

Steven A Mccarroll

List of Publications by Year in descending order

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Version: 2024-02-01

159
papers

111,990
citations

3515

90
h-index

6282

158
g-index

208
all docs

208
docs citations

208
times ranked

123567
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	13.7	9,051
3	Finding the missing heritability of complex diseases. <i>Nature</i> , 2009, 461, 747-753.	13.7	7,490
4	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	13.7	6,140
5	Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets. <i>Cell</i> , 2015, 161, 1202-1214.	13.5	5,908
6	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.	13.7	4,761
7	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
8	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. <i>New England Journal of Medicine</i> , 2014, 371, 2477-2487.	13.9	2,669
9	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
10	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	9.4	2,421
11	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	9.4	2,067
12	Genes that act downstream of DAF-16 to influence the lifespan of <i>Caenorhabditis elegans</i> . <i>Nature</i> , 2003, 424, 277-283.	13.7	1,998
13	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	13.7	1,994
14	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	9.4	1,982
15	Schizophrenia risk from complex variation of complement component 4. <i>Nature</i> , 2016, 530, 177-183.	13.7	1,915
16	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	13.7	1,788
17	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009, 41, 25-34.	9.4	1,572
18	De novo mutations in schizophrenia implicate synaptic networks. <i>Nature</i> , 2014, 506, 179-184.	13.7	1,510

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19	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013, 45, 1150-1159.	9.4	1,395
20	Single-Cell RNA Sequencing of Microglia throughout the Mouse Lifespan and in the Injured Brain Reveals Complex Cell-State Changes. <i>Immunity</i> , 2019, 50, 253-271.e6.	6.6	1,351
21	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. <i>Nature Genetics</i> , 2018, 50, 381-389.	9.4	1,332
22	A polygenic burden of rare disruptive mutations in schizophrenia. <i>Nature</i> , 2014, 506, 185-190.	13.7	1,305
23	Molecular Diversity and Specializations among the Cells of the Adult Mouse Brain. <i>Cell</i> , 2018, 174, 1015-1030.e16.	13.5	1,231
24	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. <i>Science</i> , 2012, 335, 823-828.	6.0	1,095
25	Comprehensive Classification of Retinal Bipolar Neurons by Single-Cell Transcriptomics. <i>Cell</i> , 2016, 166, 1308-1323.e30.	13.5	1,010
26	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65.	13.7	991
27	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. <i>Nature Genetics</i> , 2009, 41, 334-341.	9.4	990
28	Mapping and sequencing of structural variation from eight human genomes. <i>Nature</i> , 2008, 453, 56-64.	13.7	983
29	Cell diversity and network dynamics in photosensitive human brain organoids. <i>Nature</i> , 2017, 545, 48-53.	13.7	933
30	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	13.7	929
31	Integrated detection and population-genetic analysis of SNPs and copy number variation. <i>Nature Genetics</i> , 2008, 40, 1166-1174.	9.4	838
32	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	9.4	838
33	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
34	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629.	9.4	807
35	Integrated genotype calling and association analysis of SNPs, common copy number polymorphisms and rare CNVs. <i>Nature Genetics</i> , 2008, 40, 1253-1260.	9.4	712
36	Copy number variation: New insights in genome diversity. <i>Genome Research</i> , 2006, 16, 949-961.	2.4	697

