

# Eric M Sobel

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3217870/publications.pdf>

Version: 2024-02-01

41  
papers

1,789  
citations

687363

13  
h-index

330143

37  
g-index

41  
all docs

41  
docs citations

41  
times ranked

3119  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analysis by lasso penalized logistic regression. <i>Bioinformatics</i> , 2009, 25, 714-721.	4.1	639
2	Detection and Integration of Genotyping Errors in Statistical Genetics. <i>American Journal of Human Genetics</i> , 2002, 70, 496-508.	6.2	317
3	Integrated Weighted Gene Co-expression Network Analysis with an Application to Chronic Fatigue Syndrome. <i>BMC Systems Biology</i> , 2008, 2, 95.	3.0	167
4	Mendel: the Swiss army knife of genetic analysis programs. <i>Bioinformatics</i> , 2013, 29, 1568-1570.	4.1	104
5	Genome-wide ultraconserved elements exhibit higher phylogenetic informativeness than traditional gene markers in percomorph fishes. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 140-146.	2.7	68
6	Association testing with Mendel. <i>Genetic Epidemiology</i> , 2005, 29, 36-50.	1.3	57
7	Shared Molecular Pathways and Gene Networks for Cardiovascular Disease and Type 2 Diabetes Mellitus in Women Across Diverse Ethnicities. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 911-919.	5.1	48
8	Linkage analysis without defined pedigrees. <i>Genetic Epidemiology</i> , 2011, 35, 360-370.	1.3	40
9	Next-Generation Statistical Genetics: Modeling, Penalization, and Optimization in High-Dimensional Data. <i>Annual Review of Statistics and Its Application</i> , 2014, 1, 279-300.	7.0	40
10	Fine mapping of a multiple sclerosis locus to 2.5 Mb on chromosome 17q22-q24. <i>Human Molecular Genetics</i> , 2002, 11, 2257-2267.	2.9	39
11	OpenMendel: a cooperative programming project for statistical genetics. <i>Human Genetics</i> , 2020, 139, 61-71.	3.8	29
12	Haplotyping Algorithms. , 1996, , 89-110.		29
13	Replication and refinement of linkage of posterior polymorphous corneal dystrophy to the posterior polymorphous corneal dystrophy 1 locus on chromosome 20. <i>Genetics in Medicine</i> , 2007, 9, 228-234.	2.4	25
14	Genome-Wide Meta-analysis of Gene-Environment Interaction for Insulin Resistance Phenotypes and Breast Cancer Risk in Postmenopausal Women. <i>Cancer Prevention Research</i> , 2019, 12, 31-42.	1.5	15
15	Breast Cancer Risk and Insulin Resistance: Post Genome-Wide Gene-Environment Interaction Study Using a Random Survival Forest. <i>Cancer Research</i> , 2019, 79, 2784-2794.	0.9	13
16	Genome-wide Association Analysis of Proinflammatory Cytokines and Gene-lifestyle Interaction for Invasive Breast Cancer Risk: The WHI dbGaP Study. <i>Cancer Prevention Research</i> , 2021, 14, 41-54.	1.5	13
17	Ataxia-telangiectasia: linkage analysis of chromosome 11q22-q23 markers in Turkish families. <i>FASEB Journal</i> , 1992, 6, 2848-2852.	0.5	11
18	Mendel-GPU: haplotyping and genotype imputation on graphics processing units. <i>Bioinformatics</i> , 2012, 28, 2979-2980.	4.1	11

