

Cristiane Rocha

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

1,344
citations

516710

16
h-index

395702

33
g-index

48
all docs

48
docs citations

48
times ranked

3403
citing authors

#	ARTICLE	IF	CITATIONS
1	The genetic architecture of the human cerebral cortex. <i>Science</i> , 2020, 367, .	12.6	450
2	White matter abnormalities across different epilepsy syndromes in adults: an ENIGMA-Epilepsy study. <i>Brain</i> , 2020, 143, 2454-2473.	7.6	123
3	Transcription Profiling of Signal Transduction-Related Genes in Sugarcane Tissues. <i>DNA Research</i> , 2005, 12, 27-38.	3.4	77
4	MicroRNAs-424 and 206 are potential prognostic markers in spinal onset amyotrophic lateral sclerosis. <i>Journal of the Neurological Sciences</i> , 2016, 368, 19-24.	0.6	76
5	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	12.8	61
6	Toward a better definition of focal cortical dysplasia: An iterative histopathological and genetic agreement trial. <i>Epilepsia</i> , 2021, 62, 1416-1428.	5.1	54
7	International Multicenter Analysis of Brain Structure Across Clinical Stages of Parkinson's Disease. <i>Movement Disorders</i> , 2021, 36, 2583-2594.	3.9	54
8	The <sc>ENIGMAâ€Epilepsy</sc> working group: Mapping disease from large data sets. <i>Human Brain Mapping</i> , 2022, 43, 113-128.	3.6	47
9	MicroRNA Expression Profile in Murine Central Nervous System Development. <i>Journal of Molecular Neuroscience</i> , 2008, 35, 331-337.	2.3	46
10	PBMCs express a transcriptome signature predictor of oxygen uptake responsiveness to endurance exercise training in men. <i>Physiological Genomics</i> , 2015, 47, 13-23.	2.3	33
11	Genetic variability in COVID-19-related genes in the Brazilian population. <i>Human Genome Variation</i> , 2021, 8, 15.	0.7	29
12	The Brazilian Initiative on Precision Medicine (BIPMed): fostering genomic data-sharing of underrepresented populations. <i>Npj Genomic Medicine</i> , 2020, 5, 42.	3.8	25
13	Distribution of local ancestry and evidence of adaptation in admixed populations. <i>Scientific Reports</i> , 2019, 9, 13900.	3.3	24
14	Circulating lymphocytes and monocytes transcriptomic analysis of patients with type 2 diabetes mellitus, dyslipidemia and periodontitis. <i>Scientific Reports</i> , 2020, 10, 8145.	3.3	23
15	Downregulation of 14q32 microRNAs in Primary Human Desmoplastic Medulloblastoma. <i>Frontiers in Oncology</i> , 2013, 3, 254.	2.8	22
16	RNA sequencing reveals region-specific molecular mechanisms associated with epileptogenesis in a model of classical hippocampal sclerosis. <i>Scientific Reports</i> , 2016, 6, 22416.	3.3	18
17	Multi-omics analysis suggests enhanced epileptogenesis in the <i>Cornu Ammonis</i> 3 of the pilocarpine model of mesial temporal lobe epilepsy. <i>Hippocampus</i> , 2021, 31, 122-139.	1.9	18
18	Inflexible ethanol intake: A putative link with the Lrrk2 pathway. <i>Behavioural Brain Research</i> , 2016, 313, 30-37.	2.2	15

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19	A comparison between different reference genes for expression studies in human hippocampal tissue. <i>Journal of Neuroscience Methods</i> , 2012, 208, 44-47.	2.5	14
20	Risk factors for acquisition of Methicillin-resistant <i>Staphylococcus aureus</i> among patients from a burn unit in Brazil. <i>Burns</i> , 2009, 35, 1104-1111.	1.9	12
21	Transcriptome of the Wistar audiogenic rat (WAR) strain following audiogenic seizures. <i>Epilepsy Research</i> , 2018, 147, 22-31.	1.6	11
22	Strand Analysis, a free online program for the computational identification of the best RNA interference (RNAi) targets based on Gibbs free energy. <i>Genetics and Molecular Biology</i> , 2007, 30, 1206-1208.	1.3	9
23	Junctional instability in neuroepithelium and network hyperexcitability in a focal cortical dysplasia human model. <i>Brain</i> , 2022, 145, 1962-1977.	7.6	9
24	LINKGEN: A new algorithm to process data in genetic linkage studies. <i>Genomics</i> , 2008, 91, 544-547.	2.9	8
25	Expression Profile of Genes Potentially Associated with Adequate Glycemic Control in Patients with Type 2 Diabetes Mellitus. <i>Journal of Diabetes Research</i> , 2017, 2017, 1-9.	2.3	8
26	ISER: selection of differentially expressed genes from DNA array data by non-linear data transformations and local fitting. <i>Bioinformatics</i> , 2005, 21, 4427-4429.	4.1	7
27	Using association rule mining to jointly detect clinical features and differentially expressed genes related to chronic inflammatory diseases. <i>PLoS ONE</i> , 2020, 15, e0240269.	2.5	7
28	Loss of control over the ethanol consumption: differential transcriptional regulation in prefrontal cortex. <i>Journal of Neurogenetics</i> , 2017, 31, 170-177.	1.4	6
29	Benchmarking the proteomic profile of animal models of mesial temporal epilepsy. <i>Annals of Clinical and Translational Neurology</i> , 2022, 9, 454-467.	3.7	6
30	Exploring a Region on Chromosome 8p23.1 Displaying Positive Selection Signals in Brazilian Admixed Populations: Additional Insights Into Predisposition to Obesity and Related Disorders. <i>Frontiers in Genetics</i> , 2021, 12, 636542.	2.3	4
31	Placental transcriptome profile of women with sickle cell disease reveals differentially expressed genes involved in migration, trophoblast differentiation and inflammation. <i>Blood Cells, Molecules, and Diseases</i> , 2020, 84, 102458.	1.4	3
32	Methodological differences can affect sequencing depth with a possible impact on the accuracy of genetic diagnosis. <i>Genetics and Molecular Biology</i> , 2020, 43, e20190270.	1.3	2
33	MicroRNA expression profile in epilepsy: breaking molecular barriers. <i>Journal of Epilepsy and Clinical Neurophysiology</i> , 2012, 18, 57-59.	0.1	1
34	A caracterização do perfil de expressão gênica em larga escala em modelos genéticos de epilepsia fornece elementos para entender os mecanismos envolvidos na epileptogênese em roedores. <i>Journal of Epilepsy and Clinical Neurophysiology</i> , 2012, 18, 50-52.	0.1	1
35	Identificação de genes envolvidos na síntese de proteínas de células musculares lisas com expressão aumentada em placas ateromatosas associados a hiperplasia neointimal após implante de stents não-farmacológicos: estudo GENESIS-R. <i>Revista Brasileira De Cardiologia Invasiva</i> , 2012, 20, 140-145.	0.1	0
36	The impact of post-alignment processing procedures on whole-exome sequencing data. <i>Genetics and Molecular Biology</i> , 2020, 43, e20200047.	1.3	0

#	ARTICLE	IF	CITATIONS
37	Title is missing!. , 2020, 15, e0240269.		0
38	Title is missing!. , 2020, 15, e0240269.		0
39	Title is missing!.. , 2020, 15, e0240269.		0
40	Title is missing!.. , 2020, 15, e0240269.		0