Bernie Devlin

List of Publications by Year
in descending order

136 papers	33,202 citations	16451 64 h-index	11308 136 g-index
159 all docs	159 docs citations	159 times ranked	31428 citing authors

#	Article	IF	Citations
1	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	27.8	2,254
2	De novo mutations revealed by whole-exome sequencing are strongly associated with autism. Nature, 2012, 485, 237-241.	27.8	1,863
3	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
4	Patterns and rates of exonic de novo mutations in autism spectrum disorders. Nature, 2012, 485, 242-245.	27.8	1,597
5	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	21.4	1,538
6	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	28.9	1,422
7	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328.	21.4	1,272
8	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. Nature, 2009, 459, 569-573.	27.8	1,270
9	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	8.1	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.	8.1	1,146
11	Most genetic risk for autism resides with common variation. Nature Genetics, 2014, 46, 881-885.	21.4	977
12	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	14.8	952
13	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	21.4	943
14	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	12.6	851
15	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	28.9	825
16	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	6.2	819
17	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	2.9	538
18	Testing for an Unusual Distribution of Rare Variants. PLoS Genetics, 2011, 7, e1001322.	3.5	530

#	ARTICLE	IF	CITATIONS
19	Spatial and Temporal Mapping of De Novo Mutations in Schizophrenia to a Fetal Prefrontal Cortical Network. Cell, 2013, 154, 518-529.	28.9	507
20	Identification of common variants influencing risk of the tauopathy progressive supranuclear palsy. Nature Genetics, 2011, 43, 699-705.	21.4	502
21	Genetic architecture in autism spectrum disorder. Current Opinion in Genetics and Development, 2012, 22, 229-237.	3.3	445
22	Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders. Nature Genetics, 2017, 49, 978-985.	21.4	401
23	Common genetic variants, acting additively, are a major source of risk for autism. Molecular Autism, 2012, 3, 9.	4.9	357
24	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	2.9	334
25	Association and linkage analyses of RGS4 polymorphisms in schizophrenia. Human Molecular Genetics, 2002, 11, 1373-1380.	2.9	318
26	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nature Communications, 2015, 6, 6404.	12.8	316
27	Common genetic variants in the CLDN2 and PRSS1-PRSS2 loci alter risk for alcohol-related and sporadic pancreatitis. Nature Genetics, 2012, 44, 1349-1354.	21.4	303
28	Refining the role of de novo protein-truncating variants in neurodevelopmental disorders by using population reference samples. Nature Genetics, 2017, 49, 504-510.	21.4	298
29	Integrated Model of De Novo and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. PLoS Genetics, 2013, 9, e1003671.	3.5	253
30	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. Neuron, 2013, 77, 235-242.	8.1	242
31	An analytical framework for whole-genome sequence association studies and its implications for autism spectrum disorder. Nature Genetics, 2018, 50, 727-736.	21.4	235
32	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	12.6	234
33	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	6.2	225
34	Alcohol Use Disorder Comorbidity in Eating Disorders. Journal of Clinical Psychiatry, 2004, 65, 1000-1006.	2.2	200
35	Temperament and Character in Women with Anorexia Nervosa. Journal of Nervous and Mental Disease, 2000, 188, 559-567.	1.0	178
36	Circadian Phase Variation in Bipolar I Disorder. Chronobiology International, 2005, 22, 571-584.	2.0	177

