

Federico Manuel Giorgi

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75
papers

4,192
citations

27
h-index

64
g-index

97
ext. papers

5,835
ext. citations

9.5
avg, IF

6.54
L-index

#	Paper	IF	Citations
75	Oxygen sensing in plants is mediated by an N-end rule pathway for protein destabilization. <i>Nature</i> , 2011 , 479, 419-22	50.4	480
74	Co-expression tools for plant biology: opportunities for hypothesis generation and caveats. <i>Plant, Cell and Environment</i> , 2009 , 32, 1633-51	8.4	373
73	Geographic and Genomic Distribution of SARS-CoV-2 Mutations. <i>Frontiers in Microbiology</i> , 2020 , 11, 1800-7	5.7	333
72	Functional characterization of somatic mutations in cancer using network-based inference of protein activity. <i>Nature Genetics</i> , 2016 , 48, 838-47	36.3	328
71	Genomic variance of the 2019-nCoV coronavirus. <i>Journal of Medical Virology</i> , 2020 , 92, 522-528	19.7	257
70	An extensive evaluation of read trimming effects on Illumina NGS data analysis. <i>PLoS ONE</i> , 2013 , 8, e85034	3.4	252
69	PlaNet: combined sequence and expression comparisons across plant networks derived from seven species. <i>Plant Cell</i> , 2011 , 23, 895-910	11.6	245
68	Genomic and transcriptomic analysis of the AP2/ERF superfamily in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2010 , 11, 719	4.5	209
67	Measurement of the muon reconstruction performance of the ATLAS detector using 2011 and 2012 LHC proton-proton collision data. <i>European Physical Journal C</i> , 2014 , 74, 3130	4.2	166
66	ARACNe-AP: gene network reverse engineering through adaptive partitioning inference of mutual information. <i>Bioinformatics</i> , 2016 , 32, 2233-5	7.2	141
65	Master Regulator Analysis of the SARS-CoV-2/Human Interactome. <i>Journal of Clinical Medicine</i> , 2020 , 9,	5.1	106
64	Robin: an intuitive wizard application for R-based expression microarray quality assessment and analysis. <i>Plant Physiology</i> , 2010 , 153, 642-51	6.6	90
63	Comparative study of RNA-seq- and microarray-derived coexpression networks in <i>Arabidopsis thaliana</i> . <i>Bioinformatics</i> , 2013 , 29, 717-24	7.2	76
62	Histone Deacetylases (HDACs): Evolution, Specificity, Role in Transcriptional Complexes, and Pharmacological Actionability. <i>Genes</i> , 2020 , 11,	4.2	70
61	Structural analysis of the RZZ complex reveals common ancestry with multisubunit vesicle tethering machinery. <i>Structure</i> , 2010 , 18, 616-26	5.2	63
60	Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in <i>Brachypodium distachyon</i> . <i>New Phytologist</i> , 2017 , 215, 1009-1025	9.8	60
59	Preliminary report on severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Spike mutation T478K. <i>Journal of Medical Virology</i> , 2021 , 93, 5638-5643	19.7	59

