

# Kathryn M Roeder

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6639737/publications.pdf>

Version: 2024-02-01

147  
papers

35,903  
citations

11608

70  
h-index

9839

141  
g-index

178  
all docs

178  
docs citations

178  
times ranked

39361  
citing authors

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

#	ARTICLE	IF	CITATIONS
19	The heritability of IQ. <i>Nature</i> , 1997, 388, 468-471.	13.7	484
20	Genomic Control, a New Approach to Genetic-Based Association Studies. <i>Theoretical Population Biology</i> , 2001, 60, 155-166.	0.5	465
21	Practical Bayesian Density Estimation Using Mixtures of Normals. <i>Journal of the American Statistical Association</i> , 1997, 92, 894-902.	1.8	370
22	Ulcerative colitis risk loci on chromosomes 1p36 and 12q15 found by genome-wide association study. <i>Nature Genetics</i> , 2009, 41, 216-220.	9.4	364
23	Common genetic variants, acting additively, are a major source of risk for autism. <i>Molecular Autism</i> , 2012, 3, 9.	2.6	357
24	High-dimensional variable selection. <i>Annals of Statistics</i> , 2009, 37, 2178-2201.	1.4	344
25	The Power of Genomic Control. <i>American Journal of Human Genetics</i> , 2000, 66, 1933-1944.	2.6	338
26	Individual common variants exert weak effects on the risk for autism spectrum disorders. <i>Human Molecular Genetics</i> , 2012, 21, 4781-4792.	1.4	334
27	Modeling Uncertainty in Latent Class Membership: A Case Study in Criminology. <i>Journal of the American Statistical Association</i> , 1999, 94, 766-776.	1.8	319
28	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. <i>Nature Communications</i> , 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. <i>Nature Genetics</i> , 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. <i>Nature Genetics</i> , 2017, 49, 504-510.	9.4	298
31	Integrated Model of De Novo and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. <i>PLoS Genetics</i> , 2013, 9, e1003671.	1.5	253
32	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. <i>Neuron</i> , 2013, 77, 235-242.	3.8	242
33	False discovery control with p-value weighting. <i>Biometrika</i> , 2006, 93, 509-524.	1.3	238
34	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. <i>Nature Genetics</i> , 2018, 50, 727-736.	9.4	235
35	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. <i>Science</i> , 2018, 362, .	6.0	234
36	Modeling Uncertainty in Latent Class Membership: A Case Study in Criminology. , 0, .		202

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

#	ARTICLE	IF	CITATIONS
55	Evolutionary-based association analysis using haplotype data. <i>Genetic Epidemiology</i> , 2003, 25, 48-58.	0.6	106
56	Screen and clean: a tool for identifying interactions in genome-wide association studies. <i>Genetic Epidemiology</i> , 2010, 34, 275-285.	0.6	105
57	Association studies for quantitative traits in structured populations. <i>Genetic Epidemiology</i> , 2002, 22, 78-93.	0.6	104
58	Transmission/Disequilibrium Test Meets Measured Haplotype Analysis: Family-Based Association Analysis Guided by Evolution of Haplotypes. <i>American Journal of Human Genetics</i> , 2001, 68, 1250-1263.	2.6	102
59	Characterization of multilocus linkage disequilibrium. <i>Genetic Epidemiology</i> , 2005, 28, 193-206.	0.6	101
60	African ancestry and lung function in Puerto Rican children. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 129, 1484-1490.e6.	1.5	96
61	Do common variants play a role in risk for autism? Evidence and theoretical musings. <i>Brain Research</i> , 2011, 1380, 78-84.	1.1	95
62	Genome-Wide Significance Levels and Weighted Hypothesis Testing. <i>Statistical Science</i> , 2009, 24, 398-413.	1.6	94
63	Global spectral clustering in dynamic networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 927-932.	3.3	93
64	Flexible Parametric Measurement Error Models. <i>Biometrics</i> , 1999, 55, 44-54.	0.8	92
65	Analysis of single-locus tests to detect gene/disease associations. <i>Genetic Epidemiology</i> , 2005, 28, 207-219.	0.6	92
66	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. <i>Cell Reports</i> , 2020, 31, 107489.	2.9	91
67	Practical Bayesian Density Estimation Using Mixtures of Normals. , 0, .		91
68	A Graphical Technique for Determining the Number of Components in a Mixture of Normals. <i>Journal of the American Statistical Association</i> , 1994, 89, 487-495.	1.8	90
69	Disequilibrium Mapping: Composite Likelihood for Pairwise Disequilibrium. <i>Genomics</i> , 1996, 36, 1-16.	1.3	90
70	Improving power in genome-wide association studies: weights tip the scale. <i>Genetic Epidemiology</i> , 2007, 31, 741-747.	0.6	90
71	Discovering genetic ancestry using spectral graph theory. <i>Genetic Epidemiology</i> , 2010, 34, 51-59.	0.6	90
72	A Semiparametric Mixture Approach to Case-Control Studies with Errors in Covariables. <i>Journal of the American Statistical Association</i> , 1996, 91, 722-732.	1.8	87

