Olga Vitek

List of Publications by Year
in descending order

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	Skyline Batch: An Intuitive User Interface for Batch Processing with Skyline. Journal of Proteome Research, 2022, 21, 289-294.	3.7	4
2	Do-calculus enables estimation of causal effects in partially observed biomolecular pathways. Bioinformatics, 2022, 38, i350-i358.	4.1	0
3	Moving translational mass spectrometry imaging towards transparent and reproducible data analyses: a case study of an urothelial cancer cohort analyzed in the Galaxy framework. Clinical Proteomics, 2022, 19, 8.	2.1	8
4	Leveraging Structured Biological Knowledge for Counterfactual Inference: A Case Study of Viral Pathogenesis. IEEE Transactions on Big Data, 2021, 7, 25-37.	6.1	12
5	Multiplexed proteomics of autophagy-deficient murine macrophages reveals enhanced antimicrobial immunity via the oxidative stress response. ELife, 2021, 10, .	6.0	10
6	MSstatsTMT: Statistical Detection of Differentially Abundant Proteins in Experiments with Isobaric Labeling and Multiple Mixtures. Molecular and Cellular Proteomics, 2020, 19, 1706-1723.	3.8	89
7	Deep multiple instance learning classifies subtissue locations in mass spectrometry images from tissue-level annotations. Bioinformatics, 2020, 36, i300-i308.	4.1	19
8	Verification of a Blood-Based Targeted Proteomics Signature for Malignant Pleural Mesothelioma. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1973-1982.	2.5	6
9	MassIVE.quant: a community resource of quantitative mass spectrometry–based proteomics datasets. Nature Methods, 2020, 17, 981-984.	19.0	66
10	Selection of Features with Consistent Profiles Improves Relative Protein Quantification in Mass Spectrometry Experiments. Molecular and Cellular Proteomics, 2020, 19, 944-959.	3.8	25
11	Combining Precursor and Fragment Information for Improved Detection of Differential Abundance in Data Independent Acquisition. Molecular and Cellular Proteomics, 2020, 19, 421-430.	3.8	40
12	New mixture models for decoy-free false discovery rate estimation in mass spectrometry proteomics. Bioinformatics, 2020, 36, i745-i753.	4.1	8
13	Statistical detection of differentially abundant ions in mass spectrometry-based imaging experiments with complex designs. International Journal of Mass Spectrometry, 2019, 437, 49-57.	1.5	8
14	A Targeted Mass Spectrometry Strategy for Developing Proteomic Biomarkers: A Case Study of Epithelial Ovarian Cancer. Molecular and Cellular Proteomics, 2019, 18, 1836-1850.	3.8	42
15	Unsupervised segmentation of mass spectrometric ion images characterizes morphology of tissues. Bioinformatics, 2019, 35, i208-i217.	4.1	9
16	Benchmarking comes of age. Genome Biology, 2019, 20, 205.	8.8	6
17	Improving Precursor Selectivity in Data-Independent Acquisition Using Overlapping Windows. Journal of the American Society for Mass Spectrometry, 2019, 30, 669-684.	2.8	101
18	Comparison of Protein Quantification in a Complex Background by DIA and TMT Workflows with Fixed Instrument Time. Journal of Proteome Research, 2019, 18, 1340-1351.	3.7	107

