# Mikhail V Gorshkov

List of Publications by Year
in descending order

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|---|---|---|---|
| 123 papers | 2,917 citations | 172207 29 h-index | 223531 46 g-index |
| 130 all docs | 130 docs citations | 130 times ranked | 2424 citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------| 
| 1 | Zeptomole-Sensitivity Electrospray IonizationˆˋFourier Transform Ion Cyclotron Resonance Mass Spectrometry of Proteins. Analytical Chemistry, 2000, 72, 2271-2279. | 3.2 | 160 |
| 2 | Pyteomicsâ€"a Python Framework for Exploratory Data Analysis and Rapid Software Prototyping in Proteomics. Journal of the American Society for Mass Spectrometry, 2013, 24, 301-304. | 1.2 | 153 |
| 3 | Pyteomics 4.0: Five Years of Development of a Python Proteomics Framework. Journal of Proteome Research, 2019, 18, 709-714. | 1.8 | 116 |
| 4 | Improved low-energy electron injection systems for high rate electron capture dissociation in Fourier transform ion cyclotron resonance mass spectrometry. Rapid Communications in Mass Spectrometry, 2001, 15, 1849-1854. | 0.7 | 112 |
| 5 | C??C Backbone Fragmentation Dominates in Electron Detachment Dissociation of Gas-Phase Polypeptide Polyanions. Chemistry - A European Journal, 2005, 11, 1803-1812. | 1.7 | 112 |
| 6 | Design and Performance of an ESI Interface for Selective External Ion Accumulation Coupled to a Fourier Transform Ion Cyclotron Mass Spectrometer. Analytical Chemistry, 2001, 73, 253-261. | 3.2 | 84 |
| 7 | Initial implementation of an electrodynamic ion funnel with fourier transform ion cyclotron resonance mass spectrometry. Journal of the American Society for Mass Spectrometry, 2000, 11, 19-23. | 1.2 | 74 |
| 8 | Liquid Chromatography at Critical Conditions:Â Comprehensive Approach to Sequence-Dependent Retention Time Prediction. Analytical Chemistry, 2006, 78, 7770-7777. | 3.2 | 73 |
| 9 | Observation of ion coalescence in Orbitrap Fourier transform mass spectrometry. Rapid Communications in Mass Spectrometry, 2012, 26, 1711-1717. | 0.7 | 65 |
| 10 | Dynamics of ion motion in an elongated cylindrical cell of an ICR spectrometer and the shape of the signal registered. International Journal of Mass Spectrometry and Ion Processes, 1985, 64, 115-125. | 1.9 | 62 |
| 11 | Ion cyclotron resonance signal-detection at multiples of the cyclotron frequency. Rapid Communications in Mass Spectrometry, 1990, 4, 144-146. | 0.7 | 62 |
| 12 | Empirical Multidimensional Space for Scoring Peptide Spectrum Matches in Shotgun Proteomics. Journal of Proteome Research, 2014, 13, 1911-1920. | 1.8 | 62 |
| 13 | Unbiased False Discovery Rate Estimation for Shotgun Proteomics Based on the Target-Decoy Approach. Journal of Proteome Research, 2017, 16, 393-397. | 1.8 | 56 |
| 14 | IdentiPy: An Extensible Search Engine for Protein Identification in Shotgun Proteomics. Journal of Proteome Research, 2018, 17, 2249-2255. | 1.8 | 52 |
| 15 | Protein corona formed on silver nanoparticles in blood plasma is highly selective and resistant to physicochemical changes of the solution. Environmental Science: Nano, 2019, 6, 1089-1098. | 2.2 | 52 |
| 16 | Scavager: A Versatile Postsearch Validation Algorithm for Shotgun Proteomics Based on Gradient Boosting. Proteomics, 2019, 19, e1800280. | 1.3 | 51 |
| 17 | Sequence Scrambling in Shotgun Proteomics is Negligible. Journal of the American Society for Mass Spectrometry, 2011, 22, 1121-1124. | 1.2 | 48 |
| 18 | Analysis and elimination of systematic errors originating from coulomb mutual interaction and image charge in Fourier transform ion cyclotron resonance precise mass difference measurements. Journal of the American Society for Mass Spectrometry, 1993, 4, 855-868. | 1.2 | 47 |

