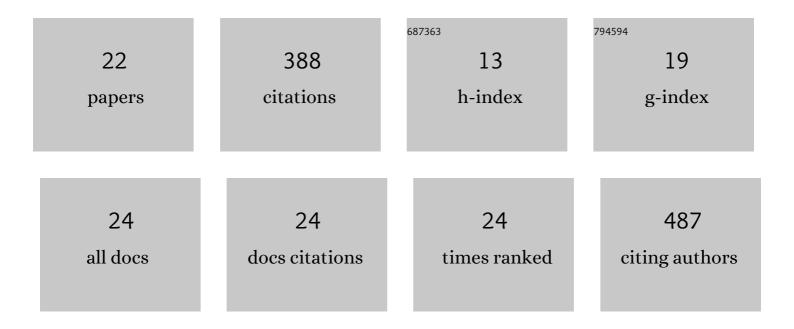
Gelio Alves

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3159122/publications.pdf Version: 2024-02-01



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

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| # | 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 |