

Olga Vitek

List of Publications by Year in descending order

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72
papers

6,985
citations

109321

35
h-index

85541

71
g-index

77
all docs

77
docs citations

77
times ranked

11340
citing authors

#	ARTICLE	IF	CITATIONS
1	Extending the Limits of Quantitative Proteome Profiling with Data-Independent Acquisition and Application to Acetaminophen-Treated Three-Dimensional Liver Microtissues. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1400-1410.	3.8	873
2	MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments. <i>Bioinformatics</i> , 2014, 30, 2524-2526.	4.1	832
3	Analysis and validation of proteomic data generated by tandem mass spectrometry. <i>Nature Methods</i> , 2007, 4, 787-797.	19.0	585
4	A Coastal Cline in Sodium Accumulation in <i>Arabidopsis thaliana</i> Is Driven by Natural Variation of the Sodium Transporter AtHKT1;1. <i>PLoS Genetics</i> , 2010, 6, e1001193.	3.5	317
5	Quantitative variability of 342 plasma proteins in a human twin population. <i>Molecular Systems Biology</i> , 2015, 11, 786.	7.2	300
6	SuperHirn – a novel tool for high resolution LC-MS-based peptide/protein profiling. <i>Proteomics</i> , 2007, 7, 3470-3480.	2.2	295
7	The leaf ionome as a multivariable system to detect a plant's physiological status. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12081-12086.	7.1	288
8	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. <i>Science Signaling</i> , 2010, 3, rs4.	3.6	277
9	Statistical Design of Quantitative Mass Spectrometry-Based Proteomic Experiments. <i>Journal of Proteome Research</i> , 2009, 8, 2144-2156.	3.7	244
10	Cardinal : an R package for statistical analysis of mass spectrometry-based imaging experiments. <i>Bioinformatics</i> , 2015, 31, 2418-2420.	4.1	203
11	Reproducible and Consistent Quantification of the <i>Saccharomyces cerevisiae</i> Proteome by SWATH-mass spectrometry*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 739-749.	3.8	158
12	Multivariate statistical differentiation of renal cell carcinomas based on lipidomic analysis by ambient ionization imaging mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 398, 2969-2978.	3.7	137
13	Comparison of Protein Quantification in a Complex Background by DIA and TMT Workflows with Fixed Instrument Time. <i>Journal of Proteome Research</i> , 2019, 18, 1340-1351.	3.7	107
14	Improving Precursor Selectivity in Data-Independent Acquisition Using Overlapping Windows. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 669-684.	2.8	101
15	Multivariate Statistical Identification of Human Bladder Carcinomas Using Ambient Ionization Imaging Mass Spectrometry. <i>Chemistry - A European Journal</i> , 2011, 17, 2897-2902.	3.3	99
16	Protein Quantification in Label-Free LC-MS Experiments. <i>Journal of Proteome Research</i> , 2009, 8, 5275-5284.	3.7	94
17	MSstatsTMT: Statistical Detection of Differentially Abundant Proteins in Experiments with Isobaric Labeling and Multiple Mixtures. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1706-1723.	3.8	89
18	Prediction of colorectal cancer diagnosis based on circulating plasma proteins. <i>EMBO Molecular Medicine</i> , 2015, 7, 1166-1178.	6.9	80

