

Yury O Tsybin

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.

121
papers

3,722
citations

35
h-index

54
g-index

127
ext. papers

4,222
ext. citations

5.2
avg, IF

5.33
L-index

#	Paper	IF	Citations
121	The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021 , 7, eabk0734	14.3	19
120	Metabolic profiling of Peperoni di Senise PGI bell peppers with ultra-high resolution absorption mode Fourier transform ion cyclotron resonance mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2021 , 470, 116722	1.9	1
119	Improved Uranium Isotope Ratio Analysis in Liquid Sampling-Atmospheric Pressure Glow Discharge/Orbitrap FTMS Coupling through the Use of an External Data Acquisition System. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1224-1236	3.5	9
118	Untargeted analysis of pure snail slime and snail slime-induced Au nanoparticles metabolome with MALDI FT-ICR MS. <i>Journal of Mass Spectrometry</i> , 2021 , 56, e4722	2.2	3
117	Vacuum Laser Photoionization inside the C-trap of an Orbitrap Mass Spectrometer: Resonance-Enhanced Multiphoton Ionization High-Resolution Mass Spectrometry. <i>Analytical Chemistry</i> , 2021 , 93, 9418-9427	7.8	2
116	Fast Afucosylation Profiling of Glycoengineered Antibody Subunits by Middle-Up Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021 , 2271, 73-83	1.4	1
115	Spatially-distributed cyclotron oscillators approach to FT-ICR MS at the true cyclotron frequency: Computational evaluation of sensitivity. <i>International Journal of Mass Spectrometry</i> , 2021 , 466, 116604	1.9	0
114	Drug-to-Antibody Ratio Estimation via Proteoform Peak Integration in the Analysis of Antibody-Oligonucleotide Conjugates with Orbitrap Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2021 , 93, 12930-12937	7.8	2
113	Trace-Level Persistent Organic Pollutant Analysis with Gas-Chromatography Orbitrap Mass Spectrometry-Enhanced Performance by Complementary Acquisition and Processing of Time-Domain Data. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 257-266	3.5	10
112	Monitoring glycation levels of a bispecific monoclonal antibody at subunit level by ultrahigh-resolution MALDI FT-ICR mass spectrometry. <i>MAbs</i> , 2020 , 12, 1682403	6.6	20
111	Imaging of Triglycerides in Tissues Using Nanospray Desorption Electrospray Ionization (Nano-DESI) Mass Spectrometry. <i>International Journal of Mass Spectrometry</i> , 2020 , 448,	1.9	16
110	Narrow Aperture Detection Electrodes ICR Cell with Quadrupolar Ion Detection for FT-ICR MS at the Cyclotron Frequency. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 2258-2269	3.5	2
109	Transient-Mediated Simulations of FTMS Isotopic Distributions and Mass Spectra to Guide Experiment Design and Data Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1927-1942	3.5	7
108	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1783-1802	3.5	32
107	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019 , 16, 939-940	21.6	25
106	Advanced fundamentals in Fourier transform mass spectrometry 2019 , 113-132		8
105	Increased throughput and ultra-high mass resolution in DESI FT-ICR MS imaging through new-generation external data acquisition system and advanced data processing approaches. <i>Scientific Reports</i> , 2019 , 9, 8	4.9	37

