

# Mark V Ivanov

## 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.

29  
papers

520  
citations

12  
h-index

22  
g-index

39  
ext. papers

777  
ext. citations

4.2  
avg, IF

3.84  
L-index

#	Paper	IF	Citations
29	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> , <b>2021</b> , 20, 1864-1873	5.6	5
28	Improving the Protein Inference from Bottom-Up Proteomic Data Using Identifications from MS1 Spectra. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2021</b> , 32, 1258-1262	3.5	
27	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> , <b>2021</b> , e9045	2.2	3
26	DirectMS1: MS/MS-Free Identification of 1000 Proteins of Cellular Proteomes in 5 Minutes. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 4326-4333	7.8	14
25	Proteome-Wide Analysis of ADAR-Mediated Messenger RNA Editing during Fruit Fly Ontogeny. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 4046-4060	5.6	0
24	Adenosine-to-Inosine RNA Editing in Mouse and Human Brain Proteomes. <i>Proteomics</i> , <b>2019</b> , 19, e190019	4.8	6
23	Pyteomics 4.0: Five Years of Development of a Python Proteomics Framework. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 709-714	5.6	57
22	Scavenger: A Versatile Postsearch Validation Algorithm for Shotgun Proteomics Based on Gradient Boosting. <i>Proteomics</i> , <b>2019</b> , 19, e1800280	4.8	23
21	IdentiPy: An Extensible Search Engine for Protein Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 2249-2255	5.6	26
20	Proteogenomics of Malignant Melanoma Cell Lines: The Effect of Stringency of Exome Data Filtering on Variant Peptide Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 1801-1811	5.6	10
19	Brute-Force Approach for Mass Spectrometry-Based Variant Peptide Identification in Proteogenomics without Personalized Genomic Data. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2018</b> , 29, 435-438	3.5	2
18	Comparative proteomics as a tool for identifying specific alterations within interferon response pathways in human glioblastoma multiforme cells. <i>Oncotarget</i> , <b>2018</b> , 9, 1785-1802	3.3	7
17	Proteogenomics of Adenosine-to-Inosine RNA Editing in the Fruit Fly. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 3889-3903	5.6	5
16	Validation of Peptide Identification Results in Proteomics Using Amino Acid Counting. <i>Proteomics</i> , <b>2018</b> , 18, e1800117	4.8	5
15	Comparative evaluation of label-free quantification methods for shotgun proteomics. <i>Rapid Communications in Mass Spectrometry</i> , <b>2017</b> , 31, 606-612	2.2	32
14	Unbiased False Discovery Rate Estimation for Shotgun Proteomics Based on the Target-Decoy Approach. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 393-397	5.6	33
13	Comparison of False Discovery Rate Control Strategies for Variant Peptide Identifications in Shotgun Proteogenomics. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 1936-1943	5.6	11

12	MS/MS-Free Protein Identification in Complex Mixtures Using Multiple Enzymes with Complementary Specificity. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 3989-3999	5.6	6
11	Adaptation of Decoy Fusion Strategy for Existing Multi-Stage Search Workflows. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2016</b> , 27, 1579-82	3.5	3
10	Exome-based proteogenomics of HEK-293 human cell line: Coding genomic variants identified at the level of shotgun proteome. <i>Proteomics</i> , <b>2016</b> , 16, 1980-91	4.8	18
9	Depletion of human serum albumin in embryo culture media for in vitro fertilization using monolithic columns with immobilized antibodies. <i>Electrophoresis</i> , <b>2016</b> , 37, 2322-7	3.6	8
8	GroupFilter: A software tool for efficient filtering of Morpheus search engine results. <i>Journal of Analytical Chemistry</i> , <b>2016</b> , 71, 1275-1279	1.1	1
7	Methionine to isothreonine conversion as a source of false discovery identifications of genetically encoded variants in proteogenomics. <i>Journal of Proteomics</i> , <b>2015</b> , 120, 169-78	3.9	19
6	PepxmltkB format converter for peptide identification results obtained from tandem mass spectrometry data using X!Tandem search engine. <i>Journal of Analytical Chemistry</i> , <b>2015</b> , 70, 1598-1599	1.1	8
5	Peptide identification in BshotgunB proteomics using tandem mass spectrometry: Comparison of search engine algorithms. <i>Journal of Analytical Chemistry</i> , <b>2015</b> , 70, 1614-1619	1.1	2
4	Exome-driven characterization of the cancer cell lines at the proteome level: the NCI-60 case study. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 5551-60	5.6	27
3	Empirical multidimensional space for scoring peptide spectrum matches in shotgun proteomics. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 1911-20	5.6	38
2	Breath analysis in real time by mass spectrometry in chronic obstructive pulmonary disease. <i>Respiration</i> , <b>2014</b> , 87, 301-10	3.7	39
1	Pyteomics--a Python framework for exploratory data analysis and rapid software prototyping in proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2013</b> , 24, 301-4	3.5	110