Kathryn M Roeder

List of Publications by Year
in descending order

147 papers	35,903 citations	10373 72 h-index	8618 146 g-index
178 all docs	178 docs citations	178 times ranked	39361 citing authors

#	Article	IF	Citations
1	Genomic Control for Association Studies. Biometrics, 1999, 55, 997-1004.	0.8	2,722
2	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	13.7	2,254
3	A SAS Procedure Based on Mixture Models for Estimating Developmental Trajectories. Sociological Methods and Research, 2001, 29, 374-393.	4.3	1,869
4	De novo mutations revealed by whole-exome sequencing are strongly associated with autism. Nature, 2012, 485, 237-241.	13.7	1,863
5	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	13.7	1,803
6	Patterns and rates of exonic de novo mutations in autism spectrum disorders. Nature, 2012, 485, 242-245.	13.7	1,597
7	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
8	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
9	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	3.8	1,219
10	Multiple Recurrent De Novo CNVs, Including Duplications of the 7q11.23 Williams Syndrome Region, Are Strongly Associated with Autism. Neuron, 2011, 70, 863-885.	3.8	1,146
11	Most genetic risk for autism resides with common variation. Nature Genetics, 2014, 46, 881-885.	9.4	977
12	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
13	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	9.4	943
14	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
15	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	13.5	825
16	Genome-wide association identifies multiple ulcerative colitis susceptibility loci. Nature Genetics, 2010, 42, 332-337.	9.4	572
17	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	1.4	538
18	Testing for an Unusual Distribution of Rare Variants. PLoS Genetics, 2011, 7, e1001322.	1.5	530

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19	The heritability of IQ. Nature, 1997, 388, 468-471.	13.7	484
20	Genomic Control, a New Approach to Genetic-Based Association Studies. Theoretical Population Biology, 2001, 60, 155-166.	0.5	465
21	Practical Bayesian Density Estimation Using Mixtures of Normals. Journal of the American Statistical Association, 1997, 92, 894-902.	1.8	370
22	Ulcerative colitisâ€“risk loci on chromosomes 1p36 and 12q15 found by genome-wide association study. Nature Genetics, 2009, 41, 216-220.	9.4	364
23	Common genetic variants, acting additively, are a major source of risk for autism. Molecular Autism, 2012, 3, 9.	2.6	357
24	High-dimensional variable selection. Annals of Statistics, 2009, 37, 2178-2201.	1.4	344
25	The Power of Genomic Control. American Journal of Human Genetics, 2000, 66, 1933-1944.	2.6	338
26	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	1.4	334
27	Modeling Uncertainty in Latent Class Membership: A Case Study in Criminology. Journal of the American Statistical Association, 1999, 94, 766-776.	1.8	319
28	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nature Communications, 2015, 6, 6404.	5.8	316
29	Common genetic variants in the CLDN2 and PRSS1-PRSS2 loci alter risk for alcohol-related and sporadic pancreatitis. Nature Genetics, 2012, 44, 1349-1354.	9.4	303
30	Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples. Nature Genetics, 2017, 49, 504-510.	9.4	298
31	Integrated Model of De Novo and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. PLoS Genetics, 2013, 9, e1003671.	1.5	253
32	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. Neuron, 2013, 77, 235-242.	3.8	242
33	False discovery control with p-value weighting. Biometrika, 2006, 93, 509-524.	1.3	238
34	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	9.4	235
35	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	6.0	234
36	Modeling Uncertainty in Latent Class Membership: A Case Study in Criminology. Journal of the American Statistical Association, 1999, 94, 766.	1.8	202

