Jennifer L Moran

List of Publications by Year
in descending order

74 papers	23,726 citations	50276 46 h-index	74163 75 g-index
80 all docs	80 docs citations	80 times ranked	32424 citing authors

#	Article	IF	Citations
1	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. New England Journal of Medicine, 2014, 371, 2477-2487.	27.0	2,669
2	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
3	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	21.4	1,594
4	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	21.4	1,538
5	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	27.8	1,510
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	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	21.4	1,395
8	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	27.8	1,305
9	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	28.9	935
10	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
11	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	12.6	851
12	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
13	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.	21.4	629
14	Discovery and Statistical Genotyping of Copy-Number Variation from Whole-Exome Sequencing Depth. American Journal of Human Genetics, 2012, 91, 597-607.	6.2	513
15	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	14.8	427
16	Analysis of copy number variations at 15 schizophrenia-associated loci. British Journal of Psychiatry, 2014, 204, 108-114.	2.8	380
17	Agouti C57BL/6N embryonic stem cells for mouse genetic resources. Nature Methods, 2009, 6, 493-495.	19.0	340
18	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	21.4	340

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19	The Penetrance of Copy Number Variations for Schizophrenia and Developmental Delay. Biological Psychiatry, 2014, 75, 378-385.	1.3	321
20	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. Nature Genetics, 2012, 44, 631-635.	21.4	239
21	zCall: a rare variant caller for array-based genotyping. Bioinformatics, 2012, 28, 2543-2545.	4.1	195
22	The IFT-A complex regulates Shh signaling through cilia structure and membrane protein trafficking. Journal of Cell Biology, 2012, 197, 789-800.	5.2	194
23	Novel Findings from CNVs Implicate Inhibitory and Excitatory Signaling Complexes in Schizophrenia. Neuron, 2015, 86, 1203-1214.	8.1	173
24	Latent TGF-Î²â€“binding protein 4 modifies muscular dystrophy in mice. Journal of Clinical Investigation, 2009, 119, 3703-3712.	8.2	172
25	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds ofDrosophilaandCaenorhabditis elegansTranscription Factors. Genetics, 2018, 208, 937-949.	2.9	164
26	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	1.3	146
27	Exome sequencing in schizophrenia-affected parentâ€“offspring trios reveals risk conferred by protein-coding de novo mutations. Nature Neuroscience, 2020, 23, 185-193.	14.8	125
28	Lethal Skeletal Dysplasia in Mice and Humans Lacking the Golgin GMAP-210. New England Journal of Medicine, 2010, 362, 206-216.	27.0	122
29	Validation of Electronic Health Record Phenotyping of Bipolar Disorder Cases and Controls. American Journal of Psychiatry, 2015, 172, 363-372.	7.2	116
30	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. Lancet Psychiatry,the, 2016, 3, 350-357.	7.4	107
31	Evidence of Common Genetic Overlap Between Schizophrenia and Cognition. Schizophrenia Bulletin, 2016, 42, 832-842.	4.3	102
32	Gene expression changes during mouse skeletal myoblast differentiation revealed by transcriptional profiling. Physiological Genomics, 2002, 10, 103-111.	2.3	97
33	Exome Sequencing of Familial Bipolar Disorder. JAMA Psychiatry, 2016, 73, 590.	11.0	97
34	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	12.8	95
35	A Rare Functional Noncoding Variant at the GWAS-Implicated MIR137/MIR2682 Locus Might Confer Risk to Schizophrenia and Bipolar Disorder. American Journal of Human Genetics, 2014, 95, 744-753.	6.2	91
36	Utilization of a whole genome SNP panel for efficient genetic mapping in the mouse. Genome Research, 2006, 16, 436-440.	5.5	89

