

Carmen Amador

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

934
citations

567281

15
h-index

526287

27
g-index

38
all docs

38
docs citations

38
times ranked

2457
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. <i>Molecular Psychiatry</i> , 2018, 23, 2347-2362.	7.9	131
2	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
3	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. <i>Genome Medicine</i> , 2017, 9, 23.	8.2	110
4	Identification of epigenome-wide DNA methylation differences between carriers of APOE ϵ 4 and APOE ϵ 2 alleles. <i>Genome Medicine</i> , 2021, 13, 1.	8.2	76
5	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. <i>PLoS Genetics</i> , 2016, 12, e1005804.	3.5	72
6	Recent genomic heritage in Scotland. <i>BMC Genomics</i> , 2015, 16, 437.	2.8	46
7	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	12.8	37
8	Genomic selection for recovery of original genetic background from hybrids of endangered and common breeds. <i>Evolutionary Applications</i> , 2014, 7, 227-237.	3.1	33
9	Genetic Stratification to Identify Risk Groups for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2017, 57, 275-283.	2.6	33
10	Shared Genetics and Couple-Associated Environment Are Major Contributors to the Risk of Both Clinical and Self-Declared Depression. <i>EBioMedicine</i> , 2016, 14, 161-167.	6.1	32
11	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. <i>PLoS Genetics</i> , 2020, 16, e1008785.	3.5	29
12	Removing exogenous information using pedigree data. <i>Conservation Genetics</i> , 2011, 12, 1565-1573.	1.5	26
13	The genetic landscape of Scotland and the Isles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19064-19070.	7.1	24
14	The purge of genetic load through restricted panmixia in a <i>Drosophila</i> experiment. <i>Journal of Evolutionary Biology</i> , 2010, 23, 1937-1946.	1.7	23
15	Advantages of using molecular coancestry in the removal of introgressed genetic material. <i>Genetics Selection Evolution</i> , 2013, 45, 13.	3.0	22
16	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. <i>Wellcome Open Research</i> , 2018, 3, 11.	1.8	19
17	Regional variation in health is predominantly driven by lifestyle rather than genetics. <i>Nature Communications</i> , 2017, 8, 801.	12.8	15
18	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. <i>Wellcome Open Research</i> , 2018, 3, 11.	1.8	15

#	ARTICLE	IF	CITATIONS
19	Use of different sources of information for the recovery and genetic management of endangered populations: Example with the extreme case of Iberian pig Dorado strain. <i>Livestock Science</i> , 2012, 149, 282-288.	1.6	11
20	Regeneration of the variance of metric traits by spontaneous mutation in a <i>Drosophila</i> population. <i>Genetical Research</i> , 2010, 92, 91-102.	0.9	10
21	Molecular Markers Allow to Remove Introgressed Genetic Background: A Simulation Study. <i>PLoS ONE</i> , 2012, 7, e49409.	2.5	10
22	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. <i>Molecular Psychiatry</i> , 2022, 27, 1647-1657.	7.9	10
23	Epigenome-wide analyses identify DNA methylation signatures of dementia risk. <i>Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring</i> , 2020, 12, e12078.	2.4	8
24	Methylome-wide association study of early life stressors and adult mental health. <i>Human Molecular Genetics</i> , 2022, 31, 651-664.	2.9	7
25	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. <i>PLoS Genetics</i> , 2021, 17, e1009750.	3.5	7
26	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730.	6.1	5
27	Complex trait methylation scores in the prediction of major depressive disorder. <i>EBioMedicine</i> , 2022, 79, 104000.	6.1	4
28	Epigenome-wide association study of global cortical volumes in generation Scotland: Scottish family health study. <i>Epigenetics</i> , 2022, 17, 1143-1158.	2.7	3