

Alexander R Ivanov

List of Publications by Year in descending order

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57
papers

4,721
citations

201674

27
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144013

57
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docs citations

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times ranked

8479
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of Microflow and Analytical Flow Liquid Chromatography Coupled to Mass Spectrometry Global Metabolomics Methods Using a Urea Cycle Disorder Mouse Model. <i>Journal of Proteome Research</i> , 2022, 21, 151-163.	3.7	6
2	Capillary Electrophoresis Coupled to Electrospray Ionization Tandem Mass Spectrometry for Ultra-Sensitive Proteomic Analysis of Limited Samples. <i>Analytical Chemistry</i> , 2022, 94, 704-713.	6.5	18
3	MPAPASS software enables stitched multiplex, multidimensional EV repertoire analysis and a standard framework for reporting bead-based assays. <i>Cell Reports Methods</i> , 2022, 2, 100136.	2.9	8
4	High-Sensitivity Glycan Profiling of Blood-Derived Immunoglobulin G, Plasma, and Extracellular Vesicle Isolates with Capillary Zone Electrophoresis-Mass Spectrometry. <i>Analytical Chemistry</i> , 2021, 93, 1991-2002.	6.5	23
5	Lipidome-based Targeting of STAT3-driven Breast Cancer Cells Using Poly-<sc> </sc>-glutamic Acid-coated Layer-by-Layer Nanoparticles. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 726-738.	4.1	4
6	Simple and Efficient Microsolid-Phase Extraction Tip-Based Sample Preparation Workflow to Enable Sensitive Proteomic Profiling of Limited Samples (200 to 10,000 Cells). <i>Journal of Proteome Research</i> , 2021, 20, 1676-1688.	3.7	16
7	A systematic approach to development of analytical scale and microflow-based liquid chromatography coupled to mass spectrometry metabolomics methods to support drug discovery and development. <i>Journal of Chromatography A</i> , 2021, 1642, 462047.	3.7	4
8	Rapid Highly-Efficient Digestion and Peptide Mapping of Adeno-Associated Viruses. <i>Analytical Chemistry</i> , 2021, 93, 10403-10410.	6.5	16
9	Channeling macrophage polarization by rocaglates increases macrophage resistance to <i>Mycobacterium tuberculosis</i> . <i>IScience</i> , 2021, 24, 102845.	4.1	14
10	High-throughput microfluidic 3D biomimetic model enabling quantitative description of the human breast tumor microenvironment. <i>Acta Biomaterialia</i> , 2021, 132, 473-488.	8.3	20
11	A simple, high-throughput method of protein and label removal from extracellular vesicle samples. <i>Nanoscale</i> , 2021, 13, 3737-3745.	5.6	6
12	The integrated stress response mediates necrosis in murine <i>Mycobacterium tuberculosis</i> granulomas. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	27
13	Improved Sensitivity of Ultralow Flow LC-MS-Based Proteomic Profiling of Limited Samples Using Monolithic Capillary Columns and FAIMS Technology. <i>Analytical Chemistry</i> , 2020, 92, 14702-14712.	6.5	52
14	Machine learning-aided quantification of antibody-based cancer immunotherapy by natural killer cells in microfluidic droplets. <i>Lab on A Chip</i> , 2020, 20, 2317-2327.	6.0	24
15	Multi-omics Reveals Impact of Cysteine Feed Concentration and Resulting Redox Imbalance on Cellular Energy Metabolism and Specific Productivity in CHO Cell Bioprocessing. <i>Biotechnology Journal</i> , 2020, 15, e1900565.	3.5	17
16	Technologies and Standardization in Research on Extracellular Vesicles. <i>Trends in Biotechnology</i> , 2020, 38, 1066-1098.	9.3	250
17	New mixture models for decoy-free false discovery rate estimation in mass spectrometry proteomics. <i>Bioinformatics</i> , 2020, 36, i745-i753.	4.1	8
18	A nanoscale, multi-parametric flow cytometry-based platform to study mitochondrial heterogeneity and mitochondrial DNA dynamics. <i>Communications Biology</i> , 2019, 2, 258.	4.4	32

