

# Michael C Turchin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8889564/publications.pdf>

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	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
2	Evidence of widespread selection on standing variation in Europe at height-associated SNPs. <i>Nature Genetics</i> , 2012, 44, 1015-1019.	9.4	315
3	The deleterious mutation load is insensitive to recent population history. <i>Nature Genetics</i> , 2014, 46, 220-224.	9.4	279
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	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
6	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
7	Genome-wide polygenic score to predict chronic kidney disease across ancestries. <i>Nature Medicine</i> , 2022, 28, 1412-1420.	15.2	48
8	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. <i>PLoS Genetics</i> , 2019, 15, e1008431.	1.5	14
9	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
10	Gencrypt: one-way cryptographic hashes to detect overlapping individuals across samples. <i>Bioinformatics</i> , 2012, 28, 886-888.	1.8	10
11	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
12	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
13	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
14	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
15	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
16	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0
17	Bayesian multivariate reanalysis of large genetic studies identifies many new associations. , 2019, 15, e1008431.		0