Mark V Ivanov

List of Publications by Citations

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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	Pyteomics--a Python framework for exploratory data analysis and rapid software prototyping in proteomics. *Journal of the American Society for Mass Spectrometry*, **2013**, 24, 301-4	3.5	110
28	Pyteomics 4.0: Five Years of Development of a Python Proteomics Framework. *Journal of Proteome Research*, **2019**, 18, 709-714	5.6	57
27	Breath analysis in real time by mass spectrometry in chronic obstructive pulmonary disease. *Respiration*, **2014**, 87, 301-10	3.7	39
26	Empirical multidimensional space for scoring peptide spectrum matches in shotgun proteomics. *Journal of Proteome Research*, **2014**, 13, 1911-20	5.6	38
25	Unbiased False Discovery Rate Estimation for Shotgun Proteomics Based on the Target-Decoy Approach. *Journal of Proteome Research*, **2017**, 16, 393-397	5.6	33
24	Comparative evaluation of label-free quantification methods for shotgun proteomics. *Rapid Communications in Mass Spectrometry*, **2017**, 31, 606-612	2.2	32
23	Exome-driven characterization of the cancer cell lines at the proteome level: the NCI-60 case study. *Journal of Proteome Research*, **2014**, 13, 5551-60	5.6	27
22	IdentiPy: An Extensible Search Engine for Protein Identification in Shotgun Proteomics. *Journal of Proteome Research*, **2018**, 17, 2249-2255	5.6	26
21	Scavager: A Versatile Postsearch Validation Algorithm for Shotgun Proteomics Based on Gradient Boosting. *Proteomics*, **2019**, 19, e1800280	4.8	23
20	Methionine to isothreonine conversion as a source of false discovery identifications of genetically encoded variants in proteogenomics. *Journal of Proteomics*, **2015**, 120, 169-78	3.9	19
19	Exome-based proteogenomics of HEK-293 human cell line: Coding genomic variants identified at the level of shotgun proteome. *Proteomics*, **2016**, 16, 1980-91	4.8	18
18	DirectMS1: MS/MS-Free Identification of 1000 Proteins of Cellular Proteomes in 5 Minutes. *Analytical Chemistry*, **2020**, 92, 4326-4333	7.8	14
17	Comparison of False Discovery Rate Control Strategies for Variant Peptide Identifications in Shotgun Proteogenomics. *Journal of Proteome Research*, **2017**, 16, 1936-1943	5.6	11
16	Proteogenomics of Malignant Melanoma Cell Lines: The Effect of Stringency of Exome Data Filtering on Variant Peptide Identification in Shotgun Proteomics. *Journal of Proteome Research*, **2018**, 17, 1801-1811	5.6	10
15	Pepxmltk□ format converter for peptide identification results obtained from tandem mass spectrometry data using X!Tandem search engine. *Journal of Analytical Chemistry*, **2015**, 70, 1598-1599	1.1	8
14	Depletion of human serum albumin in embryo culture media for in vitro fertilization using monolithic columns with immobilized antibodies. *Electrophoresis*, **2016**, 37, 2322-7	3.6	8
13	Comparative proteomics as a tool for identifying specific alterations within interferon response pathways in human glioblastoma multiforme cells. *Oncotarget*, **2018**, 9, 1785-1802	3.3	7

12	Adenosine-to-Inosine RNA Editing in Mouse and Human Brain Proteomes. *Proteomics*, **2019**, 19, e1900195	4.8	6
11	MS/MS-Free Protein Identification in Complex Mixtures Using Multiple Enzymes with Complementary Specificity. *Journal of Proteome Research*, **2017**, 16, 3989-3999	5.6	6
10	Boosting MS1-only Proteomics with Machine Learning Allows 2000 Protein Identifications in Single-Shot Human Proteome Analysis Using 5 min HPLC Gradient. *Journal of Proteome Research*, **2021**, 20, 1864-1873	5.6	5
9	Proteogenomics of Adenosine-to-Inosine RNA Editing in the Fruit Fly. *Journal of Proteome Research*, **2018**, 17, 3889-3903	5.6	5
8	Validation of Peptide Identification Results in Proteomics Using Amino Acid Counting. *Proteomics*, **2018**, 18, e1800117	4.8	5
7	Adaptation of Decoy Fusion Strategy for Existing Multi-Stage Search Workflows. *Journal of the American Society for Mass Spectrometry*, **2016**, 27, 1579-82	3.5	3
6	Biosaur: An open-source Python software for liquid chromatography-mass spectrometry peptide feature detection with ion mobility support. *Rapid Communications in Mass Spectrometry*, **2021**, e9045	2.2	3
5	Brute-Force Approach for Mass Spectrometry-Based Variant Peptide Identification in Proteogenomics without Personalized Genomic Data. *Journal of the American Society for Mass Spectrometry*, **2018**, 29, 435-438	3.5	2
4	Peptide identification in shotgun proteomics using tandem mass spectrometry: Comparison of search engine algorithms. *Journal of Analytical Chemistry*, **2015**, 70, 1614-1619	1.1	2
3	GroupFilter: A software tool for efficient filtering of Morpheus search engine results. *Journal of Analytical Chemistry*, **2016**, 71, 1275-1279	1.1	1
2	Proteome-Wide Analysis of ADAR-Mediated Messenger RNA Editing during Fruit Fly Ontogeny. *Journal of Proteome Research*, **2020**, 19, 4046-4060	5.6	0
1	Improving the Protein Inference from Bottom-Up Proteomic Data Using Identifications from MS1 Spectra. *Journal of the American Society for Mass Spectrometry*, **2021**, 32, 1258-1262	3.5	