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	Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. Biological Psychiatry, 2022, 91, 92-101.	1.3	38
2	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
3	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
4	Bayesian estimation of cell typeâ€“specific gene expression with prior derived from single-cell data. Genome Research, 2021, 31, 1807-1818.	5.5	40
5	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
6	Genome-wide association identifies the first risk loci for psychosis in Alzheimer disease. Molecular Psychiatry, 2021, 26, 5797-5811.	7.9	30
7	An approach to gene-based testing accounting for dependence of tests among nearby genes. Briefings in Bioinformatics, 2021, 22, .	6.5	0
8	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
9	Hâ€MAGMA, inheriting a shaky statistical foundation, yields excess false positives. Annals of Human Genetics, 2021, 85, 97-100.	0.8	15
10	How rare and common risk variation jointly affect liability for autism spectrum disorder. Molecular Autism, 2021, 12, 66.	4.9	20
11	Prevalence and phenotypic impact of rare potentially damaging variants in autism spectrum disorder. Molecular Autism, 2021, 12, 65.	4.9	22
12	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
13	Using multiple measurements of tissue to estimate subject- and cell-type-specific gene expression. Bioinformatics, 2020, 36, 782-788.	4.1	28
14	Cohort profile: Epidemiology and Genetics of Obsessiveâ€“compulsive disorder and chronic tic disorders in Sweden (EGOS). Social Psychiatry and Psychiatric Epidemiology, 2020, 55, 1383-1393.	3.1	13
15	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.	4.9	19
16	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
17	Not All Autism Genes Are Created Equal: A Response to Myers etÂal.. American Journal of Human Genetics, 2020, 107, 1000-1003.	6.2	11
18	Functional annotation of rare structural variation in the human brain. Nature Communications, 2020, 11, 2990.	12.8	32

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19	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
20	Age dependent association of inbreeding with risk for schizophrenia in Egypt. Schizophrenia Research, 2020, 216, 450-459.	2.0	1
21	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
22	Maternal Effects as Causes of Risk for Obsessive-Compulsive Disorder. Biological Psychiatry, 2020, 87, 1045-1051.	1.3	18
23	Whole-Genome and RNA Sequencing Reveal Variation and Transcriptomic Coordination in the Developing Human Prefrontal Cortex. Cell Reports, 2020, 31, 107489.	6.4	91
24	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
25	Global landscape and genetic regulation of RNA editing in cortical samples from individuals with schizophrenia. Nature Neuroscience, 2019, 22, 1402-1412.	14.8	63
26	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	5.3	149
27	Variations in Genes Related to Sleep Patterns in Children With Autism Spectrum Disorder. Biological Research for Nursing, 2019, 21, 335-342.	1.9	9
28	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	21.4	154
29	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	21.4	1,538
30	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
31	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	12.6	851
32	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
33	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
34	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
35	Genome-wide de novo risk score implicates promoter variation in autism spectrum disorder. Science, 2018, 362, .	12.6	234
36	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

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37	A unified statistical framework for single cell and bulk RNA sequencing data. Annals of Applied Statistics, 2018, 12, 609-632.	1.1	82
38	An interactome perturbation framework prioritizes damaging missense mutations for developmental disorders. Nature Genetics, 2018, 50, 1032-1040.	21.4	64
39	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
40	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
41	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
42	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
43	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	6.2	91
44	Testing high-dimensional covariance matrices, with application to detecting schizophrenia risk genes. Annals of Applied Statistics, 2017, 11, 1810-1831.	1.1	20
45	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
46	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	14.8	952
47	A Pleiotropic Missense Variant in SLC39A8 Is Associated With Crohnâ€™s Disease and Human Gut Microbiome Composition. Gastroenterology, 2016, 151, 724-732.	1.3	109
48	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
49	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
50	The autism-associated chromatin modifier CHD8 regulates other autism risk genes during human neurodevelopment. Nature Communications, 2015, 6, 6404.	12.8	316
51	Insights into Autism Spectrum Disorder Genomic Architecture and Biology from 71 Risk Loci. Neuron, 2015, 87, 1215-1233.	8.1	1,219
52	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
53	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
54	De Novo Insertions and Deletions of Predominantly Paternal Origin Are Associated with Autism Spectrum Disorder. Cell Reports, 2014, 9, 16-23.	6.4	151

