

Michael C Turchin

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

2,890
citations

1162367

8
h-index

1281420

11
g-index

22
all docs

22
docs citations

22
times ranked

7862
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide polygenic score to predict chronic kidney disease across ancestries. <i>Nature Medicine</i> , 2022, 28, 1412-1420.	15.2	48
2	Leveraging health systems data to characterize a large effect variant conferring risk for liver disease in Puerto Ricans. <i>American Journal of Human Genetics</i> , 2021, 108, 2099-2111.	2.6	4
3	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. <i>PLoS Genetics</i> , 2019, 15, e1008431.	1.5	14
4	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	2.8	276
5	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
6	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
7	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
8	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
9	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
10	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
11	The deleterious mutation load is insensitive to recent population history. <i>Nature Genetics</i> , 2014, 46, 220-224.	9.4	279
12	Gencrypt: one-way cryptographic hashes to detect overlapping individuals across samples. <i>Bioinformatics</i> , 2012, 28, 886-888.	1.8	10
13	Temporally Variable Selection on Proteolysis-Related Reproductive Tract Proteins in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 229-238.	3.5	12
14	Evidence of widespread selection on standing variation in Europe at height-associated SNPs. <i>Nature Genetics</i> , 2012, 44, 1015-1019.	9.4	315
15	Genome-wide Association of Copy-Number Variation Reveals an Association between Short Stature and the Presence of Low-Frequency Genomic Deletions. <i>American Journal of Human Genetics</i> , 2011, 89, 751-759.	2.6	63
16	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	18.7	1,789
17	Evidence for Positive Selection on <i>Drosophila melanogaster</i> Seminal Fluid Protease Homologs. <i>Molecular Biology and Evolution</i> , 2008, 25, 497-506.	3.5	54