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19	MSstatsQC 2.0: R/Bioconductor Package for Statistical Quality Control of Mass Spectrometry-Based Proteomics Experiments. Journal of Proteome Research, 2019, 18, 678-686.	3.7	13
20	Nonlinear Regression Improves Accuracy of Characterization of Multiplexed Mass Spectrometric Assays. Molecular and Cellular Proteomics, 2018, 17, 913-924.	3.8	18
21	Infection-Induced Peroxisome Biogenesis Is a Metabolic Strategy for Herpesvirus Replication. Cell Host and Microbe, 2018, 24, 526-541.e7.	11.0	65
22	A Bayesian Active Learning Experimental Design for Inferring Signaling Networks. Journal of Computational Biology, 2018, 25, 709-725.	1.6	1
23	Sex Determination in <i>Ceratopteris richardii</i> Is Accompanied by Transcriptome Changes That Drive Epigenetic Reprogramming of the Young Gametophyte. G3: Genes, Genomes, Genetics, 2018, 8, 2205-2214.	1.8	22
24	New Guidelines for Publication of Manuscripts Describing Development and Application of Targeted Mass Spectrometry Measurements of Peptides and Proteins. Molecular and Cellular Proteomics, 2017, 16, 327-328.	3.8	33
25	MSstatsQC: Longitudinal System Suitability Monitoring and Quality Control for Targeted Proteomic Experiments. Molecular and Cellular Proteomics, 2017, 16, 1335-1347.	3.8	21
26	ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LCâ€"MS/MS Experiments. Journal of Proteome Research, 2017, 16, 945-957.	3.7	42
27	System-Wide Quantitative Proteomics of the Metabolic Syndrome in Mice: Genotypic and Dietary Effects. Journal of Proteome Research, 2017, 16, 831-841.	3.7	11
28	matter: an R package for rapid prototyping with larger-than-memory datasets on disk. Bioinformatics, 2017, 33, 3142-3144.	4.1	3
29	Statistical characterization of therapeutic protein modifications. Scientific Reports, 2017, 7, 7896.	3.3	4
30	Protein biomarkers on tissue as imaged via MALDI mass spectrometry: A systematic approach to study the limits of detection. Proteomics, 2016, 16, 1660-1669.	2.2	12
31	From Correlation to Causality: Statistical Approaches to Learning Regulatory Relationships in Large-Scale Biomolecular Investigations. Journal of Proteome Research, 2016, 15, 683-690.	3.7	17
32	Probabilistic Segmentation of Mass Spectrometry (MS) Images Helps Select Important Ions and Characterize Confidence in the Resulting Segments. Molecular and Cellular Proteomics, 2016, 15, 1761-1772.	3.8	54
33	Challenges in Large-Scale Computational Mass Spectrometry and Multiomics. Journal of Proteome Research, 2016, 15, 681-682.	3.7	0
34	Protein-Based Classifier to Predict Conversion from Clinically Isolated Syndrome to Multiple Sclerosis. Molecular and Cellular Proteomics, 2016, 15, 318-328.	3.8	28
35	Prediction of colorectal cancer diagnosis based onÂcirculating plasma proteins. EMBO Molecular Medicine, 2015, 7, 1166-1178.	6.9	80
36	Nonâ€invasive prognostic protein biomarker signatures associated with colorectal cancer. EMBO Molecular Medicine, 2015, 7, 1153-1165.	6.9	49

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37	Using collective expert judgements to evaluate quality measures of mass spectrometry images. Bioinformatics, 2015, 31, i375-i384.	4.1	16
38	Reproducible and Consistent Quantification of the Saccharomyces cerevisiae Proteome by SWATH-mass spectrometry *. Molecular and Cellular Proteomics, 2015, 14, 739-749.	3.8	158
39	*Cardinal*: an R package for statistical analysis of mass spectrometry-based imaging experiments. Bioinformatics, 2015, 31, 2418-2420.	4.1	203
40	Extending the Limits of Quantitative Proteome Profiling with Data-Independent Acquisition and Application to Acetaminophen-Treated Three-Dimensional Liver Microtissues. Molecular and Cellular Proteomics, 2015, 14, 1400-1410.	3.8	873
41	MS1 Peptide Ion Intensity Chromatograms in MS2 (SWATH) Data Independent Acquisitions. Improving Post Acquisition Analysis of Proteomic Experiments. Molecular and Cellular Proteomics, 2015, 14, 2405-2419.	3.8	57
42	Quantitative variability of 342 plasma proteins in a human twin population. Molecular Systems Biology, 2015, 11, 786.	7.2	300
43	MSstats: an R package for statistical analysis of quantitative mass spectrometry-based proteomic experiments. Bioinformatics, 2014, 30, 2524-2526.	4.1	832
44	A framework for installable external tools in Skyline. Bioinformatics, 2014, 30, 2521-2523.	4.1	36
45	Targeted protein quantification using sparse reference labeling. Nature Methods, 2014, 11, 301-304.	19.0	9
46	Automated selected reaction monitoring data analysis workflow for large-scale targeted proteomic studies. Nature Protocols, 2013, 8, 1602-1619.	12.0	71
47	Targeted proteomics reveals strain€specific changes in the mouse insulin and central metabolic pathways after a sustained high€fat diet. Molecular Systems Biology, 2013, 9, 681.	7.2	36
48	Developmental Changes in the Metabolic Network of Snapdragon Flowers. PLoS ONE, 2012, 7, e40381.	2.5	72
49	€œAdd to Subtract€ A Simple Method to Remove Complex Background Signals from the ^{1}H Nuclear Magnetic Resonance Spectra of Mixtures. Analytical Chemistry, 2012, 84, 994-1002.	6.5	18
50	Evaluation of label-free quantitative proteomics in a plant matrix: A case study of the night-to-day transition in corn leaf. Analytical Methods, 2011, 3, 2733.	2.7	8
51	Statistical Design and Analysis of Label-free LC-MS Proteomic Experiments: A Case Study of Coronary Artery Disease. Methods in Molecular Biology, 2011, 728, 293-319.	0.9	6
52	Multivariate Statistical Identification of Human Bladder Carcinomas Using Ambient Ionization Imaging Mass Spectrometry. Chemistry - A European Journal, 2011, 17, 2897-2902.	3.3	99
53	Computational Mass Spectrometry€"Based Proteomics. PLoS Computational Biology, 2011, 7, e1002277.	3.2	55
54	Multivariate statistical differentiation of renal cell carcinomas based on lipidomic analysis by ambient ionization imaging mass spectrometry. Analytical and Bioanalytical Chemistry, 2010, 398, 2969-2978.	3.7	137

