

Mirana Ramialison

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

1,961
citations

304743

22
h-index

276875

41
g-index

67
all docs

67
docs citations

67
times ranked

3812
citing authors

#	ARTICLE	IF	CITATIONS
1	3D-cardiomics: A spatial transcriptional atlas of the mammalian heart. <i>Journal of Molecular and Cellular Cardiology</i> , 2022, 163, 20-32.	1.9	16
2	The RNA-binding protein SRSF3 has an essential role in megakaryocyte maturation and platelet production. <i>Blood</i> , 2022, 139, 1359-1373.	1.4	9
3	Spatially resolved transcriptomics in immersive environments. <i>Visual Computing for Industry, Biomedicine, and Art</i> , 2022, 5, 2.	3.7	2
4	Detection and identification of cis-regulatory elements using change-point and classification algorithms. <i>BMC Genomics</i> , 2022, 23, 78.	2.8	1
5	Comparative Analysis of Packages and Algorithms for the Analysis of Spatially Resolved Transcriptomics Data. , 2022, , 165-186.		2
6	MonaGO: a novel gene ontology enrichment analysis visualisation system. <i>BMC Bioinformatics</i> , 2022, 23, 69.	2.6	12
7	Adult mouse fibroblasts retain organ-specific transcriptomic identity. <i>ELife</i> , 2022, 11, .	6.0	14
8	CD90 Marks a Mesenchymal Program in Human Thymic Epithelial Cells In Vitro and In Vivo. <i>Frontiers in Immunology</i> , 2022, 13, 846281.	4.8	5
9	Transcriptomic profile dataset of embryonic stem cells (Wild-type and IPO13-Knock Out) with and without oxidative stress. <i>Data in Brief</i> , 2022, 42, 108099.	1.0	3
10	Activation of Nkx2.5 transcriptional program is required for adult myocardial repair. <i>Nature Communications</i> , 2022, 13, .	12.8	7
11	Human Cardiac Transcription Factor Networks. , 2021, , 429-453.		5
12	Towards spatio-temporally resolved developmental cardiac gene regulatory networks in zebrafish. <i>Briefings in Functional Genomics</i> , 2021, , .	2.7	2
13	A cis-regulatory-directed pipeline for the identification of genes involved in cardiac development and disease. <i>Genome Biology</i> , 2021, 22, 335.	8.8	4
14	Transcriptome analysis of the zebrafish <i>atoh7</i> Mutant, <i>lakritz</i> , highlights Atoh7-dependent genetic networks with potential implications for human eye diseases. <i>FASEB BioAdvances</i> , 2020, 2, 434-448.	2.4	2
15	Integrated Value of Influence: An Integrative Method for the Identification of the Most Influential Nodes within Networks. <i>Patterns</i> , 2020, 1, 100052.	5.9	49
16	From whole-mount to single-cell spatial assessment of gene expression in 3D. <i>Communications Biology</i> , 2020, 3, 602.	4.4	82
17	β -catenin drives distinct transcriptional networks in proliferative and non-proliferative cardiomyocytes. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	24
18	Navigating the non-coding genome in heart development and Congenital Heart Disease. <i>Differentiation</i> , 2019, 107, 11-23.	1.9	17

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19	Variable outcomes of human heart attack recapitulated in genetically diverse mice. <i>Npj Regenerative Medicine</i> , 2019, 4, 5.	5.2	20
20	Metformin intervention prevents cardiac dysfunction in a murine model of adult congenital heart disease. <i>Molecular Metabolism</i> , 2019, 20, 102-114.	6.5	11
21	TrawlerWeb: an online de novo motif discovery tool for next-generation sequencing datasets. <i>BMC Genomics</i> , 2018, 19, 238.	2.8	12
22	Control of cardiac jelly dynamics by NOTCH1 and NRG1 defines the building plan for trabeculation. <i>Nature</i> , 2018, 557, 439-445.	27.8	144
23	A gene regulatory network anchored by LIM homeobox 1 for embryonic head development. <i>Genesis</i> , 2018, 56, e23246.	1.6	6
24	Analysis of steric effects in DamID profiling of transcription factor target genes. <i>Genomics</i> , 2017, 109, 75-82.	2.9	8
25	Germline Stem Cell Activity Is Sustained by SALL4-Dependent Silencing of Distinct Tumor Suppressor Genes. <i>Stem Cell Reports</i> , 2017, 9, 956-971.	4.8	50
26	Multicellular Transcriptional Analysis of Mammalian Heart Regeneration. <i>Circulation</i> , 2017, 136, 1123-1139.	1.6	222
27	Cell Type of Origin Dictates the Route to Pluripotency. <i>Cell Reports</i> , 2017, 21, 2649-2660.	6.4	49
28	Combinatorial Ranking of Gene Sets to Predict Disease Relapse: The Retinoic Acid Pathway in Early Prostate Cancer. <i>Frontiers in Oncology</i> , 2017, 7, 30.	2.8	5
29	Point mutations in murine Nkx2-5 phenocopy human congenital heart disease and induce pathogenic Wnt signaling. <i>JCI Insight</i> , 2017, 2, e88271.	5.0	24
30	Formation of the Embryonic Head in the Mouse. <i>Current Topics in Developmental Biology</i> , 2016, 117, 497-521.	2.2	5
31	A novel conditional mouse model for Nkx2-5 reveals transcriptional regulation of cardiac ion channels. <i>Differentiation</i> , 2016, 91, 29-41.	1.9	25
32	Cardiac gene expression data and in silico analysis provide novel insights into human and mouse taste receptor gene regulation. <i>Naunyn-Schmiedeberg's Archives of Pharmacology</i> , 2015, 388, 1009-1027.	3.0	23
33	Asymmetric inheritance of the apical domain and self-renewal of retinal ganglion cell progenitors depend on Anillin function. <i>Development (Cambridge)</i> , 2015, 142, 832-9.	2.5	27
34	<i>Drosophila</i> Hrp48 Is Required for Mushroom Body Axon Growth, Branching and Guidance. <i>PLoS ONE</i> , 2015, 10, e0136610.	2.5	7
35	NKX2-5 mutations causative for congenital heart disease retain functionality and are directed to hundreds of targets. <i>ELife</i> , 2015, 4, .	6.0	54
36	Imp Promotes Axonal Remodeling by Regulating profilin mRNA during Brain Development. <i>Current Biology</i> , 2014, 24, 793-800.	3.9	58