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37	Common deletion polymorphisms in the human genome. <i>Nature Genetics</i> , 2006, 38, 86-92.	9.4	656
38	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	5.8	636
39	A molecular census of arcuate hypothalamus and median eminence cell types. <i>Nature Neuroscience</i> , 2017, 20, 484-496.	7.1	635
40	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	9.4	629
41	Deletion polymorphism upstream of IRGM associated with altered IRGM expression and Crohn's disease. <i>Nature Genetics</i> , 2008, 40, 1107-1112.	9.4	604
42	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. <i>American Journal of Human Genetics</i> , 2014, 95, 535-552.	2.6	569
43	Copy-number variation and association studies of human disease. <i>Nature Genetics</i> , 2007, 39, S37-S42.	9.4	531
44	Discovery and Statistical Genotyping of Copy-Number Variation from Whole-Exome Sequencing Depth. <i>American Journal of Human Genetics</i> , 2012, 91, 597-607.	2.6	513
45	Whole-Genome Sequencing in Autism Identifies Hot Spots for De Novo Germline Mutation. <i>Cell</i> , 2012, 151, 1431-1442.	13.5	501
46	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019, 51, 1670-1678.	9.4	440
47	Comparing genomic expression patterns across species identifies shared transcriptional profile in aging. <i>Nature Genetics</i> , 2004, 36, 197-204.	9.4	434
48	Lymphatic and Other Vascular Malformative/Overgrowth Disorders Are Caused by Somatic Mutations in PIK3CA. <i>Journal of Pediatrics</i> , 2015, 166, 1048-1054.e5.	0.9	429
49	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1433-1441.	7.1	427
50	Human pluripotent stem cells recurrently acquire and expand dominant negative P53 mutations. <i>Nature</i> , 2017, 545, 229-233.	13.7	409
51	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. <i>Nature Genetics</i> , 2018, 50, 538-548.	9.4	406
52	Pathways Disrupted in Human ALS Motor Neurons Identified through Genetic Correction of Mutant SOD1. <i>Cell Stem Cell</i> , 2014, 14, 781-795.	5.2	392
53	Analysis of copy number variations at 15 schizophrenia-associated loci. <i>British Journal of Psychiatry</i> , 2014, 204, 108-114.	1.7	380
54	De novo copy number variants identify new genes and loci in isolated sporadic tetralogy of Fallot. <i>Nature Genetics</i> , 2009, 41, 931-935.	9.4	373

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55	Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , 2021, 598, 111-119.	13.7	361
56	Large multiallelic copy number variations in humans. <i>Nature Genetics</i> , 2015, 47, 296-303.	9.4	357
57	Rare coding variants in ten genes confer substantial risk for schizophrenia. <i>Nature</i> , 2022, 604, 509-516.	13.7	326
58	The Penetrance of Copy Number Variations for Schizophrenia and Developmental Delay. <i>Biological Psychiatry</i> , 2014, 75, 378-385.	0.7	321
59	A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , 2021, 598, 86-102.	13.7	316
60	Discovery and genotyping of genome structural polymorphism by sequencing on a population scale. <i>Nature Genetics</i> , 2011, 43, 269-276.	9.4	299
61	Increased neutrophil extracellular trap formation promotes thrombosis in myeloproliferative neoplasms. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	299
62	Quantifying prion disease penetrance using large population control cohorts. <i>Science Translational Medicine</i> , 2016, 8, 322ra9.	5.8	289
63	Linkage Disequilibrium and Heritability of Copy-Number Polymorphisms within Duplicated Regions of the Human Genome. <i>American Journal of Human Genetics</i> , 2006, 79, 275-290.	2.6	283
64	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
65	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. <i>Nature</i> , 2018, 559, 350-355.	13.7	279
66	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
67	Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals. <i>American Journal of Human Genetics</i> , 2019, 105, 267-282.	2.6	237
68	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
69	Differential Relationship of DNA Replication Timing to Different Forms of Human Mutation and Variation. <i>American Journal of Human Genetics</i> , 2012, 91, 1033-1040.	2.6	220
70	Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of multiple myeloma. <i>Nature Cancer</i> , 2020, 1, 493-506.	5.7	209
71	Innovations present in the primate interneuron repertoire. <i>Nature</i> , 2020, 586, 262-269.	13.7	206
72	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019, 575, 652-657.	13.7	198

