Kathryn M Roeder

List of Publications by Year in Descending Order

156 papers	26,395 citations	69 h-index	162 g-index
178 ext. papers	32,223 ext. citations	10.9 avg, IF	6.51 L-index

#	Paper	IF	Citations
156	H-MAGMA, inheriting a shaky statistical foundation, yields excess false positives. *Annals of Human Genetics*, **2021**, 85, 97-100	2.2	7
155	The Genetic Architecture of Obsessive-Compulsive Disorder: Contribution of Liability to OCD From Alleles Across the Frequency Spectrum. *American Journal of Psychiatry*, **2021**, appiajp202121010101	11.9	2
154	How rare and common risk variation jointly affect liability for autism spectrum disorder. *Molecular Autism*, **2021**, 12, 66	6.5	2
153	Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. *Molecular Autism*, **2021**, 12, 65	6.5	4
152	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	2.8	2
151	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,	11.5	7
150	Bayesian estimation of cell type-specific gene expression with prior derived from single-cell data. *Genome Research*, **2021**, 31, 1807-1818	9.7	0
149	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	2.8	
148	Cell type hierarchy reconstruction via reconciliation of multi-resolution cluster tree. *Nucleic Acids Research*, **2021**, 49, e91	20.1	1
147	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	2.8	1
146	ESCO: single cell expression simulation incorporating gene co-expression. *Bioinformatics*, **2021**,	7.2	4
145	SCEPTRE improves calibration and sensitivity in single-cell CRISPR screen analysis.. *Genome Biology*, **2021**, 22, 344	18.3	2
144	Not All Autism Genes Are Created Equal: A Response to Myers et al. *American Journal of Human Genetics*, **2020**, 107, 1000-1003	11	5
143	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	11.5	4
142	Functional connectome fingerprinting accuracy in youths and adults is similar when examined on the same day and 1.5-years apart. *Human Brain Mapping*, **2020**, 41, 4187-4199	5.9	11
141	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. *Cell*, **2020**, 180, 568-584.e23	56.2	578
140	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. *Cell Reports*, **2020**, 31, 107489	10.6	43

139	Resting-State Functional Network Organization Is Stable Across Adolescent Development for Typical and Psychosis Spectrum Youth. *Schizophrenia Bulletin*, **2020**, 46, 395-407	1.3	2
138	De novo missense variants disrupting protein-protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. *Molecular Autism*, **2020**, 11, 76	6.5	8
137	APOE and TREM2 regulate amyloid-responsive microglia in Alzheimer's disease. *Acta Neuropathologica*, **2020**, 140, 477-493	14.3	31
136	Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. *Bioinformatics*, **2020**, 36, 782-788	7.2	13
135	Identification of common genetic risk variants for autism spectrum disorder. *Nature Genetics*, **2019**, 51, 431-444	36.3	746
134	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. *Molecular Psychiatry*, **2019**, 24, 1685-1695	15.1	20
133	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. *Cell*, **2019**, 179, 1469-1482.e11	56.2	402
132	Semisoft clustering of single-cell data. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 466-471	11.5	36
131	Global spectral clustering in dynamic networks. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 927-932	11.5	65
130	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. *Nature Genetics*, **2018**, 50, 727-736	36.3	156
129	Heritable Variation, With Little or No Maternal Effect, Accounts for Recurrence Risk to Autism Spectrum Disorder in Sweden. *Biological Psychiatry*, **2018**, 83, 589-597	7.9	28
128	A UNIFIED STATISTICAL FRAMEWORK FOR SINGLE CELL AND BULK RNA SEQUENCING DATA. *Annals of Applied Statistics*, **2018**, 12, 609-632	2.1	42
127	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. *Nature Genetics*, **2018**, 50, 1032-1040	36.3	44
126	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. *Science* , **2018**, 362,	33.3	134
125	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. *American Journal of Human Genetics*, **2018**, 102, 1169-1184	11	73
124	Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples. *Nature Genetics*, **2017**, 49, 504-510	36.3	203
123	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	9.7	31
122	TESTING HIGH-DIMENSIONAL COVARIANCE MATRICES, WITH APPLICATION TO DETECTING SCHIZOPHRENIA RISK GENES. *Annals of Applied Statistics*, **2017**, 11, 1810-1831	2.1	10