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| 19 | Electrospray ionization—Fourier transform ion cyclotron resonance mass spectrometry at 11.5 tesla: Instrument design and initial results. Journal of the American Society for Mass Spectrometry, 1998, 9, 692-700. | 1.2 | 46 |
| 20 | Proteome Digestion Specificity Analysis for Rational Design of Extended Bottom-up and Middle-down Proteomics Experiments. Journal of Proteome Research, 2013, 12, 5558-5569. | 1.8 | 43 |
| 21 | High-Resolution Fourier Transform Ion Cyclotron Resonance Mass Spectrometry with Increased Throughput for Biomolecular Analysis. Analytical Chemistry, 2014, 86, 9020-9028. | 3.2 | 43 |
| 22 | Comparative evaluation of label–free quantification methods for shotgun proteomics. Rapid Communications in Mass Spectrometry, 2017, 31, 606-612. | 0.7 | 41 |
| 23 | Dyanmic ion trapping for Fourier-transform ion cyclotron resonance mass spectrometry: Simultaneous positive- and negative-ion detection. Rapid Communications in Mass Spectrometry, 1992, 6, 166-172. | 0.7 | 38 |
| 24 | Multiplexed Middle-Down Mass Spectrometry as a Method for Revealing Light and Heavy Chain Connectivity in a Monoclonal Antibody. Analytical Chemistry, 2018, 90, 12527-12535. | 3.2 | 38 |
| 25 | Calibration function for the orbitrap FTMS accounting for the space charge effect. Journal of the American Society for Mass Spectrometry, 2010, 21, 1846-1851. | 1.2 | 36 |
| 26 | Positive and negative analyte ion yield in matrix-assisted laser desorption/ionization. International Journal of Mass Spectrometry, 2007, 268, 122-130. | 0.7 | 35 |
| 27 | Letter: Characteristics of Photoelectrons Emitted in Matrix-Assisted Laser Desorption/Ionization Fourier Transform Ion Cyclotron Resonance Experiments. European Journal of Mass Spectrometry, 2002, 8, 67-69. | 0.5 | 33 |
| 28 | Predictive chromatography of peptides and proteins as a complementary tool for proteomics. Analyst, The, 2016, 141, 4816-4832. | 1.7 | 33 |
| 29 | Optimal cyclotron radius for high resolution FT-ICR spectrometry. International Journal of Mass Spectrometry and Ion Processes, 1993, 125, 1-8. | 1.9 | 32 |
| 30 | On the Utility of Isotopic Fine Structure Mass Spectrometry in Protein Identification. Analytical Chemistry, 2012, 84, 4042-4051. | 3.2 | 31 |
| 31 | DirectMS1: MS/MS-Free Identification of 1000 Proteins of Cellular Proteomes in 5 Minutes. Analytical Chemistry, 2020, 92, 4326-4333. | 3.2 | 31 |
| 32 | Exome-Driven Characterization of the Cancer Cell Lines at the Proteome Level: The NCI-60 Case Study. Journal of Proteome Research, 2014, 13, 5551-5560. | 1.8 | 30 |
| 33 | Enhancing the Cytotoxic Activity of Anticancer Pt<sup>IV</sup> Complexes by Introduction of Lonidamine as an Axial Ligand. European Journal of Inorganic Chemistry, 2017, 2017, 1785-1791. | 1.0 | 29 |
| 34 | Controlled ion fragmentation in a 2-D quadrupole ion trap for external ion accumulation in ESI FTICR mass spectrometry. Journal of the American Society for Mass Spectrometry, 2001, 12, 1312-1319. | 1.2 | 28 |
| 35 | Considerations for electron capture dissociation efficiency in FTICR mass spectrometry. International Journal of Mass Spectrometry, 2004, 234, 131-136. | 0.7 | 28 |
| 36 | Exome-based proteogenomics of HEK-293 human cell line: Coding genomic variants identified at the level of shotgun proteome. Proteomics, 2016, 16, 1980-1991. | 1.3 | 28 |

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| 37 | Masses of stable neon isotopes determined at parts per billion precision by Fourier transform ion cyclotron resonance mass spectrometry. International Journal of Mass Spectrometry and Ion Processes, 1993, 128, 47-60. | 1.9 | 27 |
| 38 | A novel high-performance Fourier transform ion cyclotron resonance cell for improved biopolymer characterization. , 2000, 35, 85-94. | | 27 |
| 39 | Retention time prediction using the model of liquid chromatography of biomacromolecules at critical conditions in LC–MS phosphopeptide analysis. Proteomics, 2010, 10, 3458-3468. | 1.3 | 27 |
