## Laurent Gatto

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Modular and Expandable Ecosystem for Metabolomics Data Annotation in R. Metabolites, 2022, 12, 173.	2.9	43
2	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
3	The intra-mitochondrial O-GlcNAcylation system rapidly modulates OXPHOS function and ROS release in the heart. Communications Biology, 2022, 5, 349.	4.4	17
4	HYGIEIA: HYpothesizing the Genesis of Infectious Diseases and Epidemics through an Integrated Systems Biology Approach. Viruses, 2022, 14, 1373.	3.3	2
5	MSnbase, Efficient and Elegant R-Based Processing and Visualization of Raw Mass Spectrometry Data. Journal of Proteome Research, 2021, 20, 1063-1069.	3.7	68
6	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
7	Replication of single-cell proteomics data reveals important computational challenges. Expert Review of Proteomics, 2021, 18, 835-843.	3.0	19
8	Inflammation-Induced Coagulopathy Substantially Differs Between COVID-19 and Septic Shock: A Prospective Observational Study. Frontiers in Medicine, 2021, 8, 780750.	2.6	9
9	Aberrant Membrane Composition and Biophysical Properties Impair Erythrocyte Morphology and Functionality in Elliptocytosis. Biomolecules, 2020, 10, 1120.	4.0	10
10	Molecular networks in Network Medicine: Development and applications. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1489.	6.6	128
11	A semi-supervised Bayesian approach for simultaneous protein sub-cellular localisation assignment and novelty detection. PLoS Computational Biology, 2020, 16, e1008288.	3.2	16
12	Reproducibility and Transparency by Design. Molecular and Cellular Proteomics, 2019, 18, S202-S204.	3.8	5
13	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. Plant Physiology, 2019, 181, 1721-1738.	4.8	58
14	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. Nature Communications, 2019, 10, 331.	12.8	146
15	ensembldb: an R package to create and use Ensembl-based annotation resources. Bioinformatics, 2019, 35, 3151-3153.	4.1	90
16	Assessing sub-cellular resolution in spatial proteomics experiments. Current Opinion in Chemical Biology, 2019, 48, 123-149.	6.1	31
17	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
18	A Bioconductor workflow for the Bayesian analysis of spatial proteomics. F1000Research, 2019, 8, 446.	1.6	27

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19	A Bayesian mixture modelling approach for spatial proteomics. PLoS Computational Biology, 2018, 14, e1006516.	3.2	53
20	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
21	Negative feedback via RSK modulates Erkâ€dependent progression from naÃ⁻ve pluripotency. EMBO Reports, 2018, 19, .	4.5	28
22	hiPSC hepatocyte model demonstrates the role of unfolded protein response and inflammatory networks in α1-antitrypsin deficiency. Journal of Hepatology, 2018, 69, 851-860.	3.7	48
23	A subcellular map of the human proteome. Science, 2017, 356, .	12.6	2,079
24	Using hyperLOPIT to perform high-resolution mapping of the spatial proteome. Nature Protocols, 2017, 12, 1110-1135.	12.0	113
25	BioContainers: an open-source and community-driven framework for software standardization. Bioinformatics, 2017, 33, 2580-2582.	4.1	205
26	DAPAR & ProStaR: software to perform statistical analyses in quantitative discovery proteomics. Bioinformatics, 2017, 33, 135-136.	4.1	245
27	Analysis of <i>Drosophila melanogaster</i> proteome dynamics during embryonic development by a combination of labelâ€free proteomics approaches. Proteomics, 2016, 16, 2068-2080.	2.2	24
28	A draft map of the mouse pluripotent stem cell spatial proteome. Nature Communications, 2016, 7, 8992.	12.8	197
29	Testing and Validation of Computational Methods for Mass Spectrometry. Journal of Proteome Research, 2016, 15, 809-814.	3.7	34
30	Accounting for the Multiple Natures of Missing Values in Label-Free Quantitative Proteomics Data Sets to Compare Imputation Strategies. Journal of Proteome Research, 2016, 15, 1116-1125.	3.7	345
31	A Bioconductor workflow for processing and analysing spatial proteomics data. F1000Research, 2016, 5, 2926.	1.6	34
32	A Bioconductor workflow for processing and analysing spatial proteomics data. F1000Research, 2016, 5, 2926.	1.6	26
33	Learning from Heterogeneous Data Sources: An Application in Spatial Proteomics. PLoS Computational Biology, 2016, 12, e1004920.	3.2	47
34	Ten Simple Rules for Taking Advantage of Git and GitHub. PLoS Computational Biology, 2016, 12, e1004947.	3.2	96
35	Dynamic Proteomic Profiling of Extra-Embryonic Endoderm Differentiation in Mouse Embryonic Stem Cells, 2015, 33, 2712-2725.	3.2	16
36	Visualization of proteomics data using R and Bioconductor. Proteomics, 2015, 15, 1375-1389.	2.2	47