121	Analysis of Shared Haplotypes amongst Palauans Maps Loci for Psychotic Disorders to 4q28 and 5q23-q31. *Molecular Neuropsychiatry*, **2017**, 2, 173-184	4.9	1
120	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. *American Journal of Human Genetics*, **2016**, 98, 857-868	11	14
119	Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nature Neuroscience*, **2016**, 19, 1442-1453	25.5	622
118	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. *Nature Communications*, **2015**, 6, 6404	17.4	218
117	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. *Neuron*, **2015**, 87, 1215-1233	13.9	806
116	NETWORK ASSISTED ANALYSIS TO REVEAL THE GENETIC BASIS OF AUTISM. *Annals of Applied Statistics*, **2015**, 9, 1571-1600	2.1	24
115	Synaptic, transcriptional and chromatin genes disrupted in autism. *Nature*, **2014**, 515, 209-15	50.4	1581
114	A framework for the interpretation of de novo mutation in human disease. *Nature Genetics*, **2014**, 46, 944-50	36.3	656
113	Most genetic risk for autism resides with common variation. *Nature Genetics*, **2014**, 46, 881-5	36.3	734
112	Transcriptional consequences of 16p11.2 deletion and duplication in mouse cortex and multiplex autism families. *American Journal of Human Genetics*, **2014**, 94, 870-83	11	78
111	MIRA: mutual information-based reporter algorithm for metabolic networks. *Bioinformatics*, **2014**, 30, i175-84	7.2	3
110	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**, 165B, 521-30	3.5	4
109	Positive Semidefinite Rank-based Correlation Matrix Estimation with Application to Semiparametric Graph Estimation. *Journal of Computational and Graphical Statistics*, **2014**, 23, 895-922	1.4	20
108	De novo insertions and deletions of predominantly paternal origin are associated with autism spectrum disorder. *Cell Reports*, **2014**, 9, 16-23	10.6	118
107	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. *Molecular Autism*, **2014**, 5, 22	6.5	89
106	Coexpression networks implicate human midfetal deep cortical projection neurons in the pathogenesis of autism. *Cell*, **2013**, 155, 997-1007	56.2	591
105	Whole exome sequencing reveals minimal differences between cell line and whole blood derived DNA. *Genomics*, **2013**, 102, 270-7	4.3	11
104	Rare complete knockouts in humans: population distribution and significant role in autism spectrum disorders. *Neuron*, **2013**, 77, 235-42	13.9	190

103	Clustering and alignment of polymorphic sequences for HLA-DRB1 genotyping. *PLoS ONE*, **2013**, 8, e59835	37	6
102	Integrated model of de novo and inherited genetic variants yields greater power to identify risk genes. *PLoS Genetics*, **2013**, 9, e1003671	6	168
101	Analysis of rare, exonic variation amongst subjects with autism spectrum disorders and population controls. *PLoS Genetics*, **2013**, 9, e1003443	6	108
100	REFINING GENETICALLY INFERRED RELATIONSHIPS USING TREELET COVARIANCE SMOOTHING. *Annals of Applied Statistics*, **2013**, 7, 669-690	2.1	8
99	The autism sequencing consortium: large-scale, high-throughput sequencing in autism spectrum disorders. *Neuron*, **2012**, 76, 1052-6	13.9	124
98	Common genetic variants in the CLDN2 and PRSS1-PRSS2 loci alter risk for alcohol-related and sporadic pancreatitis. *Nature Genetics*, **2012**, 44, 1349-54	36.3	223
97	Patterns and rates of exonic de novo mutations in autism spectrum disorders. *Nature*, **2012**, 485, 242-5	50.4	1300
96	African ancestry and lung function in Puerto Rican children. *Journal of Allergy and Clinical Immunology*, **2012**, 129, 1484-90.e6	11.5	73
95	Vitamin D insufficiency and severe asthma exacerbations in Puerto Rican children. *American Journal of Respiratory and Critical Care Medicine*, **2012**, 186, 140-6	10.2	154
94	Common genetic variants, acting additively, are a major source of risk for autism. *Molecular Autism*, **2012**, 3, 9	6.5	294
93	De novo mutations revealed by whole-exome sequencing are strongly associated with autism. *Nature*, **2012**, 485, 237-41	50.4	1470
92	Individual common variants exert weak effects on the risk for autism spectrum disorders. *Human Molecular Genetics*, **2012**, 21, 4781-92	5.6	279
91	The huge Package for High-dimensional Undirected Graph Estimation in R. *Journal of Machine Learning Research*, **2012**, 13, 1059-1062	28.6	141
90	Copy number variants for schizophrenia and related psychotic disorders in Oceanic Palau: risk and transmission in extended pedigrees. *Biological Psychiatry*, **2011**, 70, 1115-21	7.9	23
89	TOMM40 poly-T repeat lengths, age of onset and psychosis risk in Alzheimer disease. *Neurobiology of Aging*, **2011**, 32, 2328.e1-9	5.6	28
88	Multiple recurrent de novo CNVs, including duplications of the 7q11.23 Williams syndrome region, are strongly associated with autism. *Neuron*, **2011**, 70, 863-85	13.9	932
87	Testing for an unusual distribution of rare variants. *PLoS Genetics*, **2011**, 7, e1001322	6	465
86	STRUCTURED, SPARSE REGRESSION WITH APPLICATION TO HIV DRUG RESISTANCE. *Annals of Applied Statistics*, **2011**, 5, 628-644	2.1	5