104	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019 , 16, 587-594	21.6	137
103	Top or Middle? Up or Down? Toward a Standard Lexicon for Protein Top-Down and Allied Mass Spectrometry Approaches. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 1149-1157	3.5	59
102	Detection of Proteoforms Using Top-Down Mass Spectrometry and Diagnostic Ions. <i>Methods in Molecular Biology</i> , 2019 , 1959, 173-183	1.4	4
101	The Russian Mass Spectrometry Interest Group at ASMS: Over 20 Years of Science and Water Polo. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 2178-2182	3.5	
100	Clinical method evaluation of hemoglobin S and C identification by top-down selected reaction monitoring and electron transfer dissociation. <i>Clinical Proteomics</i> , 2019 , 16, 41	5	1
99	Structural Analysis of Monoclonal Antibodies by Ultrahigh Resolution MALDI In-Source Decay FT-ICR Mass Spectrometry. <i>Analytical Chemistry</i> , 2019 , 91, 2079-2085	7.8	28
98	<i>Drosophila melanogaster</i> cloak their eggs with pheromones, which prevents cannibalism. <i>PLoS Biology</i> , 2019 , 17, e2006012	9.7	9
97	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018 , 17, 1321-1325	5.6	27
96	Chemical-Mediated Digestion: An Alternative Realm for Middle-down Proteomics?. <i>Journal of Proteome Research</i> , 2018 , 17, 2005-2016	5.6	8
95	Multiparticle Simulations of Quadrupolar Ion Detection in an Ion Cyclotron Resonance Cell with Four Narrow Aperture Detection Electrodes. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 51-62	3.5	6
94	Cyclotron Phase-Coherent Ion Spatial Dispersion in a Non-Quadratic Trapping Potential is Responsible for FT-ICR MS at the Cyclotron Frequency. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 63-77	3.5	4
93	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
92	Fourier Transform Ion Cyclotron Resonance Mass Spectrometry at the Cyclotron Frequency. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 768-780	3.5	12
91	Top-down analysis of immunoglobulin G isotypes 1 and 2 with electron transfer dissociation on a high-field Orbitrap mass spectrometer. <i>Journal of Proteomics</i> , 2017 , 159, 67-76	3.9	36
90	Intensity-Independent Noise Filtering in FT MS and FT MS/MS Spectra for Shotgun Lipidomics. <i>Analytical Chemistry</i> , 2017 , 89, 7046-7052	7.8	34
89	Monitoring Membrane Lipidome Turnover by Metabolic N Labeling and Shotgun Ultra-High-Resolution Orbitrap Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 12857-12865	7.8	28
88	On-Chip Mesoporous Functionalized Magnetic Microspheres for Protein Sequencing by Extended Bottom-up Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 1775-84	7.8	14
87	Identification of hemoglobin variants by top-down mass spectrometry using selected diagnostic product ions. <i>Analytical and Bioanalytical Chemistry</i> , 2015 , 407, 2837-45	4.4	11

86	Ion trap with narrow aperture detection electrodes for Fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 741-51	3.5	18
85	Gold finger formation studied by high-resolution mass spectrometry and in silico methods. <i>Chemical Communications</i> , 2015 , 51, 1612-5	5.8	37
84	A Functional Group Approach for Prediction of APPI Response of Organic Synthetic Targets. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 1221-32	3.5	4
83	On the use of electron capture rate constants to describe electron capture dissociation mass spectrometry of peptides. <i>European Journal of Mass Spectrometry</i> , 2015 , 21, 451-8	1.1	2
82	Producing absorption mode Fourier transform ion cyclotron resonance mass spectra with non-quadratic phase correction functions. <i>Rapid Communications in Mass Spectrometry</i> , 2015 , 29, 1087-93	3.2	17
81	Time-dependent frequency of ion motion in Fourier transform mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015 , 376, 75-84	1.9	3
80	Distinguishing analyte from noise components in mass spectra of complex samples: where to cut the noise?. <i>Analytical Chemistry</i> , 2014 , 86, 3308-16	7.8	33
79	On the viability of heterolytic peptide N-C(=O) bond cleavage in electron capture and transfer dissociation mass spectrometry. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 2985-92	3.4	8
78	Ping-pong protons: how hydrogen-bonding networks facilitate heterolytic bond cleavage in peptide radical cations. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 2628-37	3.4	6
77	Advantages of extended bottom-up proteomics using Sap9 for analysis of monoclonal antibodies. <i>Analytical Chemistry</i> , 2014 , 86, 9945-53	7.8	44
76	Empirical multidimensional space for scoring peptide spectrum matches in shotgun proteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 1911-20	5.6	38
75	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
74	Least-squares fitting of time-domain signals for Fourier transform mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2014 , 25, 1263-73	3.5	15
73	Middle-down analysis of monoclonal antibodies with electron transfer dissociation orbitrap Fourier transform mass spectrometry. <i>Analytical Chemistry</i> , 2014 , 86, 3005-12	7.8	129
72	Extended bottom-up proteomics with secreted aspartic protease Sap9. <i>Journal of Proteomics</i> , 2014 , 110, 20-31	3.9	21
71	Structural Analysis of Complex Molecular Systems by High-Resolution and Tandem Mass Spectrometry 2014 , 63-90		1
70	From high- to super-resolution mass spectrometry. <i>Chimia</i> , 2014 , 68, 168-74	1.3	13
69	Self-assembly of a giant molecular Solomon link from 30 subcomponents. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 11261-5	16.4	74