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37	Using Linkage Genome Scans to Improve Power of Association in Genome Scans. American Journal of Human Genetics, 2006, 78, 243-252.	2.6	197
38	Vitamin D Insufficiency and Severe Asthma Exacerbations in Puerto Rican Children. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 140-146.	2.5	183
39	The huge Package for High-dimensional Undirected Graph Estimation in R. Journal of Machine Learning Research, 2012, 13, 1059-1062.	62.4	183
40	Density Estimation with Confidence Sets Exemplified by Superclusters and Voids in the Galaxies. Journal of the American Statistical Association, 1990, 85, 617-624.	1.8	181
41	The Autism Sequencing Consortium: Large-Scale, High-Throughput Sequencing in Autism Spectrum Disorders. Neuron, 2012, 76, 1052-1056.	3.8	153
42	De Novo Insertions and Deletions of Predominantly Paternal Origin Are Associated with Autism Spectrum Disorder. Cell Reports, 2014, 9, 16-23.	2.9	151
43	Genomic Control to the extreme. Nature Genetics, 2004, 36, 1129-1130.	9.4	148
44	Analysis of Rare, Exonic Variation amongst Subjects with Autism Spectrum Disorders and Population Controls. PLoS Genetics, 2013, 9, e1003443.	1.5	133
45	Unbiased methods for population-based association studies. Genetic Epidemiology, 2001, 21, 273-284.	0.6	132
46	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	2.6	128
47	On the Identification of Disease Mutations by the Analysis of Haplotype Similarity and Goodness of Fit. American Journal of Human Genetics, 2003, 72, 891-902.	2.6	127
48	Pleiotropy and principal components of heritability combine to increase power for association analysis. Genetic Epidemiology, 2008, 32, 9-19.	0.6	123
49	SNP-Based Analysis of Genetic Substructure in the German Population. Human Heredity, 2006, 62, 20-29.	0.4	121
50	On the Use of General Control Samples for Genome-wide Association Studies: Genetic Matching Highlights Causal Variants. American Journal of Human Genetics, 2008, 82, 453-463.	2.6	120
51	APOE and TREM2 regulate amyloid-responsive microglia in Alzheimerâ€™s disease. Acta Neuropathologica, 2020, 140, 477-493.	3.9	117
52	Transcriptional Consequences of 16p11.2 Deletion and Duplication in Mouse Cortex and Multiplex Autism Families. American Journal of Human Genetics, 2014, 94, 870-883.	2.6	116
53	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. Molecular Autism, 2014, 5, 22.	2.6	111
54	Stability Approach to Regularization Selection (StARS) for High Dimensional Graphical Models. Advances in Neural Information Processing Systems, 2010, 24, 1432-1440.	2.8	110

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55	Evolutionary-based association analysis using haplotype data. Genetic Epidemiology, 2003, 25, 48-58.	0.6	106
56	Screen and clean: a tool for identifying interactions in genomeâ€wide association studies. Genetic Epidemiology, 2010, 34, 275-285.	0.6	105
57	Association studies for quantitative traits in structured populations. Genetic Epidemiology, 2002, 22, 78-93.	0.6	104
58	Transmission/Disequilibrium Test Meets Measured Haplotype Analysis: Family-Based Association Analysis Guided by Evolution of Haplotypes. American Journal of Human Genetics, 2001, 68, 1250-1263.	2.6	102
59	Characterization of multilocus linkage disequilibrium. Genetic Epidemiology, 2005, 28, 193-206.	0.6	101
60	African ancestry and lung function in Puerto Rican children. Journal of Allergy and Clinical Immunology, 2012, 129, 1484-1490.e6.	1.5	96
61	Do common variants play a role in risk for autism? Evidence and theoretical musings. Brain Research, 2011, 1380, 78-84.	1.1	95
62	Genome-Wide Significance Levels and Weighted Hypothesis Testing. Statistical Science, 2009, 24, 398-413.	1.6	94
63	Global spectral clustering in dynamic networks. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 927-932.	3.3	93
64	Flexible Parametric Measurement Error Models. Biometrics, 1999, 55, 44-54.	0.8	92
65	Analysis of single-locus tests to detect gene/disease associations. Genetic Epidemiology, 2005, 28, 207-219.	0.6	92
66	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489.	2.9	91
67	Practical Bayesian Density Estimation Using Mixtures of Normals. Journal of the American Statistical Association, 1997, 92, 894.	1.8	91
68	A Graphical Technique for Determining the Number of Components in a Mixture of Normals. Journal of the American Statistical Association, 1994, 89, 487-495.	1.8	90
69	Disequilibrium Mapping: Composite Likelihood for Pairwise Disequilibrium. Genomics, 1996, 36, 1-16.	1.3	90
70	Improving power in genome-wide association studies: weights tip the scale. Genetic Epidemiology, 2007, 31, 741-747.	0.6	90
71	Discovering genetic ancestry using spectral graph theory. Genetic Epidemiology, 2010, 34, 51-59.	0.6	90
72	A Semiparametric Mixture Approach to Case-Control Studies with Errors in Covariables. Journal of the American Statistical Association, 1996, 91, 722-732.	1.8	87