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19	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019, 16, 587-594.	19.0	241
20	Genetically Encoded Fluorescent Proteins Enable High-Throughput Assignment of Cell Cohorts Directly from MALDI-MS Images. <i>Analytical Chemistry</i> , 2019, 91, 3810-3817.	6.5	3
21	Multi-Omics Study on the Impact of Cysteine Feed Level on Cell Viability and mAb Production in a CHO Bioprocess. <i>Biotechnology Journal</i> , 2019, 14, e1800352.	3.5	30
22	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
23	Complementary middle-down and intact monoclonal antibody proteoform characterization by capillary zone electrophoresis mass spectrometry. <i>Electrophoresis</i> , 2018, 39, 2069-2082.	2.4	67
24	Host Cell Protein Profiling by Targeted and Untargeted Analysis of Data Independent Acquisition Mass Spectrometry Data with Parallel Reaction Monitoring Verification. <i>Analytical Chemistry</i> , 2017, 89, 5294-5302.	6.5	53
25	Binding Site Characterization of AM1336, a Novel Covalent Inverse Agonist at Human Cannabinoid 2 Receptor, Using Mass Spectrometric Analysis. <i>Journal of Proteome Research</i> , 2017, 16, 2419-2428.	3.7	12
26	Rapid Isolation of Extracellular Vesicles from Blood Plasma with Size-Exclusion Chromatography Followed by Mass Spectrometry-Based Proteomic Profiling. <i>Methods in Molecular Biology</i> , 2017, 1660, 295-302.	0.9	24
27	Analysis of Proteins, Protein Complexes, and Organellar Proteomes Using Sheathless Capillary Zone Electrophoresis - Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2614-2634.	2.8	71
28	Diurnal Variations of Circulating Extracellular Vesicles Measured by Nano Flow Cytometry. <i>PLoS ONE</i> , 2016, 11, e0144678.	2.5	58
29	Combined metabolomics and proteomics reveals hypoxia as a cause of lower productivity on scale-up to a 5000-liter CHO bioprocess. <i>Biotechnology Journal</i> , 2016, 11, 1190-1200.	3.5	63
30	Advanced Precursor Ion Selection Algorithms for Increased Depth of Bottom-Up Proteomic Profiling. <i>Journal of Proteome Research</i> , 2016, 15, 3563-3573.	3.7	20
31	Comparative studies of peak intensities and chromatographic separation of proteolytic digests, PTMs, and intact proteins obtained by nanoLC-ESI MS analysis at room and elevated temperatures. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 3953-3968.	3.7	5
32	High Resolution CZE-MS Quantitative Characterization of Intact Biopharmaceutical Proteins: Proteoforms of Interferon- β . <i>Analytical Chemistry</i> , 2016, 88, 1138-1146.	6.5	76
33	Ligation of Glycophorin A Generates Reactive Oxygen Species Leading to Decreased Red Blood Cell Function. <i>PLoS ONE</i> , 2016, 11, e0141206.	2.5	19
34	Application of Statistical Thermodynamics To Predict the Adsorption Properties of Polypeptides in Reversed-Phase HPLC. <i>Analytical Chemistry</i> , 2015, 87, 6562-6569.	6.5	8
35	Physical detection of influenza A epitopes identifies a stealth subset on human lung epithelium evading natural CD8 immunity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2151-2156.	7.1	48
36	An Integrated Platform for Isolation, Processing, and Mass Spectrometry-based Proteomic Profiling of Rare Cells in Whole Blood*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1672-1683.	3.8	134

