Janet S Sinsheimer

List of Publications by Year
in descending order

72 papers	2,812 citations	236925 25 h-index	197818 49 g-index
79 all docs	79 docs citations	79 times ranked	6144 citing authors

#	Article	IF	Citations
1	Prioritizing GWAS Results: A Review of Statistical Methods and Recommendations for Their Application. American Journal of Human Genetics, 2010, 86, 6-22.	6.2	531
2	Normal/Independent Distributions and Their Applications in Robust Regression. Journal of Computational and Graphical Statistics, 1993, 2, 175-198.	1.7	181
3	Structural variants in genes associated with human Williams-Beuren syndrome underlie stereotypical hypersociability in domestic dogs. Science Advances, 2017, 3, e1700398.	10.3	139
4	Diagnostic utility of transcriptome sequencing for rare Mendelian diseases. Genetics in Medicine, 2020, 22, 490-499.	2.4	136
5	Association screening of common and rare genetic variants by penalized regression. Bioinformatics, 2010, 26, 2375-2382.	4.1	120
6	Mendel: the Swiss army knife of genetic analysis programs. Bioinformatics, 2013, 29, 1568-1570.	4.1	104
7	Acceleration of Age-Associated Methylation Patterns in HIV-1-Infected Adults. PLoS ONE, 2015, 10, e0119201.	2.5	101
8	Detecting genotype combinations that increase risk for disease: Maternal-Fetal genotype incompatibility test. Genetic Epidemiology, 2003, 24, 1-13.	1.3	84
9	Amerindian-specific regions under positive selection harbour new lipid variants in Latinos. Nature Communications, 2014, 5, 3983.	12.8	81
10	Integration of human adipocyte chromosomal interactions with adipose gene expression prioritizes obesity-related genes from GWAS. Nature Communications, 2018, 9, 1512.	12.8	75
11	Pooled analysis of iron-related genes in Parkinson's disease: Association with transferrin. Neurobiology of Disease, 2014, 62, 172-178.	4.4	74
12	The concerted impact of domestication and transposon insertions on methylation patterns between dogs and grey wolves. Molecular Ecology, 2016, 25, 1838-1855.	3.9	73
13	Inferring Spatial Phylogenetic Variation Along Nucleotide Sequences. Journal of the American Statistical Association, 2003, 98, 427-437.	3.1	70
14	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
15	Gene-environment interactions linking air pollution and inflammation in Parkinson's disease. Environmental Research, 2016, 151, 713-720.	7.5	55
16	APOE, MAPT, and COMT and Parkinsonâ€™s Disease Susceptibility and Cognitive Symptom Progression. Journal of Parkinson's Disease, 2016, 6, 349-359.	2.8	53
17	Organophosphate pesticides and PON1 L55M in Parkinson's disease progression. Environment International, 2017, 107, 75-81.	10.0	43
18	Histone H3.3 beyond cancer: Germline mutations in Histone 3 Family 3A and 3B cause a previously unidentified neurodegenerative disorder in 46 patients. Science Advances, 2020, 6, .	10.3	43

