

Mark V Ivanov

List of Publications by Year in descending order

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32
papers

887
citations

687220

13
h-index

526166

27
g-index

39
all docs

39
docs citations

39
times ranked

1003
citing authors

#	ARTICLE	IF	CITATIONS
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> , 2013, 24, 301-304.	1.2	153
2	Pyteomics 4.0: Five Years of Development of a Python Proteomics Framework. <i>Journal of Proteome Research</i> , 2019, 18, 709-714.	1.8	116
3	Empirical Multidimensional Space for Scoring Peptide Spectrum Matches in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 1911-1920.	1.8	62
4	Unbiased False Discovery Rate Estimation for Shotgun Proteomics Based on the Target-Decoy Approach. <i>Journal of Proteome Research</i> , 2017, 16, 393-397.	1.8	56
5	IdentiPy: An Extensible Search Engine for Protein Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2249-2255.	1.8	52
6	Scavenger: A Versatile Postsearch Validation Algorithm for Shotgun Proteomics Based on Gradient Boosting. <i>Proteomics</i> , 2019, 19, e1800280.	1.3	51
7	Breath Analysis in Real Time by Mass Spectrometry in Chronic Obstructive Pulmonary Disease. <i>Respiration</i> , 2014, 87, 301-310.	1.2	49
8	Comparative evaluation of label-free quantification methods for shotgun proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2017, 31, 606-612.	0.7	41
9	DirectMS1: MS/MS-Free Identification of 1000 Proteins of Cellular Proteomes in 5 Minutes. <i>Analytical Chemistry</i> , 2020, 92, 4326-4333.	3.2	31
10	Exome-Driven Characterization of the Cancer Cell Lines at the Proteome Level: The NCI-60 Case Study. <i>Journal of Proteome Research</i> , 2014, 13, 5551-5560.	1.8	30
11	Exome-based proteogenomics of HEK-293 human cell line: Coding genomic variants identified at the level of shotgun proteome. <i>Proteomics</i> , 2016, 16, 1980-1991.	1.3	28
12	Methionine to isothreonine conversion as a source of false discovery identifications of genetically encoded variants in proteogenomics. <i>Journal of Proteomics</i> , 2015, 120, 169-178.	1.2	24
13	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.	0.7	19
14	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.	1.8	18
15	MS/MS-Free Protein Identification in Complex Mixtures Using Multiple Enzymes with Complementary Specificity. <i>Journal of Proteome Research</i> , 2017, 16, 3989-3999.	1.8	17
16	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> , 2018, 17, 1801-1811.	1.8	17
17	Adenosine-to-Inosine RNA Editing in Mouse and Human Brain Proteomes. <i>Proteomics</i> , 2019, 19, 1900195.	1.3	17
18	Proteogenomics of Adenosine-to-Inosine RNA Editing in the Fruit Fly. <i>Journal of Proteome Research</i> , 2018, 17, 3889-3903.	1.8	16

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19	Depletion of human serum albumin in embryo culture media for in vitro fertilization using monolithic columns with immobilized antibodies. <i>Electrophoresis</i> , 2016, 37, 2322-2327.	1.3	13
20	Comparison of False Discovery Rate Control Strategies for Variant Peptide Identifications in Shotgun Proteogenomics. <i>Journal of Proteome Research</i> , 2017, 16, 1936-1943.	1.8	13
21	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.	0.8	12
22	Validation of Peptide Identification Results in Proteomics Using Amino Acid Counting. <i>Proteomics</i> , 2018, 18, e1800117.	1.3	9
23	Pepxmltkâ€”a format converter for peptide identification results obtained from tandem mass spectrometry data using X!Tandem search engine. <i>Journal of Analytical Chemistry</i> , 2015, 70, 1598-1599.	0.4	8
24	Adaptation of Decoy Fusion Strategy for Existing Multi-Stage Search Workflows. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1579-1582.	1.2	7
25	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> , 2018, 29, 435-438.	1.2	7
26	Proteome-Wide Analysis of ADAR-Mediated Messenger RNA Editing during Fruit Fly Ontogeny. <i>Journal of Proteome Research</i> , 2020, 19, 4046-4060.	1.8	6
27	Validating Amino Acid Variants in Proteogenomics Using Sequence Coverage by Multiple Reads. <i>Journal of Proteome Research</i> , 2022, 21, 1438-1448.	1.8	6
28	Multimic Profiling Identified EGF Receptor Signaling as a Potential Inhibitor of Type I Interferon Response in Models of Oncolytic Therapy by Vesicular Stomatitis Virus. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5244.	1.8	3
29	Peptide identification in â€œshotgunâ€•proteomics using tandem mass spectrometry: Comparison of search engine algorithms. <i>Journal of Analytical Chemistry</i> , 2015, 70, 1614-1619.	0.4	2
30	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1566-1574.	1.8	2
31	GroupFilter: A software tool for efficient filtering of Morpheus search engine results. <i>Journal of Analytical Chemistry</i> , 2016, 71, 1275-1279.	0.4	1
32	Improving the Protein Inference from Bottom-Up Proteomic Data Using Identifications from MS1 Spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1258-1262.	1.2	0