , 2015 , 70, 1614-1619	1.1	2
59	Exome-driven characterization of the cancer cell lines at the proteome level: the NCI-60 case study. <i>Journal of Proteome Research</i> , 2014 , 13, 5551-60	5.6	27
58	Empirical multidimensional space for scoring peptide spectrum matches in shotgun proteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 1911-20	5.6	38
57	High-resolution Fourier transform ion cyclotron resonance mass spectrometry with increased throughput for biomolecular analysis. <i>Analytical Chemistry</i> , 2014 , 86, 9020-8	7.8	35
56	Proteome digestion specificity analysis for rational design of extended bottom-up and middle-down proteomics experiments. <i>Journal of Proteome Research</i> , 2013 , 12, 5558-69	5.6	30
55	Pyteomics--a Python framework for exploratory data analysis and rapid software prototyping in proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2013 , 24, 301-4	3.5	110
54	Combination of Edman degradation of peptides with liquid chromatography/mass spectrometry workflow for peptide identification in bottom-up proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2013 , 27, 391-400	2.2	13
53	On the utility of predictive chromatography to complement mass spectrometry based intact protein identification. <i>Analytical and Bioanalytical Chemistry</i> , 2012 , 402, 2521-9	4.4	5
52	Inversion of chromatographic elution orders of peptides and its importance for proteomics. <i>Journal of Analytical Chemistry</i> , 2012 , 67, 1014-1025	1.1	9
51	On the utility of isotopic fine structure mass spectrometry in protein identification. <i>Analytical Chemistry</i> , 2012 , 84, 4042-51	7.8	27
50	Probing the mechanisms of ambient ionization by laser-induced fluorescence spectroscopy. <i>Rapid Communications in Mass Spectrometry</i> , 2012 , 26, 1567-72	2.2	14
49	Observation of ion coalescence in Orbitrap Fourier transform mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2012 , 26, 1711-7	2.2	46

48	Limitation of predictive 2-D liquid chromatography in reducing the database search space in shotgun proteomics: in silico studies. <i>Journal of Separation Science</i> , 2012 , 35, 1771-8	3.4	4
47	Towards data acquisition throughput increase in Fourier transform mass spectrometry of proteins using double frequency measurements. <i>International Journal of Mass Spectrometry</i> , 2011 , 306, 227-231	1.9	16
46	Applicability of the critical-chromatography concept to analysis of proteins: Dependence of retention times on the sequence of amino acid residues in a chain. <i>Polymer Science - Series A</i> , 2011 , 53, 1227-1241	1.2	3
45	An atmospheric pressure ionization source based on desorption electrospray ionization technology (DESI) for ion cyclotron resonance mass spectrometry. <i>Journal of Analytical Chemistry</i> , 2011 , 66, 1376-1384	1.1	2
44	Sequence scrambling in shotgun proteomics is negligible. <i>Journal of the American Society for Mass Spectrometry</i> , 2011 , 22, 1121-4	3.5	44
43	Sequence-specific predictive chromatography to assist mass spectrometric analysis of asparagine deamidation and aspartate isomerization in peptides. <i>Electrophoresis</i> , 2011 , 32, 1962-9	3.6	13
42	Critical chromatography and mass spectrometry of macromolecules: Determination of the position of a functional group in a chain. <i>Polymer Science - Series A</i> , 2010 , 52, 340-347	1.2	
41	Critical chromatography of macromolecules as a tool for reading the amino acid sequence of biomacromolecules: Reality or science fiction?. <i>Journal of Analytical Chemistry</i> , 2010 , 65, 2-11	1.1	5
40	Alternative methods for verifying the results of the mass spectrometric identification of peptides in shotgun proteomics. <i>Journal of Analytical Chemistry</i> , 2010 , 65, 1462-1468	1.1	1
39	Calibration function for the Orbitrap FTMS accounting for the space charge effect. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 1846-51	3.5	26
38	Retention time prediction using the model of liquid chromatography of biomacromolecules at critical conditions in LC-MS phosphopeptide analysis. <i>Proteomics</i> , 2010 , 10, 3458-68	4.8	24
37	Empirical approach to false discovery rate estimation in shotgun proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2010 , 24, 454-62	2.2	13
36	Use of models of biomacromolecule separation in AMT database generation for shotgun proteomics. <i>Biochemistry (Moscow)</i> , 2009 , 74, 1195-202	2.9	8
35	Standardization of retention time data for AMT tag proteomics database generation. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009 , 877, 433-40	3.2	19
34	Applicability of the critical chromatography concept to proteomics problems: Experimental study of the dependence of peptide retention time on the sequence of amino acids in the chain. <i>Polymer Science - Series A</i> , 2008 , 50, 309-321	1.2	18
33	Positive and negative analyte ion yield in matrix-assisted laser desorption/ionization. <i>International Journal of Mass Spectrometry</i> , 2007 , 268, 122-130	1.9	32
32	Atmospheric pressure ionization permanent magnet fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2007 , 18, 1552-8	3.5	15
31	Applicability of the critical chromatography concept to proteomics problems: Dependence of retention time on the sequence of amino acids. <i>Polymer Science - Series B</i> , 2007 , 49, 93-107	0.8	19