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73	A unified statistical framework for single cell and bulk RNA sequencing data. Annals of Applied Statistics, 2018, 12, 609-632.	0.5	82
74	Application of Maximum Likelihood Methods to Population Genetic Data for the Estimation of Individual Fertilities. Biometrics, 1989, 45, 363.	0.8	81
75	Semisoft clustering of single-cell data. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 466-471.	3.3	71
76	Analysis of multilocus models of association. Genetic Epidemiology, 2003, 25, 36-47.	0.6	70
77	DNA Fingerprinting: A Review of the Controversy. Statistical Science, 1994, 9, .	1.6	68
78	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Nature Genetics, 2018, 50, 1032-1040.	9.4	64
79	A Bayesian semiparametric model for case-control studies with errors in variables. Biometrika, 1997, 84, 523-537.	1.3	63
80	A statistical model for locating regulatory regions in genomic DNA. Journal of Molecular Biology, 1997, 268, 8-14.	2.0	62
81	Residual Diagnostics for Mixture Models. Journal of the American Statistical Association, 1992, 87, 785-794.	1.8	61
82	Haplotype Fine Mapping by Evolutionary Trees. American Journal of Human Genetics, 2000, 66, 659-673.	2.6	58
83	High-Density Association Study of 383 Candidate Genes for Volumetric BMD at the Femoral Neck and Lumbar Spine Among Older Men. Journal of Bone and Mineral Research, 2009, 24, 2039-2049.	3.1	57
84	Candidate gene analysis of femoral neck trabecular and cortical volumetric bone mineral density in older men. Journal of Bone and Mineral Research, 2010, 25, 330-338.	3.1	50
85	Forensic Inference from DNA Fingerprints. Journal of the American Statistical Association, 1992, 87, 337-350.	1.8	49
86	Genomic control for association studies: a semiparametric test to detect excess-haplotype sharing. Biostatistics, 2000, 1, 369-387.	0.9	49
87	Mixture models for linkage analysis of affected sibling pairs and covariates. Genetic Epidemiology, 2002, 22, 52-65.	0.6	48
88	The Yin and Yang of Autism Genetics: How Rare De Novo and Common Variations Affect Liability. Annual Review of Genomics and Human Genetics, 2017, 18, 167-187.	2.5	44
89	Network assisted analysis to reveal the genetic basis of autism. Annals of Applied Statistics, 2015, 9, 1571-1600.	0.5	43
90	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. Molecular Psychiatry, 2019, 24, 1685-1695.	4.1	40

