Eric M Sobel

List of Publications by Year
in descending order

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 of Proinflammatory Cytokines and Gene–lifestyle Interaction for Invasive Breast Cancer Risk: The WHI dbGaP Study. Cancer Prevention Research, 2021, 14, 41-54.	1.5	13
2	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. Scientific Reports, 2021, 11, 1058.	3.3	6
3	Modern simulation utilities for genetic analysis. BMC Bioinformatics, 2021, 22, 228.	2.6	3
4	A fast data-driven method for genotype imputation, phasing and local ancestry inference: MendelImpute.jl. Bioinformatics, 2021, 37, 4756-4763.	4.1	4
5	Molecular Biology Networks and Key Gene Regulators for Inflammatory Biomarkers Shared by Breast Cancer Development: Multi-Omics Systems Analysis. Biomolecules, 2021, 11, 1379.	4.0	2
6	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. Frontiers in Oncology, 2021, 11, 760243.	2.8	1
7	Genetically determined elevated C-reactive protein associated with primary colorectal cancer risk: Mendelian randomization with lifestyle interactions. American Journal of Cancer Research, 2021, 11, 1733-1753.	1.4	1
8	OpenMendel: a cooperative programming project for statistical genetics. Human Genetics, 2020, 139, 61-71.	3.8	29
9	Mendelian Randomization Study: The Association Between Metabolic Pathways and Colorectal Cancer Risk. Frontiers in Oncology, 2020, 10, 1005.	2.8	8
10	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. GigaScience, 2020, 9, .	6.4	10
11	Genetically Predicted C-Reactive Protein Associated With Postmenopausal Breast Cancer Risk: Interrelation With Estrogen and Cancer Molecular Subtypes Using Mendelian Randomization. Frontiers in Oncology, 2020, 10, 630994.	2.8	3
12	Pro-inflammatory cytokine polymorphisms in ONECUT2 and HNF4A and primary colorectal carcinoma: a post genome-wide gene-lifestyle interaction study. American Journal of Cancer Research, 2020, 10, 2955-2976.	1.4	1
13	Post genome-wide gene-environment interaction study: The effect of genetically driven insulin resistance on breast cancer risk using Mendelian randomization. PLoS ONE, 2019, 14, e0218917.	2.5	8
14	Breast Cancer Risk and Insulin Resistance: Post Genome-Wide Gene–Environment Interaction Study Using a Random Survival Forest. Cancer Research, 2019, 79, 2784-2794.	0.9	13
15	Post Genome-Wide Gene–Environment Interaction Study Using Random Survival Forest: Insulin Resistance, Lifestyle Factors, and Colorectal Cancer Risk. Cancer Prevention Research, 2019, 12, 877-890.	1.5	3
16	Genome-Wide Meta-analysis of Gene–Environmental Interaction for Insulin Resistance Phenotypes and Breast Cancer Risk in Postmenopausal Women. Cancer Prevention Research, 2019, 12, 31-42.	1.5	15
17	Genetic Variants in Metabolic Signaling Pathways and Their Interaction with Lifestyle Factors on Breast Cancer Risk: A Random Survival Forest Analysis. Cancer Prevention Research, 2018, 11, 44-51.	1.5	4
18	Interaction of insulin-like growth factor-I and insulin resistance-related genetic variants with lifestyle factors on postmenopausal breast cancer risk. Breast Cancer Research and Treatment, 2017, 164, 475-495.	2.5	11

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19	Fast Genome–Wide QTL Association Mapping on Pedigree and Population Data. Genetic Epidemiology, 2017, 41, 174-186.	1.3	10
20	Effect of genetic variants and traits related to glucose metabolism and their interaction with obesity on breast and colorectal cancer risk among postmenopausal women. BMC Cancer, 2017, 17, 290.	2.6	8
21	The Quantitative-MFG Test: A Linear Mixed Effect Model to Detect Maternal-Offspring Gene Interactions. Annals of Human Genetics, 2016, 80, 63-80.	0.8	3
22	Genome-wide QTL and eQTL analyses using Mendel. BMC Proceedings, 2016, 10, 239-244.	1.6	0
23	Obesity and associated lifestyles modify the effect of glucose metabolism–related genetic variants on impaired glucose homeostasis among postmenopausal women. Genetic Epidemiology, 2016, 40, 520-530.	1.3	10
24	Genome-wide ultraconserved elements exhibit higher phylogenetic informativeness than traditional gene markers in percomorph fishes. Molecular Phylogenetics and Evolution, 2015, 92, 140-146.	2.7	68
25	Shared Molecular Pathways and Gene Networks for Cardiovascular Disease and Type 2 Diabetes Mellitus in Women Across Diverse Ethnicities. Circulation: Cardiovascular Genetics, 2014, 7, 911-919.	5.1	48
26	Next-Generation Statistical Genetics: Modeling, Penalization, and Optimization in High-Dimensional Data. Annual Review of Statistics and Its Application, 2014, 1, 279-300.	7.0	40
27	Fast genome-wide pedigree quantitative trait loci analysis using MENDEL. BMC Proceedings, 2014, 8, S93.	1.6	5
28	Mendel: the Swiss army knife of genetic analysis programs. Bioinformatics, 2013, 29, 1568-1570.	4.1	104
29	Mendel-GPU: haplotyping and genotype imputation on graphics processing units. Bioinformatics, 2012, 28, 2979-2980.	4.1	11
30	Quantitative Trait Loci Association Mapping by Imputation of Strain Origins in Multifounder Crosses. Genetics, 2012, 190, 459-473.	2.9	8
31	Linkage analysis without defined pedigrees. Genetic Epidemiology, 2011, 35, 360-370.	1.3	40
32	Detection of Intergenerational Genetic Effects with Application to *HLA-B* Matching as a Risk Factor for Schizophrenia. Human Heredity, 2011, 72, 161-172.	0.8	10
33	Genome-wide association analysis by lasso penalized logistic regression. Bioinformatics, 2009, 25, 714-721.	4.1	639
34	Integrated Weighted Gene Co-expression Network Analysis with an Application to Chronic Fatigue Syndrome. BMC Systems Biology, 2008, 2, 95.	3.0	167
35	Replication and refinement of linkage of posterior polymorphous corneal dystrophy to the posterior polymorphous corneal dystrophy 1 locus on chromosome 20. Genetics in Medicine, 2007, 9, 228-234.	2.4	25
36	Fine mapping of the multiple sclerosis susceptibility locus on 5p14–p12. Journal of Neuroimmunology, 2005, 170, 122-133.	2.3	5

#	Article	IF	Citations
37	Association testing with Mendel. Genetic Epidemiology, 2005, 29, 36-50.	1.3	57
38	Fine mapping of a multiple sclerosis locus to 2.5 Mb on chromosome 17q22-q24. Human Molecular Genetics, 2002, 11, 2257-2267.	2.9	39
39	Detection and Integration of Genotyping Errors in Statistical Genetics. American Journal of Human Genetics, 2002, 70, 496-508.	6.2	317
40	Haplotyping Algorithms. , 1996, , 89-110.		29
41	Ataxiaâ€telangiectasia: linkage analysis of chromosome 11q22â€23 markers in Turkish families. FASEB Journal, 1992, 6, 2848-2852.	0.5	11