Elena Carnero-Montoro

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3328308/publications.pdf

Version: 2024-02-01

24 papers 898 citations

16 h-index 24 g-index

29 all docs 29 docs citations

times ranked

29

2145 citing authors

#	Article	IF	CITATIONS
1	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
2	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. Clinical Epigenetics, 2018, 10, 126.	4.1	110
3	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. Arthritis and Rheumatology, 2021, 73, 1073-1085.	5.6	81
4	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62
5	Epigenome-wide association studies for systemic autoimmune diseases: The road behind and the road ahead. Clinical Immunology, 2018, 196, 21-33.	3.2	37
6	Epigenetic discrimination of identical twins from blood under the forensic scenario. Forensic Science International: Genetics, 2017, 31, 67-80.	3.1	35
7	Extreme Population Differences in the Human Zinc Transporter ZIP4 (SLC39A4) Are Explained by Positive Selection in Sub-Saharan Africa. PLoS Genetics, 2014, 10, e1004128.	3.5	34
8	IgG glycosylation and DNA methylation are interconnected with smoking. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 637-648.	2.4	33
9	2SNP heritability and effects of genetic variants for neutrophil-to-lymphocyte and platelet-to-lymphocyte ratio. Journal of Human Genetics, 2017, 62, 979-988.	2.3	32
10	Genetic and environmental impacts on DNA methylation levels in twins. Epigenomics, 2016, 8, 105-117.	2.1	31
11	Epigenome-Wide Comparative Study Reveals Key Differences Between Mixed Connective Tissue Disease and Related Systemic Autoimmune Diseases. Frontiers in Immunology, 2019, 10, 1880.	4.8	26
12	COPD GWAS variant at 19q13.2 in relation with DNA methylation and gene expression. Human Molecular Genetics, 2018, 27, 396-405.	2.9	24
13	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. Nature Communications, 2018, 9, 3738.	12.8	24
14	Understanding the role of the chromosome 15q25.1 in COPD through epigenetics and transcriptomics. European Journal of Human Genetics, 2018, 26, 709-722.	2.8	21
15	Evolutionary and Functional Evidence for Positive Selection at the Human CD5 Immune Receptor Gene. Molecular Biology and Evolution, 2012, 29, 811-823.	8.9	20
16	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	12.8	18
17	Investigating the Epigenetic Discrimination of Identical Twins Using Buccal Swabs, Saliva, and Cigarette Butts in the Forensic Setting. Genes, 2018, 9, 252.	2.4	17
18	Integrative epigenomics in SjögrenÂ's syndrome reveals novel pathways and a strong interaction between the HLA, autoantibodies and the interferon signature. Scientific Reports, 2021, 11, 23292.	3.3	16

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19	Analysis of Ancestral and Functionally Relevant CD5 Variants in Systemic Lupus Erythematosus Patients. PLoS ONE, 2014, 9, e113090.	2.5	15
20	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. Human Molecular Genetics, 2016, 25, 4339-4349.	2.9	11
21	Expression Quantitative Trait Locus Analysis in Systemic Sclerosis Identifies New Candidate Genes Associated With Multiple Aspects of Disease Pathology. Arthritis and Rheumatology, 2021, 73, 1288-1300.	5.6	9
22	Impact of the functional CD5 polymorphism A471V on the response of chronic lymphocytic leukaemia to conventional chemotherapy regimens. British Journal of Haematology, 2017, 177, 147-150.	2.5	8
23	Analysis of Five Gene Sets in Chimpanzees Suggests Decoupling between the Action of Selection on Protein-Coding and on Noncoding Elements. Genome Biology and Evolution, 2015, 7, 1490-1505.	2.5	1
24	Epigenetics in systemic lupus erythematosus and the integration of molecular pathways., 2021,, 35-61.		0