58	Low duplicability and network fragility of cancer genes. <i>Trends in Genetics</i> , 2008 , 24, 427-30	8.5	56
57	Inhibition of polyamine synthesis and uptake reduces tumor progression and prolongs survival in mouse models of neuroblastoma. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	55
56	Correcting under-reported COVID-19 case numbers: estimating the true scale of the pandemic		48
55	Algorithm-driven artifacts in median polish summarization of microarray data. <i>BMC Bioinformatics</i> , 2010 , 11, 553	3.6	42
54	Coronapp: A web application to annotate and monitor SARS-CoV-2 mutations. <i>Journal of Medical Virology</i> , 2021 , 93, 3238-3245	19.7	42
53	High-definition CpG methylation of novel genes in gastric carcinogenesis identified by next-generation sequencing. <i>Modern Pathology</i> , 2016 , 29, 182-93	9.8	35
52	Transcriptional wiring of cell wall-related genes in Arabidopsis. <i>Molecular Plant</i> , 2009 , 2, 1015-24	14.4	35
51	Age-dependent regulation of ERF-VII transcription factor activity in Arabidopsis thaliana. <i>Plant, Cell and Environment</i> , 2017 , 40, 2333-2346	8.4	33
50	Transcriptome sequencing and microarray design for functional genomics in the extremophile Arabidopsis relative <i>Thellungiella salsuginea</i> (<i>Eutrema salsugineum</i>). <i>BMC Genomics</i> , 2013 , 14, 793	4.5	30
49	Gene regulatory network inference resources: A practical overview. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020 , 1863, 194430	6	28
48	Misexpression of a chloroplast aspartyl protease leads to severe growth defects and alters carbohydrate metabolism in Arabidopsis. <i>Plant Physiology</i> , 2012 , 160, 1237-50	6.6	26
47	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. <i>Cell Stem Cell</i> , 2018 , 22, 575-588.e7	18	24
46	LASSO modeling of the Arabidopsis thaliana seed/seedling transcriptome: a model case for detection of novel mucilage and pectin metabolism genes. <i>Molecular BioSystems</i> , 2012 , 8, 2566-74		24
45	HRE-type genes are regulated by growth-related changes in internal oxygen concentrations during the normal development of potato (<i>Solanum tuberosum</i>) tubers. <i>Plant and Cell Physiology</i> , 2011 , 52, 1957-72	4.9	23
44	SLocX: Predicting Subcellular Localization of Arabidopsis Proteins Leveraging Gene Expression Data. <i>Frontiers in Plant Science</i> , 2011 , 2, 43	6.2	22
43	Measurement of distributions sensitive to the underlying event in inclusive Z-boson production in [Formula: see text] collisions at [Formula: see text] TeV with the ATLAS detector. <i>European Physical Journal C</i> , 2014 , 74, 3195	4.2	21
42	Structural genetics of circulating variants affecting the SARS-CoV-2 spike/human ACE2 complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 1-11	3.6	21
41	Web tools to fight pandemics: the COVID-19 experience. <i>Briefings in Bioinformatics</i> , 2021 , 22, 690-700	13.4	20

40	A modular master regulator landscape controls cancer transcriptional identity. <i>Cell</i> , 2021 , 184, 334-351.e302	20
39	Intratumoral Copper Modulates PD-L1 Expression and Influences Tumor Immune Evasion. <i>Cancer Research</i> , 2020 , 80, 4129-4144	10.1 19
38	Measurements of jet vetoes and azimuthal decorrelations in dijet events produced in [Formula: see text] collisions at [Formula: see text] using the ATLAS detector. <i>European Physical Journal C</i> , 2014 , 74, 3117	4.2 17
37	Geographic and Genomic Distribution of SARS-CoV-2 Mutations	17
36	Inferring protein modulation from gene expression data using conditional mutual information. <i>PLoS ONE</i> , 2014 , 9, e109569	3.7 16
35	Molecular and biochemical responses to wounding in mesocarp of ripe peach (<i>Prunus persica</i> L. Batsch) fruit. <i>Postharvest Biology and Technology</i> , 2014 , 90, 40-51	6.2 14
34	Differential submergence tolerance between juvenile and adult Arabidopsis plants involves the ANAC017 transcription factor. <i>Plant Journal</i> , 2020 , 104, 979-994	6.9 14
33	VULCAN integrates ChIP-seq with patient-derived co-expression networks to identify GRHL2 as a key co-regulator of ERa at enhancers in breast cancer. <i>Genome Biology</i> , 2019 , 20, 91	18.3 13
32	Pan-Cancer and Single-Cell Modeling of Genomic Alterations Through Gene Expression. <i>Frontiers in Genetics</i> , 2019 , 10, 671	4.5 13
31	CEBPA-regulated lncRNAs, new players in the study of acute myeloid leukemia. <i>Journal of Hematology and Oncology</i> , 2014 , 7, 69	22.4 13
30	GENOMIC APPROACHES TO UNVEIL THE PHYSIOLOGICAL PATHWAYS ACTIVATED IN ARABIDOPSIS TREATED WITH PLANT-DERIVED RAW EXTRACTS. <i>Acta Horticulturae</i> , 2013 , 161-174	0.3 13
29	Predicting the response of the dental pulp to SARS-CoV2 infection: a transcriptome-wide effect cross-analysis. <i>Genes and Immunity</i> , 2020 , 21, 360-363	4.4 13
28	corto: a lightweight R package for gene network inference and master regulator analysis. <i>Bioinformatics</i> , 2020 , 36, 3916-3917	7.2 12
27	Detection and removal of spatial bias in multiwell assays. <i>Bioinformatics</i> , 2016 , 32, 1959-65	7.2 11
26	Genomic variance of the 2019-nCoV coronavirus	11
25	The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. <i>Briefings in Bioinformatics</i> , 2013 , 14, 548-55	13.4 7
24	coronapp: A Web Application to Annotate and Monitor SARS-CoV-2 Mutations	7
23	DNA Repair Biomarker for Lung Cancer Risk and its Correlation With Airway Cells Gene Expression. <i>JNCI Cancer Spectrum</i> , 2020 , 4, pkz067	4.6 6