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37	CNV analysis in a large schizophrenia sample implicates deletions at 16p12.1 and SLC1A1 and duplications at 1p36.33 and CGNL1. Human Molecular Genetics, 2014, 23, 1669-1676.	2.9	82
38	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. Molecular Psychiatry, 2020, 25, 2455-2467.	7.9	82
39	De novo CNVs in bipolar affective disorder and schizophrenia. Human Molecular Genetics, 2014, 23, 6677-6683.	2.9	70
40	Bile duct proliferation in Jag1/fringe heterozygous mice identifies candidate modifiers of the alagille syndrome hepatic phenotype. Hepatology, 2008, 48, 1989-1997.	7.3	69
41	Implication of a Rare Deletion at Distal 16p11.2 in Schizophrenia. JAMA Psychiatry, 2013, 70, 253.	11.0	69
42	Genome-wide association study identifies SESTD1 as a novel risk gene for lithium-responsive bipolar disorder. Molecular Psychiatry, 2016, 21, 1290-1297.	7.9	69
43	The genomic psychiatry cohort: Partners in discovery. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 306-312.	1.7	66
44	ERG Measurements of the Spectral Sensitivity of Common Chimpanzee (Pan troglodytes). Vision Research, 1996, 36, 2587-2594.	1.4	52
45	A Mouse Mutation in the 12R-Lipoxygenase, Alox12b, Disrupts Formation of the Epidermal Permeability Barrier. Journal of Investigative Dermatology, 2007, 127, 1893-1897.	0.7	52
46	Limbs move beyond the Radical fringe. Nature, 1999, 399, 742-743.	27.8	48
47	Contribution of Rare Copy Number Variants toÂBipolar Disorder Risk Is Limited to Schizoaffective Cases. Biological Psychiatry, 2019, 86, 110-119.	1.3	45
48	Cholesterol Metabolism Is Required for Intracellular Hedgehog Signal Transduction In Vivo. PLoS Genetics, 2011, 7, e1002224.	3.5	42
49	A HUMANIZED ANTI-CD3 ANTIBODY, HuM291, WITH LOW MITOGENIC ACTIVITY, MEDIATES COMPLETE AND REVERSIBLE T-CELL DEPLETION IN CHIMPANZEES. Transplantation, 1999, 68, 545-554.	1.0	42
50	Manic fringe is not required for embryonic development, and fringe family members do not exhibit redundant functions in the axial skeleton, limb, or hindbrain. Developmental Dynamics, 2009, 238, 1803-1812.	1.8	41
51	A forward genetic screen with a thalamocortical axon reporter mouse yields novel neurodevelopment mutants and a distinct emx2 mutant phenotype. Neural Development, 2011, 6, 3.	2.4	40
52	Analysis of genetic deletions and duplications in the University College London bipolar disorder case control sample. European Journal of Human Genetics, 2011, 19, 588-592.	2.8	38
53	Screening for novel risk factors related to peripherally inserted central catheterâ€associated complications. Journal of Hospital Medicine, 2014, 9, 481-489.	1.4	29
54	Genomic structure, mapping, and expression analysis of the mammalian Lunatic, Manic, and Radical fringe genes. Mammalian Genome, 1999, 10, 535-541.	2.2	24

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55	High resolution mapping and positional cloning of ENU-induced mutations in the Rw region of mouse chromosome 5. BMC Genetics, 2010, 11, 106.	2.7	23
56	The Mouse Spam1 maps to proximal Chromosome 6 and is a candidate for the sperm dysfunction in Rb(6.16)24Lub and Rb(6.15)lAld heterozygotes. Mammalian Genome, 1997, 8, 94-97.	2.2	22
57	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. European Journal of Human Genetics, 2015, 23, 555-557.	2.8	21
58	Concurrent Lpin1 and Nrcam Mouse Mutations Result in Severe Peripheral Neuropathy with Transitory Hindlimb Paralysis. Journal of Neuroscience, 2009, 29, 12089-12100.	3.6	19
59	Genome-wide identification of mouse congenital heart disease loci. Human Molecular Genetics, 2010, 19, 3105-3113.	2.9	19
60	Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 724-731.	1.7	19
61	ENU mutagenesis in mice identifies candidate genes for hypogonadism. Mammalian Genome, 2012, 23, 346-355.	2.2	16
62	A genome wide survey supports the involvement of large copy number variants in schizophrenia with and without intellectual disability. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 847-854.	1.7	16
63	Mosaic copy number variation in schizophrenia. European Journal of Human Genetics, 2013, 21, 1007-1011.	2.8	15
64	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	7.9	15
65	Description and genetic mapping of Polypodia: an X-linked dominant mouse mutant with ectopic caudal limbs and other malformations. Mammalian Genome, 2006, 17, 903-913.	2.2	14
66	De Novo Exon Duplication in a New Allele of Mouse Glra1 (Spasmodic). Genetics, 2006, 174, 2245-2247.	2.9	14
67	Residents Examine Factors Associated With 30-Day, Same-Cause Hospital Readmissions on an Internal Medicine Service. American Journal of Medical Quality, 2013, 28, 492-501.	0.5	11
68	A Spontaneous Fatp4/Scl27a4 Splice Site Mutation in a New Murine Model for Congenital Ichthyosis. PLoS ONE, 2012, 7, e50634.	2.5	11
69	A mouse model of Waardenburg syndrome type IV resulting from an ENU-induced mutation in endothelin 3. Pigment Cell & Melanoma Research, 2007, 20, 210-215.	3.6	8
70	An N-ethyl-N-nitrosourea mutagenesis recessive screen identifies two candidate regions for murine cardiomyopathy that map to chromosomes 1 and 15. Mammalian Genome, 2009, 20, 296-304.	2.2	6
71	Polymorphisms in Toll-Like Receptor 4 Underlie Susceptibility to Tumor Induction by the Mouse Polyomavirus. Journal of Virology, 2012, 86, 11541-11547.	3.4	6
72	Rescue of the Mouse DDK Syndrome by Parent-of-Origin-Dependent Modifiers1. Biology of Reproduction, 2007, 76, 286-293.	2.7	5

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73	Three loci on mouse chromosome 5 and 10 modulate sex determination in XX Ods/+ mice. Genesis, 2007, 45, 452-455.	1.6	2
74	Genomeâ€wide significant locus for Research Diagnostic Criteria Schizoaffective Disorder Bipolar type. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 767-771.	1.7	1