68	Self-Assembly of a Giant Molecular Solomon Link from 30 Subcomponents. <i>Angewandte Chemie</i> , 2014 , 126, 11443-11447	3.6	29
67	Top-down analysis of 30-80 kDa proteins by electron transfer dissociation time-of-flight mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2013 , 405, 8505-14	4.4	31
66	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
65	Hexagonal class representation for fingerprinting and facile comparison of petroleomic samples. <i>Analytical Chemistry</i> , 2013 , 85, 5311-5	7.8	8
64	Principles of electron capture and transfer dissociation mass spectrometry applied to peptide and protein structure analysis. <i>Chemical Society Reviews</i> , 2013 , 42, 5014-30	58.5	146
63	Iterative method for mass spectra recalibration via empirical estimation of the mass calibration function for Fourier transform mass spectrometry-based petroleomics. <i>Analytical Chemistry</i> , 2013 , 85, 6437-45	7.8	34
62	Evaluation of High-Field Orbitrap Fourier Transform Mass Spectrometer for Petroleomics. <i>Energy & Fuels</i> , 2013 , 27, 2974-2983	4.1	69
61	Practical considerations for improving the productivity of mass spectrometry-based proteomics. <i>Chimia</i> , 2013 , 67, 244-9	1.3	9
60	Glycan variability on a recombinant IgG antibody transiently produced in HEK-293E cells. <i>New Biotechnology</i> , 2012 , 29, 471-6	6.4	26
59	Statistical analysis of ion mobility spectrometry. I. Unbiased and guided replica-exchange molecular dynamics. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 386-96	3.5	17
58	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
57	Fragmentation methods on the balance: unambiguous top-down mass spectrometric characterization of oxaliplatin-ubiquitin binding sites. <i>Analytical and Bioanalytical Chemistry</i> , 2012 , 402, 2655-62	4.4	38
56	Analysis of intact monoclonal antibody IgG1 by electron transfer dissociation Orbitrap FTMS. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1758-67	7.6	124
55	Sidebands in Fourier transform ion cyclotron resonance mass spectra. <i>International Journal of Mass Spectrometry</i> , 2012 , 325-327, 10-18	1.9	16
54	In-spray supercharging of peptides and proteins in electrospray ionization mass spectrometry. <i>Analytical Chemistry</i> , 2012 , 84, 4647-51	7.8	67
53	Heterolytic N-C bond cleavage in electron capture and transfer dissociation of peptide cations. <i>Journal of Physical Chemistry B</i> , 2012 , 116, 10807-15	3.4	19
52	Electron transfer dissociation mass spectrometry of hemoglobin on clinical samples. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 1750-6	3.5	22
51	Filter diagonalization method-based mass spectrometry for molecular and macromolecular structure analysis. <i>Analytical Chemistry</i> , 2012 , 84, 2850-6	7.8	33

