

Federico Manuel Giorgi

List of Publications by Year in Descending Order

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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 | The R Language: An Engine for Bioinformatics and Data Science. <i>Life</i> , 2022 , 12, 648 | 3 | 2 |
| 74 | 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 | |
| 73 | svpluscnv: analysis and visualization of complex structural variation data. <i>Bioinformatics</i> , 2021 , 37, 1912-1914 | 4.14 | 4 |
| 72 | A G316A Polymorphism in the Ornithine Decarboxylase Gene Promoter Modulates MYCN-Driven Childhood Neuroblastoma. <i>Cancers</i> , 2021 , 13, | 6.6 | 1 |
| 71 | 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 |
| 70 | 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 |
| 69 | 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 |
| 68 | Copper: An Intracellular AchillesUHeel Allowing the Targeting of Epigenetics, Kinase Pathways, and Cell Metabolism in Cancer Therapeutics. <i>ChemMedChem</i> , 2021 , 16, 2315-2329 | 3.7 | 5 |
| 67 | Web tools to fight pandemics: the COVID-19 experience. <i>Briefings in Bioinformatics</i> , 2021 , 22, 690-700 | 13.4 | 20 |
| 66 | 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 |
| 65 | Oncoprotein-specific molecular interaction maps (SigMaps) for cancer network analyses. <i>Nature Biotechnology</i> , 2021 , 39, 215-224 | 44.5 | 4 |
| 64 | Single-Cell Gene Network Analysis and Transcriptional Landscape of MYCN-Amplified Neuroblastoma Cell Lines. <i>Biomolecules</i> , 2021 , 11, | 5.9 | 4 |
| 63 | 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 |
| 62 | 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 |
| 61 | A modular master regulator landscape controls cancer transcriptional identity. <i>Cell</i> , 2021 , 184, 334-351.e20 | 32.2 | 20 |
| 60 | Histone Deacetylases (HDACs): Evolution, Specificity, Role in Transcriptional Complexes, and Pharmacological Actionability. <i>Genes</i> , 2020 , 11, | 4.2 | 70 |
| 59 | Spatial: an R package for the evolutionary analysis of biological data. <i>Bioinformatics</i> , 2020 , 36, 4664-4667 | 7.2 | 2 |

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| 58 | 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 |
| 57 | Genomic variance of the 2019-nCoV coronavirus. <i>Journal of Medical Virology</i> , 2020 , 92, 522-528 | 19.7 | 257 |
| 56 | Master Regulator Analysis of the SARS-CoV-2/Human Interactome. <i>Journal of Clinical Medicine</i> , 2020 , 9, | 5.1 | 106 |
| 55 | corto: a lightweight R package for gene network inference and master regulator analysis. <i>Bioinformatics</i> , 2020 , 36, 3916-3917 | 7.2 | 12 |
| 54 | Gene regulatory network inference resources: A practical overview. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020 , 1863, 194430 | 6 | 28 |
| 53 | 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 |
| 52 | 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 |
| 51 | Geographic and Genomic Distribution of SARS-CoV-2 Mutations. <i>Frontiers in Microbiology</i> , 2020 , 11, 180057 | 5.7 | 333 |
| 50 | 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 |
| 49 | Intratumoral Copper Modulates PD-L1 Expression and Influences Tumor Immune Evasion. <i>Cancer Research</i> , 2020 , 80, 4129-4144 | 10.1 | 19 |
| 48 | 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 |
| 47 | VULCAN integrates ChIP-seq with patient-derived co-expression networks to identify GRHL2 as a key co-regulator of ERα at enhancers in breast cancer. <i>Genome Biology</i> , 2019 , 20, 91 | 18.3 | 13 |
| 46 | Pan-Cancer and Single-Cell Modeling of Genomic Alterations Through Gene Expression. <i>Frontiers in Genetics</i> , 2019 , 10, 671 | 4.5 | 13 |
| 45 | 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 |
| 44 | 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 |
| 43 | Age-dependent regulation of ERF-VII transcription factor activity in <i>Arabidopsis thaliana</i> . <i>Plant, Cell and Environment</i> , 2017 , 40, 2333-2346 | 8.4 | 33 |
| 42 | 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 |
| 41 | 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 |