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37	Rare Copy Number Variants in Tourette Syndrome Disrupt Genes in Histaminergic Pathways and Overlap with Autism. Biological Psychiatry, 2012, 71, 392-402.	1.3	167
38	Personality characteristics of women before and after recovery from an eating disorder. Psychological Medicine, 2004, 34, 1407-1418.	4.5	165
39	Genome-wide Transcriptome Profiling Reveals the Functional Impact of Rare De Novo and Recurrent CNVs in Autism Spectrum Disorders. American Journal of Human Genetics, 2012, 91, 38-55.	6.2	160
40	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	21.4	154
41	The Autism Sequencing Consortium: Large-Scale, High-Throughput Sequencing in Autism Spectrum Disorders. Neuron, 2012, 76, 1052-1056.	8.1	153
42	De Novo Insertions and Deletions of Predominantly Paternal Origin Are Associated with Autism Spectrum Disorder. Cell Reports, 2014, 9, 16-23.	6.4	151
43	Comprehensive analysis of APOE and selected proximate markers for late-onset Alzheimer's disease: Patterns of linkage disequilibrium and disease/marker association. Genomics, 2007, 89, 655-665.	2.9	149
44	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	5.3	149
45	Linkage analysis of anorexia nervosa incorporating behavioral covariates. Human Molecular Genetics, 2002, 11, 689-696.	2.9	144
46	Association study of 21 circadian genes with bipolar I disorder, schizoaffective disorder, and schizophrenia. Bipolar Disorders, 2009, 11, 701-710.	1.9	133
47	Trajectories of cognitive decline in Alzheimer's disease. International Psychogeriatrics, 2010, 22, 281-290.	1.0	133
48	Analysis of Rare, Exonic Variation amongst Subjects with Autism Spectrum Disorders and Population Controls. PLoS Genetics, 2013, 9, e1003443.	3.5	133
49	A Genome-wide Association Study of Autism Using the Simons Simplex Collection: Does Reducing Phenotypic Heterogeneity in Autism Increase Genetic Homogeneity?. Biological Psychiatry, 2015, 77, 775-784.	1.3	133
50	Association of FKBP5 Polymorphisms With Suicidal Events in the Treatment of Resistant Depression in Adolescents (TORDIA) Study. American Journal of Psychiatry, 2010, 167, 190-197.	7.2	128
51	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	6.2	128
52	Association of Multiple DRD2 Polymorphisms with Anorexia Nervosa. Neuropsychopharmacology, 2005, 30, 1703-1710.	5.4	127
53	A network of dopaminergic gene variations implicated as risk factors for schizophrenia. Human Molecular Genetics, 2008, 17, 747-758.	2.9	124
54	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.	6.2	120

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55	Transcriptional Consequences of 16p11.2 Deletion and Duplication in Mouse Cortex and Multiplex Autism Families. American Journal of Human Genetics, 2014, 94, 870-883.	6.2	116
56	A search for susceptibility loci for anorexia nervosa: methods and sample description. Biological Psychiatry, 2000, 47, 794-803.	1.3	113
57	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. Molecular Autism, 2014, 5, 22.	4.9	111
58	A Pleiotropic Missense Variant in SLC39A8 Is Associated With Crohn's Disease and Human Gut Microbiome Composition. Gastroenterology, 2016, 151, 724-732.	1.3	109
59	Do common variants play a role in risk for autism? Evidence and theoretical musings. Brain Research, 2011, 1380, 78-84.	2.2	95
60	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	6.2	91
61	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489.	6.4	91
62	Discovering genetic ancestry using spectral graph theory. Genetic Epidemiology, 2010, 34, 51-59.	1.3	90
63	Evaluation of a Susceptibility Gene for Schizophrenia: Genotype Based Meta-Analysis of RGS4 Polymorphisms from Thirteen Independent Samples. Biological Psychiatry, 2006, 60, 152-162.	1.3	87
64	A unified statistical framework for single cell and bulk RNA sequencing data. Annals of Applied Statistics, 2018, 12, 609-632.	1.1	82
65	Alleles of a reelin CGG repeat do not convey liability to autism in a sample from the CPEA network. American Journal of Medical Genetics Part A, 2004, 126B, 46-50.	2.4	72
66	Semisoft clustering of single-cell data. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 466-471.	7.1	71
67	Adjusting Head Circumference for Covariates in Autism: Clinical Correlates of a Highly Heritable Continuous Trait. Biological Psychiatry, 2013, 74, 576-584.	1.3	70
68	Heritability of Psychosis in Alzheimer Disease. American Journal of Geriatric Psychiatry, 2005, 13, 624-627.	1.2	64
69	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Nature Genetics, 2018, 50, 1032-1040.	21.4	64
70	Intellectual Disability Is Associated with Increased Runs of Homozygosity in Simplex Autism. American Journal of Human Genetics, 2013, 93, 103-109.	6.2	63
71	Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. Nature Neuroscience, 2019, 22, 1402-1412.	14.8	63
72	Novel, Replicated Associations Between Dopamine D3 Receptor Gene Polymorphisms and Schizophrenia in Two Independent Samples. Biological Psychiatry, 2006, 60, 570-577.	1.3	62