50	On the utility of isotopic fine structure mass spectrometry in protein identification. <i>Analytical Chemistry</i> , 2012 , 84, 4042-51	7.8	27
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	Maleimide-functionalised organoruthenium anticancer agents and their binding to thiol-containing biomolecules. <i>Chemical Communications</i> , 2012 , 48, 1475-7	5.8	82
47	UV radiation induces genome-mediated, site-specific cleavage in viral proteins. <i>ChemBioChem</i> , 2012 , 13, 837-45	3.8	25
46	Statistical analysis of ion mobility spectrometry. II. Adaptively biased methods and shape correlations. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 1279-88	3.5	18
45	Coronene Fusion by Heat Treatment: Road to Nanographenes. <i>Journal of Physical Chemistry C</i> , 2011 , 115, 13207-13214	3.8	45
44	Metal-based inhibition of poly(ADP-ribose) polymerase--the guardian angel of DNA. <i>Journal of Medicinal Chemistry</i> , 2011 , 54, 2196-206	8.3	124
43	Reaction of C60 with Hydrogen Gas: In Situ Monitoring and Pathways. <i>Journal of Physical Chemistry C</i> , 2011 , 115, 11484-11492	3.8	26
42	High-resolution and tandem mass spectrometry--the indispensable tools of the XXI century. <i>Chimia</i> , 2011 , 65, 641-5	1.3	4
41	Repeatability and reproducibility of product ion abundances in electron capture dissociation mass spectrometry of peptides. <i>European Journal of Mass Spectrometry</i> , 2011 , 17, 321-31	1.1	12
40	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
39	Deamidation and transamidation of substance P by tissue transglutaminase revealed by electron-capture dissociation fourier transform mass spectrometry. <i>Chemistry - A European Journal</i> , 2011 , 17, 486-97	4.8	11
38	Structural preferences of gas-phase M2TMP monomers upon sequence variations. <i>Journal of Physical Chemistry A</i> , 2011 , 115, 4711-8	2.8	8
37	Structural analysis of intact monoclonal antibodies by electron transfer dissociation mass spectrometry. <i>Analytical Chemistry</i> , 2011 , 83, 8919-27	7.8	111
36	Tissue transglutaminase-mediated glutamine deamidation of beta-amyloid peptide increases peptide solubility, whereas enzymatic cross-linking and peptide fragmentation may serve as molecular triggers for rapid peptide aggregation. <i>Journal of Biological Chemistry</i> , 2011 , 286, 12172-88	5.4	27
35	Conformation of polyalanine and polyglycine dications in the gas phase: insight from ion mobility spectrometry and replica-exchange molecular dynamics. <i>Journal of Physical Chemistry A</i> , 2010 , 114, 6888-96	2.8	42
34	Ruthenium versus platinum: interactions of anticancer metallodrugs with duplex oligonucleotides characterised by electrospray ionisation mass spectrometry. <i>Journal of Biological Inorganic Chemistry</i> , 2010 , 15, 677-88	3.7	75
33	Radical stability directs electron capture and transfer dissociation of amino acids in peptides. <i>Chemistry - A European Journal</i> , 2010 , 16, 4612-22	4.8	15