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19	Subtypes of Native American ancestry and leading causes of death: Mapuche ancestry-specific associations with gallbladder cancer risk in Chile. PLoS Genetics, 2017, 13, e1006756.	3.5	41
20	Ordered multinomial regression for genetic association analysis of ordinal phenotypes at Biobank scale. Genetic Epidemiology, 2020, 44, 248-260.	1.3	37
21	Genetic variability in ABCB1, occupational pesticide exposure, and Parkinsonâ€™s disease. Environmental Research, 2015, 143, 98-106.	7.5	34
22	Vitamin D receptor gene polymorphisms and cognitive decline in Parkinson's disease. Journal of the Neurological Sciences, 2016, 370, 100-106.	0.6	34
23	Dopamine receptors and BDNF -haplotypes predict dyskinesia in Parkinson's disease. Parkinsonism and Related Disorders, 2018, 47, 39-44.	2.2	33
24	Association ofLOXL1Polymorphisms With Pseudoexfoliation, Glaucoma, Intraocular Pressure, and Systemic Diseases in a Greek Population. The Thessaloniki Eye Study. , 2014, 55, 4238.		30
25	OpenMendel: a cooperative programming project for statistical genetics. Human Genetics, 2020, 139, 61-71.	3.8	29
26	Increased Menopausal Age Reduces the Risk of Parkinson's Disease: A Mendelian Randomization Approach. Movement Disorders, 2021, 36, 2264-2272.	3.9	28
27	Human liver single nucleus and singleÂcell RNA sequencing identify a hepatocellular carcinoma-associated cell-type affecting survival. Genome Medicine, 2022, 14, 50.	8.2	27
28	Bilingual approach to online cancer genetics education for Deaf American Sign Language users produces greater knowledge and confidence than English text only: A randomized study. Disability and Health Journal, 2017, 10, 23-32.	2.8	26
29	Apolipoprotein-E genotype and human immunodeficiency virus-associated neurocognitive disorder: the modulating effects of older age and disease severity. Neurobehavioral HIV Medicine, 2013, 5, 11.	2.0	25
30	Vitamin D receptor gene polymorphisms and Parkinson's disease in a population with high ultraviolet radiation exposure. Journal of the Neurological Sciences, 2015, 352, 88-93.	0.6	25
31	Activity of Genes with Functions in Human Williamsâ€“Beuren Syndrome Is Impacted by Mobile Element Insertions in the Gray Wolf Genome. Genome Biology and Evolution, 2018, 10, 1546-1553.	2.5	25
32	Identification of TBX15 as an adipose master trans regulator of abdominal obesity genes. Genome Medicine, 2021, 13, 123.	8.2	23
33	Genetic analysis of hyperemesis gravidarum reveals association with intracellular calcium release channel (RYR2). Molecular and Cellular Endocrinology, 2017, 439, 308-316.	3.2	22
34	Filtering nucleotide sites by phylogenetic signal to noise ratio increases confidence in the Neoaves phylogeny generated from ultraconserved elements. Molecular Phylogenetics and Evolution, 2018, 126, 116-128.	2.7	19
35	Heritability of interpack aggression in a wild pedigreed population of North American grey wolves. Molecular Ecology, 2020, 29, 1764-1775.	3.9	19
36	Fine mapping of Hyplip1 and the human homolog, a potential locus for FCHL. Mammalian Genome, 2001, 12, 238-245.	2.2	17

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37	Commonalities across computational workflows for uncovering explanatory variants in undiagnosed cases. Genetics in Medicine, 2021, 23, 1075-1085.	2.4	16
38	An examination of school reopening strategies during the SARS-CoV-2 pandemic. PLoS ONE, 2021, 16, e0251242.	2.5	16
39	Regulation of Sex Determination in Mice by a Non-coding Genomic Region. Genetics, 2014, 197, 885-897.	2.9	14
40	Reverse geneâ€“environment interaction approach to identify variants influencing body-mass index in humans. Nature Metabolism, 2019, 1, 630-642.	11.9	14
41	Associations of regional amyloid-Î² plaque and phospho-tau pathology with biological factors and neuropsychological functioning among HIV-infected adults. Journal of NeuroVirology, 2019, 25, 741-753.	2.1	13
42	GWAS of longitudinal trajectories at biobank scale. American Journal of Human Genetics, 2022, 109, 433-445.	6.2	13
43	Fast and accurate site frequency spectrum estimation from low coverage sequence data. Bioinformatics, 2015, 31, 720-727.	4.1	12
44	Understanding Adult Participant and Parent Empowerment Prior to Evaluation in the Undiagnosed Diseases Network. Journal of Genetic Counseling, 2018, 27, 1087-1101.	1.6	12
45	BioSimulator.jl: Stochastic simulation in Julia. Computer Methods and Programs in Biomedicine, 2018, 167, 23-35.	4.7	12
46	Evolutionary Similarity Among Genes. Journal of the American Statistical Association, 2003, 98, 653-662.	3.1	11
47	Detection of a mosaic CDKL5 deletion and inversion by optical genome mapping ends an exhaustive diagnostic odyssey. Molecular Genetics & Genomic Medicine, 2021, 9, e1665.	1.2	11
48	Genetic variants in nicotinic receptors and smoking cessation in Parkinson's disease. Parkinsonism and Related Disorders, 2019, 62, 57-61.	2.2	10
49	Iterative hard thresholding in genome-wide association studies: Generalized linear models, prior weights, and double sparsity. GigaScience, 2020, 9, .	6.4	10
50	Identification of 90 NAFLD GWAS loci and establishment of NAFLD PRS and causal role of NAFLD in coronary artery disease. Human Genetics and Genomics Advances, 2022, 3, 100056.	1.7	10
51	Reuse, recycle, reweigh: Combating influenza through efficient sequential Bayesian computation for massive data. Annals of Applied Statistics, 2010, 4, 1722-1748.	1.1	9
52	Bilingual Cancer Genetic Education Modules for the Deaf Community: Development and Evaluation of the Online Video Material. Journal of Genetic Counseling, 2018, 27, 457-469.	1.6	9
53	Impact of Genetic Counseling and Connexin-26 and Connexin-30 Testing on Deaf Identity and Comprehension of Genetic Test Results in a Sample of Deaf Adults: A Prospective, Longitudinal Study. PLoS ONE, 2014, 9, e111512.	2.5	8
54	NFE2L2, PPARGC1Î±, and pesticides and Parkinsonâ€™s disease risk and progression. Mechanisms of Ageing and Development, 2018, 173, 1-8.	4.6	8