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55	DAWN: a framework to identify autism genes and subnetworks using gene expression and genetics. Molecular Autism, 2014, 5, 22.	4.9	111
56	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	6.2	819
57	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	27.8	2,254
58	Modest Impact on Risk for Autism Spectrum Disorder of Rare Copy Number Variants at 15<scp>q</scp>11.2, Specifically Breakpoints 1 to 2. Autism Research, 2014, 7, 355-362.	3.8	59
59	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	21.4	943
60	Most genetic risk for autism resides with common variation. Nature Genetics, 2014, 46, 881-885.	21.4	977
61	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
62	Intellectual Disability Is Associated with Increased Runs of Homozygosity in Simplex Autism. American Journal of Human Genetics, 2013, 93, 103-109.	6.2	63
63	Spatial and Temporal Mapping of De Novo Mutations in Schizophrenia to a Fetal Prefrontal Cortical Network. Cell, 2013, 154, 518-529.	28.9	507
64	Adjusting Head Circumference for Covariates in Autism: Clinical Correlates of a Highly Heritable Continuous Trait. Biological Psychiatry, 2013, 74, 576-584.	1.3	70
65	Coexpression Networks Implicate Human Midfetal Deep Cortical Projection Neurons in the Pathogenesis of Autism. Cell, 2013, 155, 997-1007.	28.9	825
66	Whole exome sequencing reveals minimal differences between cell line and whole blood derived DNA. Genomics, 2013, 102, 270-277.	2.9	13
67	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. Neuron, 2013, 77, 235-242.	8.1	242
68	Integrated Model of De Novo and Inherited Genetic Variants Yields Greater Power to Identify Risk Genes. PLoS Genetics, 2013, 9, e1003671.	3.5	253
69	Analysis of Rare, Exonic Variation amongst Subjects with Autism Spectrum Disorders and Population Controls. PLoS Genetics, 2013, 9, e1003443.	3.5	133
70	Principal Components of Heritability From Neurocognitive Domains Differ Between Families With Schizophrenia and Control Subjects. Schizophrenia Bulletin, 2013, 39, 464-471.	4.3	12
71	Refining genetically inferred relationships using treelet covariance smoothing. Annals of Applied Statistics, 2013, 7, 669-690.	1.1	9
72	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	2.9	334

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73	The Autism Sequencing Consortium: Large-Scale, High-Throughput Sequencing in Autism Spectrum Disorders. Neuron, 2012, 76, 1052-1056.	8.1	153
74	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
75	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
76	Evaluation of HLA Polymorphisms in Relation to Schizophrenia Risk and Infectious Exposure. Schizophrenia Bulletin, 2012, 38, 1149-1154.	4.3	22
77	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
78	Genetic architecture in autism spectrum disorder. Current Opinion in Genetics and Development, 2012, 22, 229-237.	3.3	445
79	Patterns and rates of exonic de novo mutations in autism spectrum disorders. Nature, 2012, 485, 242-245.	27.8	1,597
80	Common genetic variants, acting additively, are a major source of risk for autism. Molecular Autism, 2012, 3, 9.	4.9	357
81	De novo mutations revealed by whole-exome sequencing are strongly associated with autism. Nature, 2012, 485, 237-241.	27.8	1,863
82	The AVPR1A Gene and Substance Use Disorders: Association, Replication, and Functional Evidence. Biological Psychiatry, 2011, 70, 519-527.	1.3	45
83	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
84	Identification of common variants influencing risk of the tauopathy progressive supranuclear palsy. Nature Genetics, 2011, 43, 699-705.	21.4	502
85	No association of psychosis in Alzheimer disease with neurodegenerative pathway genes. Neurobiology of Aging, 2011, 32, 555.e9-555.e11.	3.1	18
86	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
87	Testing for an Unusual Distribution of Rare Variants. PLoS Genetics, 2011, 7, e1001322.	3.5	530
88	Do common variants play a role in risk for autism? Evidence and theoretical musings. Brain Research, 2011, 1380, 78-84.	2.2	95
89	Discovering genetic ancestry using spectral graph theory. Genetic Epidemiology, 2010, 34, 51-59.	1.3	90
90	Trajectories of cognitive decline in Alzheimer's disease. International Psychogeriatrics, 2010, 22, 281-290.	1.0	133

