Jennifer Asimit

List of Publications by Year
in descending order

25	1,381	623734 14	677142 22
papers	citations	h-index	g-index

28	28	28	4152
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Flashfm-ivis: interactive visualization for fine-mapping of multiple quantitative traits. Bioinformatics, 2022, 38, 4238-4242.	4.1	2
2	The flashfm approach for fine-mapping multiple quantitative traits. Nature Communications, 2021, 12, 6147.	12.8	14
3	Fine-mapping genetic associations. Human Molecular Genetics, 2020, 29, R81-R88.	2.9	32
4	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
5	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
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	Trans-ethnic study design approaches for fine-mapping. European Journal of Human Genetics, 2016, 24, 1330-1336.	2.8	75
8	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
9	A Bayesian Approach to the Overlap Analysis of Epidemiologically Linked Traits. Genetic Epidemiology, 2015, 39, 624-634.	1.3	4
10	The African Genome Variation Project shapes medical genetics in Africa. Nature, 2015, 517, 327-332.	27.8	473
11	Collapsing Approaches for the Association Analysis of Rare Variants. , 2015, , 135-148.		0
12	Rare variants in PPARG 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
13	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
14	A Combined Functional Annotation Score for Non-Synonymous Variants. Human Heredity, 2012, 73, 47-51.	0.8	90
15	ARIEL and AMELIA: Testing for an Accumulation of Rare Variants Using Next-Generation Sequencing Data. Human Heredity, 2012, 73, 84-94.	0.8	51
16	Genomeâ€Wide Association Analysis of Imputed Rare Variants: Application to Seven Common Complex Diseases. Genetic Epidemiology, 2012, 36, 785-796.	1.3	36
17	Imputation of Rare Variants in Next-Generation Association Studies. Human Heredity, 2012, 74, 196-204.	0.8	22
18	Testing for rare variant associations in complex diseases. Genome Medicine, 2011, 3, 24.	8.2	11

#	Article	IF	Citations
19	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
20	Defining the power limits of genomeâ€wide association scan metaâ€analyses. Genetic Epidemiology, 2011, 35, 781-789.	1.3	18
21	Rare Variant Association Analysis Methods for Complex Traits. Annual Review of Genetics, 2010, 44, 293-308.	7.6	238
22	AN EVALUATION OF POWER TO DETECT LOW-FREQUENCY VARIANT ASSOCIATIONS USING ALLELE-MATCHING TESTS THAT ACCOUNT FOR UNCERTAINTY. , 2010, , 100-105.		1
23	Region-based analysis in genome-wide association study of Framingham Heart Study blood lipid phenotypes. BMC Proceedings, 2009, 3, S127.	1.6	10
24	Third order point process intensity estimation for reaction time experiment data. Canadian Journal of Statistics, 2005, 33, 243-257.	0.9	0
25	Parametric Modeling of Reaction Time Experiment Data. Biometrics, 2003, 59, 661-669.	1.4	5