

# Chiara Sabatti

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/397225/publications.pdf>

Version: 2024-02-01

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	Variance component model to account for sample structure in genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 348-354.	21.4	2,287
2	Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. <i>Nature Genetics</i> , 2009, 41, 35-46.	21.4	676
3	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	27.8	161
4	SLOPE: Adaptive variable selection via convex optimization. <i>Annals of Applied Statistics</i> , 2015, 9, 1103-1140.	1.1	146
5	False Discovery Rate in Linkage and Association Genome Screens for Complex Disorders. <i>Genetics</i> , 2003, 164, 829-833.	2.9	138
6	Revealing enzyme functional architecture via high-throughput microfluidic enzyme kinetics. <i>Science</i> , 2021, 373, .	12.6	105
7	Controlling the Rate of GWAS False Discoveries. <i>Genetics</i> , 2017, 205, 61-75.	2.9	93
8	Gene hunting with hidden Markov model knockoffs. <i>Biometrika</i> , 2019, 106, 1-18.	2.4	78
9	Homozygosity and Linkage Disequilibrium. <i>Genetics</i> , 2002, 160, 1707-1719.	2.9	69
10	Many Phenotypes Without Many False Discoveries: Error Controlling Strategies for Multitrait Association Studies. <i>Genetic Epidemiology</i> , 2016, 40, 45-56.	1.3	62
11	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. <i>Nature Genetics</i> , 2017, 49, 1714-1721.	21.4	57
12	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. <i>PLoS Genetics</i> , 2014, 10, e1004147.	3.5	50
13	Understanding the Hidden Complexity of Latin American Population Isolates. <i>American Journal of Human Genetics</i> , 2018, 103, 707-726.	6.2	48
14	Multi-resolution localization of causal variants across the genome. <i>Nature Communications</i> , 2020, 11, 1093.	12.8	37
15	TreeQTL: hierarchical error control for eQTL findings. <i>Bioinformatics</i> , 2016, 32, 2556-2558.	4.1	35
16	False discovery rate control in genome-wide association studies with population structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	33
17	Causal inference in genetic trio studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24117-24126.	7.1	25
18	Distinct and shared contributions of diagnosis and symptom domains to cognitive performance in severe mental illness in the Paisa population: a case-control study. <i>Lancet Psychiatry</i> , 2020, 7, 411-419.	7.4	24

#	ARTICLE	IF	CITATIONS
19	Multilayer knockoff filter: Controlled variable selection at multiple resolutions. <i>Annals of Applied Statistics</i> , 2019, 13, 1-33.	1.1	23
20	Genomewide motif identification using a dictionary model. <i>Proceedings of the IEEE</i> , 2002, 90, 1803-1810.	21.3	21
21	Rejoinder: "Gene hunting with hidden Markov model knockoffs" <sup>TM</sup> . <i>Biometrika</i> , 2019, 106, 35-45.	2.4	15
22	Multivariate Linear Models for GWAS. , 2013, , 188-207.		10
23	Exploratory Gene Ontology Analysis with Interactive Visualization. <i>Scientific Reports</i> , 2019, 9, 7793.	3.3	10
24	Hypotheses on a tree: new error rates and testing strategies. <i>Biometrika</i> , 2021, 108, 575-590.	2.4	10
25	Searching for robust associations with a multi-environment knockoff filter. <i>Biometrika</i> , 2022, 109, 611-629.	2.4	9
26	Bayesian Gaussian Mixture Models for High-Density Genotyping Arrays. <i>Journal of the American Statistical Association</i> , 2008, 103, 89-100.	3.1	7
27	Selection-adjusted inference: an application to confidence intervals for <i>cis</i> -eQTL effect sizes. <i>Biostatistics</i> , 2021, 22, 181-197.	1.5	6
28	Filtering the Rejection Set While Preserving False Discovery Rate Control. <i>Journal of the American Statistical Association</i> , 2023, 118, 165-176.	3.1	6
29	Characterization of Expression Quantitative Trait Loci in Pedigrees from Colombia and Costa Rica Ascertained for Bipolar Disorder. <i>PLoS Genetics</i> , 2016, 12, e1006046.	3.5	4
30	Genome-wide mapping of brain phenotypes in extended pedigrees with strong genetic loading for bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5229-5238.	7.9	4
31	Genetic Variant Selection: Learning Across Traits and Sites. <i>Genetics</i> , 2016, 202, 439-455.	2.9	3
32	Bayesian Gaussian Mixture Models for High-Density Genotyping Arrays. <i>Journal of the American Statistical Association</i> , 2008, 103, 89-100.	3.1	3
33	Multiregion Quantification of Extracellular Signal-regulated Kinase Activity in Renal Cell Carcinoma. <i>European Urology Oncology</i> , 2020, 3, 360-364.	5.4	2
34	Response to the Letter "Gametic and Zygotic Associations" by Rong-Cai Yang. <i>Genetics</i> , 2003, 165, 451-452.	2.9	1
35	Data Science in a Time of Crisis: Lessons from the Pandemic. <i>Statistical Science</i> , 2022, 37, .	2.8	1
36	Discussion of the Paper "Prediction, Estimation, and Attribution" by B. Efron. <i>Journal of the American Statistical Association</i> , 2020, 115, 656-658.	3.1	0

#	ARTICLE	IF	CITATIONS
37	Discussion of the Paper "Prediction, Estimation, and Attribution" by B. Efron. International Statistical Review, 2020, 88, .	1.9	0