| 40 | Methionine to isothreonine conversion as a source of false discovery identifications of genetically encoded variants in proteogenomics. Journal of Proteomics, 2015, 120, 169-178. | 1.2 | 24 |
| 41 | Applicability of the critical chromatography concept to proteomics problems: Dependence of retention time on the sequence of amino acids. Polymer Science - Series B, 2007, 49, 93-107. | 0.3 | 23 |
| 42 | High Speed Intact Protein Characterization Using 4X Frequency Multiplication, Ion Trap Harmonization, and 21 Tesla FTICR-MS. Analytical Chemistry, 2018, 90, 5557-5562. | 3.2 | 23 |
| 43 | Standardization of retention time data for AMT tag proteomics database generation. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 433-440. | 1.2 | 22 |
| 44 | Advanced Precursor Ion Selection Algorithms for Increased Depth of Bottom-Up Proteomic Profiling. Journal of Proteome Research, 2016, 15, 3563-3573. | 1.8 | 20 |
| 45 | Biosaur: An open–source Python software for liquid chromatography–mass spectrometry peptide feature detection with ion mobility support. Rapid Communications in Mass Spectrometry, 2021, , e9045. | 0.7 | 19 |
| 46 | 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. Polymer Science - Series A, 2008, 50, 309-321. | 0.4 | 18 |
| 47 | Towards data acquisition throughput increase in Fourier transform mass spectrometry of proteins using double frequency measurements. International Journal of Mass Spectrometry, 2011, 306, 227-231. | 0.7 | 18 |
| 48 | Boosting MS1-only Proteomics with Machine Learning Allows 2000 Protein Identifications in Single-Shot Human Proteome Analysis Using 5 min HPLC Gradient. Journal of Proteome Research, 2021, 20, 1864-1873. | 1.8 | 18 |
| 49 | MS/MS-Free Protein Identification in Complex Mixtures Using Multiple Enzymes with Complementary Specificity. Journal of Proteome Research, 2017, 16, 3989-3999. | 1.8 | 17 |
| 50 | Proteogenomics of Malignant Melanoma Cell Lines: The Effect of Stringency of Exome Data Filtering on Variant Peptide Identification in Shotgun Proteomics. Journal of Proteome Research, 2018, 17, 1801-1811. | 1.8 | 17 |
| 51 | Adenosine–to–Inosine RNA Editing in Mouse and Human Brain Proteomes. Proteomics, 2019, 19, 1900195. | 1.3 | 17 |
| 52 | Atmospheric pressure ionization permanent magnet fourier transform ion cyclotron resonance mass spectrometry. Journal of the American Society for Mass Spectrometry, 2007, 18, 1552-1558. | 1.2 | 16 |
| 53 | Proteogenomics of Adenosine-to-Inosine RNA Editing in the Fruit Fly. Journal of Proteome Research, 2018, 17, 3889-3903. | 1.8 | 16 |
| 54 | Cysteine alkylation methods in shotgun proteomics and their possible effects on methionine residues. Journal of Proteomics, 2021, 231, 104022. | 1.2 | 16 |

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| 55 | Multi-Omics Analysis of Glioblastoma Cells' Sensitivity to Oncolytic Viruses. Cancers, 2021, 13, 5268. | 1.7 | 16 |
| 56 | Empirical approach to false discovery rate estimation in shotgun proteomics. Rapid Communications in Mass Spectrometry, 2010, 24, 454-462. | 0.7 | 15 |
| 57 | Probing the mechanisms of ambient ionization by laser-induced fluorescence spectroscopy. Rapid Communications in Mass Spectrometry, 2012, 26, 1567-1572. | 0.7 | 15 |
| 58 | Combination of Edman degradation of peptides with liquid chromatography/mass spectrometry workflow for peptide identification in bottom-up proteomics. Rapid Communications in Mass Spectrometry, 2013, 27, 391-400. | 0.7 | 15 |
| 59 | Circularly polarized quadrature excitation for Fourier-transform ion cyclotron resonance mass spectrometry. Chemical Physics Letters, 1992, 198, 143-148. | 1.2 | 14 |
| 60 | A dynamic ion cooling technique for FTICR mass spectrometry. Journal of the American Society for Mass Spectrometry, 2001, 12, 1169-1173. | 1.2 | 14 |