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73	Project Among African-Americans to Explore Risks for Schizophrenia (PAARTNERS): Evidence for Impairment and Heritability of Neurocognitive Functioning in Families of Schizophrenia Patients. American Journal of Psychiatry, 2010, 167, 459-472.	7.2	59
74	Modest Impact on Risk for Autism Spectrum Disorder of Rare Copy Number Variants at 15q11.2, Specifically Breakpoints 1 to 2. Autism Research, 2014, 7, 355-362.	3.8	59
75	De novo structural mutation rates and gamete-of-origin biases revealed through genome sequencing of 2,396 families. American Journal of Human Genetics, 2021, 108, 597-607.	6.2	57
76	Linkage analysis of anorexia and bulimia nervosa cohorts using selected behavioral phenotypes as quantitative traits or covariates. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 139B, 61-68.	1.7	55
77	The MAOA promoter polymorphism, disruptive behavior disorders, and early onset substance use disorder: gene–environment interaction. Psychiatric Genetics, 2007, 17, 323-332.	1.1	53
78	Consanguinity and increased risk for schizophrenia in Egypt. Schizophrenia Research, 2010, 120, 108-112.	2.0	53
79	Genetic analysis of bulimia nervosa: Methods and sample description. International Journal of Eating Disorders, 2004, 35, 556-570.	4.0	50
80	Investigating Shared Genetic Basis Across Tourette Syndrome and Comorbid Neurodevelopmental Disorders Along the Impulsivity-Compulsivity Spectrum. Biological Psychiatry, 2021, 90, 317-327.	1.3	49
81	Mixture models for linkage analysis of affected sibling pairs and covariates. Genetic Epidemiology, 2002, 22, 52-65.	1.3	48
82	The genetics of anorexia nervosa collaborative study: Methods and sample description. International Journal of Eating Disorders, 2008, 41, 289-300.	4.0	48
83	Heritability of Psychosis in Alzheimer Disease. American Journal of Geriatric Psychiatry, 2005, 13, 624-627.	1.2	47
84	The AVPR1A Gene and Substance Use Disorders: Association, Replication, and Functional Evidence. Biological Psychiatry, 2011, 70, 519-527.	1.3	45
85	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.	6.2	44
86	Fine Mapping of the Split-Hand/Split-Foot Locus (SHFM3) at 10q24: Evidence for Anticipation and Segregation Distortion. American Journal of Human Genetics, 1999, 64, 1646-1654.	6.2	40
87	Polymorphisms in MICB are associated with human herpes virus seropositivity and schizophrenia risk. Schizophrenia Research, 2007, 94, 342-353.	2.0	40
88	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. Molecular Psychiatry, 2019, 24, 1685-1695.	7.9	40
89	Bayesian estimation of cell type–specific gene expression with prior derived from single-cell data. Genome Research, 2021, 31, 1807-1818.	5.5	40
90	Heritable Variation, With Little or No Maternal Effect, Accounts for Recurrence Risk to Autism Spectrum Disorder in Sweden. Biological Psychiatry, 2018, 83, 589-597.	1.3	38

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91	Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. Biological Psychiatry, 2022, 91, 92-101.	1.3	38
92	Personality in men with eating disorders. Journal of Psychosomatic Research, 2004, 57, 273-278.	2.6	34
93	No evidence for linkage of liability to autism toHOXA1 in a sample from the CPEA network. American Journal of Medical Genetics Part A, 2002, 114, 667-672.	2.4	33
94	Project among African-Americans to explore risks for schizophrenia (PAARTNERS): Recruitment and assessment methods. Schizophrenia Research, 2006, 87, 32-44.	2.0	33
95	Functional annotation of rare structural variation in the human brain. Nature Communications, 2020, 11, 2990.	12.8	32
96	Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. Molecular Psychiatry, 2021, 26, 5797-5811.	7.9	30
97	Are exposure to cytomegalovirus and genetic variation on chromosome 6p joint risk factors for schizophrenia?. Annals of Medicine, 2007, 39, 145-153.	3.8	28
98	Copy Number Variants for Schizophrenia and Related Psychotic Disorders in Oceanic Palau: Risk and Transmission in Extended Pedigrees. Biological Psychiatry, 2011, 70, 1115-1121.	1.3	28
99	Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. Bioinformatics, 2020, 36, 782-788.	4.1	28
100	Selection of eating-disorder phenotypes for linkage analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 139B, 81-87.	1.7	25
101	Linkage analysis of a completely ascertained sample of familial schizophrenics and bipolars from Palau, Micronesia. Human Genetics, 2005, 117, 349-356.	3.8	22
102	Sequence Variation in the Primate Dopamine Transporter Gene and Its Relationship to Social Dominance. Molecular Biology and Evolution, 2007, 25, 18-28.	8.9	22
103	Evaluation of HLA Polymorphisms in Relation to Schizophrenia Risk and Infectious Exposure. Schizophrenia Bulletin, 2012, 38, 1149-1154.	4.3	22
104	Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. Molecular Autism, 2021, 12, 65.	4.9	22
105	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. American Journal of Human Genetics, 2016, 98, 857-868.	6.2	21
106	Testing high-dimensional covariance matrices, with application to detecting schizophrenia risk genes. Annals of Applied Statistics, 2017, 11, 1810-1831.	1.1	20
107	How rare and common risk variation jointly affect liability for autism spectrum disorder. Molecular Autism, 2021, 12, 66.	4.9	20
108	ADLAPH: A molecular haplotyping method based on allele-discriminating long-range PCR. Genomics, 2004, 84, 600-612.	2.9	19

