

Federico Gaiti

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

1,333
citations

687220

13
h-index

752573

20
g-index

36
all docs

36
docs citations

36
times ranked

2365
citing authors

#	ARTICLE	IF	CITATIONS
1	Early metazoan cell type diversity and the evolution of multicellular gene regulation. <i>Nature Ecology and Evolution</i> , 2018, 2, 1176-1188.	3.4	226
2	Genome-wide cell-free DNA mutational integration enables ultra-sensitive cancer monitoring. <i>Nature Medicine</i> , 2020, 26, 1114-1124.	15.2	216
3	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580.	13.7	195
4	DNA methylation disruption reshapes the hematopoietic differentiation landscape. <i>Nature Genetics</i> , 2020, 52, 378-387.	9.4	154
5	Epigenetic encoding, heritability and plasticity of glioma transcriptional cell states. <i>Nature Genetics</i> , 2021, 53, 1469-1479.	9.4	100
6	Deep conservation of the enhancer regulatory code in animals. <i>Science</i> , 2020, 370, .	6.0	89
7	Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity. <i>Molecular Biology and Evolution</i> , 2015, 32, 2367-2382.	3.5	66
8	Corrupted coordination of epigenetic modifications leads to diverging chromatin states and transcriptional heterogeneity in CLL. <i>Nature Communications</i> , 2019, 10, 1874.	5.8	63
9	Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. <i>ELife</i> , 2017, 6, .	2.8	51
10	Origin and evolution of the metazoan non-coding regulatory genome. <i>Developmental Biology</i> , 2017, 427, 193-202.	0.9	42
11	Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , 2021, 16, 4004-4030.	5.5	34
12	De novo transcriptome assembly reveals high transcriptional complexity in <i>Pisum sativum</i> axillary buds and shows rapid changes in expression of diurnally regulated genes. <i>BMC Genomics</i> , 2017, 18, 221.	1.2	24
13	Sex Determination in <i>Ceratopteris richardii</i> Is Accompanied by Transcriptome Changes That Drive Epigenetic Reprogramming of the Young Gametophyte. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2205-2214.	0.8	22
14	Long non-coding regulatory RNAs in sponges and insights into the origin of animal multicellularity. <i>RNA Biology</i> , 2018, 15, 1-7.	1.5	14
15	Pre-introduction introgression contributes to parallel differentiation and contrasting hybridization outcomes between invasive and native marine mussels. <i>Journal of Evolutionary Biology</i> , 2021, 34, 175-192.	0.8	10
16	De Novo Plant Transcriptome Assembly and Annotation Using Illumina RNA-Seq Reads. <i>Methods in Molecular Biology</i> , 2019, 1933, 265-275.	0.4	9
17	Sponge Long Non-Coding RNAs Are Expressed in Specific Cell Types and Conserved Networks. <i>Non-coding RNA</i> , 2018, 4, 6.	1.3	8
18	Single cell biology – a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 74-97.	1.8	3

#	ARTICLE	IF	CITATIONS
19	Single-Cell Multi-Omics Defines the Cell-Type Specific Impact of SF3B1 Splicing Factor Mutations on Hematopoietic Differentiation in Human Clonal Hematopoiesis and Myelodysplastic Syndromes. <i>Blood</i> , 2021, 138, 145-145.	0.6	3
20	Single-Cell Multi-Omics in Human Clonal Hematopoiesis Reveals That <i>DNMT3A</i> R882 Mutations Perturb Early Progenitor States through Selective Hypomethylation. <i>Blood</i> , 2020, 136, 1-2.	0.6	1
21	Multimodal Single-Cell Profiling Defines the Epigenetic Determinants of Chronic Lymphocytic Leukemia Evolution. <i>Blood</i> , 2018, 132, 1312-1312.	0.6	0
22	Single-Cell Multi-Omics Reveals Distinct Paths to Survival of Admixed BTKC481 Mutant Vs. Wild-Type Cells in Clinically Progressing Chronic Lymphocytic Leukemia. <i>Blood</i> , 2020, 136, 40-42.	0.6	0
23	EPCO-14. DECIPHERING DIFFERENTIATION HIERARCHIES, HERITABILITY AND PLASTICITY IN HUMAN GLIOMAS VIA SINGLE-CELL MULTI-OMICS. <i>Neuro-Oncology</i> , 2020, 22, ii72-ii72.	0.6	0