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55	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. Science Signaling, 2010, 3, rs4.	3.6	277
56	A Coastal Cline in Sodium Accumulation in Arabidopsis thaliana Is Driven by Natural Variation of the Sodium Transporter AtHKT1;1. PLoS Genetics, 2010, 6, e1001193.	3.5	317
57	Getting Started in Computational Mass Spectrometry–Based Proteomics. PLoS Computational Biology, 2009, 5, e1000366.	3.2	13
58	Interdependence of Signal Processing and Analysis of Urine ^{1}H NMR Spectra for Metabolic Profiling. Analytical Chemistry, 2009, 81, 6080-6088.	6.5	48
59	Statistical Design of Quantitative Mass Spectrometry-Based Proteomic Experiments. Journal of Proteome Research, 2009, 8, 2144-2156.	3.7	244
60	Correlation between y-Type Ions Observed in Ion Trap and Triple Quadrupole Mass Spectrometers. Journal of Proteome Research, 2009, 8, 4243-4251.	3.7	51
61	Protein Quantification in Label-Free LC-MS Experiments. Journal of Proteome Research, 2009, 8, 5275-5284.	3.7	94
62	Differential Plasma Glycoproteome of p19ARF Skin Cancer Mouse Model Using the Corra Label-Free LC-MS Proteomics Platform. Clinical Proteomics, 2008, 4, 105-116.	2.1	11
63	The leaf ionome as a multivariable system to detect a plant's physiological status. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 12081-12086.	7.1	288
64	Quantification of the Compositional Information Provided by Immonium Ions on a Quadrupole-Time-of-Flight Mass Spectrometer. Analytical Chemistry, 2008, 80, 5596-5606.	6.5	40
65	**_SuperHirn_** – a novel tool for high resolution LC–MS–based peptide/protein profiling. Proteomics, 2007, 7, 3470-3480.	2.2	295
66	Analysis and validation of proteomic data generated by tandem mass spectrometry. Nature Methods, 2007, 4, 787-797.	19.0	585
67	Functional evolution within a protein superfamily. Proteins: Structure, Function and Bioinformatics, 2006, 63, 697-708.	2.6	2
68	Inferential backbone assignment for sparse data. Journal of Biomolecular NMR, 2006, 35, 187-208.	2.8	15
69	Statistical design of experiments as a tool in mass spectrometry. Journal of Mass Spectrometry, 2005, 40, 565-579.	1.6	72
70	Reconsidering complete search algorithms for protein backbone NMR assignment. Bioinformatics, 2005, 21, ii230-ii236.	4.1	15
71	Gene expression profiling of Caco-2 BBe cells suggests a role for specific signaling pathways during intestinal differentiation. Physiological Genomics, 2003, 13, 57-68.	2.3	59
72	Screening for pressure ulcer risk in an acute care hospital. Journal of Clinical Epidemiology, 2002, 55, 498-504.	5.0	68