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109	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.	4.9	19
110	No association of psychosis in Alzheimer disease with neurodegenerative pathway genes. Neurobiology of Aging, 2011, 32, 555.e9-555.e11.	3.1	18
111	Maternal Effects as Causes of Risk for Obsessive-Compulsive Disorder. Biological Psychiatry, 2020, 87, 1045-1051.	1.3	18
112	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.	7.1	16
113	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.	7.2	16
114	Convergent patterns of association between phenylalanine hydroxylase variants and schizophrenia in four independent samples. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 560-569.	1.7	15
115	Using ancestry matching to combine family–based and unrelated samples for genome–wide association studies. Statistics in Medicine, 2010, 29, 2932-2945.	1.6	15
116	H–MAGMA, inheriting a shaky statistical foundation, yields excess false positives. Annals of Human Genetics, 2021, 85, 97-100.	0.8	15
117	Whole exome sequencing reveals minimal differences between cell line and whole blood derived DNA. Genomics, 2013, 102, 270-277.	2.9	13
118	Cohort profile: Epidemiology and Genetics of Obsessive–compulsive disorder and chronic tic disorders in Sweden (EGOS). Social Psychiatry and Psychiatric Epidemiology, 2020, 55, 1383-1393.	3.1	13
119	Transcriptome alterations are enriched for synapse-associated genes in the striatum of subjects with obsessive-compulsive disorder. Translational Psychiatry, 2021, 11, 171.	4.8	13
120	Genetic liability to schizophrenia in Oceanic Palau: a search in the affected and maternal generation. Human Genetics, 2007, 121, 675-684.	3.8	12
121	Principal Components of Heritability From Neurocognitive Domains Differ Between Families With Schizophrenia and Control Subjects. Schizophrenia Bulletin, 2013, 39, 464-471.	4.3	12
122	Not All Autism Genes Are Created Equal: A Response to Myers etÂal.. American Journal of Human Genetics, 2020, 107, 1000-1003.	6.2	11
123	Refining genetically inferred relationships using treelet covariance smoothing. Annals of Applied Statistics, 2013, 7, 669-690.	1.1	9
124	Variations in Genes Related to Sleep Patterns in Children With Autism Spectrum Disorder. Biological Research for Nursing, 2019, 21, 335-342.	1.9	9
125	Joint evaluation of serum C-Reactive Protein levels and polygenic risk scores as risk factors for schizophrenia. Psychiatry Research, 2018, 261, 148-153.	3.3	6
126	Galton Redux: Eugenics, Intelligence, Race, and Society: A Review of the Bell Curve: Intelligence and Class Structure in American Life.. Journal of the American Statistical Association, 1995, 90, 1483.	3.1	5

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127	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.	1.7	5
128	Runs of homozygosity, copy number variation, and risk for depression and suicidal behavior in an Arab Bedouin kindred. Psychiatric Genetics, 2017, 27, 169-177.	1.1	5
129	Resting-State Functional Network Organization Is Stable Across Adolescent Development for Typical and Psychosis Spectrum Youth. Schizophrenia Bulletin, 2020, 46, 395-407.	4.3	5
130	Wringing The Bell Curve: A Cautionary Tale about the Relationships among Race, Genes, and IQ. Chance, 1995, 8, 27-36.	0.2	4
131	Shedding new light on genetic dark matter. Genome Medicine, 2010, 2, 79.	8.2	3
132	Analysis of Shared Haplotypes amongst Palauans Maps Loci for Psychotic Disorders to 4q28 and 5q23-q31. Molecular Neuropsychiatry, 2016, 2, 173-184.	2.9	2
133	Heterogeneous Trajectories of Problematic Alcohol Use, Depressive Symptoms, and their Co-Occurrence in Young Adults with and without Childhood ADHD. Journal of Abnormal Child Psychology, 2020, 48, 1265-1277.	3.5	1
134	Age dependent association of inbreeding with risk for schizophrenia in Egypt. Schizophrenia Research, 2020, 216, 450-459.	2.0	1
135	Architecture of the Genetic Risk for Autism. Key Issues in Mental Health, 0, , 80-96.	0.6	0
136	An approach to gene-based testing accounting for dependence of tests among nearby genes. Briefings in Bioinformatics, 2021, 22, .	6.5	0