85	Do common variants play a role in risk for autism? Evidence and theoretical musings. *Brain Research*, **2011**, 1380, 78-84	3.7	80
84	Functional impact of global rare copy number variation in autism spectrum disorders. *Nature*, **2010**, 466, 368-72	50.4	1499
83	Genome-wide association identifies multiple ulcerative colitis susceptibility loci. *Nature Genetics*, **2010**, 42, 332-7	36.3	491
82	A genome-wide scan for common alleles affecting risk for autism. *Human Molecular Genetics*, **2010**, 19, 4072-82	5.6	443
81	Discovering genetic ancestry using spectral graph theory. *Genetic Epidemiology*, **2010**, 34, 51-9	2.6	74
80	A SPECTRAL GRAPH APPROACH TO DISCOVERING GENETIC ANCESTRY. *Annals of Applied Statistics*, **2010**, 4, 179-202	2.1	19
79	Candidate gene analysis of femoral neck trabecular and cortical volumetric bone mineral density in older men. *Journal of Bone and Mineral Research*, **2010**, 25, 330-8	6.3	44
78	Screen and clean: a tool for identifying interactions in genome-wide association studies. *Genetic Epidemiology*, **2010**, 34, 275-85	2.6	87
77	Using ancestry matching to combine family-based and unrelated samples for genome-wide association studies. *Statistics in Medicine*, **2010**, 29, 2932-45	2.3	13
76	Stability Approach to Regularization Selection (StARS) for High Dimensional Graphical Models. *Advances in Neural Information Processing Systems*, **2010**, 24, 1432-1440	2.2	98
75	Ulcerative colitis-risk loci on chromosomes 1p36 and 12q15 found by genome-wide association study. *Nature Genetics*, **2009**, 41, 216-20	36.3	325
74	Depression and mental health help-seeking behaviors in a predominantly African American population of children and adolescents with epilepsy. *Epilepsia*, **2009**, 50, 1943-52	6.4	30
73	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, 2039-49	6.3	54
72	Searching for disease susceptibility variants in structured populations. *Genomics*, **2009**, 93, 1-4	4.3	14
71	Genome-Wide Significance Levels and Weighted Hypothesis Testing. *Statistical Science*, **2009**, 24, 398-413	2.4	74
70	HIGH DIMENSIONAL VARIABLE SELECTION. *Annals of Statistics*, **2009**, 37, 2178-2201	3.2	260
69	Pleiotropy and principal components of heritability combine to increase power for association analysis. *Genetic Epidemiology*, **2008**, 32, 9-19	2.6	105
68	On the use of general control samples for genome-wide association studies: genetic matching highlights causal variants. *American Journal of Human Genetics*, **2008**, 82, 453-63	11	106