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37	Orchestrating high-throughput genomic analysis with Bioconductor. Nature Methods, 2015, 12, 115-121.	19.0	3,070
38	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. Molecular and Cellular Proteomics, 2014, 13, 1905-1913.	3.8	42
39	Mass-spectrometry-based spatial proteomics data analysis using <tt>pRoloc</tt> and <tt>pRolocdata</tt> . Bioinformatics, 2014, 30, 1322-1324.	4.1	85
40	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. Molecular and Cellular Proteomics, 2014, 13, 2765-2775.	3.8	130
41	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	17.5	2,505
42	Human Urinary Exosomes as Innate Immune Effectors. Journal of the American Society of Nephrology: JASN, 2014, 25, 2017-2027.	6.1	127
43	A Foundation for Reliable Spatial Proteomics Data Analysis. Molecular and Cellular Proteomics, 2014, 13, 1937-1952.	3.8	49
44	Identification of Trans-Golgi Network Proteins in <i>Arabidopsis thaliana</i> Root Tissue. Journal of Proteome Research, 2014, 13, 763-776.	3.7	65
45	Label-Free Protein Quantification for Plant Golgi Protein Localization and Abundance. Plant Physiology, 2014, 166, 1033-1043.	4.8	48
46	Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach. Molecular and Cellular Proteomics, 2014, 13, 2147-2167.	3.8	96
47	Using R and Bioconductor for proteomics data analysis. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 42-51.	2.3	60
48	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
49	Improving Qualitative and Quantitative Performance for MS <sup>E</sup> -based Label-free Proteomics. Journal of Proteome Research, 2013, 12, 2340-2353.	3.7	64
50	RNA-seq reveals the RNA binding proteins, Hfq and RsmA, play various roles in virulence, antibiotic production and genomic flux in Serratia sp. ATCC 39006. BMC Genomics, 2013, 14, 822.	2.8	50
51	Effects of Traveling Wave Ion Mobility Separation on Data Independent Acquisition in Proteomics Studies. Journal of Proteome Research, 2013, 12, 2323-2339.	3.7	81
52	MSnbase-an R/Bioconductor package for isobaric tagged mass spectrometry data visualization, processing and quantitation. Bioinformatics, 2012, 28, 288-289.	4.1	288
53	A cross-platform toolkit for mass spectrometry and proteomics. Nature Biotechnology, 2012, 30, 918-920.	17.5	2,794
54	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

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55	A posteriori quality control for the curation and reuse of public proteomics data. Proteomics, 2011, 11, 2182-2194.	2.2	29
56	Challenges for proteomics core facilities. Proteomics, 2011, 11, 1017-1025.	2.2	8
57	Organelle proteomics experimental designs and analysis. Proteomics, 2010, 10, 3957-3969.	2.2	54
58	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
59	Towards reproducible MSMS data preprocessing, quality control and quantification. Nature Precedings, 2010, , .	0.1	0
60	Interferon regulatory factor 7â€mediated responses are defective in cord blood plasmacytoid dendritic cells. European Journal of Immunology, 2008, 38, 507-517.	2.9	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. Biological Journal of the Linnean Society, 2008, 94, 105-114.	1.6	1
62	Exploiting the DepMap cancer dependency data using the depmap R package. F1000Research, 0, 10, 416.	1.6	7
63	Data Management Plan for a Biotechnology and Biological Sciences Research Council (BBSRC) Tools and ResourcesÂDevelopment Fund (TRDF) Grant. Research Ideas and Outcomes, 0, 3, e11624.	1.0	2