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| 40 | Detection and removal of spatial bias in multiwell assays. <i>Bioinformatics</i> , 2016 , 32, 1959-65 | 7.2 | 11 |
| 39 | Wage rigidities and business cycle fluctuations: a linked employer-employee analysis. <i>IZA Journal of Labor Policy</i> , 2016 , 5, | 1.8 | 2 |
| 38 | ARACNe-AP: gene network reverse engineering through adaptive partitioning inference of mutual information. <i>Bioinformatics</i> , 2016 , 32, 2233-5 | 7.2 | 141 |
| 37 | 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 |
| 36 | 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 |
| 35 | 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 |
| 34 | 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 |
| 33 | 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 |
| 32 | Inferring protein modulation from gene expression data using conditional mutual information. <i>PLoS ONE</i> , 2014 , 9, e109569 | 3.7 | 16 |
| 31 | Transcriptome sequencing and microarray design for functional genomics in the extremophile <i>Arabidopsis</i> relative <i>Thellungiella salsuginea</i> (<i>Eutrema salsugineum</i>). <i>BMC Genomics</i> , 2013 , 14, 793 | 4.5 | 30 |
| 30 | 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 |
| 29 | 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 |
| 28 | 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 |
| 27 | An extensive evaluation of read trimming effects on Illumina NGS data analysis. <i>PLoS ONE</i> , 2013 , 8, e85034 | 3.7 | 252 |
| 26 | LASSO modeling of the <i>Arabidopsis thaliana</i> seed/seedling transcriptome: a model case for detection of novel mucilage and pectin metabolism genes. <i>Molecular BioSystems</i> , 2012 , 8, 2566-74 | | 24 |
| 25 | Misexpression of a chloroplast aspartyl protease leads to severe growth defects and alters carbohydrate metabolism in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2012 , 160, 1237-50 | 6.6 | 26 |
| 24 | 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 |
| 23 | SLocX: Predicting Subcellular Localization of <i>Arabidopsis</i> Proteins Leveraging Gene Expression Data. <i>Frontiers in Plant Science</i> , 2011 , 2, 43 | 6.2 | 22 |

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| 22 | 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 |
| 21 | PlaNet: combined sequence and expression comparisons across plant networks derived from seven species. <i>Plant Cell</i> , 2011 , 23, 895-910 | 11.6 | 245 |
| 20 | 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 |
| 19 | Structural analysis of the RZZ complex reveals common ancestry with multisubunit vesicle tethering machinery. <i>Structure</i> , 2010 , 18, 616-26 | 5.2 | 63 |
| 18 | Algorithm-driven artifacts in median polish summarization of microarray data. <i>BMC Bioinformatics</i> , 2010 , 11, 553 | 3.6 | 42 |
| 17 | Genomic and transcriptomic analysis of the AP2/ERF superfamily in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2010 , 11, 719 | 4.5 | 209 |
| 16 | Transcriptional wiring of cell wall-related genes in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2009 , 2, 1015-24 | 14.4 | 35 |
| 15 | 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 |
| 14 | Low duplicability and network fragility of cancer genes. <i>Trends in Genetics</i> , 2008 , 24, 427-30 | 8.5 | 56 |
| 13 | Genomic variance of the 2019-nCoV coronavirus | | 11 |
| 12 | corto: a lightweight R package for Gene Network Inference and Master Regulator Analysis | | 1 |
| 11 | Geographic and Genomic Distribution of SARS-CoV-2 Mutations | | 17 |
| 10 | Intersection between ageing-related Genes and SARS-CoV-2 Interactome: Is it higher than expected? | | 2 |
| 9 | A Modular Master Regulator Landscape Determines the Impact of Genetic Alterations on the Transcriptional Identity of Cancer Cells | | 2 |
| 8 | Differential submergence tolerance between juvenile and adult <i>Arabidopsis</i> plants involves the ANAC017 transcription factor | | 1 |
| 7 | Correcting under-reported COVID-19 case numbers: estimating the true scale of the pandemic | | 48 |
| 6 | Master Regulator Analysis of the SARS-CoV-2/Human interactome | | 6 |
| 5 | coronapp: A Web Application to Annotate and Monitor SARS-CoV-2 Mutations | | 7 |

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| 4 | Structural Genetics of circulating variants affecting the SARS-CoV-2 Spike / human ACE2 complex | 3 |
| 3 | Network analysis of CHIP-seq data by VULCAN identifies GRHL2 as a key co-regulator of ERα in luminal breast cancer | 2 |
| 2 | Pan-Cancer and Single-Cell modelling of genomic alterations through gene expression | 1 |
| 1 | Preliminary report on SARS-CoV-2 Spike mutation T478K | 4 |