Douglas M Ruderfer

List of Publications by Year
in descending order

135 papers	65,886 citations	11235 73 h-index	14012 133 g-index
162 all docs	162 docs citations	162 times ranked	71735 citing authors

#	Article	IF	Citations
1	Genomics-driven screening for causal determinants of suicide attempt. Australian and New Zealand Journal of Psychiatry, 2023, 57, 423-431.	1.3	3
2	Leveraging electronic health records to inform genetic counseling practice surrounding psychiatric disorders. Journal of Genetic Counseling, 2022, , .	0.9	1
3	A genome-wide association study of suicide attempts in the million veterans program identifies evidence of pan-ancestry and ancestry-specific risk loci. Molecular Psychiatry, 2022, 27, 2264-2272.	4.1	35
4	Sex differences in the genetic architecture of cognitive resilience to Alzheimerâ€™s disease. Brain, 2022, 145, 2541-2554.	3.7	26
5	Genetic risk for major depressive disorder and loneliness in sex-specific associations with coronary artery disease. Molecular Psychiatry, 2021, 26, 4254-4264.	4.1	26
6	Clinical laboratory test-wide association scan of polygenic scores identifies biomarkers of complex disease. Genome Medicine, 2021, 13, 6.	3.6	49
7	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	0.7	103
8	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
9	Phenotypic signatures in clinical data enable systematic identification of patients for genetic testing. Nature Medicine, 2021, 27, 1097-1104.	15.2	21
10	Characterisation of age and polarity at onset in bipolar disorder. British Journal of Psychiatry, 2021, 219, 659-669.	1.7	20
11	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15
12	VEGF-family brain protein abundance: Associations with Alzheimer's disease pathology and cognitive decline.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e052984.	0.4	0
13	Sex differences in the genetic architecture underlying resilience in AD.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e055010.	0.4	0
14	Significant shared heritability underlies suicide attempt and clinically predicted probability of attempting suicide. Molecular Psychiatry, 2020, 25, 2422-2430.	4.1	91
15	Characterization of Single Gene Copy Number Variants in Schizophrenia. Biological Psychiatry, 2020, 87, 736-744.	0.7	10
16	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
17	APOE Îµ4-specific associations of VEGF gene family expression with cognitive aging and Alzheimer's disease. Neurobiology of Aging, 2020, 87, 18-25.	1.5	24
18	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. Cell Reports, 2020, 31, 107716.	2.9	44

#	Article	IF	Citations
19	Genetic variants and functional pathways associated with resilience to Alzheimerâ€™s disease. Brain, 2020, 143, 2561-2575.	3.7	93
20	Functional annotation of rare structural variation in the human brain. Nature Communications, 2020, 11, 2990.	5.8	32
21	Expanding cultural and ancestral representation in psychiatric genetic studies. Neuropsychopharmacology, 2020, 45, 1593-1594.	2.8	1
22	Penetrance and Pleiotropy of Polygenic Risk Scores for Schizophrenia in 106,160 Patients Across Four Health Care Systems. American Journal of Psychiatry, 2019, 176, 846-855.	4.0	168
23	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
24	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
25	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.1	2
26	Contribution of Rare Copy Number Variants toÂBipolar Disorder Risk Is Limited to Schizoaffective Cases. Biological Psychiatry, 2019, 86, 110-119.	0.7	45
27	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. Nature Communications, 2018, 9, 989.	5.8	136
28	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	9.4	1,332
29	Genetic validation of bipolar disorder identified by automated phenotyping using electronic health records. Translational Psychiatry, 2018, 8, 86.	2.4	24
30	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
31	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	6.0	164
32	Genetic risk for schizophrenia and autism, social impairment and developmental pathways to psychosis. Translational Psychiatry, 2018, 8, 204.	2.4	16
33	20.4 MODELING THE CONTRIBUTION OF COMMON VARIANTS TO SCHIZOPHRENIA RISK. Schizophrenia Bulletin, 2018, 44, S34-S34.	2.3	0
34	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
35	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	2.6	119
36	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623

