Chiara Sabatti

List of Publications by Year
in descending order

37 papers	4,283 citations	430874 18 h-index	361022 35 g-index
48 all docs	48 docs citations	48 times ranked	9145 citing authors

#	Article	IF	Citations
1	Filtering the Rejection Set While Preserving False Discovery Rate Control. Journal of the American Statistical Association, 2023, 118, 165-176.	3.1	6
2	Searching for robust associations with a multi-environment knockoff filter. Biometrika, 2022, 109, 611-629.	2.4	9
3	Data Science in a Time of Crisis: Lessons from the Pandemic. Statistical Science, 2022, 37, .	2.8	1
4	Genome-wide mapping of brain phenotypes in extended pedigrees with strong genetic loading for bipolar disorder. Molecular Psychiatry, 2021, 26, 5229-5238.	7.9	4
5	Selection-adjusted inference: an application to confidence intervals for cis-eQTL effect sizes. Biostatistics, 2021, 22, 181-197.	1.5	6
6	Revealing enzyme functional architecture via high-throughput microfluidic enzyme kinetics. Science, 2021, 373, .	12.6	105
7	False discovery rate control in genome-wide association studies with population structure. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	33
8	Hypotheses on a tree: new error rates and testing strategies. Biometrika, 2021, 108, 575-590.	2.4	10
9	Multiregion Quantification of Extracellular Signal-regulated Kinase Activity in Renal Cell Carcinoma. European Urology Oncology, 2020, 3, 360-364.	5.4	2
10	Distinct and shared contributions of diagnosis and symptom domains to cognitive performance in severe mental illness in the Paisa population: a case-control study. Lancet Psychiatry,the, 2020, 7, 411-419.	7.4	24
11	Causal inference in genetic trio studies. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24117-24126.	7.1	25
12	Discussion of the Paper â€œPrediction, Estimation, and Attributionâ€•by B. Efron. Journal of the American Statistical Association, 2020, 115, 656-658.	3.1	0
13	Multi-resolution localization of causal variants across the genome. Nature Communications, 2020, 11, 1093.	12.8	37
14	Discussion of the Paper â€œPrediction, Estimation, and Attributionâ€•by B. Efron. International Statistical Review, 2020, 88, .	1.9	0
15	Gene hunting with hidden Markov model knockoffs. Biometrika, 2019, 106, 1-18.	2.4	78
16	Multilayer knockoff filter: Controlled variable selection at multiple resolutions. Annals of Applied Statistics, 2019, 13, 1-33.	1.1	23
17	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	27.8	161
18	Exploratory Gene Ontology Analysis with Interactive Visualization. Scientific Reports, 2019, 9, 7793.	3.3	10

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19	Rejoinder: â€˜Gene hunting with hidden Markov model knockoffsâ€™. Biometrika, 2019, 106, 35-45.	2.4	15
20	Understanding the Hidden Complexity of Latin American Population Isolates. American Journal of Human Genetics, 2018, 103, 707-726.	6.2	48
21	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. Nature Genetics, 2017, 49, 1714-1721.	21.4	57
22	Controlling the Rate of GWAS False Discoveries. Genetics, 2017, 205, 61-75.	2.9	93
23	Characterization of Expression Quantitative Trait Loci in Pedigrees from Colombia and Costa Rica Ascertained for Bipolar Disorder. PLoS Genetics, 2016, 12, e1006046.	3.5	4
24	Many Phenotypes Without Many False Discoveries: Error Controlling Strategies for Multitrait Association Studies. Genetic Epidemiology, 2016, 40, 45-56.	1.3	62
25	TreeQTL: hierarchical error control for eQTL findings. Bioinformatics, 2016, 32, 2556-2558.	4.1	35
26	Genetic Variant Selection: Learning Across Traits and Sites. Genetics, 2016, 202, 439-455.	2.9	3
27	SLOPEâ€”Adaptive variable selection via convex optimization. Annals of Applied Statistics, 2015, 9, 1103-1140.	1.1	146
28	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	3.5	50
29	Multivariate Linear Models for GWAS. , 2013, , 188-207.		10
30	Variance component model to account for sample structure in genome-wide association studies. Nature Genetics, 2010, 42, 348-354.	21.4	2,287
31	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. Nature Genetics, 2009, 41, 35-46.	21.4	676
32	Bayesian Gaussian Mixture Models for High-Density Genotyping Arrays. Journal of the American Statistical Association, 2008, 103, 89-100.	3.1	7
33	Bayesian Gaussian Mixture Models for High-Density Genotyping Arrays. Journal of the American Statistical Association, 2008, 103, 89-100.	3.1	3
34	False Discovery Rate in Linkage and Association Genome Screens for Complex Disorders. Genetics, 2003, 164, 829-833.	2.9	138
35	Response to the Letter â€œGametic and Zygotic Associationsâ€•by Rong-Cai Yang. Genetics, 2003, 165, 451-452.	2.9	1
36	Genomewide motif identification using a dictionary model. Proceedings of the IEEE, 2002, 90, 1803-1810.	21.3	21

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37	Homozygosity and Linkage Disequilibrium. Genetics, 2002, 160, 1707-1719.	2.9	69