32	Comparative dissociation of peptide polyanions by electron impact and photo-induced electron detachment. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 670-80	3.5	29
31	Electron capture and transfer dissociation: Peptide structure analysis at different ion internal energy levels. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 567-75	3.5	39
30	Periodic sequence distribution of product ion abundances in electron capture dissociation of amphipathic peptides and proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 1182-92	3.5	41
29	Electron capture dissociation product ion abundances at the X amino acid in RAAAA-X-AAAK peptides correlate with amino acid polarity and radical stability. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 2273-83	3.5	16
28	Thermal Decomposition of C60H18. <i>Journal of Physical Chemistry C</i> , 2009 , 113, 13133-13138	3.8	13
27	Characterization of platinum anticancer drug protein-binding sites using a top-down mass spectrometric approach. <i>Inorganic Chemistry</i> , 2008 , 47, 17-9	5.1	87
26	High resolution mass spectrometry for studying the interactions of cisplatin with oligonucleotides. <i>Inorganic Chemistry</i> , 2008 , 47, 10626-33	5.1	55
25	Amide-I relaxation-induced hydrogen bond distortion: An intermediate in electron capture dissociation mass spectrometry of alpha-helical peptides?. <i>Journal of Chemical Physics</i> , 2008 , 129, 095106	3.9	31
24	Synthesis and structural characterization of C70H38. <i>Angewandte Chemie - International Edition</i> , 2008 , 47, 2796-9	16.4	16
23	Electron capture dissociation implementation progress in Fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2008 , 19, 762-71	3.5	30
22	Stability of an organometallic ruthenium-ubiquitin adduct in the presence of glutathione: relevance to antitumour activity. <i>Journal of Inorganic Biochemistry</i> , 2008 , 102, 2136-41	4.2	57
21	Ion activation in electron capture dissociation to distinguish between N-terminal and C-terminal product ions. <i>Analytical Chemistry</i> , 2007 , 79, 7596-602	7.8	62
20	Identification of single and double sites of phosphorylation by ECD FT-ICR/MS in peptides related to the phosphorylation site domain of the myristoylated alanine-rich C kinase protein. <i>Journal of the American Society for Mass Spectrometry</i> , 2007 , 18, 2137-45	3.5	11
19	Hydrogenation of C60 at 2GPa pressure and high temperature. <i>Chemical Physics</i> , 2006 , 325, 445-451	2.3	25
18	Impact of ion magnetron motion on electron capture dissociation Fourier transform ion cyclotron resonance mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2006 , 255-256, 144-149	1.9	31
17	Reaction of hydrogen gas with C60 at elevated pressure and temperature: hydrogenation and cage fragmentation. <i>Journal of Physical Chemistry A</i> , 2006 , 110, 8528-34	2.8	46
16	Solution-phase deuterium/hydrogen exchange at a specific residue using nozzle-skimmer and electron capture dissociation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2006 , 20, 661-5	2.2	10
15	Charge location directs electron capture dissociation of peptide dications. <i>Journal of the American Society for Mass Spectrometry</i> , 2006 , 17, 1704-11	3.5	31

14	Composition of hydrofullerene mixtures produced by C(60) reaction with hydrogen gas revealed by high-resolution mass spectrometry. <i>Journal of Physical Chemistry B</i> , 2005 , 109, 12742-7	3.4	36
13	Synthesis of C ₅₉ H _x and C ₅₈ H _x fullerenes stabilized by hydrogen. <i>Journal of Physical Chemistry B</i> , 2005 , 109, 5403-5	3.4	31
12	Selective synthesis of the C _{3v} isomer of C ₆₀ H ₁₈ . <i>Organic Letters</i> , 2005 , 7, 5557-60	6.2	26
11	Electron capture dissociation Fourier transform ion cyclotron resonance mass spectrometry in the electron energy range 0-50 eV. <i>Rapid Communications in Mass Spectrometry</i> , 2004 , 18, 1607-13	2.2	23
10	Peptide and protein characterization by high-rate electron capture dissociation Fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2004 , 39, 719-29	2.2	40
9	Shifted-basis technique improves accuracy of peak position determination in Fourier transform mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2004 , 15, 457-61	3.5	11
8	A novel mass spectrometric approach to the analysis of hormonal peptides in extracts of mouse pancreatic islets. <i>FEBS Journal</i> , 2003 , 270, 3146-52		13
7	Combined infrared multiphoton dissociation and electron capture dissociation with a hollow electron beam in Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2003 , 17, 1759-68	2.2	105
6	Ionization energies of multiply protonated polypeptides obtained by tandem ionization in Fourier transform mass spectrometers. <i>Journal of Mass Spectrometry</i> , 2002 , 37, 1141-4	2.2	41
5	Liquid chromatography and electron-capture dissociation in Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2002 , 16, 988-92	2.2	44
4	A Theoretical Investigation of the Kinetic Energy of Ions Trapped in a Radio-Frequency Hexapole Ion Trap. <i>European Journal of Mass Spectrometry</i> , 2002 , 8, 181-189	1.1	12
3	Capillary Electrophoresis and Electron Capture Dissociation Fourier Transform Ion Cyclotron Resonance Mass Spectrometry for Peptide Mixture and Protein Digest Analysis. <i>European Journal of Mass Spectrometry</i> , 2002 , 8, 389-395	1.1	20
2	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
1	The Human Proteoform Project: A Plan to Define the Human Proteome		7