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19	Statistical design of experiments as a tool in mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2005, 40, 565-579.	1.6	72
20	Developmental Changes in the Metabolic Network of Snapdragon Flowers. <i>PLoS ONE</i> , 2012, 7, e40381.	2.5	72
21	Automated selected reaction monitoring data analysis workflow for large-scale targeted proteomic studies. <i>Nature Protocols</i> , 2013, 8, 1602-1619.	12.0	71
22	Screening for pressure ulcer risk in an acute care hospital. <i>Journal of Clinical Epidemiology</i> , 2002, 55, 498-504.	5.0	68
23	MassIVE.quant: a community resource of quantitative mass spectrometry-based proteomics datasets. <i>Nature Methods</i> , 2020, 17, 981-984.	19.0	66
24	Infection-Induced Peroxisome Biogenesis Is a Metabolic Strategy for Herpesvirus Replication. <i>Cell Host and Microbe</i> , 2018, 24, 526-541.e7.	11.0	65
25	Gene expression profiling of Caco-2 BBe cells suggests a role for specific signaling pathways during intestinal differentiation. <i>Physiological Genomics</i> , 2003, 13, 57-68.	2.3	59
26	MS1 Peptide Ion Intensity Chromatograms in MS2 (SWATH) Data Independent Acquisitions. Improving Post Acquisition Analysis of Proteomic Experiments. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2405-2419.	3.8	57
27	Computational Mass Spectrometry-Based Proteomics. <i>PLoS Computational Biology</i> , 2011, 7, e1002277.	3.2	55
28	Probabilistic Segmentation of Mass Spectrometry (MS) Images Helps Select Important Ions and Characterize Confidence in the Resulting Segments. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1761-1772.	3.8	54
29	Correlation between γ -Type Ions Observed in Ion Trap and Triple Quadrupole Mass Spectrometers. <i>Journal of Proteome Research</i> , 2009, 8, 4243-4251.	3.7	51
30	Non-invasive prognostic protein biomarker signatures associated with colorectal cancer. <i>EMBO Molecular Medicine</i> , 2015, 7, 1153-1165.	6.9	49
31	Interdependence of Signal Processing and Analysis of Urine ¹ H NMR Spectra for Metabolic Profiling. <i>Analytical Chemistry</i> , 2009, 81, 6080-6088.	6.5	48
32	ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LC-MS/MS Experiments. <i>Journal of Proteome Research</i> , 2017, 16, 945-957.	3.7	42
33	A Targeted Mass Spectrometry Strategy for Developing Proteomic Biomarkers: A Case Study of Epithelial Ovarian Cancer. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1836-1850.	3.8	42
34	Quantification of the Compositional Information Provided by Immonium Ions on a Quadrupole-Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2008, 80, 5596-5606.	6.5	40
35	Combining Precursor and Fragment Information for Improved Detection of Differential Abundance in Data Independent Acquisition. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 421-430.	3.8	40
36	Targeted proteomics reveals strain-specific changes in the mouse insulin and central metabolic pathways after a sustained high-fat diet. <i>Molecular Systems Biology</i> , 2013, 9, 681.	7.2	36

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37	A framework for installable external tools in Skyline. <i>Bioinformatics</i> , 2014, 30, 2521-2523.	4.1	36
38	New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 327-328.	3.8	33
39	Protein-Based Classifier to Predict Conversion from Clinically Isolated Syndrome to Multiple Sclerosis. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 318-328.	3.8	28
40	Selection of Features with Consistent Profiles Improves Relative Protein Quantification in Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 944-959.	3.8	25
41	Sex Determination in <i>Ceratopteris richardii</i> Is Accompanied by Transcriptome Changes That Drive Epigenetic Reprogramming of the Young Gametophyte. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2205-2214.	1.8	22
42	MSstatsQC: Longitudinal System Suitability Monitoring and Quality Control for Targeted Proteomic Experiments. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1335-1347.	3.8	21
43	Deep multiple instance learning classifies subtissue locations in mass spectrometry images from tissue-level annotations. <i>Bioinformatics</i> , 2020, 36, i300-i308.	4.1	19
44	“Add to Subtract” A Simple Method to Remove Complex Background Signals from the ¹ H Nuclear Magnetic Resonance Spectra of Mixtures. <i>Analytical Chemistry</i> , 2012, 84, 994-1002.	6.5	18
45	Nonlinear Regression Improves Accuracy of Characterization of Multiplexed Mass Spectrometric Assays. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 913-924.	3.8	18
46	From Correlation to Causality: Statistical Approaches to Learning Regulatory Relationships in Large-Scale Biomolecular Investigations. <i>Journal of Proteome Research</i> , 2016, 15, 683-690.	3.7	17
47	Using collective expert judgements to evaluate quality measures of mass spectrometry images. <i>Bioinformatics</i> , 2015, 31, i375-i384.	4.1	16
48	Reconsidering complete search algorithms for protein backbone NMR assignment. <i>Bioinformatics</i> , 2005, 21, ii230-ii236.	4.1	15
49	Inferential backbone assignment for sparse data. <i>Journal of Biomolecular NMR</i> , 2006, 35, 187-208.	2.8	15
50	Getting Started in Computational Mass Spectrometry-Based Proteomics. <i>PLoS Computational Biology</i> , 2009, 5, e1000366.	3.2	13
51	MSstatsQC 2.0: R/Bioconductor Package for Statistical Quality Control of Mass Spectrometry-Based Proteomics Experiments. <i>Journal of Proteome Research</i> , 2019, 18, 678-686.	3.7	13
52	Protein biomarkers on tissue as imaged via MALDI mass spectrometry: A systematic approach to study the limits of detection. <i>Proteomics</i> , 2016, 16, 1660-1669.	2.2	12
53	Leveraging Structured Biological Knowledge for Counterfactual Inference: A Case Study of Viral Pathogenesis. <i>IEEE Transactions on Big Data</i> , 2021, 7, 25-37.	6.1	12
54	Differential Plasma Glycoproteome of p19ARF Skin Cancer Mouse Model Using the Corra Label-Free LC-MS Proteomics Platform. <i>Clinical Proteomics</i> , 2008, 4, 105-116.	2.1	11

