Marco Antonio Mendoza-Parra

List of Publications by Year
in descending order

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	Senescence-associated reprogramming promotes cancer stemness. Nature, 2018, 553, 96-100.	27.8	714
2	Spo11-Accessory Proteins Link Double-Strand Break Sites to the Chromosome Axis in Early Meiotic Recombination. Cell, 2011, 146, 372-383.	28.9	330
3	Transferring the Concept of Multinuclearity to Ruthenium Complexes for Improvement of Anticancer Activity. Journal of Medicinal Chemistry, 2009, 52, 916-925.	6.4	168
4	Single-tube linear DNA amplification (LinDA) for robust ChIP-seq. Nature Methods, 2011, 8, 565-567.	19.0	120
5	The inactive X chromosome is epigenetically unstable and transcriptionally labile in breast cancer. Genome Research, 2015, 25, 488-503.	5.5	106
6	Dissecting the retinoidâ€induced differentiation of F9 embryonal stem cells by integrative genomics. Molecular Systems Biology, 2011, 7, 538.	7.2	76
7	A quality control system for profiles obtained by ChIP sequencing. Nucleic Acids Research, 2013, 41, e196-e196.	14.5	40
8	Single-tube linear DNA amplification for genome-wide studies using a few thousand cells. Nature Protocols, 2012, 7, 328-339.	12.0	37
9	Reconstructed cell fateâ€"regulatory programs in stem cells reveal hierarchies and key factors of neurogenesis. Genome Research, 2016, 26, 1505-1519.	5.5	25
10	CDYL2 Epigenetically Regulates MIR124 to Control NF-Î°B/STAT3-Dependent Breast Cancer Cell Plasticity. IScience, 2020, 23, 101141.	4.1	22
11	Reconstruction of gene regulatory networks reveals chromatin remodelers and key transcription factors in tumorigenesis. Genome Medicine, 2016, 8, 57.	8.2	20
12	Genome-wide studies of nuclear receptors in cell fate decisions. Seminars in Cell and Developmental Biology, 2013, 24, 706-715.	5.0	18
13	Inferring biologically relevant molecular tissue substructures by agglomerative clustering of digitized spatial transcriptomes with multilayer. Cell Systems, 2021, 12, 694-705.e3.	6.2	18
14	Senescenceâ€secreted factors activate M yc and sensitize pretransformed cells to TRAILâ€induced apoptosis. Aging Cell, 2014, 13, 487-496.	6.7	16
15	Characterising ChIP-seq binding patterns by model-based peak shape deconvolution. BMC Genomics, 2013, 14, 834.	2.8	15
16	Modeling gene-regulatory networks to describe cell fate transitions and predict master regulators. Npj Systems Biology and Applications, 2018, 4, 29.	3.0	15
17	NGS-QC Generator: A Quality Control System for ChIP-Seq and Related Deep Sequencing-Generated Datasets. Methods in Molecular Biology, 2016, 1418, 243-265.	0.9	14
18	Real-time SARS-CoV-2 diagnostic and variants tracking over multiple candidates using nanopore DNA sequencing. Scientific Reports, 2021, 11, 15869.	3.3	11

#	ARTICLE	IF	CITATIONS
19	POLYPHEMUS: R package for comparative analysis of RNA polymerase II ChIP-seq profiles by non-linear normalization. Nucleic Acids Research, 2012, 40, e30-e30.	14.5	7
20	Assessing quality standards for ChIP-seq and related massive parallel sequencing-generated datasets: When rating goes beyond avoiding the crisis. Genomics Data, 2014, 2, 268-273.	1.3	7
21	RARÎ² Agonist Drug (C286) Demonstrates Efficacy in a Pre-clinical Neuropathic Pain Model Restoring Multiple Pathways via DNA Repair Mechanisms. IScience, 2019, 20, 554-566.	4.1	7
22	Epimetheus - a multi-profile normalizer for epigenomic sequencing data. BMC Bioinformatics, 2017, 18, 259.	2.6	5
23	Protocol for using MULTILAYER to reveal molecular tissue substructures from digitized spatial transcriptomes. STAR Protocols, 2021, 2, 100823.	1.2	5
24	A comprehensive resource for retrieving, visualizing, and integrating functional genomics data. Life Science Alliance, 2020, 3, e201900546.	2.8	5
25	LOGIQA: a database dedicated to long-range genome interactions quality assessment. BMC Genomics, 2016, 17, 355.	2.8	3
26	Integrative Genomics to Dissect Retinoid Functions. Sub-Cellular Biochemistry, 2014, 70, 181-202.	2.4	2
27	Development of biotin-retinoid conjugates as chemical probes for analysis of retinoid function. Bioorganic and Medicinal Chemistry Letters, 2018, 28, 2442-2445.	2.2	2
28	The NANOTUMOR consortium â€" Towards the Tumor Cell Atlas. Biology of the Cell, 2021, 113, 272-280.	2.0	1
29	A Core Transcription Regulatory Circuitry Defining Microglia Cell Identity Inferred from the Reanalysis of Multiple Human Microglia Differentiation Protocols. Brain Sciences, 2021, 11, 1338.	2.3	1
30	About the variability, quality and reproducibility of ChIP-seq data. ScienceOpen Research, 0, , .	0.6	0
31	Systems Biology Perspectives for Studying Neurodevelopmental Events. , 0, , .		0
32	Patient-matched analysis identifies deregulated networks in prostate cancer to guide personalized therapeutic intervention. American Journal of Cancer Research, 2021, 11, 5299-5318.	1.4	0