#	Article	IF	Citations
37	Learning Opportunities for Drug Repositioning via GWAS and PheWAS Findings. AMIA Summits on Translational Science Proceedings, 2018, 2017, 237-246.	0.4	5
38	The ExAC browser: displaying reference data information from over 60 000 exomes. Nucleic Acids Research, 2017, 45, D840-D845.	6.5	587
39	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	1.6	98
40	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. American Journal of Human Genetics, 2017, 100, 885-894.	2.6	91
41	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
42	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	3.0	39
43	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
44	Transcriptional signatures of schizophrenia in hiPSC-derived NPCs and neurons are concordant with post-mortem adult brains. Nature Communications, 2017, 8, 2225.	5.8	143
45	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. Genome Medicine, 2017, 9, 114.	3.6	86
46	Genetic identification of a common collagen disease in Puerto Ricans via identity-by-descent mapping in a health system. ELife, 2017, 6, .	2.8	65
47	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
48	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	7.1	427
49	Deep phenotyping predicts Huntington's genotype. Nature Biotechnology, 2016, 34, 823-824.	9.4	3
50	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
51	Patterns of genic intolerance of rare copy number variation in 59,898 human exomes. Nature Genetics, 2016, 48, 1107-1111.	9.4	167
52	Dysregulation of miRNA-9 in a Subset of Schizophrenia Patient-Derived Neural Progenitor Cells. Cell Reports, 2016, 15, 1024-1036.	2.9	107
53	Genomeâ€wide association study reveals greater polygenic loading for schizophrenia in cases with a family history of illness. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 276-289.	1.1	28
54	Schizophrenia risk from complex variation of complement component 4. Nature, 2016, 530, 177-183.	13.7	1,915

#	Article	IF	Citations
55	Quantifying prion disease penetrance using large population control cohorts. Science Translational Medicine, 2016, 8, 322ra9.	5.8	289
56	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. Lancet Psychiatry,the, 2016, 3, 350-357.	3.7	107
57	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
58	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
59	Genome-wide association study identifies SESTD1 as a novel risk gene for lithium-responsive bipolar disorder. Molecular Psychiatry, 2016, 21, 1290-1297.	4.1	69
60	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. PLoS Genetics, 2016, 12, e1006343.	1.5	24
61	Vaccine-Preventable Outbreaks: Still with Us After All These Years. Pediatric Annals, 2015, 44, e76-81.	0.3	17
62	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	9.4	88
63	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.	2.6	225
64	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. Nature Genetics, 2015, 47, 291-295.	9.4	3,905
65	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
66	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. European Journal of Human Genetics, 2015, 23, 555-557.	1.4	21
67	Analysis of exome sequence in 604 trios for recessive genotypes in schizophrenia. Translational Psychiatry, 2015, 5, e607-e607.	2.4	35
68	Validation of Electronic Health Record Phenotyping of Bipolar Disorder Cases and Controls. American Journal of Psychiatry, 2015, 172, 363-372.	4.0	116
69	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
70	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
71	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. Nature Genetics, 2015, 47, 1385-1392.	9.4	431
72	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	0.9	53

#	Article	IF	Citations
73	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
74	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	2.9	225
75	Genetic modifiers and subtypes in schizophrenia: Investigations of age at onset, severity, sex and family history. Schizophrenia Research, 2014, 154, 48-53.	1.1	68
76	Identification of Pathways for Bipolar Disorder. JAMA Psychiatry, 2014, 71, 657.	6.0	204
77	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
78	Variability in Working Memory Performance Explained by Epistasis vs Polygenic Scores in theZNF804APathway. JAMA Psychiatry, 2014, 71, 778.	6.0	28
79	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
80	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	1,305
81	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
82	Copy number variation in schizophrenia in Sweden. Molecular Psychiatry, 2014, 19, 762-773.	4.1	257
83	Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. Molecular Psychiatry, 2014, 19, 1017-1024.	4.1	333
84	Biological insights from 108 schizophrenia-associated genetic loci. Nature, 2014, 511, 421-427.	13.7	6,934
85	Rare Copy Number Variation in Treatment-Resistant Major Depressive Disorder. Biological Psychiatry, 2014, 76, 536-541.	0.7	67
86	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
87	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
88	Implication of a Rare Deletion at Distal 16p11.2 in Schizophrenia. JAMA Psychiatry, 2013, 70, 253.	6.0	69
89	Mosaic copy number variation in schizophrenia. European Journal of Human Genetics, 2013, 21, 1007-1011.	1.4	15
90	Rare Complete Knockouts in Humans: Population Distribution and Significant Role in Autism Spectrum Disorders. Neuron, 2013, 77, 235-242.	3.8	242