| 61 | Ion Coalescence in Fourier Transform Mass Spectrometry: Should We Worry about This in Shotgun Proteomics?. European Journal of Mass Spectrometry, 2015, 21, 459-470. | 0.5 | 14 |
| 62 | Resonant excitation of relativistic-ion cyclotron orbital motion. Physical Review A, 1993, 47, 2730-2737. | 1.0 | 13 |
| 63 | A Dual-Trap Design and Its Applications in Electrospray Ionization FTICR Mass Spectrometry. Analytical Chemistry, 1997, 69, 1307-1314. | 3.2 | 13 |
| 64 | Optimal pressure conditions for unbiased external ion accumulation in a two-dimensional radio-frequency quadrupole for Fourier transform ion cyclotron resonance mass spectrometry. Rapid Communications in Mass Spectrometry, 2001, 15, 1988-1996. | 0.7 | 13 |
| 65 | Sequence-specific predictive chromatography to assist mass spectrometric analysis of asparagine deamidation and aspartate isomerization in peptides. Electrophoresis, 2011, 32, 1962-1969. | 1.3 | 13 |
| 66 | Depletion of human serum albumin in embryo culture media for in vitro fertilization using monolithic columns with immobilized antibodies. Electrophoresis, 2016, 37, 2322-2327. | 1.3 | 13 |
| 67 | Comparison of False Discovery Rate Control Strategies for Variant Peptide Identifications in Shotgun Proteogenomics. Journal of Proteome Research, 2017, 16, 1936-1943. | 1.8 | 13 |
| 68 | On the accuracy of polypeptide masses measured in a linear ion trap. Rapid Communications in Mass Spectrometry, 2005, 19, 3755-3758. | 0.7 | 12 |
| 69 | Chemical-Mediated Digestion: An Alternative Realm for Middle-down Proteomics?. Journal of Proteome Research, 2018, 17, 2005-2016. | 1.8 | 12 |
| 70 | Comparative proteomics as a tool for identifying specific alterations within interferon response pathways in human glioblastoma multiforme cells. Oncotarget, 2018, 9, 1785-1802. | 0.8 | 12 |
| 71 | Deuterium atomic mass from Fourier-transform–ion-cyclotron-resonance measurement of the mass difference between $H_21O^+$ and $HO^+2$. Physical Review A, 1993, 47, 3433-3436. | 1.0 | 11 |
| 72 | Rpn4 and proteasome-mediated yeast resistance to ethanol includes regulation of autophagy. Applied Microbiology and Biotechnology, 2020, 104, 4027-4041. | 1.7 | 11 |

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| 73 | Dynamically assisted gated trapping for Fourier transform ion cyclotron mass spectrometry. Rapid Communications in Mass Spectrometry, 2001, 15, 1558-1561. | 0.7 | 10 |
| 74 | Inversion of chromatographic elution orders of peptides and its importance for proteomics. Journal of Analytical Chemistry, 2012, 67, 1014-1025. | 0.4 | 10 |
| 75 | Identification of Single Amino Acid Substitutions in Proteogenomics. Biochemistry (Moscow), 2018, 83, 250-258. | 0.7 | 10 |
| 76 | Profiling modifications for glioblastoma proteome using ultra-tolerant database search: Are the peptide mass shifts biologically relevant or chemically induced?. Journal of Proteomics, 2019, 191, 16-21. | 1.2 | 10 |
| 77 | Validation of Peptide Identification Results in Proteomics Using Amino Acid Counting. Proteomics, 2018, 18, e1800117. | 1.3 | 9 |
| 78 | A high performance low magnetic field internal electrospray ionization-fourier transform ion cyclotron resonance mass spectrometer. Journal of the American Society for Mass Spectrometry, 1996, 7, 915-922. | 1.2 | 8 |
| 79 | Pressure limited sustained off-resonance irradiation for collision-activated dissociation in Fourier transform mass spectrometry. Journal of the American Society for Mass Spectrometry, 1999, 10, 15-18. | 1.2 | 8 |
| 80 | Use of models of biomacromolecule separation in AMT database generation for shotgun proteomics. Biochemistry (Moscow), 2009, 74, 1195-1202. | 0.7 | 8 |
| 81 | Application of Statistical Thermodynamics To Predict the Adsorption Properties of Polypeptides in Reversed-Phase HPLC. Analytical Chemistry, 2015, 87, 6562-6569. | 3.2 | 8 |
