

Robert M Maier

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

4,046
citations

949033

11
h-index

1113639

15
g-index

20
all docs

20
docs citations

20
times ranked

10328
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrative skeletal and paleogenomic analysis of stature variation suggests relatively reduced health for early European farmers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2106743119.	3.3	21
2	Response to Comment on "Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior". <i>Science</i> , 2021, 371, .	6.0	5
3	Genomic evidence consistent with antagonistic pleiotropy may help explain the evolutionary maintenance of same-sex sexual behaviour in humans. <i>Nature Human Behaviour</i> , 2021, 5, 1251-1258.	6.2	27
4	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	0.7	137
5	No statistical evidence for an effect of CCR5- $\Delta 32$ on lifespan in the UK Biobank cohort. <i>Nature Medicine</i> , 2020, 26, 178-180.	15.2	16
6	Genetic contributions to variation in human stature in prehistoric Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21484-21492.	3.3	64
7	Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior. <i>Science</i> , 2019, 365, .	6.0	245
8	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	2.8	276
9	Genome studies must account for history"Response. <i>Science</i> , 2019, 366, 1461-1462.	6.0	4
10	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. <i>Nature Communications</i> , 2018, 9, 989.	5.8	136
11	Causal associations between risk factors and common diseases inferred from GWAS summary data. <i>Nature Communications</i> , 2018, 9, 224.	5.8	629
12	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
13	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. <i>American Journal of Human Genetics</i> , 2015, 96, 283-294.	2.6	225