Mirana Ramialison

List of Publications by Year
in descending order

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	Multicellular Transcriptional Analysis of Mammalian Heart Regeneration. Circulation, 2017, 136, 1123-1139.	1.6	222
2	Control of cardiac jelly dynamics by NOTCH1 and NRG1 defines the building plan for trabeculation. Nature, 2018, 557, 439-445.	27.8	144
3	A systematic genome-wide screen for mutations affecting organogenesis in Medaka, Oryzias latipes. Mechanisms of Development, 2004, 121, 647-658.	1.7	126
4	Haematopoietic stem cell induction by somite-derived endothelial cells controlled by meox1. Nature, 2014, 512, 314-318.	27.8	122
5	Defining the earliest step of cardiovascular progenitor specification during embryonic stem cell differentiation. Journal of Cell Biology, 2011, 192, 751-765.	5.2	114
6	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). Nature Biotechnology, 2008, 26, 305-312.	17.5	111
7	From whole-mount to single-cell spatial assessment of gene expression in 3D. Communications Biology, 2020, 3, 602.	4.4	82
8	Trawler: de novo regulatory motif discovery pipeline for chromatin immunoprecipitation. Nature Methods, 2007, 4, 563-565.	19.0	71
9	Imp Promotes Axonal Remodeling by Regulating profilin mRNA during Brain Development. Current Biology, 2014, 24, 793-800.	3.9	58
10	NKX2-5 mutations causative for congenital heart disease retain functionality and are directed to hundreds of targets. ELife, 2015, 4, .	6.0	54
11	Large-scale expression screening by automated whole-mount in situ hybridization. Mechanisms of Development, 2004, 121, 971-976.	1.7	50
12	Germline Stem Cell Activity Is Sustained by SALL4-Dependent Silencing ofÂDistinct Tumor Suppressor Genes. Stem Cell Reports, 2017, 9, 956-971.	4.8	50
13	Cell Type of Origin Dictates the Route to Pluripotency. Cell Reports, 2017, 21, 2649-2660.	6.4	49
14	Integrated Value of Influence: An Integrative Method for the Identification of the Most Influential Nodes within Networks. Patterns, 2020, 1, 100052.	5.9	49
15	Nlcam modulates midline convergence during anterior neural plate morphogenesis. Developmental Biology, 2010, 339, 14-25.	2.0	46
16	Genetic Networks Governing Heart Development. Cold Spring Harbor Perspectives in Medicine, 2014, 4, a013839-a013839.	6.2	46
17	New genes in the evolution of the neural crest differentiation program. Genome Biology, 2007, 8, R36.	9.6	42
18	Tyrosine phosphorylation of <scp>LRP</scp>6 by Src and Fer inhibits Wnt/Î²â€catenin signalling. EMBO Reports, 2014, 15, 1254-1267.	4.5	34

#	Article	IF	Citations
19	Identification of <i>starmaker–like</i> in medaka as a putative target gene of Pax2 in the otic vesicle. Developmental Dynamics, 2009, 238, 2860-2866.	1.8	27
20	Asymmetric inheritance of the apical domain and self-renewal of retinal ganglion cell progenitors depend on Anillin function. Development (Cambridge), 2015, 142, 832-9.	2.5	27
21	A novel conditional mouse model for Nkx2-5 reveals transcriptional regulation of cardiac ion channels. Differentiation, 2016, 91, 29-41.	1.9	25
22	MEPD: a resource for medaka gene expression patterns. Bioinformatics, 2005, 21, 3195-3197.	4.1	24
23	Î²-catenin drives distinct transcriptional networks in proliferative and non-proliferative cardiomyocytes. Development (Cambridge), 2020, 147, .	2.5	24
24	Point mutations in murine Nkx2-5 phenocopy human congenital heart disease and induce pathogenic Wnt signaling. JCI Insight, 2017, 2, e88271.	5.0	24
25	MEPD: a Medaka gene expression pattern database. Nucleic Acids Research, 2003, 31, 72-74.	14.5	23
26	Cardiac gene expression data and in silico analysis provide novel insights into human and mouse taste receptor gene regulation. Naunyn-Schmiedeberg's Archives of Pharmacology, 2015, 388, 1009-1027.	3.0	23
27	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
28	Variable outcomes of human heart attack recapitulated in genetically diverse mice. Npj Regenerative Medicine, 2019, 4, 5.	5.2	20
29	Development of the Minimum Information Specification forIn SituHybridization and Immunohistochemistry Experiments (MISFISHIE). OMICS A Journal of Integrative Biology, 2006, 10, 205-208.	2.0	19
30	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
31	Navigating the non-coding genome in heart development and Congenital Heart Disease. Differentiation, 2019, 107, 11-23.	1.9	17
32	Evolutionary relationships and diversification of barhl genes within retinal cell lineages. BMC Evolutionary Biology, 2011, 11, 340.	3.2	16
33	3D-cardiomics: A spatial transcriptional atlas of the mammalian heart. Journal of Molecular and Cellular Cardiology, 2022, 163, 20-32.	1.9	16
34	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
35	Adult mouse fibroblasts retain organ-specific transcriptomic identity. ELife, 2022, 11, .	6.0	14
36	TrawlerWeb: an online de novo motif discovery tool for next-generation sequencing datasets. BMC Genomics, 2018, 19, 238.	2.8	12

