

Gelio Alves

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

388
citations

687363

13
h-index

794594

19
g-index

24
all docs

24
docs citations

24
times ranked

487
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of Antibiotic Resistance Proteins via MiCIdâ€™s Augmented Workflow. A Mass Spectrometry-Based Proteomics Approach. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 917-931.	2.8	3
2	Novel Insights into Quantitative Proteomics from an Innovative Bottom-Up Simple Light Isotope Metabolic (bSLIM) Labeling Data Processing Strategy. <i>Journal of Proteome Research</i> , 2021, 20, 1476-1487.	3.7	7
3	Robust Accurate Identification and Biomass Estimates of Microorganisms via Tandem Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 85-102.	2.8	6
4	RAId: Knowledgeâ€™Integrated Proteomics Web Service with Accurate Statistical Significance Assignment. <i>Proteomics</i> , 2019, 19, 1800367.	2.2	1
5	A graphical user interface for RAId, a knowledge integrated proteomics analysis suite with accurate statistics. <i>BMC Research Notes</i> , 2018, 11, 182.	1.4	0
6	Rapid Classification and Identification of Multiple Microorganisms with Accurate Statistical Significance via High-Resolution Tandem Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1721-1737.	2.8	26
7	Confidence assignment for mass spectrometry based peptide identifications via the extreme value distribution. <i>Bioinformatics</i> , 2016, 32, 2642-2649.	4.1	4
8	Identification of Microorganisms by High Resolution Tandem Mass Spectrometry with Accurate Statistical Significance. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 194-210.	2.8	20
9	Mass spectrometry-based protein identification with accurate statistical significance assignment. <i>Bioinformatics</i> , 2015, 31, 699-706.	4.1	17
10	Accuracy Evaluation of the Unified P-Value from Combining Correlated P-Values. <i>PLoS ONE</i> , 2014, 9, e91225.	2.5	23
11	Molecular Isotopic Distribution Analysis (MIDAs) with Adjustable Mass Accuracy. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 57-70.	2.8	16
12	Improving Peptide Identification Sensitivity in Shotgun Proteomics by Stratification of Search Space. <i>Journal of Proteome Research</i> , 2013, 12, 2571-2581.	3.7	24
13	Combining Independent, Weighted P-Values: Achieving Computational Stability by a Systematic Expansion with Controllable Accuracy. <i>PLoS ONE</i> , 2011, 6, e22647.	2.5	14
14	Assigning statistical significance to proteotypic peptides via database searches. <i>Journal of Proteomics</i> , 2011, 74, 199-211.	2.4	12
15	RAId_aPS: MS/MS Analysis with Multiple Scoring Functions and Spectrum-Specific Statistics. <i>PLoS ONE</i> , 2010, 5, e15438.	2.5	20
16	Statistical characterization of a 1D random potential problemâ€™With applications in score statistics of MS-based peptide sequencing. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008, 387, 6538-6544.	2.6	16
17	RAId_DbS: mass-spectrometry based peptide identification web server with knowledge integration. <i>BMC Genomics</i> , 2008, 9, 505.	2.8	19
18	Detection of co-eluted peptides using database search methods. <i>Biology Direct</i> , 2008, 3, 27.	4.6	22

#	ARTICLE	IF	CITATIONS
19	Enhancing Peptide Identification Confidence by Combining Search Methods. Journal of Proteome Research, 2008, 7, 3102-3113.	3.7	66
20	RAId_DbS: Peptide Identification using Database Searches with Realistic Statistics. Biology Direct, 2007, 2, 25.	4.6	26
21	Calibrating E-values for MS2 database search methods. Biology Direct, 2007, 2, 26.	4.6	24
22	Robust accurate identification of peptides (RAId): deciphering MS2 data using a structured library search with de novo based statistics. Bioinformatics, 2005, 21, 3726-3732.	4.1	22