

Laurent Gatto

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

14,938
citations

125106

35
h-index

145109

60
g-index

82
all docs

82
docs citations

82
times ranked

34253
citing authors

#	ARTICLE	IF	CITATIONS
1	A Modular and Expandable Ecosystem for Metabolomics Data Annotation in R. <i>Metabolites</i> , 2022, 12, 173.	1.3	43
2	BRAFV600E Induction in Thyrocytes Triggers Important Changes in the miRNAs Content and the Populations of Extracellular Vesicles Released in Thyroid Tumor Microenvironment. <i>Biomedicines</i> , 2022, 10, 755.	1.4	4
3	The intra-mitochondrial O-GlcNAcylation system rapidly modulates OXPHOS function and ROS release in the heart. <i>Communications Biology</i> , 2022, 5, 349.	2.0	17
4	HYGIEIA: HYpothesizing the Genesis of Infectious Diseases and Epidemics through an Integrated Systems Biology Approach. <i>Viruses</i> , 2022, 14, 1373.	1.5	2
5	MSnbase, Efficient and Elegant R-Based Processing and Visualization of Raw Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2021, 20, 1063-1069.	1.8	68
6	Spatiotemporal proteomic profiling of the pro-inflammatory response to lipopolysaccharide in the THP-1 human leukaemia cell line. <i>Nature Communications</i> , 2021, 12, 5773.	5.8	29
7	Replication of single-cell proteomics data reveals important computational challenges. <i>Expert Review of Proteomics</i> , 2021, 18, 835-843.	1.3	19
8	Inflammation-Induced Coagulopathy Substantially Differs Between COVID-19 and Septic Shock: A Prospective Observational Study. <i>Frontiers in Medicine</i> , 2021, 8, 780750.	1.2	9
9	Aberrant Membrane Composition and Biophysical Properties Impair Erythrocyte Morphology and Functionality in Elliptocytosis. <i>Biomolecules</i> , 2020, 10, 1120.	1.8	10
10	Molecular networks in Network Medicine: Development and applications. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2020, 12, e1489.	6.6	128
11	A semi-supervised Bayesian approach for simultaneous protein sub-cellular localisation assignment and novelty detection. <i>PLoS Computational Biology</i> , 2020, 16, e1008288.	1.5	16
12	Reproducibility and Transparency by Design. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S202-S204.	2.5	5
13	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. <i>Plant Physiology</i> , 2019, 181, 1721-1738.	2.3	58
14	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , 2019, 10, 331.	5.8	146
15	ensemldb: an R package to create and use Ensembl-based annotation resources. <i>Bioinformatics</i> , 2019, 35, 3151-3153.	1.8	90
16	Assessing sub-cellular resolution in spatial proteomics experiments. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 123-149.	2.8	31
17	Fast approximate inference for variable selection in Dirichlet process mixtures, with an application to pan-cancer proteomics. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2019, 18, .	0.2	6
18	A Bioconductor workflow for the Bayesian analysis of spatial proteomics. <i>F1000Research</i> , 2019, 8, 446.	0.8	27

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19	A Bayesian mixture modelling approach for spatial proteomics. <i>PLoS Computational Biology</i> , 2018, 14, e1006516.	1.5	53
20	Recent developments in scholarly publishing to improve research practices in the life sciences. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 775-778.	1.1	5
21	Negative feedback via RSK modulates Erk-dependent progression from naïve pluripotency. <i>EMBO Reports</i> , 2018, 19, .	2.0	28
22	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in Î±1-antitrypsin deficiency. <i>Journal of Hepatology</i> , 2018, 69, 851-860.	1.8	48
23	A subcellular map of the human proteome. <i>Science</i> , 2017, 356, .	6.0	2,079
24	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. <i>Nature Protocols</i> , 2017, 12, 1110-1135.	5.5	113
25	BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , 2017, 33, 2580-2582.	1.8	205
26	DAPAR & ProStar: software to perform statistical analyses in quantitative discovery proteomics. <i>Bioinformatics</i> , 2017, 33, 135-136.	1.8	245
27	Analysis of <i>Drosophila melanogaster</i> proteome dynamics during embryonic development by a combination of label-free proteomics approaches. <i>Proteomics</i> , 2016, 16, 2068-2080.	1.3	24
28	A draft map of the mouse pluripotent stem cell spatial proteome. <i>Nature Communications</i> , 2016, 7, 8992.	5.8	197
29	Testing and Validation of Computational Methods for Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 809-814.	1.8	34
30	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.	1.8	345
31	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	0.8	34
32	A Bioconductor workflow for processing and analysing spatial proteomics data. <i>F1000Research</i> , 2016, 5, 2926.	0.8	26
33	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. <i>PLoS Computational Biology</i> , 2016, 12, e1004920.	1.5	47
34	Ten Simple Rules for Taking Advantage of Git and GitHub. <i>PLoS Computational Biology</i> , 2016, 12, e1004947.	1.5	96
35	Dynamic Proteomic Profiling of Extra-Embryonic Endoderm Differentiation in Mouse Embryonic Stem Cells. <i>Stem Cells</i> , 2015, 33, 2712-2725.	1.4	16
36	Visualization of proteomics data using R and Bioconductor. <i>Proteomics</i> , 2015, 15, 1375-1389.	1.3	47