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73	zCall: a rare variant caller for array-based genotyping. <i>Bioinformatics</i> , 2012, 28, 2543-2545.	1.8	195
74	The Genetic Landscape of Diamond-Blackfan Anemia. <i>American Journal of Human Genetics</i> , 2018, 103, 930-947.	2.6	184
75	Evaluation of Common Variants in the Six Known Maturity-Onset Diabetes of the Young (MODY) Genes for Association With Type 2 Diabetes. <i>Diabetes</i> , 2007, 56, 685-693.	0.3	178
76	Single-Tissue and Cross-Tissue Heritability of Gene Expression Via Identity-by-Descent in Related or Unrelated Individuals. <i>PLoS Genetics</i> , 2011, 7, e1001317.	1.5	173
77	Novel Findings from CNVs Implicate Inhibitory and Excitatory Signaling Complexes in Schizophrenia. <i>Neuron</i> , 2015, 86, 1203-1214.	3.8	173
78	Phenotypic Landscape of Schizophrenia-Associated Genes Defines Candidates and Their Shared Functions. <i>Cell</i> , 2019, 177, 478-491.e20.	13.5	159
79	Complement genes contribute sex-biased vulnerability in diverse disorders. <i>Nature</i> , 2020, 582, 577-581.	13.7	158
80	Overexpression of schizophrenia susceptibility factor human complement C4A promotes excessive synaptic loss and behavioral changes in mice. <i>Nature Neuroscience</i> , 2021, 24, 214-224.	7.1	158
81	Extending genome-wide association studies to copy-number variation. <i>Human Molecular Genetics</i> , 2008, 17, R135-R142.	1.4	154
82	Genetic Variation in Human DNA Replication Timing. <i>Cell</i> , 2014, 159, 1015-1026.	13.5	149
83	Genetically Distinct Parallel Pathways in the Entopeduncular Nucleus for Limbic and Sensorimotor Output of the Basal Ganglia. <i>Neuron</i> , 2017, 94, 138-152.e5.	3.8	146
84	Accurately Assessing the Risk of Schizophrenia Conferred by Rare Copy-Number Variation Affecting Genes with Brain Function. <i>PLoS Genetics</i> , 2010, 6, e1001097.	1.5	134
85	DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage. <i>Nature</i> , 2006, 440, 1045-1049.	13.7	130
86	Exome sequencing in schizophrenia-affected parent-offspring trios reveals risk conferred by protein-coding de novo mutations. <i>Nature Neuroscience</i> , 2020, 23, 185-193.	7.1	125
87	Structural haplotypes and recent evolution of the human 17q21.31 region. <i>Nature Genetics</i> , 2012, 44, 881-885.	9.4	124
88	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. <i>Nature Neuroscience</i> , 2017, 20, 1661-1668.	7.1	122
89	Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. <i>Nature Genetics</i> , 2015, 47, 921-925.	9.4	120
90	Monogenic and polygenic inheritance become instruments for clonal selection. <i>Nature</i> , 2020, 584, 136-141.	13.7	119

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91	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. <i>Nature Medicine</i> , 2021, 27, 1012-1024.	15.2	109
92	Evidence of Common Genetic Overlap Between Schizophrenia and Cognition. <i>Schizophrenia Bulletin</i> , 2016, 42, 832-842.	2.3	102
93	Chromosomal alterations among age-related haematopoietic clones in Japan. <i>Nature</i> , 2020, 584, 130-135.	13.7	102
94	Protein-coding repeat polymorphisms strongly shape diverse human phenotypes. <i>Science</i> , 2021, 373, 1499-1505.	6.0	96
95	Recurring exon deletions in the HP (haptoglobin) gene contribute to lower blood cholesterol levels. <i>Nature Genetics</i> , 2016, 48, 359-366.	9.4	93
96	Donor-recipient mismatch for common gene deletion polymorphisms in graft-versus-host disease. <i>Nature Genetics</i> , 2009, 41, 1341-1344.	9.4	91
97	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. <i>Nature Neuroscience</i> , 2016, 19, 1563-1565.	7.1	90
98	CNV analysis in a large schizophrenia sample implicates deletions at 16p12.1 and SLC1A1 and duplications at 1p36.33 and CGNL1. <i>Human Molecular Genetics</i> , 2014, 23, 1669-1676.	1.4	82
99	Genome-scale neurogenetics: methodology and meaning. <i>Nature Neuroscience</i> , 2014, 17, 756-763.	7.1	82
100	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. <i>Molecular Psychiatry</i> , 2020, 25, 2455-2467.	4.1	82
101	Genetic association analysis highlights new loci that modulate hematological trait variation in Caucasians and African Americans. <i>Human Genetics</i> , 2011, 129, 307-317.	1.8	81
102	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	5.8	79
103	Progress in the Genetics of Polygenic Brain Disorders: Significant New Challenges for Neurobiology. <i>Neuron</i> , 2013, 80, 578-587.	3.8	74
104	A whole-genome sequence study identifies genetic risk factors for neuromyelitis optica. <i>Nature Communications</i> , 2018, 9, 1929.	5.8	73
105	Insights into variation in meiosis from 31,228 human sperm genomes. <i>Nature</i> , 2020, 583, 259-264.	13.7	73
106	De novo CNVs in bipolar affective disorder and schizophrenia. <i>Human Molecular Genetics</i> , 2014, 23, 6677-6683.	1.4	70
107	Genome-wide association study identifies SESTD1 as a novel risk gene for lithium-responsive bipolar disorder. <i>Molecular Psychiatry</i> , 2016, 21, 1290-1297.	4.1	69
108	Random replication of the inactive X chromosome. <i>Genome Research</i> , 2014, 24, 64-69.	2.4	65