| 82 | Pepxmltkâ€"a format converter for peptide identification results obtained from tandem mass spectrometry data using X!Tandem search engine. Journal of Analytical Chemistry, 2015, 70, 1598-1599. | 0.4 | 8 |
| 83 | FractionOptimizer: a method for optimal peptide fractionation in bottom-up proteomics. Analytical and Bioanalytical Chemistry, 2018, 410, 3827-3833. | 1.9 | 8 |
| 84 | Identification of isoforms of aspartic acid residues in peptides by 2D UV-MS fingerprinting of cold ions. Analyst, The, 2018, 143, 833-836. | 1.7 | 8 |
| 85 | Data Reflection Algorithm for Spectral Enhancement in Fourier Transform ICR and NMR Spectroscopies. Analytical Chemistry, 1995, 67, 3412-3420. | 3.2 | 7 |
| 86 | Adaptation of Decoy Fusion Strategy for Existing Multi-Stage Search Workflows. Journal of the American Society for Mass Spectrometry, 2016, 27, 1579-1582. | 1.2 | 7 |
| 87 | Brute-Force Approach for Mass Spectrometry-Based Variant Peptide Identification in Proteogenomics without Personalized Genomic Data. Journal of the American Society for Mass Spectrometry, 2018, 29, 435-438. | 1.2 | 7 |
| 88 | PhosphoShield: Improving Trypsin Digestion of Phosphoproteins by Shielding the Negatively Charged Phosphate Moiety. Journal of the American Society for Mass Spectrometry, 2020, 31, 2053-2060. | 1.2 | 7 |
| 89 | New Insectotoxin from Tibellus Oblongus Spider Venom Presents Novel Adaptation of ICK Fold. Toxins, 2021, 13, 29. | 1.5 | 7 |
| 90 | High Performance Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry at Low Magnetic Field. European Journal of Mass Spectrometry, 2002, 8, 169-176. | 0.5 | 6 |

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| 91 | Critical chromatography of macromolecules as a tool for reading the amino acid sequence of biomacromolecules: Reality or science fiction?. Journal of Analytical Chemistry, 2010, 65, 2-11. | 0.4 | 6 |
| 92 | On the utility of predictive chromatography to complement mass spectrometry based intact protein identification. Analytical and Bioanalytical Chemistry, 2012, 402, 2521-2529. | 1.9 | 6 |
| 93 | Proteome-Wide Analysis of ADAR-Mediated Messenger RNA Editing during Fruit Fly Ontogeny. Journal of Proteome Research, 2020, 19, 4046-4060. | 1.8 | 6 |
| 94 | Single Cell Proteogenomics â€" Immediate Prospects. Biochemistry (Moscow), 2020, 85, 140-146. | 0.7 | 6 |
| 95 | Validating Amino Acid Variants in Proteogenomics Using Sequence Coverage by Multiple Reads. Journal of Proteome Research, 2022, 21, 1438-1448. | 1.8 | 6 |
| 96 | Influence of the Number of Axial Bexarotene Ligands on the Cytotoxicity of Pt(IV) Analogs of Oxaliplatin. Bioinorganic Chemistry and Applications, 2017, 2017, 1-6. | 1.8 | 5 |
| 97 | Semi-supervised quality control method for proteome analyses based on tandem mass spectrometry. International Journal of Mass Spectrometry, 2018, 427, 59-64. | 0.7 | 5 |
| 98 | Method for Identification of Threonine Isoforms in Peptides by Ultraviolet Photofragmentation of Cold Ions. Analytical Chemistry, 2019, 91, 6709-6715. | 3.2 | 5 |
| 99 | Applicability of the critical-chromatography concept to analysis of proteins: Dependence of retention times on the sequence of amino acid residues in a chain. Polymer Science - Series A, 2011, 53, 1227-1241. | 0.4 | 4 |
| 100 | Limitation of predictive 2â€‹<scp>D</scp> liquid chromatography in reducing the database search space in shotgun proteomics: <i>In silico</i> studies. Journal of Separation Science, 2012, 35, 1771-1778. | 1.3 | 4 |
| 101 | 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. Journal of Analytical Chemistry, 2016, 71, 110-125. | 0.4 | 4 |
| 102 | viQC: Visual and Intuitive Quality Control for Mass Spectrometry-Based Proteome Analysis. Journal of Analytical Chemistry, 2019, 74, 1363-1370. | 0.4 | 4 |
| 103 | Identification-Free Control over the Precursor Isotopic Mass Misassignment in Orbitrap-Based Proteomics. Journal of the American Society for Mass Spectrometry, 2021, 32, 218-224. | 1.2 | 4 |
