Jennifer Asimit

List of Publications by Year
in descending order

25 papers	1,381 citations	623734 14 h-index	677142 22 g-index
28 all docs	28 docs citations	28 times ranked	4152 citing authors

#	Article	IF	Citations
1	The African Genome Variation Project shapes medical genetics in Africa. Nature, 2015, 517, 327-332.	27.8	473
2	Rare Variant Association Analysis Methods for Complex Traits. Annual Review of Genetics, 2010, 44, 293-308.	7.6	238
3	Rare variants in <i>PPARG</i> with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	7.1	152
4	A Combined Functional Annotation Score for Non-Synonymous Variants. Human Heredity, 2012, 73, 47-51.	0.8	90
5	Trans-ethnic study design approaches for fine-mapping. European Journal of Human Genetics, 2016, 24, 1330-1336.	2.8	75
6	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927.	12.8	64
7	ARIEL and AMELIA: Testing for an Accumulation of Rare Variants Using Next-Generation Sequencing Data. Human Heredity, 2012, 73, 84-94.	0.8	51
8	Genome‐Wide Association Analysis of Imputed Rare Variants: Application to Seven Common Complex Diseases. Genetic Epidemiology, 2012, 36, 785-796.	1.3	36
9	Fine-mapping genetic associations. Human Molecular Genetics, 2020, 29, R81-R88.	2.9	32
10	Stochastic search and joint fine-mapping increases accuracy and identifies previously unreported associations in immune-mediated diseases. Nature Communications, 2019, 10, 3216.	12.8	24
11	Imputation of Rare Variants in Next-Generation Association Studies. Human Heredity, 2012, 74, 196-204.	0.8	22
12	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
13	Defining the power limits of genome‐wide association scan meta‐analyses. Genetic Epidemiology, 2011, 35, 781-789.	1.3	18
14	An evaluation of different meta-analysis approaches in the presence of allelic heterogeneity. European Journal of Human Genetics, 2012, 20, 709-712.	2.8	14
15	The flashfm approach for fine-mapping multiple quantitative traits. Nature Communications, 2021, 12, 6147.	12.8	14
16	Testing for rare variant associations in complex diseases. Genome Medicine, 2011, 3, 24.	8.2	11
17	Region-based analysis in genome-wide association study of Framingham Heart Study blood lipid phenotypes. BMC Proceedings, 2009, 3, S127.	1.6	10
18	Regression models, scan statistics and reappearance probabilities to detect regions of association between gene expression and copy number. Statistics in Medicine, 2011, 30, 1157-1178.	1.6	6

#	Article	IF	Citations
19	Parametric Modeling of Reaction Time Experiment Data. Biometrics, 2003, 59, 661-669.	1.4	5
20	A Bayesian Approach to the Overlap Analysis of Epidemiologically Linked Traits. Genetic Epidemiology, 2015, 39, 624-634.	1.3	4
21	<i>Flashfm-ivis</i>: interactive visualization for fine-mapping of multiple quantitative traits. Bioinformatics, 2022, 38, 4238-4242.	4.1	2
22	AN EVALUATION OF POWER TO DETECT LOW-FREQUENCY VARIANT ASSOCIATIONS USING ALLELE-MATCHING TESTS THAT ACCOUNT FOR UNCERTAINTY. , 2010, , 100-105.		1
23	Third order point process intensity estimation for reaction time experiment data. Canadian Journal of Statistics, 2005, 33, 243-257.	0.9	0
24	A two-stage inter-rater approach for enrichment testing of variants associated with multiple traits. European Journal of Human Genetics, 2017, 25, 341-349.	2.8	0
25	Collapsing Approaches for the Association Analysis of Rare Variants. , 2015, , 135-148.		0