

Mathieu Clément-Ziza

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

2,427
citations

471509

17
h-index

677142

22
g-index

24
all docs

24
docs citations

24
times ranked

4212
citing authors

#	ARTICLE	IF	CITATIONS
1	Hirschsprung disease, associated syndromes and genetics: a review. <i>Journal of Medical Genetics</i> , 2007, 45, 1-14.	3.2	848
2	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013, 494, 266-270.	27.8	307
3	The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan. <i>Cell</i> , 2015, 163, 1539-1554.	28.9	200
4	Phenotypic spectrum of CHARGE syndrome in fetuses with CHD7 truncating mutations correlates with expression during human development. <i>Journal of Medical Genetics</i> , 2005, 43, 211-317.	3.2	199
5	Polyalanine expansions in human. <i>Human Molecular Genetics</i> , 2004, 13, R235-R243.	2.9	131
6	Clinical and Pathological Characteristics of <i>KEAP1</i> - and <i>NFE2L2</i> -Mutated Non-Small Cell Lung Carcinoma (NSCLC). <i>Clinical Cancer Research</i> , 2018, 24, 3087-3096.	7.0	116
7	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	17.5	88
8	Rokitansky Syndrome: Clinical Experience and Results of Sigmoid Vaginoplasty in 23 Young Girls. <i>Journal of Urology</i> , 2007, 177, 1107-1111.	0.4	86
9	Epistatic interactions with a common hypomorphic <i>RET</i> allele in syndromic Hirschsprung disease. <i>Human Mutation</i> , 2007, 28, 790-796.	2.5	75
10	Stabilization of RNA during laser capture microdissection by performing experiments under argon atmosphere or using ethanol as a solvent in staining solutions. <i>Rna</i> , 2008, 14, 2698-2704.	3.5	68
11	Natural genetic variation impacts expression levels of coding, non-coding, and antisense transcripts in fission yeast. <i>Molecular Systems Biology</i> , 2014, 10, 764.	7.2	65
12	Evaluation of methods for amplification of picogram amounts of total RNA for whole genome expression profiling. <i>BMC Genomics</i> , 2009, 10, 246.	2.8	54
13	Characterization of a putative type IV aminophospholipid transporter P-type ATPase. <i>Mammalian Genome</i> , 2003, 14, 21-30.	2.2	35
14	Time-dependent Gene Expression Analysis of the Developing Superior Olivary Complex. <i>Journal of Biological Chemistry</i> , 2013, 288, 25865-25879.	3.4	32
15	Epigenomics-Based Identification of Major Cell Identity Regulators within Heterogeneous Cell Populations. <i>Cell Reports</i> , 2016, 17, 3062-3076.	6.4	29
16	Homozygosity for a frequent and weakly penetrant predisposing allele at the <i>RET</i> locus in sporadic Hirschsprung disease. <i>Journal of Medical Genetics</i> , 2005, 42, e18-e18.	3.2	23
17	Stress induces remodelling of yeast interaction and co-expression networks. <i>Molecular BioSystems</i> , 2013, 9, 1697.	2.9	21
18	Genoscape: a Cytoscape plug-in to automate the retrieval and integration of gene expression data and molecular networks. <i>Bioinformatics</i> , 2009, 25, 2617-2618.	4.1	12

#	ARTICLE	IF	CITATIONS
19	Teamwork: Improved eQTL Mapping Using Combinations of Machine Learning Methods. PLoS ONE, 2012, 7, e40916.	2.5	10
20	Rational Design of Dual Peptides Targeting Ghrelin and Y ₂ Receptors to Regulate Food Intake and Body Weight. Journal of Medicinal Chemistry, 2015, 58, 4180-4193.	6.4	9
21	The impact of genomic variation on protein phosphorylation states and regulatory networks. Molecular Systems Biology, 2022, 18, e10712.	7.2	9
22	GeneRetriever: software to extract all genes and transcripts in between two genetic markers to assist design of human custom microarrays. BioTechniques, 2005, 39, 180-184.	1.8	1