#	Article	IF	Citations
91	Improved Detection of Common Variants Associated with Schizophrenia by Leveraging Pleiotropy with Cardiovascular-Disease Risk Factors. American Journal of Human Genetics, 2013, 92, 197-209.	2.6	422
92	Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. Lancet, The, 2013, 381, 1371-1379.	6.3	2,643
93	All SNPs Are Not Created Equal: Genome-Wide Association Studies Reveal a Consistent Pattern of Enrichment among Functionally Annotated SNPs. PLoS Genetics, 2013, 9, e1003449.	1.5	268
94	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. Human Molecular Genetics, 2013, 22, 2529-2538.	1.4	57
95	Cis-acting regulation of brain-specific ANK3 gene expression by a genetic variant associated with bipolar disorder. Molecular Psychiatry, 2013, 18, 922-929.	4.1	73
96	Schizophrenia genetic variants are not associated with intelligence. Psychological Medicine, 2013, 43, 2563-2570.	2.7	40
97	Network-Assisted Investigation of Combined Causal Signals from Genome-Wide Association Studies in Schizophrenia. PLoS Computational Biology, 2012, 8, e1002587.	1.5	98
98	Bipolar Disorder and a History of Suicide Attempts With a Duplication in 5HTR1A. American Journal of Psychiatry, 2012, 169, 1213-1214.	4.0	3
99	Investigation of the Genetic Association between Quantitative Measures of Psychosis and Schizophrenia: A Polygenic Risk Score Analysis. PLoS ONE, 2012, 7, e37852.	1.1	60
100	Highly Penetrant Alterations of a Critical Region Including BDNF in Human Psychopathology and Obesity. Archives of General Psychiatry, 2012, 69, 1238.	13.8	22
101	A bias-reducing pathway enrichment analysis of genome-wide association data confirmed association of the MHC region with schizophrenia. Journal of Medical Genetics, 2012, 49, 96-103.	1.5	68
102	Genome-wide association study in a Swedish population yields support for greater CNV and MHC involvement in schizophrenia compared with bipolar disorder. Molecular Psychiatry, 2012, 17, 880-886.	4.1	230
103	Translocations Disrupting PHF21A in the Potocki-Shaffer-Syndrome Region Are Associated with Intellectual Disability and Craniofacial Anomalies. American Journal of Human Genetics, 2012, 91, 56-72.	2.6	59
104	Sequencing Chromosomal Abnormalities Reveals Neurodevelopmental Loci that Confer Risk across Diagnostic Boundaries. Cell, 2012, 149, 525-537.	13.5	534
105	De novo CNV analysis implicates specific abnormalities of postsynaptic signalling complexes in the pathogenesis of schizophrenia. Molecular Psychiatry, 2012, 17, 142-153.	4.1	775
106	Discovery and Statistical Genotyping of Copy-Number Variation from Whole-Exome Sequencing Depth. American Journal of Human Genetics, 2012, 91, 597-607.	2.6	513
107	Disruption of a Large Intergenic Noncoding RNA in Subjects with Neurodevelopmental Disabilities. American Journal of Human Genetics, 2012, 91, 1128-1134.	2.6	61
108	Copy Number Variation in Subjects with Major Depressive Disorder Who Attempted Suicide. PLoS ONE, 2012, 7, e46315.	1.1	24

