

Mikhail V Gorshkov

List of Publications by Citations

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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	Zeptomole-sensitivity electrospray ionization--Fourier transform ion cyclotron resonance mass spectrometry of proteins. <i>Analytical Chemistry</i> , 2000 , 72, 2271-9	7.8	144
118	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
117	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
116	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
115	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
114	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
113	Liquid chromatography at critical conditions: comprehensive approach to sequence-dependent retention time prediction. <i>Analytical Chemistry</i> , 2006 , 78, 7770-7	7.8	68
112	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
111	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
110	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
109	Observation of ion coalescence in Orbitrap Fourier transform mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2012 , 26, 1711-7	2.2	46
108	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
107	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
106	Sequence scrambling in shotgun proteomics is negligible. <i>Journal of the American Society for Mass Spectrometry</i> , 2011 , 22, 1121-4	3.5	44
105	Empirical multidimensional space for scoring peptide spectrum matches in shotgun proteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 1911-20	5.6	38
104	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
103	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

102	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
101	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
100	Comparative evaluation of label-free quantification methods for shotgun proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2017 , 31, 606-612	2.2	32
99	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
98	Optimal cyclotron radius for high resolution FT-ICR spectrometry. <i>International Journal of Mass Spectrometry and Ion Processes</i> , 1993 , 125, 1-8		32
97	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
96	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
95	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
94	On the utility of isotopic fine structure mass spectrometry in protein identification. <i>Analytical Chemistry</i> , 2012 , 84, 4042-51	7.8	27
93	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
92	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
91	IdentiPy: An Extensible Search Engine for Protein Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 2249-2255	5.6	26
90	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
89	Considerations for electron capture dissociation efficiency in FTICR mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2004 , 234, 131-136	1.9	26
88	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
87	Predictive chromatography of peptides and proteins as a complementary tool for proteomics. <i>Analyst, The</i> , 2016 , 141, 4816-4832	5	24
86	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
85	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

84	Scavenger: A Versatile Postsearch Validation Algorithm for Shotgun Proteomics Based on Gradient Boosting. <i>Proteomics</i> , 2019 , 19, e1800280	4.8	23
83	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
82	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
81	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
80	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
79	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
78	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
77	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
76	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
75	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
74	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
73	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
72	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
71	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
70	Empirical approach to false discovery rate estimation in shotgun proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2010 , 24, 454-62	2.2	13
69	A dual-trap design and its applications in electrospray ionization FTICR mass spectrometry. <i>Analytical Chemistry</i> , 1997 , 69, 1307-14	7.8	13
68	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
67	Resonant excitation of relativistic-ion cyclotron orbital motion. <i>Physical Review A</i> , 1993 , 47, 2730-2737	2.6	13

66	Circularly polarized quadrature excitation for Fourier-transform ion cyclotron resonance mass spectrometry. <i>Chemical Physics Letters</i> , 1992 , 198, 143-148	2.5	13
65	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
64	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
63	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
62	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
61	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
60	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
59	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
58	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
57	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
56	Chemical-Mediated Digestion: An Alternative Realm for Middle-down Proteomics?. <i>Journal of Proteome Research</i> , 2018 , 17, 2005-2016	5.6	8
55	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
54	Pepxmltkã 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
53	Use of models of biomacromolecule separation in AMT database generation for shotgun proteomics. <i>Biochemistry (Moscow)</i> , 2009 , 74, 1195-202	2.9	8
52	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
51	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
50	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
49	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

48	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
47	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
46	Cysteine alkylation methods in shotgun proteomics and their possible effects on methionine residues. <i>Journal of Proteomics</i> , 2021 , 231, 104022	3.9	7
45	FractionOptimizer: a method for optimal peptide fractionation in bottom-up proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2018 , 410, 3827-3833	4.4	6
44	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
43	Adenosine-to-Inosine RNA Editing in Mouse and Human Brain Proteomes. <i>Proteomics</i> , 2019 , 19, e190019	4.8	6
42	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
41	Data Reflection Algorithm for Spectral Enhancement in Fourier Transform ICR and NMR Spectroscopies. <i>Analytical Chemistry</i> , 1995 , 67, 3412-3420	7.8	6
40	Single Cell Proteogenomics - Immediate Prospects. <i>Biochemistry (Moscow)</i> , 2020 , 85, 140-146	2.9	5
39	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
38	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
37	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
36	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
35	Proteogenomics of Adenosine-to-Inosine RNA Editing in the Fruit Fly. <i>Journal of Proteome Research</i> , 2018 , 17, 3889-3903	5.6	5
34	Validation of Peptide Identification Results in Proteomics Using Amino Acid Counting. <i>Proteomics</i> , 2018 , 18, e1800117	4.8	5
33	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
32	Identification of Single Amino Acid Substitutions in Proteogenomics. <i>Biochemistry (Moscow)</i> , 2018 , 83, 250-258	2.9	4
31	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

30	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
29	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
28	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
27	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
26	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
25	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
24	Brain Proteome of <i>Drosophila melanogaster</i> Is Enriched with Nuclear Proteins. <i>Biochemistry (Moscow)</i> , 2019 , 84, 71-78	2.9	2
23	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
22	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
21	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
20	Peptide identification in shotgun proteomics using tandem mass spectrometry: Comparison of search engine algorithms. <i>Journal of Analytical Chemistry</i> , 2015 , 70, 1614-1619	1.1	2
19	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
18	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
17	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
16	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
15	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
14	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
13	Proteomics of Cellular Response to Stress: Taking Control of False Positive Results. <i>Biochemistry (Moscow)</i> , 2021 , 86, 338-349	2.9	1

12	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
11	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
10	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
9	Accelerating photofragmentation UV Spectroscopy-Mass spectrometry fingerprinting for quantification of isomeric peptides. <i>Talanta</i> , 2021 , 232, 122412	6.2	1
8	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
7	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
6	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
5	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</i> , 2017 , 142, 2052-2053	5	
4	Correction: Predictive chromatography of peptides and proteins as a complementary tool for proteomics. <i>Analyst</i> , 2017 , 142, 2054	5	
3	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	
2	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	
1	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	