| 104 | Proteomics of Cellular Response to Stress: Taking Control of False Positive Results. Biochemistry (Moscow), 2021, 86, 338-349. | 0.7 | 4 |
| 105 | Accelerating photofragmentation UV Spectroscopyâ€"Mass spectrometry fingerprinting for quantification of isomeric peptides. Talanta, 2021, 232, 122412. | 2.9 | 4 |
| 106 | <b>Threonine versus isothreonine in synthetic peptides analyzed by highâ€resolution liquid chromatography/tandem mass spectrometry</b>. Rapid Communications in Mass Spectrometry, 2016, 30, 1323-1331. | 0.7 | 3 |
| 107 | Predictive Liquid Chromatography of Peptides Based on Hydrophilic Interactions for Mass Spectrometry-Based Proteomics. Journal of Analytical Chemistry, 2017, 72, 1375-1382. | 0.4 | 3 |
| 108 | Brain Proteome of Drosophila melanogaster Is Enriched with Nuclear Proteins. Biochemistry (Moscow), 2019, 84, 71-78. | 0.7 | 3 |

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| 109 | 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. Proteomes, 2020, 8, 12. | 1.7 | 3 |
| 110 | AA_stat: Intelligent profiling of in vivo and in vitro modifications from open search results. Journal of Proteomics, 2021, 248, 104350. | 1.2 | 3 |
| 111 | Towards increasing the performance of FTICR-MS with signal detection at frequency multiples: Signal theory and numerical study. International Journal of Mass Spectrometry, 2021, 469, 116669. | 0.7 | 3 |
| 112 | Multiomic Profiling Identified EGF Receptor Signaling as a Potential Inhibitor of Type I Interferon Response in Models of Oncolytic Therapy by Vesicular Stomatitis Virus. International Journal of Molecular Sciences, 2022, 23, 5244. | 1.8 | 3 |
| 113 | An atmospheric pressure ionization source based on desorption electrospray ionization technology (DESI) for ion cyclotron resonance mass spectrometry. Journal of Analytical Chemistry, 2011, 66, 1376-1384. | 0.4 | 2 |
| 114 | Peptide identification in â€œshotgunâ€•proteomics using tandem mass spectrometry: Comparison of search engine algorithms. Journal of Analytical Chemistry, 2015, 70, 1614-1619. | 0.4 | 2 |
| 115 | Possible applications of an external resonant circuit in Fourier transform ion cyclotron resonance. Rapid Communications in Mass Spectrometry, 1995, 9, 317-321. | 0.7 | 1 |
| 116 | Alternative methods for verifying the results of the mass spectrometric identification of peptides in shotgun proteomics. Journal of Analytical Chemistry, 2010, 65, 1462-1468. | 0.4 | 1 |
| 117 | GroupFilter: A software tool for efficient filtering of Morpheus search engine results. Journal of Analytical Chemistry, 2016, 71, 1275-1279. | 0.4 | 1 |
| 118 | Applicability of the critical-chromatography concept to proteomics problems: Separation of peptides modeled by a heterogeneous rod. Polymer Science - Series A, 2017, 59, 451-464. | 0.4 | 1 |
| 119 | Critical chromatography and mass spectrometry of macromolecules: Determination of the position of a functional group in a chain. Polymer Science - Series A, 2010, 52, 340-347. | 0.4 | 0 |
| 120 | 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. Journal of Analytical Chemistry, 2016, 71, 1188-1197. | 0.4 | 0 |
| 121 | Reply to â€˜Comparison of peptide retention prediction algorithm in reversed-phase chromatography. Comment on â€œPredictive chromatography of peptides and proteins as a complementary tool for proteomicsâ€â€™, by O. V. Krokhin, Analyst, 2017, 142, DOI: 10.1039/c6an02510b. Analyst, The, 2017, 142, 2052-2053. | 1.7 | 0 |
| 122 | Correction: Predictive chromatography of peptides and proteins as a complementary tool for proteomics. Analyst, The, 2017, 142, 2054-2054. | 1.7 | 0 |
| 123 | Improving the Protein Inference from Bottom-Up Proteomic Data Using Identifications from MS1 Spectra. Journal of the American Society for Mass Spectrometry, 2021, 32, 1258-1262. | 1.2 | 0 |