

Vladimir A Gorshkov

List of Publications by Year in descending order

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48
papers

977
citations

430874

18
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501196

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54
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54
docs citations

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times ranked

1474
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of Differentially Abundant Proteins Among Leishmania (Viannia) braziliensis Strains Isolated From Atypical or Typical Lesions. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 824968.	3.9	0
2	Proteomic analysis reveals stage-specific reprogramed metabolism for the primary breast cancer cell lines MGSO and MACL. <i>Proteomics</i> , 2022, 22, .	2.2	2
3	Phosphoproteomic studies of alamandine signaling in CHO-MrgD and human pancreatic carcinoma cells: An antiproliferative effect is unveiled. <i>Proteomics</i> , 2022, 22, .	2.2	2
4	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.	3.7	18
5	Complex-dependent histone acetyltransferase activity of KAT8 determines its role in transcription and cellular homeostasis. <i>Molecular Cell</i> , 2021, 81, 1749-1765.e8.	9.7	42
6	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.	1.5	19
7	Multi-Omics Analysis of Glioblastoma Cells™ Sensitivity to Oncolytic Viruses. <i>Cancers</i> , 2021, 13, 5268.	3.7	16
8	Biological and Molecular Effects of Trypanosoma cruzi Residence in a LAMP-Deficient Intracellular Environment. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 788482.	3.9	3
9	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.	2.8	7
10	HUMOS: How to Understand My Orbitrap Spectrum? An Interactive Web-Based Tool to Teach the Basics of Mass-Spectrometry-Based Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 3910-3918.	3.7	0
11	Rpn4 and proteasome-mediated yeast resistance to ethanol includes regulation of autophagy. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4027-4041.	3.6	11
12	Moving Pieces in a Cellular Puzzle: A Cryptic Peptide from the Scorpion Toxin Ts14 Activates AKT and ERK Signaling and Decreases Cardiac Myocyte Contractility via Dephosphorylation of Phospholamban. <i>Journal of Proteome Research</i> , 2020, 19, 3467-3477.	3.7	4
13	The Cytotoxicity of Metal Nanoparticles Depends on Their Synergistic Interactions. <i>Particle and Particle Systems Characterization</i> , 2020, 37, 2000135.	2.3	3
14	DirectMS1: MS/MS-Free Identification of 1000 Proteins of Cellular Proteomes in 5 Minutes. <i>Analytical Chemistry</i> , 2020, 92, 4326-4333.	6.5	31
15	Middle-Down Proteomic Analyses with Ion Mobility Separations of Endogenous Isomeric Proteoforms. <i>Analytical Chemistry</i> , 2020, 92, 2364-2368.	6.5	18
16	PRMT5 methylome profiling uncovers a direct link to splicing regulation in acute myeloid leukemia. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 999-1012.	8.2	105
17	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.	4.3	52
18	Silver nanoparticle-induced expression of proteins related to oxidative stress and neurodegeneration in an <i>in vitro</i> human blood-brain barrier model. <i>Nanotoxicology</i> , 2019, 13, 221-239.	3.0	51