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37	Mass-Spectrometry-Based Molecular Characterization of Extracellular Vesicles: Lipidomics and Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 2367-2384.	3.7	198
38	Reply to van de Sandt and Rimmelzwaan: Matching epitope display with functional avidity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2418-E2418.	7.1	1
39	Granulin, a novel STAT3-interacting protein, enhances STAT3 transcriptional function and correlates with poorer prognosis in breast cancer. <i>Genes and Cancer</i> , 2015, 6, 153-168.	1.9	19
40	Interlaboratory studies and initiatives developing standards for proteomics. <i>Proteomics</i> , 2013, 13, 904-909.	2.2	29
41	Malaria-Infected Erythrocyte-Derived Microvesicles Mediate Cellular Communication within the Parasite Population and with the Host Immune System. <i>Cell Host and Microbe</i> , 2013, 13, 521-534.	11.0	356
42	Alternative Methods for Characterization of Extracellular Vesicles. <i>Frontiers in Physiology</i> , 2012, 3, 354.	2.8	123
43	Comparison of in-gel protein separation techniques commonly used for fractionation in mass spectrometry-based proteomic profiling. <i>Electrophoresis</i> , 2012, 33, 2516-2526.	2.4	50
44	Proteomics under Pressure: Development of Essential Sample Preparation Techniques in Proteomics Using Ultrahigh Hydrostatic Pressure. <i>Journal of Proteome Research</i> , 2011, 10, 5536-5546.	3.7	26
45	Aberrant lipid metabolism disrupts calcium homeostasis causing liver endoplasmic reticulum stress in obesity. <i>Nature</i> , 2011, 473, 528-531.	27.8	864
46	Thermal stabilization of tissues and the preservation of protein phosphorylation states for two-dimensional gel electrophoresis. <i>Electrophoresis</i> , 2011, 32, 2206-2215.	2.4	13
47	Retention time prediction using the model of liquid chromatography of biomacromolecules at critical conditions in LC-MS phosphopeptide analysis. <i>Proteomics</i> , 2010, 10, 3458-3468.	2.2	27
48	Increased Power for the Analysis of Label-free LC-MS/MS Proteomics Data by Combining Spectral Counts and Peptide Peak Attributes. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2704-2718.	3.8	41
49	When less can yield more – Computational preprocessing of MS/MS spectra for peptide identification. <i>Proteomics</i> , 2009, 9, 4978-4984.	2.2	73
50	Zcchc11-dependent uridylation of microRNA directs cytokine expression. <i>Nature Cell Biology</i> , 2009, 11, 1157-1163.	10.3	272
51	Proteomic Analysis of the Hyaloid Vascular System Regression during Ocular Development. <i>Journal of Proteome Research</i> , 2008, 7, 4904-4913.	3.7	8
52	Tissue fractionation by hydrostatic pressure cycling technology: the unified sample preparation technique for systems biology studies. <i>Journal of Biomolecular Techniques</i> , 2008, 19, 189-99.	1.5	27
53	Comparative proteomic and transcriptomic profiling of the fission yeast <i>Schizosaccharomyces pombe</i> . <i>Molecular Systems Biology</i> , 2007, 3, 79.	7.2	106
54	Artificial Neural Network Analysis for Evaluation of Peptide MS/MS Spectra in Proteomics. <i>Analytical Chemistry</i> , 2004, 76, 1726-1732.	6.5	62

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55	High-efficiency peptide analysis on monolithic multimode capillary columns: Pressure-assisted capillary electrochromatography/capillary electrophoresis coupled to UV and electrospray ionization-mass spectrometry. <i>Electrophoresis</i> , 2003, 24, 3663-3673.	2.4	78
56	Low-Attomole Electrospray Ionization MS and MS/MS Analysis of Protein Tryptic Digests Using 20- μ m-i.d. Polystyrene- <i>divinylbenzene</i> Monolithic Capillary Columns. <i>Analytical Chemistry</i> , 2003, 75, 5306-5316.	6.5	152
57	A Universal Denoising and Peak Picking Algorithm for LC-MS Based on Matched Filtration in the Chromatographic Time Domain. <i>Analytical Chemistry</i> , 2003, 75, 6314-6326.	6.5	139