30	Liquid chromatography at critical conditions: comprehensive approach to sequence-dependent retention time prediction. <i>Analytical Chemistry</i> , 2006 , 78, 7770-7	7.8	68
29	C alpha-C backbone fragmentation dominates in electron detachment dissociation of gas-phase polypeptide polyanions. <i>Chemistry - A European Journal</i> , 2005 , 11, 1803-12	4.8	106
28	On the accuracy of polypeptide masses measured in a linear ion trap. <i>Rapid Communications in Mass Spectrometry</i> , 2005 , 19, 3755-8	2.2	9
27	Considerations for electron capture dissociation efficiency in FTICR mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2004 , 234, 131-136	1.9	26
26	Letter: Characteristics of Photoelectrons Emitted in Matrix-Assisted Laser Desorption/Ionization Fourier Transform Ion Cyclotron Resonance Experiments. <i>European Journal of Mass Spectrometry</i> , 2002 , 8, 67-69	1.1	31
25	High Performance Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry at Low Magnetic Field. <i>European Journal of Mass Spectrometry</i> , 2002 , 8, 169-176	1.1	5
24	A dynamic ion cooling technique for FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001 , 12, 1169-73	3.5	13
23	Controlled ion fragmentation in a 2-D quadrupole ion trap for external ion accumulation in ESI FTICR mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2001 , 12, 1312-9	3.5	23
22	Dynamically assisted gated trapping for Fourier transform ion cyclotron mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001 , 15, 1558-61	2.2	8
21	Improved low-energy electron injection systems for high rate electron capture dissociation in Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001 , 15, 1849-54	2.2	106
20	Optimal pressure conditions for unbiased external ion accumulation in a two-dimensional radio-frequency quadrupole for Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2001 , 15, 1988-96	2.2	11
19	Design and performance of an ESI interface for selective external ion accumulation coupled to a Fourier transform ion cyclotron mass spectrometer. <i>Analytical Chemistry</i> , 2001 , 73, 253-61	7.8	79
18	A novel high-performance fourier transform ion cyclotron resonance cell for improved biopolymer characterization. <i>Journal of Mass Spectrometry</i> , 2000 , 35, 85-94	2.2	27
17	Initial implementation of an electrodynamic ion funnel with Fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2000 , 11, 19-23	3.5	69
16	Zeptomole-sensitivity electrospray ionization--Fourier transform ion cyclotron resonance mass spectrometry of proteins. <i>Analytical Chemistry</i> , 2000 , 72, 2271-9	7.8	144
15	Pressure limited sustained off-resonance irradiation for collision-activated dissociation in fourier transform mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1999 , 10, 15-8	3.5	8
14	Electrospray ionization-Fourier transform ion cyclotron resonance mass spectrometry at 11.5 tesla: instrument design and initial results. <i>Journal of the American Society for Mass Spectrometry</i> , 1998 , 9, 692-700	3.5	45
13	A dual-trap design and its applications in electrospray ionization FTICR mass spectrometry. <i>Analytical Chemistry</i> , 1997 , 69, 1307-14	7.8	13

12	A high performance low magnetic field internal electrospray ionization-fourier transform ion cyclotron resonance mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 1996 , 7, 915-22	3.5	7
11	Possible applications of an external resonant circuit in Fourier transform ion cyclotron resonance. <i>Rapid Communications in Mass Spectrometry</i> , 1995 , 9, 317-321	2.2	1
10	Data Reflection Algorithm for Spectral Enhancement in Fourier Transform ICR and NMR Spectroscopies. <i>Analytical Chemistry</i> , 1995 , 67, 3412-3420	7.8	6
9	Deuterium atomic mass from Fourier-transform-ion-cyclotron-resonance measurement of the mass difference between $1\text{H}_2\text{O}^+$ and 2HO^+ . <i>Physical Review A</i> , 1993 , 47, 3433-3436	2.6	11
8	Resonant excitation of relativistic-ion cyclotron orbital motion. <i>Physical Review A</i> , 1993 , 47, 2730-2737	2.6	13
7	Masses of stable neon isotopes determined at parts per billion precision by Fourier transform ion cyclotron resonance mass spectrometry. <i>International Journal of Mass Spectrometry and Ion Processes</i> , 1993 , 128, 47-60		26
6	Analysis and elimination of systematic errors originating from coulomb mutual interaction and image charge in Fourier transform ion cyclotron resonance precise mass difference measurements. <i>Journal of the American Society for Mass Spectrometry</i> , 1993 , 4, 855-68	3.5	45
5	Optimal cyclotron radius for high resolution FT-ICR spectrometry. <i>International Journal of Mass Spectrometry and Ion Processes</i> , 1993 , 125, 1-8		32
4	Dyanmic ion trapping for Fourier-transform ion cyclotron resonance mass spectrometry: Simultaneous positive- and negative-ion detection. <i>Rapid Communications in Mass Spectrometry</i> , 1992 , 6, 166-172	2.2	34
3	Circularly polarized quadrature excitation for Fourier-transform ion cyclotron resonance mass spectrometry. <i>Chemical Physics Letters</i> , 1992 , 198, 143-148	2.5	13
2	Ion cyclotron resonance signal-detection at multiples of the cyclotron frequency. <i>Rapid Communications in Mass Spectrometry</i> , 1990 , 4, 144-146	2.2	56
1	Dynamics of ion motion in an elongated cylindrical cell of an ICR spectrometer and the shape of the signal registered. <i>International Journal of Mass Spectrometry and Ion Processes</i> , 1985 , 64, 115-125		55