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91	Bayesian estimation of cell typeâ€“specific gene expression with prior derived from single-cell data. Genome Research, 2021, 31, 1807-1818.	2.4	40
92	Heritable Variation, With Little or No Maternal Effect, Accounts for Recurrence Risk to Autism Spectrum Disorder in Sweden. Biological Psychiatry, 2018, 83, 589-597.	0.7	38
93	Integration of association statistics over genomic regions using Bayesian adaptive regression splines. Human Genomics, 2003, 1, 20-9.	1.4	36
94	Depression and mental health helpâ€seeking behaviors in a predominantly African American population of children and adolescents with epilepsy. Epilepsia, 2009, 50, 1943-1952.	2.6	35
95	TOMM40 poly-T repeat lengths, age of onset and psychosis risk in Alzheimer disease. Neurobiology of Aging, 2011, 32, 2328.e1-2328.e9.	1.5	34
96	A Unified Treatment of Integer Parameter Models. Journal of the American Statistical Association, 1987, 82, 758-764.	1.8	33
97	Functional connectome fingerprinting accuracy in youths and adults is similar when examined on the same day and 1.5â€years apart. Human Brain Mapping, 2020, 41, 4187-4199.	1.9	30
98	Uniqueness of estimation and identifiability in mixture models. Canadian Journal of Statistics, 1993, 21, 139-147.	0.6	29
99	Genome-wide distribution of linkage disequilibrium in the population of Palau and its implications for gene flow in Remote Oceania. Human Genetics, 2001, 108, 521-528.	1.8	29
100	Copy Number Variants for Schizophrenia and Related Psychotic Disorders in Oceanic Palau: Risk and Transmission in Extended Pedigrees. Biological Psychiatry, 2011, 70, 1115-1121.	0.7	28
101	Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. Bioinformatics, 2020, 36, 782-788.	1.8	28
102	A Graphical Technique for Determining the Number of Components in a Mixture of Normals. Journal of the American Statistical Association, 1994, 89, 487.	1.8	28
103	Outlier Detection and False Discovery Rates for Whole-Genome DNA Matching. Journal of the American Statistical Association, 2003, 98, 236-246.	1.8	27
104	A spectral graph approach to discovering genetic ancestry. Annals of Applied Statistics, 2010, 4, 179-202.	0.5	26
105	Overdispersion Diagnostics for Generalized Linear Models. Journal of the American Statistical Association, 1995, 90, 1225-1236.	1.8	23
106	Positive Semidefinite Rank-Based Correlation Matrix Estimation With Application to Semiparametric Graph Estimation. Journal of Computational and Graphical Statistics, 2014, 23, 895-922.	0.9	23
107	Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. Molecular Autism, 2021, 12, 65.	2.6	22
108	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	2.6	21

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109	ESCO: single cell expression simulation incorporating gene co-expression. Bioinformatics, 2021, 37, 2374-2381.	1.8	21
110	A Semiparametric Mixture Approach to Case-Control Studies with Errors in Covariables. , 0, .		21
111	A Bayesian hierarchical model for allele frequencies. Genetic Epidemiology, 2001, 20, 17-33.	0.6	20
112	Testing high-dimensional covariance matrices, with application to detecting schizophrenia risk genes. Annals of Applied Statistics, 2017, 11, 1810-1831.	0.5	20
113	How rare and common risk variation jointly affect liability for autism spectrum disorder. Molecular Autism, 2021, 12, 66.	2.6	20
114	De novo missense variants disrupting proteinâ€"protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. Molecular Autism, 2020, 11, 76.	2.6	19
115	Integration and transfer learning of single-cell transcriptomes via cFIT. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
116	Comments on the Statistical Aspects of the NRC's Report on DNA Typing. Journal of Forensic Sciences, 1994, 39, 28-40.	0.9	19
117	Residual Diagnostics for Mixture Models. , 0, .		19
118	SCEPTRE improves calibration and sensitivity in single-cell CRISPR screen analysis. Genome Biology, 2021, 22, 344.	3.8	19
119	Constructing local cell-specific networks from single-cell data. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	18
120	Searching for disease susceptibility variants in structured populations. Genomics, 2009, 93, 1-4.	1.3	16
121	A selective inference approach for false discovery rate control using multiomics covariates yields insights into disease risk. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15028-15035.	3.3	16
122	The Genetic Architecture of Obsessive-Compulsive Disorder: Contribution of Liability to OCD From Alleles Across the Frequency Spectrum. American Journal of Psychiatry, 2022, 179, 216-225.	4.0	16
123	Using ancestry matching to combine familyâ€based and unrelated samples for genomeâ€wide association studies. Statistics in Medicine, 2010, 29, 2932-2945.	0.8	15
124	Hâ€MAGMA, inheriting a shaky statistical foundation, yields excess false positives. Annals of Human Genetics, 2021, 85, 97-100.	0.3	15
125	Whole exome sequencing reveals minimal differences between cell line and whole blood derived DNA. Genomics, 2013, 102, 270-277.	1.3	13
126	Genetic liability to schizophrenia in Oceanic Palau: a search in the affected and maternal generation. Human Genetics, 2007, 121, 675-684.	1.8	12

