## Doulaye Dembélé

List of Publications by Year in descending order

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<u> Ο Ο ΠΑΥΕ Ο ΕΜΒΑΘΙΑΘ</u>

#	Article	IF	CITATIONS
1	AAVâ€delivered diacylglycerol kinase DGKk achieves longâ€ŧerm rescue of fragile X syndrome mouse model. EMBO Molecular Medicine, 2022, 14, e14649.	6.9	11
2	A method for computing the Perron root for primitive matrices. Numerical Linear Algebra With Applications, 2021, 28, .	1.6	3
3	Subclinical endometritis in dairy cattle is associated with distinct mRNA expression patterns in blood and endometrium. PLoS ONE, 2019, 14, e0220244.	2.5	21
4	Interleukinâ€32 Contributes to Human Nonalcoholic Fatty Liver Disease and Insulin Resistance. Hepatology Communications, 2019, 3, 1205-1220.	4.3	38
5	Co-translational assembly of mammalian nuclear multisubunit complexes. Nature Communications, 2019, 10, 1740.	12.8	90
6	Analysis of high-throughput biological data using their rank values. Statistical Methods in Medical Research, 2019, 28, 2276-2291.	1.5	3
7	Responses to climatic and pathogen threats differ in biodynamic and conventional vines. Scientific Reports, 2018, 8, 16857.	3.3	15
8	Short- and long-term gene expression profiles induced by inhaled TiO2 nanostructured aerosol in rat lung. Toxicology and Applied Pharmacology, 2018, 356, 54-64.	2.8	16
9	Hemidesmosome integrity protects the colon against colitis and colorectal cancer. Gut, 2017, 66, 1748-1760.	12.1	84
10	T Cell Zone Resident Macrophages Silently Dispose of Apoptotic Cells in the Lymph Node. Immunity, 2017, 47, 349-362.e5.	14.3	107
11	Genome-wide Analysis of RARβ Transcriptional Targets in Mouse Striatum Links Retinoic Acid Signaling with Huntington's Disease and Other Neurodegenerative Disorders. Molecular Neurobiology, 2017, 54, 3859-3878.	4.0	34
12	Comments on: fold change rank ordering statistics: a new method for detecting differentially expressed genes. BMC Bioinformatics, 2016, 17, 462.	2.6	3
13	Reduced <i>DICER1</i> Expression Bestows Rheumatoid Arthritis Synoviocytes Proinflammatory Properties and Resistance to Apoptotic Stimuli. Arthritis and Rheumatology, 2016, 68, 1839-1848.	5.6	18
14	Fragile X Mental Retardation Protein (FMRP) controls diacylglycerol kinase activity in neurons. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3619-28.	7.1	79
15	Deletion of the <i>App-Runx1</i> region in mice models human partial monosomy 21. DMM Disease Models and Mechanisms, 2015, 8, 623-634.	2.4	12
16	Opposite Phenotypes of Muscle Strength and Locomotor Function in Mouse Models of Partial Trisomy and Monosomy 21 for the Proximal Hspa13-App Region. PLoS Genetics, 2015, 11, e1005062.	3.5	39
17	Early adaptive response of the retina to a pro-diabetogenic diet: Impairment of cone response and gene expression changes in high-fructose fed rats. Experimental Eye Research, 2015, 135, 37-46.	2.6	11
18	Circulating Human Eosinophils Share a Similar Transcriptional Profile in Asthma and Other Hypereosinophilic Disorders. PLoS ONE, 2015, 10, e0141740.	2.5	30

## Doulaye Dembélé

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19	The Tumor Suppressor Ikaros Shapes the Repertoire of Notch Target Genes in T Cells. Science Signaling, 2014, 7, ra28.	3.6	63
20	Fold change rank ordering statistics: a new method for detecting differentially expressed genes. BMC Bioinformatics, 2014, 15, 14.	2.6	131
21	Mof-associated complexes have overlapping and unique roles in regulating pluripotency in embryonic stem cells and during differentiation. ELife, 2014, 3, .	6.0	43
22	Molars and incisors: show your microarray IDs. BMC Research Notes, 2013, 6, 113.	1.4	43
23	TAF15 is important for cellular proliferation and regulates the expression of a subset of cell cycle genes through miRNAs. Oncogene, 2013, 32, 4646-4655.	5.9	42
24	A Flexible Microarray Data Simulation Model. Microarrays (Basel, Switzerland), 2013, 2, 115-130.	1.4	28
25	β-Catenin activation synergizes with Pten loss and Myc overexpression in Notch-independent T-ALL. Blood, 2013, 122, 694-704.	1.4	47
26	Transcriptomic Analysis of Murine Embryos Lacking Endogenous Retinoic Acid Signaling. PLoS ONE, 2013, 8, e62274.	2.5	27
27	The App-Runx1 Region Is Critical for Birth Defects and Electrocardiographic Dysfunctions Observed in a Down Syndrome Mouse Model. PLoS Genetics, 2012, 8, e1002724.	3.5	25
28	Protracted abstinence from distinct drugs of abuse shows regulation of a common gene network. Addiction Biology, 2012, 17, 1-12.	2.6	48
29	Misregulation of miR-1 processing is associated with heart defects in myotonic dystrophy. Nature Structural and Molecular Biology, 2011, 18, 840-845.	8.2	248
30	Misregulated alternative splicing of BIN1 is associated with T tubule alterations and muscle weakness in myotonic dystrophy. Nature Medicine, 2011, 17, 720-725.	30.7	299
31	Transcriptome profile reveals AMPA receptor dysfunction in the hippocampus of the Rsk2-knockout mice, an animal model of Coffin–Lowry syndrome. Human Genetics, 2011, 129, 255-269.	3.8	23
32	A python module to normalize microarray data by the quantile adjustment method. Infection, Genetics and Evolution, 2011, 11, 765-768.	2.3	1
33	Tripartite Motif 24 (Trim24/Tif1α) Tumor Suppressor Protein Is a Novel Negative Regulator of Interferon (IFN)/Signal Transducers and Activators of Transcription (STAT) Signaling Pathway Acting through Retinoic Acid Receptor α (Rarα) Inhibition. Journal of Biological Chemistry, 2011, 286, 33369-33379.	3.4	63
34	B Cell Signature during Inactive Systemic Lupus Is Heterogeneous: Toward a Biological Dissection of Lupus. PLoS ONE, 2011, 6, e23900.	2.5	54
35	An adult tissue-specific stem cell molecular phenotype is activated in epithelial cancer stem cells and correlated to patient outcome. Cell Cycle, 2010, 9, 321-327.	2.6	17
36	Inhibition of histone deacetylases in rats selfâ€administering cocaine regulates lissencephaly geneâ€1 and reelin gene expression, as revealed by microarray technique. Journal of Neurochemistry, 2010, 113, 236-247.	3.9	12