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

#	ARTICLE	IF	CITATIONS
91	Bayesian estimation of cell type-specific gene expression with prior derived from single-cell data. <i>Genome Research</i> , 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. <i>Biological Psychiatry</i> , 2018, 83, 589-597.	0.7	38
93	Integration of association statistics over genomic regions using Bayesian adaptive regression splines. <i>Human Genomics</i> , 2003, 1, 20-9.	1.4	36
94	Depression and mental health help-seeking behaviors in a predominantly African American population of children and adolescents with epilepsy. <i>Epilepsia</i> , 2009, 50, 1943-1952.	2.6	35
95	TOMM40 poly-T repeat lengths, age of onset and psychosis risk in Alzheimer disease. <i>Neurobiology of Aging</i> , 2011, 32, 2328.e1-2328.e9.	1.5	34
96	A Unified Treatment of Integer Parameter Models. <i>Journal of the American Statistical Association</i> , 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 1.5 years apart. <i>Human Brain Mapping</i> , 2020, 41, 4187-4199.	1.9	30
98	Uniqueness of estimation and identifiability in mixture models. <i>Canadian Journal of Statistics</i> , 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. <i>Human Genetics</i> , 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. <i>Biological Psychiatry</i> , 2011, 70, 1115-1121.	0.7	28
101	Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. <i>Bioinformatics</i> , 2020, 36, 782-788.	1.8	28
102	A Graphical Technique for Determining the Number of Components in a Mixture of Normals. , 0, .		28
103	Outlier Detection and False Discovery Rates for Whole-Genome DNA Matching. <i>Journal of the American Statistical Association</i> , 2003, 98, 236-246.	1.8	27
104	A spectral graph approach to discovering genetic ancestry. <i>Annals of Applied Statistics</i> , 2010, 4, 179-202.	0.5	26
105	Overdispersion Diagnostics for Generalized Linear Models. <i>Journal of the American Statistical Association</i> , 1995, 90, 1225-1236.	1.8	23
106	Positive Semidefinite Rank-Based Correlation Matrix Estimation With Application to Semiparametric Graph Estimation. <i>Journal of Computational and Graphical Statistics</i> , 2014, 23, 895-922.	0.9	23
107	Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. <i>Molecular Autism</i> , 2021, 12, 65.	2.6	22
108	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016, 98, 857-868.	2.6	21

#	ARTICLE	IF	CITATIONS
109	ESCO: single cell expression simulation incorporating gene co-expression. <i>Bioinformatics</i> , 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. <i>Genetic Epidemiology</i> , 2001, 20, 17-33.	0.6	20
112	Testing high-dimensional covariance matrices, with application to detecting schizophrenia risk genes. <i>Annals of Applied Statistics</i> , 2017, 11, 1810-1831.	0.5	20
113	How rare and common risk variation jointly affect liability for autism spectrum disorder. <i>Molecular Autism</i> , 2021, 12, 66.	2.6	20
114	De novo missense variants disrupting protein-protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. <i>Molecular Autism</i> , 2020, 11, 76.	2.6	19
115	Integration and transfer learning of single-cell transcriptomes via cFIT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	19
116	Comments on the Statistical Aspects of the NRC's Report on DNA Typing. <i>Journal of Forensic Sciences</i> , 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. <i>Genome Biology</i> , 2021, 22, 344.	3.8	19
119	Constructing local cell-specific networks from single-cell data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	18
120	Searching for disease susceptibility variants in structured populations. <i>Genomics</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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. <i>American Journal of Psychiatry</i> , 2022, 179, 216-225.	4.0	16
123	Using ancestry matching to combine family-based and unrelated samples for genome-wide association studies. <i>Statistics in Medicine</i> , 2010, 29, 2932-2945.	0.8	15
124	H-MAGMA, inheriting a shaky statistical foundation, yields excess false positives. <i>Annals of Human Genetics</i> , 2021, 85, 97-100.	0.3	15
125	Whole exome sequencing reveals minimal differences between cell line and whole blood derived DNA. <i>Genomics</i> , 2013, 102, 270-277.	1.3	13
126	Genetic liability to schizophrenia in Oceanic Palau: a search in the affected and maternal generation. <i>Human Genetics</i> , 2007, 121, 675-684.	1.8	12



#	ARTICLE	IF	CITATIONS
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. , 0, .		11
130	Moment-based oscillation properties of mixture models. Annals of Statistics, 1997, 25, .	1.4	10
131	Overdispersion Diagnostics for Generalized Linear Models. , 0, .		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

#	ARTICLE	IF	CITATIONS
145	Avoiding stratification in association studies. , 2005, , .		0
146	Rejoinder for "Exponential-Family Embedding With Application to Cell Developmental Trajectories for Single-Cell RNA-Seq Data". 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