

Laurent Gatto

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

14,938
citations

109321

35
h-index

128289

60
g-index

82
all docs

82
docs citations

82
times ranked

31165
citing authors

#	ARTICLE	IF	CITATIONS
1	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	19.0	3,070
2	A cross-platform toolkit for mass spectrometry and proteomics. <i>Nature Biotechnology</i> , 2012, 30, 918-920.	17.5	2,794
3	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	17.5	2,505
4	A subcellular map of the human proteome. <i>Science</i> , 2017, 356, .	12.6	2,079
5	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795
6	Accounting for the Multiple Natures of Missing Values in Label-Free Quantitative Proteomics Data Sets to Compare Imputation Strategies. <i>Journal of Proteome Research</i> , 2016, 15, 1116-1125.	3.7	345
7	MSnbase-an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation. <i>Bioinformatics</i> , 2012, 28, 288-289.	4.1	288
8	DAPAR & ProStaR: software to perform statistical analyses in quantitative discovery proteomics. <i>Bioinformatics</i> , 2017, 33, 135-136.	4.1	245
9	BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , 2017, 33, 2580-2582.	4.1	205
10	A draft map of the mouse pluripotent stem cell spatial proteome. <i>Nature Communications</i> , 2016, 7, 8992.	12.8	197
11	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , 2019, 10, 331.	12.8	146
12	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2765-2775.	3.8	130
13	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1489.	6.6	128
14	Human Urinary Exosomes as Innate Immune Effectors. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2017-2027.	6.1	127
15	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. <i>Nature Protocols</i> , 2017, 12, 1110-1135.	12.0	113
16	Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2147-2167.	3.8	96
17	Ten Simple Rules for Taking Advantage of Git and GitHub. <i>PLoS Computational Biology</i> , 2016, 12, e1004947.	3.2	96
18	Interferon regulatory factor-7-mediated responses are defective in cord blood plasmacytoid dendritic cells. <i>European Journal of Immunology</i> , 2008, 38, 507-517.	2.9	91

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19	ensemblDb: an R package to create and use Ensembl-based annotation resources. <i>Bioinformatics</i> , 2019, 35, 3151-3153.	4.1	90
20	Mass-spectrometry-based spatial proteomics data analysis using <code>pRoloc</code> and <code>pRolocdata</code> . <i>Bioinformatics</i> , 2014, 30, 1322-1324.	4.1	85
21	Effects of Traveling Wave Ion Mobility Separation on Data Independent Acquisition in Proteomics Studies. <i>Journal of Proteome Research</i> , 2013, 12, 2323-2339.	3.7	81
22	MSnbase, Efficient and Elegant R-Based Processing and Visualization of Raw Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2021, 20, 1063-1069.	3.7	68
23	Identification of Trans-Golgi Network Proteins in <i>Arabidopsis thaliana</i> Root Tissue. <i>Journal of Proteome Research</i> , 2014, 13, 763-776.	3.7	65
24	Improving Qualitative and Quantitative Performance for MS ^E -based Label-free Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 2340-2353.	3.7	64
25	Using R and Bioconductor for proteomics data analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 42-51.	2.3	60
26	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. <i>Plant Physiology</i> , 2019, 181, 1721-1738.	4.8	58
27	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	2.2	54
28	A Bayesian mixture modelling approach for spatial proteomics. <i>PLoS Computational Biology</i> , 2018, 14, e1006516.	3.2	53
29	RNA-seq reveals the RNA binding proteins, Hfq and RsmA, play various roles in virulence, antibiotic production and genomic flux in <i>Serratia</i> sp. ATCC 39006. <i>BMC Genomics</i> , 2013, 14, 822.	2.8	50
30	A Foundation for Reliable Spatial Proteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1937-1952.	3.8	49
31	Label-Free Protein Quantification for Plant Golgi Protein Localization and Abundance. <i>Plant Physiology</i> , 2014, 166, 1033-1043.	4.8	48
32	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in α_1 -antitrypsin deficiency. <i>Journal of Hepatology</i> , 2018, 69, 851-860.	3.7	48
33	Visualization of proteomics data using R and Bioconductor. <i>Proteomics</i> , 2015, 15, 1375-1389.	2.2	47
34	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. <i>PLoS Computational Biology</i> , 2016, 12, e1004920.	3.2	47
35	A Modular and Expandable Ecosystem for Metabolomics Data Annotation in R. <i>Metabolites</i> , 2022, 12, 173.	2.9	43
36	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	3.8	42