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37	Tyrosine phosphorylation of <sc>LRP</sc>6 by Src and Fer inhibits Wnt/ β -catenin signalling. EMBO Reports, 2014, 15, 1254-1267.	4.5	34
38	Genetic Networks Governing Heart Development. Cold Spring Harbor Perspectives in Medicine, 2014, 4, a013839-a013839.	6.2	46
39	Haematopoietic stem cell induction by somite-derived endothelial cells controlled by meox1. Nature, 2014, 512, 314-318.	27.8	122
40	Cis-regulatory properties of medaka synexpression groups. Development (Cambridge), 2012, 139, 917-928.	2.5	9
41	Close association of olfactory placode precursors and cranial neural crest cells does not predestine cell mixing. Developmental Dynamics, 2012, 241, 1143-1154.	1.8	21
42	Defining the earliest step of cardiovascular progenitor specification during embryonic stem cell differentiation. Journal of Cell Biology, 2011, 192, 751-765.	5.2	114
43	Evolutionary relationships and diversification of barhl genes within retinal cell lineages. BMC Evolutionary Biology, 2011, 11, 340.	3.2	16
44	Defining the earliest step of cardiovascular progenitor specification during embryonic stem cell differentiation. Journal of Experimental Medicine, 2011, 208, i5-i5.	8.5	0
45	Using Trawler_standalone to discover overrepresented motifs in DNA and RNA sequences derived from various experiments including chromatin immunoprecipitation. Nature Protocols, 2010, 5, 323-334.	12.0	15
46	Nlcam modulates midline convergence during anterior neural plate morphogenesis. Developmental Biology, 2010, 339, 14-25.	2.0	46
47	Identification of <i>starmaker</i> in medaka as a putative target gene of Pax2 in the otic vesicle. Developmental Dynamics, 2009, 238, 2860-2866.	1.8	27
48	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). Nature Biotechnology, 2008, 26, 305-312.	17.5	111
49	Rapid identification of PAX2/5/8 direct downstream targets in the otic vesicle by combinatorial use of bioinformatics tools. Genome Biology, 2008, 9, R145.	9.6	18
50	New genes in the evolution of the neural crest differentiation program. Genome Biology, 2007, 8, R36.	9.6	42
51	Trawler: de novo regulatory motif discovery pipeline for chromatin immunoprecipitation. Nature Methods, 2007, 4, 563-565.	19.0	71
52	Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE). OMICS A Journal of Integrative Biology, 2006, 10, 205-208.	2.0	19
53	MEPD: a resource for medaka gene expression patterns. Bioinformatics, 2005, 21, 3195-3197.	4.1	24
54	GSD: a genetic screen database. Mechanisms of Development, 2004, 121, 959-963.	1.7	6

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55	Large-scale expression screening by automated whole-mount in situ hybridization. <i>Mechanisms of Development</i> , 2004, 121, 971-976.	1.7	50
56	A systematic genome-wide screen for mutations affecting organogenesis in Medaka, <i>Oryzias latipes</i> . <i>Mechanisms of Development</i> , 2004, 121, 647-658.	1.7	126
57	MEPD: a Medaka gene expression pattern database. <i>Nucleic Acids Research</i> , 2003, 31, 72-74.	14.5	23
58	Expression profiling in mouse fetal thymus reveals clusters of coordinately expressed genes that mark individual stages of T-cell ontogeny. <i>Immunogenetics</i> , 2002, 54, 469-478.	2.4	4