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55	System-Wide Quantitative Proteomics of the Metabolic Syndrome in Mice: Genotypic and Dietary Effects. <i>Journal of Proteome Research</i> , 2017, 16, 831-841.	3.7	11
56	Multiplexed proteomics of autophagy-deficient murine macrophages reveals enhanced antimicrobial immunity via the oxidative stress response. <i>ELife</i> , 2021, 10, .	6.0	10
57	Targeted protein quantification using sparse reference labeling. <i>Nature Methods</i> , 2014, 11, 301-304.	19.0	9
58	Unsupervised segmentation of mass spectrometric ion images characterizes morphology of tissues. <i>Bioinformatics</i> , 2019, 35, i208-i217.	4.1	9
59	Evaluation of label-free quantitative proteomics in a plant matrix: A case study of the night-to-day transition in corn leaf. <i>Analytical Methods</i> , 2011, 3, 2733.	2.7	8
60	Statistical detection of differentially abundant ions in mass spectrometry-based imaging experiments with complex designs. <i>International Journal of Mass Spectrometry</i> , 2019, 437, 49-57.	1.5	8
61	New mixture models for decoy-free false discovery rate estimation in mass spectrometry proteomics. <i>Bioinformatics</i> , 2020, 36, i745-i753.	4.1	8
62	Moving translational mass spectrometry imaging towards transparent and reproducible data analyses: a case study of an urothelial cancer cohort analyzed in the Galaxy framework. <i>Clinical Proteomics</i> , 2022, 19, 8.	2.1	8
63	Statistical Design and Analysis of Label-free LC-MS Proteomic Experiments: A Case Study of Coronary Artery Disease. <i>Methods in Molecular Biology</i> , 2011, 728, 293-319.	0.9	6
64	Benchmarking comes of age. <i>Genome Biology</i> , 2019, 20, 205.	8.8	6
65	Verification of a Blood-Based Targeted Proteomics Signature for Malignant Pleural Mesothelioma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1973-1982.	2.5	6
66	Statistical characterization of therapeutic protein modifications. <i>Scientific Reports</i> , 2017, 7, 7896.	3.3	4
67	Skyline Batch: An Intuitive User Interface for Batch Processing with Skyline. <i>Journal of Proteome Research</i> , 2022, 21, 289-294.	3.7	4
68	matter: an R package for rapid prototyping with larger-than-memory datasets on disk. <i>Bioinformatics</i> , 2017, 33, 3142-3144.	4.1	3
69	Functional evolution within a protein superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 697-708.	2.6	2
70	A Bayesian Active Learning Experimental Design for Inferring Signaling Networks. <i>Journal of Computational Biology</i> , 2018, 25, 709-725.	1.6	1
71	Challenges in Large-Scale Computational Mass Spectrometry and Multiomics. <i>Journal of Proteome Research</i> , 2016, 15, 681-682.	3.7	0
72	Do-calculus enables estimation of causal effects in partially observed biomolecular pathways. <i>Bioinformatics</i> , 2022, 38, i350-i358.	4.1	0