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37	Orchestrating high-throughput genomic analysis with Bioconductor. <i>Nature Methods</i> , 2015, 12, 115-121.	9.0	3,070
38	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	42
39	Mass-spectrometry-based spatial proteomics data analysis using <tt>pRoloc</tt> and <tt>pRolocdata</tt>. <i>Bioinformatics</i> , 2014, 30, 1322-1324.	1.8	85
40	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.	2.5	130
41	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	9.4	2,505
42	Human Urinary Exosomes as Innate Immune Effectors. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2017-2027.	3.0	127
43	A Foundation for Reliable Spatial Proteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1937-1952.	2.5	49
44	Identification of Trans-Golgi Network Proteins in <i>Arabidopsis thaliana</i> Root Tissue. <i>Journal of Proteome Research</i> , 2014, 13, 763-776.	1.8	65
45	Label-Free Protein Quantification for Plant Golgi Protein Localization and Abundance. <i>Plant Physiology</i> , 2014, 166, 1033-1043.	2.3	48
46	Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2147-2167.	2.5	96
47	Using R and Bioconductor for proteomics data analysis. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 42-51.	1.1	60
48	Spatial Proteomics: Practical Considerations for Data Acquisition and Analysis in Protein Subcellular Localisation Studies. <i>New Developments in Mass Spectrometry</i> , 2014, , 185-210.	0.2	3
49	Improving Qualitative and Quantitative Performance for MS^E-based Label-free Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 2340-2353.	1.8	64
50	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.	1.2	50
51	Effects of Traveling Wave Ion Mobility Separation on Data Independent Acquisition in Proteomics Studies. <i>Journal of Proteome Research</i> , 2013, 12, 2323-2339.	1.8	81
52	MSnbase-an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation. <i>Bioinformatics</i> , 2012, 28, 288-289.	1.8	288
53	A cross-platform toolkit for mass spectrometry and proteomics. <i>Nature Biotechnology</i> , 2012, 30, 918-920.	9.4	2,794
54	LC-MS/MS Methods for Absolute Quantification and Identification of Proteins Associated with Chimeric Plant Oil Bodies. <i>Analytical Chemistry</i> , 2011, 83, 9267-9272.	3.2	9

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55	A posteriori quality control for the curation and reuse of public proteomics data. <i>Proteomics</i> , 2011, 11, 2182-2194.	1.3	29
56	Challenges for proteomics core facilities. <i>Proteomics</i> , 2011, 11, 1017-1025.	1.3	8
57	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	1.3	54
58	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.	9.4	795
59	Towards reproducible MSMS data preprocessing, quality control and quantification. <i>Nature Precedings</i> , 2010, , .	0.1	0
60	Interferon regulatory factor-7-mediated responses are defective in cord blood plasmacytoid dendritic cells. <i>European Journal of Immunology</i> , 2008, 38, 507-517.	1.6	91
61	Morphological and mitochondrial DNA analyses indicate the presence of a hybrid zone between two species of leaf beetle (Coleoptera; Chrysomelidae) in Southern Spain. <i>Biological Journal of the Linnean Society</i> , 2008, 94, 105-114.	0.7	1
62	Exploiting the DepMap cancer dependency data using the depmap R package. <i>F1000Research</i> , 0, 10, 416.	0.8	7
63	Data Management Plan for a Biotechnology and Biological Sciences Research Council (BBSRC) Tools and Resources Development Fund (TRDF) Grant. <i>Research Ideas and Outcomes</i> , 0, 3, e11624.	1.0	2