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91	Using ancestry matching to combine familyâ€based and unrelated samples for genomeâ€wide association studies. Statistics in Medicine, 2010, 29, 2932-2945.	1.6	15
92	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
93	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	2.9	538
94	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
95	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
96	Consanguinity and increased risk for schizophrenia in Egypt. Schizophrenia Research, 2010, 120, 108-112.	2.0	53
97	Shedding new light on genetic dark matter. Genome Medicine, 2010, 2, 79.	8.2	3
98	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
99	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. Nature, 2009, 459, 569-573.	27.8	1,270
100	Association study of 21 circadian genes with bipolar I disorder, schizoaffective disorder, and schizophrenia. Bipolar Disorders, 2009, 11, 701-710.	1.9	133
101	The genetics of anorexia nervosa collaborative study: Methods and sample description. International Journal of Eating Disorders, 2008, 41, 289-300.	4.0	48
102	A network of dopaminergic gene variations implicated as risk factors for schizophrenia. Human Molecular Genetics, 2008, 17, 747-758.	2.9	124
103	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
104	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
105	The MAOA promoter polymorphism, disruptive behavior disorders, and early onset substance use disorder: geneâ€“environment interaction. Psychiatric Genetics, 2007, 17, 323-332.	1.1	53
106	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
107	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
108	Polymorphisms in MICB are associated with human herpes virus seropositivity and schizophrenia risk. Schizophrenia Research, 2007, 94, 342-353.	2.0	40

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109	Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nature Genetics, 2007, 39, 319-328.	21.4	1,272
110	Genetic liability to schizophrenia in Oceanic Palau: a search in the affected and maternal generation. Human Genetics, 2007, 121, 675-684.	3.8	12
111	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
112	Novel, Replicated Associations Between Dopamine D3 Receptor Gene Polymorphisms and Schizophrenia in Two Independent Samples. Biological Psychiatry, 2006, 60, 570-577.	1.3	62
113	Project among African-Americans to explore risks for schizophrenia (PAARTNERS): Recruitment and assessment methods. Schizophrenia Research, 2006, 87, 32-44.	2.0	33
114	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
115	Selection of eating-disorder phenotypes for linkage analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 139B, 81-87.	1.7	25
116	Linkage analysis of a completely ascertained sample of familial schizophrenics and bipolars from Palau, Micronesia. Human Genetics, 2005, 117, 349-356.	3.8	22
117	Association of Multiple DRD2 Polymorphisms with Anorexia Nervosa. Neuropsychopharmacology, 2005, 30, 1703-1710.	5.4	127
118	Circadian Phase Variation in Bipolar I Disorder. Chronobiology International, 2005, 22, 571-584.	2.0	177
119	Heritability of Psychosis in Alzheimer Disease. American Journal of Geriatric Psychiatry, 2005, 13, 624-627.	1.2	64
120	Heritability of Psychosis in Alzheimer Disease. American Journal of Geriatric Psychiatry, 2005, 13, 624-627.	1.2	47
121	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
122	Genetic analysis of bulimia nervosa: Methods and sample description. International Journal of Eating Disorders, 2004, 35, 556-570.	4.0	50
123	ADLAPH: A molecular haplotyping method based on allele-discriminating long-range PCR. Genomics, 2004, 84, 600-612.	2.9	19
124	Personality in men with eating disorders. Journal of Psychosomatic Research, 2004, 57, 273-278.	2.6	34
125	Personality characteristics of women before and after recovery from an eating disorder. Psychological Medicine, 2004, 34, 1407-1418.	4.5	165
126	Alcohol Use Disorder Comorbidity in Eating Disorders. Journal of Clinical Psychiatry, 2004, 65, 1000-1006.	2.2	200

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127	Linkage analysis of anorexia nervosa incorporating behavioral covariates. Human Molecular Genetics, 2002, 11, 689-696.	2.9	144
128	Association and linkage analyses of RGS4 polymorphisms in schizophrenia. Human Molecular Genetics, 2002, 11, 1373-1380.	2.9	318
129	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
130	Mixture models for linkage analysis of affected sibling pairs and covariates. Genetic Epidemiology, 2002, 22, 52-65.	1.3	48
131	A search for susceptibility loci for anorexia nervosa: methods and sample description. Biological Psychiatry, 2000, 47, 794-803.	1.3	113
132	Temperament and Character in Women with Anorexia Nervosa. Journal of Nervous and Mental Disease, 2000, 188, 559-567.	1.0	178
133	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
134	Wringing The Bell Curve: A Cautionary Tale about the Relationships among Race, Genes, and IQ. Chance, 1995, 8, 27-36.	0.2	4
135	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
136	Architecture of the Genetic Risk for Autism. Key Issues in Mental Health, 0, , 80-96.	0.6	0