67	Improving power in genome-wide association studies: weights tip the scale. *Genetic Epidemiology*, **2007**, 31, 741-7	2.6	76
66	Genetic liability to schizophrenia in Oceanic Palau: a search in the affected and maternal generation. *Human Genetics*, **2007**, 121, 675-84	6.3	10
65	SNP-based analysis of genetic substructure in the German population. *Human Heredity*, **2006**, 62, 20-9	1.1	109
64	False discovery control with p-value weighting. *Biometrika*, **2006**, 93, 509-524	2	174
63	Using linkage genome scans to improve power of association in genome scans. *American Journal of Human Genetics*, **2006**, 78, 243-52	11	173
62	Analysis of single-locus tests to detect gene/disease associations. *Genetic Epidemiology*, **2005**, 28, 207-19	2.6	88
61	Characterization of multilocus linkage disequilibrium. *Genetic Epidemiology*, **2005**, 28, 193-206	2.6	95
60	Genomic Control to the extreme. *Nature Genetics*, **2004**, 36, 1129-30; author reply 1131	36.3	130
59	Integration of association statistics over genomic regions using Bayesian adaptive regression splines. *Human Genomics*, **2003**, 1, 20-9	6.8	22
58	Analysis of multilocus models of association. *Genetic Epidemiology*, **2003**, 25, 36-47	2.6	65
57	Evolutionary-based association analysis using haplotype data. *Genetic Epidemiology*, **2003**, 25, 48-58	2.6	100
56	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	11	119
55	Outlier Detection and False Discovery Rates for Whole-Genome DNA Matching. *Journal of the American Statistical Association*, **2003**, 98, 236-246	2.8	23
54	Mixture models for linkage analysis of affected sibling pairs and covariates. *Genetic Epidemiology*, **2002**, 22, 52-65	2.6	44
53	Association studies for quantitative traits in structured populations. *Genetic Epidemiology*, **2002**, 22, 78-93	2.6	96
52	Reply to Olson. *Genetic Epidemiology*, **2002**, 23, 449-455	2.6	2
51	Genome-wide distribution of linkage disequilibrium in the population of Palau and its implications for gene flow in Remote Oceania. *Human Genetics*, **2001**, 108, 521-8	6.3	28
50	Unbiased methods for population-based association studies. *Genetic Epidemiology*, **2001**, 21, 273-84	2.6	119

49	A Bayesian hierarchical model for allele frequencies. *Genetic Epidemiology*, **2001**, 20, 17-33	2.6	18
48	A SAS Procedure Based on Mixture Models for Estimating Developmental Trajectories. *Sociological Methods and Research*, **2001**, 29, 374-393	2.9	1466
47	Genomic control, a new approach to genetic-based association studies. *Theoretical Population Biology*, **2001**, 60, 155-66	1.2	403
46	Transmission/disequilibrium test meets measured haplotype analysis: family-based association analysis guided by evolution of haplotypes. *American Journal of Human Genetics*, **2001**, 68, 1250-63	11	90
45	Genomic control for association studies: a semiparametric test to detect excess-haplotype sharing. *Biostatistics*, **2000**, 1, 369-87	3.7	44
44	Haplotype fine mapping by evolutionary trees. *American Journal of Human Genetics*, **2000**, 66, 659-73	11	53
43	The power of genomic control. *American Journal of Human Genetics*, **2000**, 66, 1933-44	11	294
42	Flexible parametric measurement error models. *Biometrics*, **1999**, 55, 44-54	1.8	82
41	Genomic control for association studies. *Biometrics*, **1999**, 55, 997-1004	1.8	2262
40	Modeling Uncertainty in Latent Class Membership: A Case Study in Criminology. *Journal of the American Statistical Association*, **1999**, 94, 766-776	2.8	284
39	Practical Bayesian Density Estimation Using Mixtures of Normals. *Journal of the American Statistical Association*, **1997**, 92, 894-902	2.8	303
38	Binning clones by hybridization with complex probes: statistical refinement of an inner product mapping method. *Genomics*, **1997**, 41, 141-54	4.3	2
37	A statistical model for locating regulatory regions in genomic DNA. *Journal of Molecular Biology*, **1997**, 268, 8-14	6.5	61
36	A Bayesian semiparametric model for case-control studies with errors in variables. *Biometrika*, **1997** , 84, 523-537	2	57
35	The heritability of IQ. *Nature*, **1997**, 388, 468-71	50.4	369
34	Moment-based oscillation properties of mixture models. *Annals of Statistics*, **1997**, 25,	3.2	2
33	Disequilibrium mapping: composite likelihood for pairwise disequilibrium. *Genomics*, **1996**, 36, 1-16	4.3	82
32	A Semiparametric Mixture Approach to Case-Control Studies with Errors in Covariables. *Journal of the American Statistical Association*, **1996**, 91, 722-732	2.8	73