#	Article	IF	Citations
37	MonaGO: a novel gene ontology enrichment analysis visualisation system. BMC Bioinformatics, 2022, 23, 69.	2.6	12
38	Metformin intervention prevents cardiac dysfunction in a murine model of adult congenital heart disease. Molecular Metabolism, 2019, 20, 102-114.	6.5	11
39	Cis-regulatory properties of medaka synexpression groups. Development (Cambridge), 2012, 139, 917-928.	2.5	9
40	The RNA-binding protein SRSF3 has an essential role in megakaryocyte maturation and platelet production. Blood, 2022, 139, 1359-1373.	1.4	9
41	Analysis of steric effects in DamID profiling of transcription factor target genes. Genomics, 2017, 109, 75-82.	2.9	8
42	Drosophila Hrp48 Is Required for Mushroom Body Axon Growth, Branching and Guidance. PLoS ONE, 2015, 10, e0136610.	2.5	7
43	Activation of Nkx2.5 transcriptional program is required for adult myocardial repair. Nature Communications, 2022, 13, .	12.8	7
44	GSD: a genetic screen database. Mechanisms of Development, 2004, 121, 959-963.	1.7	6
45	A gene regulatory network anchored by LIM homeobox 1 for embryonic head development. Genesis, 2018, 56, e23246.	1.6	6
46	Formation of the Embryonic Head in the Mouse. Current Topics in Developmental Biology, 2016, 117, 497-521.	2.2	5
47	Combinatorial Ranking of Gene Sets to Predict Disease Relapse: The Retinoic Acid Pathway in Early Prostate Cancer. Frontiers in Oncology, 2017, 7, 30.	2.8	5
48	Human Cardiac Transcription Factor Networks. , 2021, , 429-453.		5
49	CD90 Marks a Mesenchymal Program in Human Thymic Epithelial Cells In Vitro and In Vivo. Frontiers in Immunology, 2022, 13, 846281.	4.8	5
50	Expression profiling in mouse fetal thymus reveals clusters of coordinately expressed genes that mark individual stages of T-cell ontogeny. Immunogenetics, 2002, 54, 469-478.	2.4	4
51	A cis-regulatory-directed pipeline for the identification of genes involved in cardiac development and disease. Genome Biology, 2021, 22, 335.	8.8	4
52	Transcriptomic profile dataset of embryonic stem cells (Wild-type and IPO13-Knock Out) with and without oxidative stress. Data in Brief, 2022, 42, 108099.	1.0	3
53	Transcriptome analysis of the zebrafish<i>atoh7â˜'/â˜'</i>Mutant,<i>lakritz</i>, highlights Atoh7â€dependent genetic networks with potential implications for human eye diseases. FASEB BioAdvances, 2020, 2, 434-448.	2.4	2
54	Towards spatio-temporally resolved developmental cardiac gene regulatory networks in zebrafish. Briefings in Functional Genomics, 2021, , .	2.7	2

#	Article	IF	Citations
55	Spatially resolved transcriptomics in immersive environments. Visual Computing for Industry, Biomedicine, and Art, 2022, 5, 2.	3.7	2
56	Comparative Analysis of Packages and Algorithms for the Analysis of Spatially Resolved Transcriptomics Data. , 2022, , 165-186.		2
57	Detection and identification of cis-regulatory elements using change-point and classification algorithms. BMC Genomics, 2022, 23, 78.	2.8	1
58	Defining the earliest step of cardiovascular progenitor specification during embryonic stem cell differentiation. Journal of Experimental Medicine, 2011, 208, i5-i5.	8.5	0