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55	Cumulative effects of common genetic variants on risk of sudden cardiac death. IJC Heart and Vasculature, 2015, 7, 88-91.	1.1	7
56	Understanding the Heterogeneity of Obesity and the Relationship to the Brain-Gut Axis. Nutrients, 2020, 12, 3701.	4.1	7
57	Genetic risk scores and hallucinations in patients with Parkinson disease. Neurology: Genetics, 2020, 6, e492.	1.9	7
58	Estimating Ethnic Admixture from Pedigree Data. American Journal of Human Genetics, 2008, 82, 748-755.	6.2	6
59	Electrical impedance tomography for non-invasive identification of fatty liver infiltrate in overweight individuals. Scientific Reports, 2021, 11, 19859.	3.3	6
60	Are you my mother? Bayesian phylogenetic inference of recombination among putative parental strains. Applied Bioinformatics, 2003, 2, 131-44.	1.6	5
61	Bayesian nonparametric clustering in phylogenetics: modeling antigenic evolution in influenza. Statistics in Medicine, 2018, 37, 195-206.	1.6	4
62	Family genetic result communication in rare and undiagnosed disease communities: Understanding the practice. Journal of Genetic Counseling, 2021, 30, 439-447.	1.6	4
63	A fast data-driven method for genotype imputation, phasing and local ancestry inference: MendelImpute.jl. Bioinformatics, 2021, 37, 4756-4763.	4.1	4
64	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
65	The Roles of Physical Activity and Inflammation in Mortality, Cognition, and Depressive Symptoms Among Older Mexican Americans. American Journal of Epidemiology, 2019, 188, 1944-1952.	3.4	3
66	Modern simulation utilities for genetic analysis. BMC Bioinformatics, 2021, 22, 228.	2.6	3
67	Efficiency of Protein Production from mRNA. Journal of Statistical Theory and Practice, 2008, 2, 173-182.	0.5	2
68	Uncovering the Genomic Origins of Life. Genome Biology and Evolution, 2018, 10, 1705-1714.	2.5	2
69	Statistical Genetic Approaches for Mapping Ophthalmic Trait and Disease Genes. American Journal of Ophthalmology, 2009, 148, 183-185.	3.3	1
70	Stochastic simulation algorithms for Interacting Particle Systems. PLoS ONE, 2021, 16, e0247046.	2.5	1
71	Erratum to â€œIncreased Menopausal Age Reduces the Risk of Parkinson's Disease: A Mendelian Approachâ€• Movement Disorders, 2022, 37, 1282-1283.	3.9	1
72	Computational tools for assessing gene therapy under branching process models of mutation. Bulletin of Mathematical Biology, 2022, 84, 15.	1.9	0