#	Article	IF	Citations
109	Schizophrenia susceptibility alleles are enriched for alleles that affect gene expression in adult human brain. Molecular Psychiatry, 2012, 17, 193-201.	4.1	120
110	Genome-wide association study identifies five new schizophrenia loci. Nature Genetics, 2011, 43, 969-976.	9.4	1,758
111	Two non-synonymous markers in PTPN21, identified by genome-wide association study data-mining and replication, are associated with schizophrenia. Schizophrenia Research, 2011, 131, 43-51.	1.1	22
112	Genetic Classification of Populations Using Supervised Learning. PLoS ONE, 2011, 6, e14802.	1.1	16
113	Molecular pathways involved in neuronal cell adhesion and membrane scaffolding contribute to schizophrenia and bipolar disorder susceptibility. Molecular Psychiatry, 2011, 16, 286-292.	4.1	195
114	GWA study data mining and independent replication identify cardiomyopathy-associated 5 (CMYA5) as a risk gene for schizophrenia. Molecular Psychiatry, 2011, 16, 1117-1129.	4.1	67
115	A family-based study of common polygenic variation and risk of schizophrenia. Molecular Psychiatry, 2011, 16, 887-888.	4.1	27
116	Assessment of 2q23.1 Microdeletion Syndrome Implicates MBD5 as a Single Causal Locus of Intellectual Disability, Epilepsy, and Autism Spectrum Disorder. American Journal of Human Genetics, 2011, 89, 551-563.	2.6	195
117	Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nature Genetics, 2011, 43, 977-983.	9.4	1,283
118	Fineâ€mapping reveals novel alternative splicing of the dopamine transporter. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 1434-1447.	1.1	18
119	[S4.3]: Largeâ€scale genetic studies of rare and common variation in schizophrenia risk. International Journal of Developmental Neuroscience, 2010, 28, 647-647.	0.7	0
120	Family-based genetic risk prediction of multifactorial disease. Genome Medicine, 2010, 2, 2.	3.6	20
121	Accurately Assessing the Risk of Schizophrenia Conferred by Rare Copy-Number Variation Affecting Genes with Brain Function. PLoS Genetics, 2010, 6, e1001097.	1.5	134
122	Using Expression and Genotype to Predict Drug Response in Yeast. PLoS ONE, 2009, 4, e6907.	1.1	14
123	Comprehensive polymorphism survey elucidates population structure of Saccharomyces cerevisiae. Nature, 2009, 458, 342-345.	13.7	431
124	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. Nature, 2009, 460, 748-752.	13.7	4,345
125	Association between Microdeletion and Microduplication at 16p11.2 and Autism. New England Journal of Medicine, 2008, 358, 667-675.	13.9	1,476
126	Rare chromosomal deletions and duplications increase risk of schizophrenia. Nature, 2008, 455, 237-241.	13.7	1,387

#	Article	IF	Citations
127	Collaborative genome-wide association analysis supports a role for ANK3 and CACNA1C in bipolar disorder. Nature Genetics, 2008, 40, 1056-1058.	9.4	1,102
128	Genetic basis of proteome variation in yeast. Nature Genetics, 2007, 39, 1369-1375.	9.4	767
129	Genetic basis of individual differences in the response to small-molecule drugs in yeast. Nature Genetics, 2007, 39, 496-502.	9.4	107
130	Genome-Wide Analysis of Nucleotide-Level Variation in Commonly Used Saccharomyces cerevisiae Strains. PLoS ONE, 2007, 2, e322.	1.1	100
131	Genome-Wide Detection of Polymorphisms at Nucleotide Resolution with a Single DNA Microarray. Science, 2006, 311, 1932-1936.	6.0	242
132	Population genomic analysis of outcrossing and recombination in yeast. Nature Genetics, 2006, 38, 1077-1081.	9.4	217
133	Revealing Complex Traits with Small Molecules and Naturally Recombinant Yeast Strains. Chemistry and Biology, 2006, 13, 319-327.	6.2	38
134	Telomere Length as a Quantitative Trait: Genome-Wide Survey and Genetic Mapping of Telomere Length-Control Genes in Yeast. PLoS Genetics, 2006, 2, e35.	1.5	170
135	Analysis of Genetically Regulated Gene Expression Identifies a Trauma Type Specific PTSD Gene, SNRNP35. SSRN Electronic Journal, 0, , .	0.4	0