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109	Mapping a New Spontaneous Preterm Birth Susceptibility Gene, IGF1R, Using Linkage, Haplotype Sharing, and Association Analysis. <i>PLoS Genetics</i> , 2011, 7, e1001293.	1.5	61
110	Using population admixture to help complete maps of the human genome. <i>Nature Genetics</i> , 2013, 45, 406-414.	9.4	61
111	A Rapid Molecular Approach for Chromosomal Phasing. <i>PLoS ONE</i> , 2015, 10, e0118270.	1.1	58
112	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. <i>Human Molecular Genetics</i> , 2013, 22, 2529-2538.	1.4	57
113	Clonal Hematopoiesis and Blood-Cancer Risk. <i>New England Journal of Medicine</i> , 2015, 372, 1071-1072.	13.9	57
114	SnapShot-Seq: A Method for Extracting Genome-Wide, In Vivo mRNA Dynamics from a Single Total RNA Sample. <i>PLoS ONE</i> , 2014, 9, e89673.	1.1	53
115	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. <i>International Journal of Epidemiology</i> , 2015, 44, 1706-1721.	0.9	53
116	A Loss-of-Function Splice Acceptor Variant in <i>IGF2</i> Is Protective for Type 2 Diabetes. <i>Diabetes</i> , 2017, 66, 2903-2914.	0.3	52
117	Thy-1 Is a Component Common to Multiple Populations of Synaptic Vesicles. <i>Journal of Cell Biology</i> , 1998, 140, 685-698.	2.3	51
118	Complex and multi-allelic copy number variation in human disease. <i>Briefings in Functional Genomics</i> , 2015, 14, 329-338.	1.3	50
119	Polygenic risk for schizophrenia and measured domains of cognition in individuals with psychosis and controls. <i>Translational Psychiatry</i> , 2018, 8, 78.	2.4	49
120	Genome-Wide Association Studies of Schizophrenia and Bipolar Disorder in a Diverse Cohort of US Veterans. <i>Schizophrenia Bulletin</i> , 2021, 47, 517-529.	2.3	48
121	Cryptic and Complex Chromosomal Aberrations in Early-Onset Neuropsychiatric Disorders. <i>American Journal of Human Genetics</i> , 2014, 95, 454-461.	2.6	45
122	Common $\hat{\alpha}$ -globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. <i>PLoS Genetics</i> , 2018, 14, e1007293.	1.5	45
123	Contribution of Rare Copy Number Variants to Bipolar Disorder Risk Is Limited to Schizoaffective Cases. <i>Biological Psychiatry</i> , 2019, 86, 110-119.	0.7	45
124	Identification of Transcriptional Regulatory Elements in Chemosensory Receptor Genes by Probabilistic Segmentation. <i>Current Biology</i> , 2005, 15, 347-352.	1.8	42
125	Analyzing Copy Number Variation with Droplet Digital PCR. <i>Methods in Molecular Biology</i> , 2018, 1768, 143-160.	0.4	37
126	Mapping the Human Reference Genome's Missing Sequence by Three-Way Admixture in Latino Genomes. <i>American Journal of Human Genetics</i> , 2013, 93, 411-421.	2.6	36