31	Overdispersion Diagnostics for Generalized Linear Models. *Journal of the American Statistical Association*, **1995**, 90, 1225-1236	2.8	17
30	A Graphical Technique for Determining the Number of Components in a Mixture of Normals. *Journal of the American Statistical Association*, **1994**, 89, 487-495	2.8	77
29	DNA Fingerprinting: A Review of the Controversy. *Statistical Science*, **1994**, 9,	2.4	46
28	Comments on the Statistical Aspects of the NRC's Report on DNA Typing. *Journal of Forensic Sciences*, **1994**, 39, 13568J	1.8	11
27	Uniqueness of estimation and identifiability in mixture models. *Canadian Journal of Statistics*, **1993**, 21, 139-147	0.4	25
26	Residual Diagnostics for Mixture Models. *Journal of the American Statistical Association*, **1992**, 87, 785-79[illegible]	2.8	49
25	Forensic Inference from DNA Fingerprints. *Journal of the American Statistical Association*, **1992**, 87, 337-350	2.8	38
24	Density Estimation with Confidence Sets Exemplified by Superclusters and Voids in the Galaxies. *Journal of the American Statistical Association*, **1990**, 85, 617-624	2.8	146
23	Application of Maximum Likelihood Methods to Population Genetic Data for the Estimation of Individual Fertilities. *Biometrics*, **1989**, 45, 363	1.8	70
22	A Unified Treatment of Integer Parameter Models. *Journal of the American Statistical Association*, **1987**, 82, 758-764	2.8	28
21	Rare coding variation illuminates the allelic architecture, risk genes, cellular expression patterns, and phenotypic context of autism		4
20	How rare and common risk variation jointly affect liability for autism spectrum disorder		1
19	Residual Diagnostics for Mixture Models		19
18	Forensic Inference from DNA Fingerprints		11
17	A Graphical Technique for Determining the Number of Components in a Mixture of Normals		28
16	Overdispersion Diagnostics for Generalized Linear Models		9
15	A Semiparametric Mixture Approach to Case-Control Studies with Errors in Covariables		20
14	Modeling Uncertainty in Latent Class Membership: A Case Study in Criminology		53

13	Practical Bayesian Density Estimation Using Mixtures of Normals	89
12	Refining the role of de novo protein truncating variants in neurodevelopmental disorders using population reference samples	5
11	New mutations, old statistical challenges	1
10	Limited contribution of rare, noncoding variation to autism spectrum disorder from sequencing of 2,076 genomes in quartet families	6
9	Bayesian estimation of cell-type-specific gene expression per bulk sample with prior derived from single-cell data	2
8	Conditional resampling improves calibration and sensitivity in single-cell CRISPR screen analysis	5
7	H-MAGMA, inheriting a shaky statistical foundation, yields excess false positives	3
6	A United Statistical Framework for Single Cell and Bulk Sequencing Data	1
5	Common risk variants identified in autism spectrum disorder	32
4	Large-scale exome sequencing study implicates both developmental and functional changes in the neurobiology of autism	21
3	Functional connectome fingerprinting accuracy in youths and adults is similar when examined on the same day and 1.5 years apart	5
2	Discovery of target genes and pathways of blood trait loci using pooled CRISPR screens and single cell RNA sequencing	5
1	The genetic architecture of obsessive-compulsive disorder: alleles across the frequency spectrum contribute liability to OCD	1