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127	Not All Autism Genes Are Created Equal: A Response to Myers etÂal.. American Journal of Human Genetics, 2020, 107, 1000-1003.	2.6	11
128	Cell type hierarchy reconstruction via reconciliation of multi-resolution cluster tree. Nucleic Acids Research, 2021, 49, e91-e91.	6.5	11
129	Forensic Inference From DNA Fingerprints. Journal of the American Statistical Association, 1992, 87, 337.	1.8	11
130	Moment-based oscillation properties of mixture models. Annals of Statistics, 1997, 25, .	1.4	10
131	Overdispersion Diagnostics for Generalized Linear Models. Journal of the American Statistical Association, 1995, 90, 1225.	1.8	10
132	Refining genetically inferred relationships using treelet covariance smoothing. Annals of Applied Statistics, 2013, 7, 669-690.	0.5	9
133	Identification of cell-type-specific marker genes from co-expression patterns in tissue samples. Bioinformatics, 2021, 37, 3228-3234.	1.8	9
134	Exponential-Family Embedding With Application to Cell Developmental Trajectories for Single-Cell RNA-Seq Data. Journal of the American Statistical Association, 2021, 116, 457-470.	1.8	7
135	Clustering and Alignment of Polymorphic Sequences for HLA-DRB1 Genotyping. PLoS ONE, 2013, 8, e59835.	1.1	6
136	Structured, sparse regression with application to HIV drug resistance. Annals of Applied Statistics, 2011, 5, 628-644.	0.5	5
137	Characterizing runs of homozygosity and their impact on risk for psychosis in a population isolate. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 521-530.	1.1	5
138	Resting-State Functional Network Organization Is Stable Across Adolescent Development for Typical and Psychosis Spectrum Youth. Schizophrenia Bulletin, 2020, 46, 395-407.	2.3	5
139	MIRA: mutual information-based reporter algorithm for metabolic networks. Bioinformatics, 2014, 30, i175-i184.	1.8	3
140	Covariance-Based Sample Selection for Heterogeneous Data: Applications to Gene Expression and Autism Risk Gene Detection. Journal of the American Statistical Association, 2021, 116, 54-67.	1.8	3
141	Binning Clones by Hybridization with Complex Probes: Statistical Refinement of an Inner Product Mapping Method. Genomics, 1997, 41, 141-154.	1.3	2
142	?Reply to Olson?. Genetic Epidemiology, 2002, 23, 449-455.	0.6	2
143	Analysis of Shared Haplotypes amongst Palauans Maps Loci for Psychotic Disorders to 4q28 and 5q23-q31. Molecular Neuropsychiatry, 2016, 2, 173-184.	3.0	2
144	A data harmonization pipeline to leverage external controls and boost power in GWAS. Human Molecular Genetics, 2022, 31, 481-489.	1.4	2

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145	Avoiding stratification in association studies. , 2005, , .		0
146	Rejoinder for â€œExponential-Family Embedding With Application to Cell Developmental Trajectories for Single-Cell RNA-Seq Dataâ€• Journal of the American Statistical Association, 2021, 116, 478-480.	1.8	0
147	An approach to gene-based testing accounting for dependence of tests among nearby genes. Briefings in Bioinformatics, 2021, 22, .	3.2	0