Doulaye Dembélé

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37	SOX2 Is an Oncogene Activated by Recurrent 3q26.3 Amplifications in Human Lung Squamous Cell Carcinomas. PLoS ONE, 2010, 5, e8960.	2.5	277
38	Cyclin K and cyclin D1b are oncogenic in myeloma cells. Molecular Cancer, 2010, 9, 103.	19.2	15
39	Genomeâ€wide analysis of POU3F2/BRN2 promoter occupancy in human melanoma cells reveals Kitl as a novel regulated target gene. Pigment Cell and Melanoma Research, 2010, 23, 404-418.	3.3	48
40	A single acute pharmacological dose of γ-hydroxybutyrate modifies multiple gene expression patterns in rat hippocampus and frontal cortex. Physiological Genomics, 2010, 41, 146-160.	2.3	19
41	Gene expression profile and response to trastuzumab–docetaxel-based treatment in breast carcinoma. British Journal of Cancer, 2009, 101, 1357-1364.	6.4	27
42	Microarray Data Analysis Using Fuzzy Clustering Algorithms. Studies in Fuzziness and Soft Computing, 2009, , 83-102.	0.8	0
43	Multi-objective optimization for clustering 3-way gene expression data. Advances in Data Analysis and Classification, 2008, 2, 211-225.	1.4	5
44	<i>Gene Expression Is Altered in the Lateral Hypothalamus upon Activation of the mu Opioid Receptor</i> . Annals of the New York Academy of Sciences, 2008, 1129, 175-184.	3.8	26
45	Bcl2, a transcriptional target of p38î±, is critical for neuronal commitment of mouse embryonic stem cells. Cell Death and Differentiation, 2008, 15, 1450-1459.	11.2	32
46	Retinoic acid induces TGFβ-dependent autocrine fibroblast growth. Oncogene, 2008, 27, 477-489.	5.9	18
47	Muâ€opioid receptor activation induces transcriptional plasticity in the central extended amygdala. European Journal of Neuroscience, 2008, 27, 2973-2984.	2.6	74
48	Novel insights into the relationships between dendritic cell subsets in human and mouse revealed by genome-wide expression profiling. Genome Biology, 2008, 9, R17.	9.6	472
49	Transcriptome analysis identifies genes with enriched expression in the mouse central extended amygdala. Neuroscience, 2008, 156, 950-965.	2.3	47
50	Systematic Gene Expression Mapping Clusters Nuclear Receptors According to Their Function in the Brain. Cell, 2007, 131, 405-418.	28.9	145
51	Apoptosis and differentiation commitment: novel insights revealed by gene profiling studies in mouse embryonic stem cells. Cell Death and Differentiation, 2006, 13, 564-575.	11.2	52
52	Head and neck squamous cell carcinoma transcriptome analysis by comprehensive validated differential display. Oncogene, 2006, 25, 1821-1831.	5.9	99
53	ldentification of genes associated with tumorigenesis and metastatic potential of hypopharyngeal cancer by microarray analysis. Oncogene, 2004, 23, 2484-2498.	5.9	242
54	Fuzzy C-means method for clustering microarray data. Bioinformatics, 2003, 19, 973-980.	4.1	470

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55	Density of points clustering, application to transcriptomic data analysis. Nucleic Acids Research, 2002, 30, 3992-4000.	14.5	26
56	Quality Indicators Increase the Reliability of Microarray Data. Genomics, 2002, 80, 385-394.	2.9	23
57	Recursive estimation of fourth-order cumulants with application to identification. Signal Processing, 1998, 68, 127-139.	3.7	14
58	A new FIR system identification method based on fourth-order cumulants: Application to blind equalization. Journal of the Franklin Institute, 1997, 334, 117-133.	3.4	4