

Francesco Marabita

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

3,032
citations

361388

20
h-index

477281

29
g-index

33
all docs

33
docs citations

33
times ranked

7789
citing authors

#	ARTICLE	IF	CITATIONS
1	Multimiomics and digital monitoring during lifestyle changes reveal independent dimensions of human biology and health. <i>Cell Systems</i> , 2022, 13, 241-255.e7.	6.2	8
2	Different epigenetic clocks reflect distinct pathophysiological features of multiple sclerosis. <i>Epigenomics</i> , 2019, 11, 1429-1439.	2.1	22
3	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. <i>Scientific Data</i> , 2019, 6, 256.	5.3	26
4	An Algorithmic Information Calculus for Causal Discovery and Reprogramming Systems. <i>IScience</i> , 2019, 19, 1160-1172.	4.1	37
5	High-Throughput Functional Ex-Vivo Drug Testing and Multi-Omics Profiling in Patients with Acute Myeloid Leukemia. <i>Blood</i> , 2019, 134, 4641-4641.	1.4	1
6	Network modules uncover mechanisms of skeletal muscle dysfunction in COPD patients. <i>Journal of Translational Medicine</i> , 2018, 16, 34.	4.4	22
7	Time-resolved transcriptome and proteome landscape of human regulatory T cell (Treg) differentiation reveals novel regulators of FOXP3. <i>BMC Biology</i> , 2018, 16, 47.	3.8	23
8	DNA methylation as a mediator of HLA-DRB1*15:01 and a protective variant in multiple sclerosis. <i>Nature Communications</i> , 2018, 9, 2397.	12.8	147
9	Guidelines for Developing Successful Short Advanced Courses in Systems Medicine and Systems Biology. <i>Cell Systems</i> , 2017, 5, 168-175.	6.2	7
10	Epigenetic research in multiple sclerosis: progress, challenges, and opportunities. <i>Physiological Genomics</i> , 2017, 49, 447-461.	2.3	30
11	Expression of Transient Receptor Potential Channels in the Purified Human Pancreatic \hat{I}^2 -Cells. <i>Pancreas</i> , 2017, 46, 97-101.	1.1	25
12	Smoking induces DNA methylation changes in Multiple Sclerosis patients with exposure-response relationship. <i>Scientific Reports</i> , 2017, 7, 14589.	3.3	55
13	Transcriptomics and methylomics of CD4-positive T cells in arsenic-exposed women. <i>Archives of Toxicology</i> , 2017, 91, 2067-2078.	4.2	26
14	Comprehensive mapping of the effects of azacitidine on DNA methylation, repressive/permmissive histone marks and gene expression in primary cells from patients with MDS and MDS-related disease. <i>Oncotarget</i> , 2017, 8, 28812-28825.	1.8	42
15	Phosphoproteomics Reveals Regulatory T Cell-Mediated DEF6 Dephosphorylation That Affects Cytokine Expression in Human Conventional T Cells. <i>Frontiers in Immunology</i> , 2017, 8, 1163.	4.8	13
16	Serum microRNAs as novel biomarkers for primary sclerosing cholangitis and cholangiocarcinoma. <i>Clinical and Experimental Immunology</i> , 2016, 185, 61-71.	2.6	75
17	Normalization of circulating microRNA expression data obtained by quantitative real-time RT-PCR. <i>Briefings in Bioinformatics</i> , 2016, 17, 204-212.	6.5	211
18	Introduction to Data Types in Epigenomics. <i>Translational Bioinformatics</i> , 2015, , 3-34.	0.0	2

#	ARTICLE	IF	CITATIONS
19	An integrative analysis reveals coordinated reprogramming of the epigenome and the transcriptome in human skeletal muscle after training. <i>Epigenetics</i> , 2014, 9, 1557-1569.	2.7	184
20	Systems Medicine: from molecular features and models to the clinic in COPD. <i>Journal of Translational Medicine</i> , 2014, 12, S4.	4.4	23
21	Interaction between PNPLA3 I148M Variant and Age at Infection in Determining Fibrosis Progression in Chronic Hepatitis C. <i>PLoS ONE</i> , 2014, 9, e106022.	2.5	9
22	Network Biology Empowering Detection and Understanding of Interactions Between Genetic Factors in Development of Complex Phenotypes. , 2014, , 175-194.		0
23	A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data. <i>Bioinformatics</i> , 2013, 29, 189-196.	4.1	1,295
24	An evaluation of analysis pipelines for DNA methylation profiling using the Illumina HumanMethylation450 BeadChip platform. <i>Epigenetics</i> , 2013, 8, 333-346.	2.7	192
25	Identification of serum and tissue micro-RNA expression profiles in different stages of inflammatory bowel disease. <i>Clinical and Experimental Immunology</i> , 2013, 173, 250-258.	2.6	109
26	Intracellular Modulation, Extracellular Disposal and Serum Increase of MiR-150 Mark Lymphocyte Activation. <i>PLoS ONE</i> , 2013, 8, e75348.	2.5	66
27	Identification of New Autoantigens by Protein Array Indicates a Role for IL4 Neutralization in Autoimmune Hepatitis. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1885-1897.	3.8	38
28	Distinct microRNA signatures in human lymphocyte subsets and enforcement of the naive state in CD4+ T cells by the microRNA miR-125b. <i>Nature Immunology</i> , 2011, 12, 796-803.	14.5	222
29	Genetic variation in the <i>interleukin-28B</i> gene is not associated with fibrosis progression in patients with chronic hepatitis C and known date of infection. <i>Hepatology</i> , 2011, 54, 1127-1134.	7.3	115