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19	Maximizing Sequence Coverage in Top-Down Proteomics By Automated Multimodal Gas-Phase Protein Fragmentation. <i>Analytical Chemistry</i> , 2018, 90, 12519-12526.	6.5	25
20	Quantitative Proteome and Phosphoproteome Analyses of <i>Streptomyces coelicolor</i> Reveal Proteins and Phosphoproteins Modulating Differentiation and Secondary Metabolism. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1591-1611.	3.8	35
21	Approaching cellular resolution and reliable identification in mass spectrometry imaging of tryptic peptides. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 5825-5837.	3.7	26
22	Co-exposure to silver nanoparticles and cadmium induce metabolic adaptation in HepG2 cells. <i>Nanotoxicology</i> , 2018, 12, 781-795.	3.0	21
23	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.	1.8	12
24	SuperQuant-assisted comparative proteome analysis of glioblastoma subpopulations allows for identification of potential novel therapeutic targets and cell markers. <i>Oncotarget</i> , 2018, 9, 9400-9414.	1.8	8
25	Characterization of Complete Histone Tail Proteoforms Using Differential Ion Mobility Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 5461-5466.	6.5	41
26	Peptide de novo sequencing of mixture tandem mass spectra. <i>Proteomics</i> , 2016, 16, 2470-2479.	2.2	19
27	Protein and Peptide Composition of Male Accessory Glands of <i>Apis mellifera</i> Drones Investigated by Mass Spectrometry. <i>PLoS ONE</i> , 2015, 10, e0125068.	2.5	27
28	SuperQuant: A Data Processing Approach to Increase Quantitative Proteome Coverage. <i>Analytical Chemistry</i> , 2015, 87, 6319-6327.	6.5	26
29	Charge Inversion of Phospholipids by Dimetal Complexes for Positive Ion-Mode Electrospray Ionization Mass Spectrometry Analysis. <i>Analytical Chemistry</i> , 2015, 87, 8732-8739.	6.5	3
30	Depolymerization of lignosulfonates by submerged cultures of the basidiomycete <i>Irpex consors</i> and cloning of a putative versatile peroxidase. <i>Enzyme and Microbial Technology</i> , 2015, 81, 8-15.	3.2	9
31	Characterization of novel insect associated peptidases for hydrolysis of food proteins. <i>European Food Research and Technology</i> , 2015, 240, 431-439.	3.3	14
32	Mass spectrometric <i>de novo</i> sequencing of natural non-tryptic peptides: comparing peculiarities of collision-induced dissociation (CID) and high energy collision dissociation (HCD). <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 2595-2604.	1.5	19
33	Collision-Induced Dissociation Fragmentation Inside Disulfide C-Terminal Loops of Natural Non-Tryptic Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1037-1044.	2.8	17
34	LC-MS/MS with 2D mass mapping of skin secretions™ peptides as a reliable tool for interspecies identification inside <i>Rana esculenta</i> complex. <i>Peptides</i> , 2012, 34, 296-302.	2.4	14
35	Matrix-Assisted Laser Desorption/Ionization Post-Source Decay Fragmentation of the Cystine-Containing Amphibian Peptides with Novel Cysteine Tags. <i>European Journal of Mass Spectrometry</i> , 2011, 17, 73-83.	1.0	5
36	Investigation of skin secretory peptidome of <i>Rana lessonae</i> frog by mass spectrometry. <i>Journal of Analytical Chemistry</i> , 2011, 66, 1298-1306.	0.9	10

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37	Mass spectral study of the skin peptide of brown frog <i>Rana temporaria</i> from Zvenigorod population. <i>Journal of Analytical Chemistry</i> , 2011, 66, 1353-1360.	0.9	13
38	HPLC and MALDI investigation of the stress influence on the composition of skin secretion of the Common frog <i>Rana temporaria</i> . <i>Journal of Analytical Chemistry</i> , 2011, 66, 1361-1368.	0.9	3
39	Novel Cysteine Tags for the Sequencing of Non-Tryptic Disulfide Peptides of Anurans: ESI-MS Study of Fragmentation Efficiency. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 2246-2255.	2.8	11
40	Mass spectrometric study of bradykinin-related peptides (<sc>BRPs</sc>) from the skin secretion of Russian ranid frogs. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 933-940.	1.5	21
41	New cysteine-modifying reagents: Efficiency of derivatization and influence on the signals of the protonated molecules of disulfide-containing peptides in matrix-assisted laser desorption/ionization mass spectrometry. <i>Journal of Analytical Chemistry</i> , 2010, 65, 1320-1327.	0.9	4
42	N-terminal tagging strategy for <i>De Novo</i> sequencing of short peptides by ESI-MS/MS and MALDI-MS/MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 104-111.	2.8	37
43	Novel natural peptides from <i>Hyla arborea schelkownikowi</i> skin secretion. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 1749-1754.	1.5	12
44	Mass spectrometric study of peptides secreted by the skin glands of the brown frog <i>Rana arvalis</i> from the Moscow region. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 1241-1248.	1.5	36
45	Oxidation versus carboxamidomethylation of s-s bond in ranid frog peptides: Pro and contra for de novo MALDI-MS sequencing. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 479-487.	2.8	25
46	Bioactive peptides from the skin of ranid frogs: modern approaches to the mass spectrometric de novo sequencing. <i>Russian Chemical Bulletin</i> , 2008, 57, 1080-1091.	1.5	6
47	<i>De novo</i> sequencing of peptides secreted by the skin glands of the Caucasian Green Frog <i>Rana ridibunda</i>. <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 3517-3525.	1.5	48
48	Electrospray Ionization Tandem Mass Spectrometry Sequencing of Novel Skin Peptides from Ranid Frogs Containing Disulfide Bridges. <i>European Journal of Mass Spectrometry</i> , 2007, 13, 155-163.	1.0	32