

Marco Antonio Mendoza-Parra

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,813
citations

623734

14
h-index

501196

28
g-index

35
all docs

35
docs citations

35
times ranked

3409
citing authors

#	ARTICLE	IF	CITATIONS
1	The NANOTUMOR consortium â€œ Towards the Tumor Cell Atlas. <i>Biology of the Cell</i> , 2021, 113, 272-280.	2.0	1
2	Inferring biologically relevant molecular tissue substructures by agglomerative clustering of digitized spatial transcriptomes with multilayer. <i>Cell Systems</i> , 2021, 12, 694-705.e3.	6.2	18
3	Real-time SARS-CoV-2 diagnostic and variants tracking over multiple candidates using nanopore DNA sequencing. <i>Scientific Reports</i> , 2021, 11, 15869.	3.3	11
4	Protocol for using MULTILAYER to reveal molecular tissue substructures from digitized spatial transcriptomes. <i>STAR Protocols</i> , 2021, 2, 100823.	1.2	5
5	A Core Transcription Regulatory Circuitry Defining Microglia Cell Identity Inferred from the Reanalysis of Multiple Human Microglia Differentiation Protocols. <i>Brain Sciences</i> , 2021, 11, 1338.	2.3	1
6	Patient-matched analysis identifies deregulated networks in prostate cancer to guide personalized therapeutic intervention. <i>American Journal of Cancer Research</i> , 2021, 11, 5299-5318.	1.4	0
7	CDYL2 Epigenetically Regulates MIR124 to Control NF-Î²B/STAT3-Dependent Breast Cancer Cell Plasticity. <i>IScience</i> , 2020, 23, 101141.	4.1	22
8	A comprehensive resource for retrieving, visualizing, and integrating functional genomics data. <i>Life Science Alliance</i> , 2020, 3, e201900546.	2.8	5
9	RARÎ² Agonist Drug (C286) Demonstrates Efficacy in a Pre-clinical Neuropathic Pain Model Restoring Multiple Pathways via DNA Repair Mechanisms. <i>IScience</i> , 2019, 20, 554-566.	4.1	7
10	Senescence-associated reprogramming promotes cancer stemness. <i>Nature</i> , 2018, 553, 96-100.	27.8	714
11	Modeling gene-regulatory networks to describe cell fate transitions and predict master regulators. <i>Npj Systems Biology and Applications</i> , 2018, 4, 29.	3.0	15
12	Development of biotin-retinoid conjugates as chemical probes for analysis of retinoid function. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2018, 28, 2442-2445.	2.2	2
13	Epimetheus - a multi-profile normalizer for epigenomic sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 259.	2.6	5
14	LOGIQA: a database dedicated to long-range genome interactions quality assessment. <i>BMC Genomics</i> , 2016, 17, 355.	2.8	3
15	Reconstructed cell fateâ€œregulatory programs in stem cells reveal hierarchies and key factors of neurogenesis. <i>Genome Research</i> , 2016, 26, 1505-1519.	5.5	25
16	Reconstruction of gene regulatory networks reveals chromatin remodelers and key transcription factors in tumorigenesis. <i>Genome Medicine</i> , 2016, 8, 57.	8.2	20
17	NGS-QC Generator: A Quality Control System for ChIP-Seq and Related Deep Sequencing-Generated Datasets. <i>Methods in Molecular Biology</i> , 2016, 1418, 243-265.	0.9	14
18	The inactive X chromosome is epigenetically unstable and transcriptionally labile in breast cancer. <i>Genome Research</i> , 2015, 25, 488-503.	5.5	106

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19	Assessing quality standards for ChIP-seq and related massive parallel sequencing-generated datasets: When rating goes beyond avoiding the crisis. <i>Genomics Data</i> , 2014, 2, 268-273.	1.3	7
20	Senescence-secreted factors activate Myc and sensitize pretransformed cells to TRAIL-induced apoptosis. <i>Aging Cell</i> , 2014, 13, 487-496.	6.7	16
21	Integrative Genomics to Dissect Retinoid Functions. <i>Sub-Cellular Biochemistry</i> , 2014, 70, 181-202.	2.4	2
22	Characterising ChIP-seq binding patterns by model-based peak shape deconvolution. <i>BMC Genomics</i> , 2013, 14, 834.	2.8	15
23	Genome-wide studies of nuclear receptors in cell fate decisions. <i>Seminars in Cell and Developmental Biology</i> , 2013, 24, 706-715.	5.0	18
24	A quality control system for profiles obtained by ChIP sequencing. <i>Nucleic Acids Research</i> , 2013, 41, e196-e196.	14.5	40
25	POLYPHEMUS: R package for comparative analysis of RNA polymerase II ChIP-seq profiles by non-linear normalization. <i>Nucleic Acids Research</i> , 2012, 40, e30-e30.	14.5	7
26	Single-tube linear DNA amplification for genome-wide studies using a few thousand cells. <i>Nature Protocols</i> , 2012, 7, 328-339.	12.0	37
27	Spo11-Accessory Proteins Link Double-Strand Break Sites to the Chromosome Axis in Early Meiotic Recombination. <i>Cell</i> , 2011, 146, 372-383.	28.9	330
28	Single-tube linear DNA amplification (LinDA) for robust ChIP-seq. <i>Nature Methods</i> , 2011, 8, 565-567.	19.0	120
29	Dissecting the retinoid-induced differentiation of F9 embryonal stem cells by integrative genomics. <i>Molecular Systems Biology</i> , 2011, 7, 538.	7.2	76
30	Transferring the Concept of Multinuclearity to Ruthenium Complexes for Improvement of Anticancer Activity. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 916-925.	6.4	168
31	About the variability, quality and reproducibility of ChIP-seq data. <i>ScienceOpen Research</i> , 0, , .	0.6	0
32	Systems Biology Perspectives for Studying Neurodevelopmental Events. , 0, , .		0