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37	Testing and Validation of Computational Methods for Mass Spectrometry. Journal of Proteome Research, 2016, 15, 809-814.	3.7	34
38	A Bioconductor workflow for processing and analysing spatial proteomics data. F1000Research, 2016, 5, 2926.	1.6	34
39	Assessing sub-cellular resolution in spatial proteomics experiments. Current Opinion in Chemical Biology, 2019, 48, 123-149.	6.1	31
40	A posteriori quality control for the curation and reuse of public proteomics data. Proteomics, 2011, 11, 2182-2194.	2.2	29
41	Spatiotemporal proteomic profiling of the pro-inflammatory response to lipopolysaccharide in the THP-1 human leukaemia cell line. Nature Communications, 2021, 12, 5773.	12.8	29
42	Negative feedback via RSK modulates Erk-dependent progression from naïve pluripotency. EMBO Reports, 2018, 19, .	4.5	28
43	A Bioconductor workflow for the Bayesian analysis of spatial proteomics. F1000Research, 2019, 8, 446.	1.6	27
44	A Bioconductor workflow for processing and analysing spatial proteomics data. F1000Research, 2016, 5, 2926.	1.6	26
45	Analysis of <i>Drosophila melanogaster</i> proteome dynamics during embryonic development by a combination of label-free proteomics approaches. Proteomics, 2016, 16, 2068-2080.	2.2	24
46	Replication of single-cell proteomics data reveals important computational challenges. Expert Review of Proteomics, 2021, 18, 835-843.	3.0	19
47	The intra-mitochondrial O-GlcNAcylation system rapidly modulates OXPHOS function and ROS release in the heart. Communications Biology, 2022, 5, 349.	4.4	17
48	Dynamic Proteomic Profiling of Extra-Embryonic Endoderm Differentiation in Mouse Embryonic Stem Cells. Stem Cells, 2015, 33, 2712-2725.	3.2	16
49	A semi-supervised Bayesian approach for simultaneous protein sub-cellular localisation assignment and novelty detection. PLoS Computational Biology, 2020, 16, e1008288.	3.2	16
50	Aberrant Membrane Composition and Biophysical Properties Impair Erythrocyte Morphology and Functionality in Elliptocytosis. Biomolecules, 2020, 10, 1120.	4.0	10
51	LC-MS/MS Methods for Absolute Quantification and Identification of Proteins Associated with Chimeric Plant Oil Bodies. Analytical Chemistry, 2011, 83, 9267-9272.	6.5	9
52	Inflammation-Induced Coagulopathy Substantially Differs Between COVID-19 and Septic Shock: A Prospective Observational Study. Frontiers in Medicine, 2021, 8, 780750.	2.6	9
53	Challenges for proteomics core facilities. Proteomics, 2011, 11, 1017-1025.	2.2	8
54	Exploiting the DepMap cancer dependency data using the depmap R package. F1000Research, 0, 10, 416.	1.6	7

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55	Fast approximate inference for variable selection in Dirichlet process mixtures, with an application to pan-cancer proteomics. Statistical Applications in Genetics and Molecular Biology, 2019, 18, .	0.6	6
56	Recent developments in scholarly publishing to improve research practices in the life sciences. Emerging Topics in Life Sciences, 2018, 2, 775-778.	2.6	5
57	Reproducibility and Transparency by Design. Molecular and Cellular Proteomics, 2019, 18, S202-S204.	3.8	5
58	BRAFV600E Induction in Thyrocytes Triggers Important Changes in the miRNAs Content and the Populations of Extracellular Vesicles Released in Thyroid Tumor Microenvironment. Biomedicines, 2022, 10, 755.	3.2	4
59	Spatial Proteomics: Practical Considerations for Data Acquisition and Analysis in Protein Subcellular Localisation Studies. New Developments in Mass Spectrometry, 2014, , 185-210.	0.2	3
60	Data Management Plan for a Biotechnology and Biological Sciences Research Council (BBSRC) Tools and Resources Development Fund (TRDF) Grant. Research Ideas and Outcomes, 0, 3, e11624.	1.0	2
61	HYGIEIA: HYpothesizing the Genesis of Infectious Diseases and Epidemics through an Integrated Systems Biology Approach. Viruses, 2022, 14, 1373.	3.3	2
62	Morphological and mitochondrial DNA analyses indicate the presence of a hybrid zone between two species of leaf beetle (Coleoptera; Chrysomelidae) in Southern Spain. Biological Journal of the Linnean Society, 2008, 94, 105-114.	1.6	1
63	Towards reproducible MSMS data preprocessing, quality control and quantification. Nature Precedings, 2010, , .	0.1	0