22	Master Regulator Analysis of the SARS-CoV-2/Human interactome		6
21	Copper: An Intracellular Achilles Heel Allowing the Targeting of Epigenetics, Kinase Pathways, and Cell Metabolism in Cancer Therapeutics. <i>ChemMedChem</i> , 2021 , 16, 2315-2329	3.7	5
20	svpluscnv: analysis and visualization of complex structural variation data. <i>Bioinformatics</i> , 2021 , 37, 1912-1914	4.2	4
19	Preliminary report on SARS-CoV-2 Spike mutation T478K		4
18	Dual targeting of the epigenome via FACT complex and histone deacetylase is a potent treatment strategy for DIPG. <i>Cell Reports</i> , 2021 , 35, 108994	10.6	4
17	Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. <i>Nature Biotechnology</i> , 2021 , 39, 215-224	44.5	4
16	Single-Cell Gene Network Analysis and Transcriptional Landscape of MYCN-Amplified Neuroblastoma Cell Lines. <i>Biomolecules</i> , 2021 , 11,	5.9	4
15	Structural Genetics of circulating variants affecting the SARS-CoV-2 Spike / human ACE2 complex		3
14	A History of Heart Failure Is an Independent Risk Factor for Death in Patients Admitted with Coronavirus 19 Disease. <i>Journal of Cardiovascular Development and Disease</i> , 2021 , 8,	4.2	3
13	Spathial: an R package for the evolutionary analysis of biological data. <i>Bioinformatics</i> , 2020 , 36, 4664-4667	7.2	2
12	Intersection between ageing-related Genes and SARS-CoV-2 Interactome: Is it higher than expected?		2
11	A Modular Master Regulator Landscape Determines the Impact of Genetic Alterations on the Transcriptional Identity of Cancer Cells		2
10	Network analysis of CHIP-seq data by VULCAN identifies GRHL2 as a key co-regulator of ERa in luminal breast cancer		2
9	Transcriptional network inference and master regulator analysis of the response to ribosome-inactivating proteins in leukemia cells. <i>Toxicology</i> , 2020 , 441, 152531	4.4	2
8	Wage rigidities and business cycle fluctuations: a linked employer-employee analysis. <i>IZA Journal of Labor Policy</i> , 2016 , 5,	1.8	2
7	Exploiting the molecular basis of age and gender differences in outcomes of SARS-CoV-2 infections. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 4092-4100	6.8	2
6	The R Language: An Engine for Bioinformatics and Data Science. <i>Life</i> , 2022 , 12, 648	3	2
5	corto: a lightweight R package for Gene Network Inference and Master Regulator Analysis		1

4	Differential submergence tolerance between juvenile and adult Arabidopsis plants involves the ANAC017 transcription factor		1
3	Pan-Cancer and Single-Cell modelling of genomic alterations through gene expression		1
2	A G316A Polymorphism in the Ornithine Decarboxylase Gene Promoter Modulates MYCN-Driven Childhood Neuroblastoma. <i>Cancers</i> , 2021 , 13,	6.6	1
1	DIPG-20. Copper chelation therapy targets S-adenosylmethionine (SAM) metabolism and epigenetic regulators in diffuse intrinsic pontine glioma (DIPG). <i>Neuro-Oncology</i> , 2022 , 24, i22-i22		1