#	ARTICLE	IF	CITATIONS
19	Interaction of insulin-like growth factor-I and insulin resistance-related genetic variants with lifestyle factors on postmenopausal breast cancer risk. <i>Breast Cancer Research and Treatment</i> , 2017, 164, 475-495.	2.5	11
20	Detection of Intergenerational Genetic Effects with Application to <i>HLA-B</i> Matching as a Risk Factor for Schizophrenia. <i>Human Heredity</i> , 2011, 72, 161-172.	0.8	10
21	Obesity and associated lifestyles modify the effect of glucose metabolism-related genetic variants on impaired glucose homeostasis among postmenopausal women. <i>Genetic Epidemiology</i> , 2016, 40, 520-530.	1.3	10
22	Fast Genome-Wide QTL Association Mapping on Pedigree and Population Data. <i>Genetic Epidemiology</i> , 2017, 41, 174-186.	1.3	10
23	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. <i>GigaScience</i> , 2020, 9, .	6.4	10
24	Quantitative Trait Loci Association Mapping by Imputation of Strain Origins in Multifounder Crosses. <i>Genetics</i> , 2012, 190, 459-473.	2.9	8
25	Effect of genetic variants and traits related to glucose metabolism and their interaction with obesity on breast and colorectal cancer risk among postmenopausal women. <i>BMC Cancer</i> , 2017, 17, 290.	2.6	8
26	Post genome-wide gene-environment interaction study: The effect of genetically driven insulin resistance on breast cancer risk using Mendelian randomization. <i>PLoS ONE</i> , 2019, 14, e0218917.	2.5	8
27	Mendelian Randomization Study: The Association Between Metabolic Pathways and Colorectal Cancer Risk. <i>Frontiers in Oncology</i> , 2020, 10, 1005.	2.8	8
28	Pro-inflammatory cytokine polymorphisms and interactions with dietary alcohol and estrogen, risk factors for invasive breast cancer using a post genome-wide analysis for gene-gene and gene-lifestyle interaction. <i>Scientific Reports</i> , 2021, 11, 1058.	3.3	6
29	Fine mapping of the multiple sclerosis susceptibility locus on 5p14-p12. <i>Journal of Neuroimmunology</i> , 2005, 170, 122-133.	2.3	5
30	Fast genome-wide pedigree quantitative trait loci analysis using MENDEL. <i>BMC Proceedings</i> , 2014, 8, S93.	1.6	5
31	Genetic Variants in Metabolic Signaling Pathways and Their Interaction with Lifestyle Factors on Breast Cancer Risk: A Random Survival Forest Analysis. <i>Cancer Prevention Research</i> , 2018, 11, 44-51.	1.5	4
32	A fast data-driven method for genotype imputation, phasing and local ancestry inference: MendelImpute.jl. <i>Bioinformatics</i> , 2021, 37, 4756-4763.	4.1	4
33	The Quantitative-MFG Test: A Linear Mixed Effect Model to Detect Maternal-Offspring Gene Interactions. <i>Annals of Human Genetics</i> , 2016, 80, 63-80.	0.8	3
34	Post Genome-Wide Gene-Environment Interaction Study Using Random Survival Forest: Insulin Resistance, Lifestyle Factors, and Colorectal Cancer Risk. <i>Cancer Prevention Research</i> , 2019, 12, 877-890.	1.5	3
35	Genetically Predicted C-Reactive Protein Associated With Postmenopausal Breast Cancer Risk: Interrelation With Estrogen and Cancer Molecular Subtypes Using Mendelian Randomization. <i>Frontiers in Oncology</i> , 2020, 10, 630994.	2.8	3
36	Modern simulation utilities for genetic analysis. <i>BMC Bioinformatics</i> , 2021, 22, 228.	2.6	3

#	ARTICLE	IF	CITATIONS
37	Molecular Biology Networks and Key Gene Regulators for Inflammatory Biomarkers Shared by Breast Cancer Development: Multi-Omics Systems Analysis. <i>Biomolecules</i> , 2021, 11, 1379.	4.0	2
38	Synergistic Effects of Genetic Variants of Glucose Homeostasis and Lifelong Exposures to Cigarette Smoking, Female Hormones, and Dietary Fat Intake on Primary Colorectal Cancer Development in African and Hispanic/Latino American Women. <i>Frontiers in Oncology</i> , 2021, 11, 760243.	2.8	1
39	Pro-inflammatory cytokine polymorphisms in ONECUT2 and HNF4A and primary colorectal carcinoma: a post genome-wide gene-lifestyle interaction study. <i>American Journal of Cancer Research</i> , 2020, 10, 2955-2976.	1.4	1
40	Genetically determined elevated C-reactive protein associated with primary colorectal cancer risk: Mendelian randomization with lifestyle interactions. <i>American Journal of Cancer Research</i> , 2021, 11, 1733-1753.	1.4	1
41	Genome-wide QTL and eQTL analyses using Mendel. <i>BMC Proceedings</i> , 2016, 10, 239-244.	1.6	0