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127	Copy-number analysis goes more than skin deep. <i>Nature Genetics</i> , 2008, 40, 5-6.	9.4	35
128	Anterior thalamic dysfunction underlies cognitive deficits in a subset of neuropsychiatric disease models. <i>Neuron</i> , 2021, 109, 2590-2603.e13.	3.8	34
129	Prognostic value of polygenic risk scores for adults with psychosis. <i>Nature Medicine</i> , 2021, 27, 1576-1581.	15.2	31
130	Improved detection of global copy number variation using high density, non-polymorphic oligonucleotide probes. <i>BMC Genetics</i> , 2008, 9, 27.	2.7	27
131	Whole-genome analysis of human embryonic stem cells enables rational line selection based on genetic variation. <i>Cell Stem Cell</i> , 2022, 29, 472-486.e7.	5.2	27
132	Polygenic risk for type 2 diabetes mellitus among individuals with psychosis and their relatives. <i>Journal of Psychiatric Research</i> , 2016, 77, 52-58.	1.5	22
133	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. <i>Nature Communications</i> , 2022, 13, .	5.8	22
134	Exploring the variation within. <i>Nature Genetics</i> , 2012, 44, 614-616.	9.4	21
135	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. <i>European Journal of Human Genetics</i> , 2015, 23, 555-557.	1.4	21
136	Human DDK rescues stalled forks and counteracts checkpoint inhibition at unfired origins to complete DNA replication. <i>Molecular Cell</i> , 2021, 81, 426-441.e8.	4.5	21
137	Copy number variation and human genome maps. <i>Nature Genetics</i> , 2010, 42, 365-366.	9.4	20
138	Early role for a Na ⁺ ,K ⁺ -ATPase (<i>ATP1A3</i>) in brain development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
139	Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 724-731.	1.1	19
140	Differential excitatory vs inhibitory SCN expression at single cell level regulates brain sodium channel function in neurodevelopmental disorders. <i>European Journal of Paediatric Neurology</i> , 2020, 24, 129-133.	0.7	18
141	Publicly Available hiPSC Lines with Extreme Polygenic Risk Scores for Modeling Schizophrenia. <i>Complex Psychiatry</i> , 2020, 6, 68-82.	1.3	18
142	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	4.1	15
143	New insights into the biological basis of genomic disorders. <i>Nature Genetics</i> , 2006, 38, 1363-1364.	9.4	12
144	On the level: IRGM gene function is all about expression. <i>Autophagy</i> , 2009, 5, 96-99.	4.3	10

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145	Our Fallen Genomes. <i>Science</i> , 2013, 342, 564-565.	6.0	8
146	Using Droplet Digital PCR to Analyze Allele-Specific RNA Expression. <i>Methods in Molecular Biology</i> , 2018, 1768, 401-422.	0.4	8
147	Mapping duplicated sequences. <i>Nature Biotechnology</i> , 2009, 27, 1001-1002.	9.4	5
148	Of Rats and Men. <i>Cell</i> , 2013, 154, 481-483.	13.5	4
149	Single cell analysis of DNA in more than 10,000 individual sperm from men with abnormal reproductive outcomes. <i>Journal of Assisted Reproduction and Genetics</i> , 2021, 38, 2975-2983.	1.2	2
150	Single-Cell RNA Sequencing Reveals Compromised Immune Microenvironment in Precursor Stages of Multiple Myeloma. <i>Blood</i> , 2018, 132, 2603-2603.	0.6	1
151	Chromosomal phase improves aneuploidy detection in non-invasive prenatal testing at low fetal DNA fractions. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
152	Population Perspectives on Genome Variation and Complex Disease. , 2013, , 41-49.		0
153	Damaging Missense De Novo Coding Mutations Contribute To Schizophrenia Risk. <i>European Neuropsychopharmacology</i> , 2017, 27, S427-S428.	0.3	0
154	Ultra-Rare Protein-Altering Variants Among 4,877 Swedish Individuals with Schizophrenia. <i>European Neuropsychopharmacology</i> , 2017, 27, S426-S427.	0.3	0
155	SA122STRUCTURAL VARIATIONS OF SCHIZOPHRENIA RISK GENE COMPLEMENT COMPONENT 4 (C4) AND BRAIN MRI PHENOTYPES. <i>European Neuropsychopharmacology</i> , 2019, 29, S1255-S1256.	0.3	0
156	THE GENOMICS OF BIPOLAR AND SCHIZOPHRENIC DISORDERS IN A LARGE PEDIGREE FROM A NORTHERN SWEDISH ISOLATE. <i>European Neuropsychopharmacology</i> , 2019, 29, S902-S903.	0.3	0
157	169. New Technology for Learning About Genetic Effects on Brain Cells and Brain Tissue. <i>Biological Psychiatry</i> , 2019, 85, S70.	0.7	0
158	Single-cell RNA sequencing reveals compromised immune microenvironment in precursor stages of multiple myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e27.	0.2	0
159	Genome Variation and Donor-Recipient Compatibility in Graft-Versus-Host Disease. <i>Blood</i> , 2010, 116, SCI-12-SCI-12.	0.6	0