

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	Methylome-wide association study of early life stressors and adult mental health. <i>Human Molecular Genetics</i> , 2022, 31, 651-664.	2.9	7
2	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
3	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
4	Complex trait methylation scores in the prediction of major depressive disorder. <i>EBioMedicine</i> , 2022, 79, 104000.	6.1	4
5	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
6	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
7	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730.	6.1	5
8	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
9	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
10	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
11	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
12	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. <i>Molecular Psychiatry</i> , 2018, 23, 2347-2362.	7.9	131
13	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
14	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
15	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
16	Regional variation in health is predominantly driven by lifestyle rather than genetics. <i>Nature Communications</i> , 2017, 8, 801.	12.8	15
17	Genetic Stratification to Identify Risk Groups for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2017, 57, 275-283.	2.6	33
18	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

#	ARTICLE	IF	CITATIONS
19	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
20	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. PLoS Genetics, 2016, 12, e1005804.	3.5	72
21	Recent genomic heritage in Scotland. BMC Genomics, 2015, 16, 437.	2.8	46
22	Genomic selection for recovery of original genetic background from hybrids of endangered and common breeds. Evolutionary Applications, 2014, 7, 227-237.	3.1	33
23	Advantages of using molecular coancestry in the removal of introgressed genetic material. Genetics Selection Evolution, 2013, 45, 13.	3.0	22
24	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. Livestock Science, 2012, 149, 282-288.	1.6	11
25	Molecular Markers Allow to Remove Introgressed Genetic Background: A Simulation Study. PLoS ONE, 2012, 7, e49409.	2.5	10
26	Removing exogenous information using pedigree data. Conservation Genetics, 2011, 12, 1565-1573.	1.5	26
27	The purge of genetic load through restricted panmixia in a <i>Drosophila</i> experiment. Journal of Evolutionary Biology, 2010, 23, 1937-1946.	1.7	23
28	Regeneration of the variance of metric traits by spontaneous mutation in a <i>Drosophila</i> population. Genetical Research, 2010, 92, 91-102.	0.9	10