

Jennifer L Moran

List of Publications by Year in descending order

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74
papers

23,726
citations

50170

46
h-index

74018

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. <i>New England Journal of Medicine</i> , 2014, 371, 2477-2487.	13.9	2,669
2	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	9.4	2,067
3	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. <i>Nature Genetics</i> , 2019, 51, 63-75.	9.4	1,594
4	Identification of common genetic risk variants for autism spectrum disorder. <i>Nature Genetics</i> , 2019, 51, 431-444.	9.4	1,538
5	De novo mutations in schizophrenia implicate synaptic networks. <i>Nature</i> , 2014, 506, 179-184.	13.7	1,510
6	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. <i>Cell</i> , 2020, 180, 568-584.e23.	13.5	1,422
7	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013, 45, 1150-1159.	9.4	1,395
8	A polygenic burden of rare disruptive mutations in schizophrenia. <i>Nature</i> , 2014, 506, 185-190.	13.7	1,305
9	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. <i>Cell</i> , 2019, 179, 1469-1482.e11.	13.5	935
10	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	13.7	929
11	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018, 359, 693-697.	6.0	851
12	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
13	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
14	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
15	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
16	Analysis of copy number variations at 15 schizophrenia-associated loci. <i>British Journal of Psychiatry</i> , 2014, 204, 108-114.	1.7	380
17	Agouti C57BL/6N embryonic stem cells for mouse genetic resources. <i>Nature Methods</i> , 2009, 6, 493-495.	9.0	340
18	Exome sequencing and the genetic basis of complex traits. <i>Nature Genetics</i> , 2012, 44, 623-630.	9.4	340

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19	The Penetrance of Copy Number Variations for Schizophrenia and Developmental Delay. <i>Biological Psychiatry</i> , 2014, 75, 378-385.	0.7	321
20	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. <i>Nature Genetics</i> , 2012, 44, 631-635.	9.4	239
21	zCall: a rare variant caller for array-based genotyping. <i>Bioinformatics</i> , 2012, 28, 2543-2545.	1.8	195
22	The IFT-A complex regulates Shh signaling through cilia structure and membrane protein trafficking. <i>Journal of Cell Biology</i> , 2012, 197, 789-800.	2.3	194
23	Novel Findings from CNVs Implicate Inhibitory and Excitatory Signaling Complexes in Schizophrenia. <i>Neuron</i> , 2015, 86, 1203-1214.	3.8	173
24	Latent TGF- β binding protein 4 modifies muscular dystrophy in mice. <i>Journal of Clinical Investigation</i> , 2009, 119, 3703-3712.	3.9	172
25	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds of <i>Drosophila</i> and <i>Caenorhabditis elegans</i> Transcription Factors. <i>Genetics</i> , 2018, 208, 937-949.	1.2	164
26	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. <i>Biological Psychiatry</i> , 2018, 83, 1044-1053.	0.7	146
27	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
28	Lethal Skeletal Dysplasia in Mice and Humans Lacking the Golgin GMAP-210. <i>New England Journal of Medicine</i> , 2010, 362, 206-216.	13.9	122
29	Validation of Electronic Health Record Phenotyping of Bipolar Disorder Cases and Controls. <i>American Journal of Psychiatry</i> , 2015, 172, 363-372.	4.0	116
30	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. <i>Lancet Psychiatry</i> , 2016, 3, 350-357.	3.7	107
31	Evidence of Common Genetic Overlap Between Schizophrenia and Cognition. <i>Schizophrenia Bulletin</i> , 2016, 42, 832-842.	2.3	102
32	Gene expression changes during mouse skeletal myoblast differentiation revealed by transcriptional profiling. <i>Physiological Genomics</i> , 2002, 10, 103-111.	1.0	97
33	Exome Sequencing of Familial Bipolar Disorder. <i>JAMA Psychiatry</i> , 2016, 73, 590.	6.0	97
34	An integrative ENCODE resource for cancer genomics. <i>Nature Communications</i> , 2020, 11, 3696.	5.8	95
35	A Rare Functional Noncoding Variant at the GWAS-Implicated MIR137/MIR2682 Locus Might Confer Risk to Schizophrenia and Bipolar Disorder. <i>American Journal of Human Genetics</i> , 2014, 95, 744-753.	2.6	91
36	Utilization of a whole genome SNP panel for efficient genetic mapping in the mouse. <i>Genome Research</i> , 2006, 16, 436-440.	2.4	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. <i>Human Molecular Genetics</i> , 2014, 23, 1669-1676.	1.4	82
38	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
39	De novo CNVs in bipolar affective disorder and schizophrenia. <i>Human Molecular Genetics</i> , 2014, 23, 6677-6683.	1.4	70
40	Bile duct proliferation in Jag1/fringe heterozygous mice identifies candidate modifiers of the alagille syndrome hepatic phenotype. <i>Hepatology</i> , 2008, 48, 1989-1997.	3.6	69
41	Implication of a Rare Deletion at Distal 16p11.2 in Schizophrenia. <i>JAMA Psychiatry</i> , 2013, 70, 253.	6.0	69
42	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
43	The genomic psychiatry cohort: Partners in discovery. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 306-312.	1.1	66
44	ERG Measurements of the Spectral Sensitivity of Common Chimpanzee (<i>Pan troglodytes</i>). <i>Vision Research</i> , 1996, 36, 2587-2594.	0.7	52
45	A Mouse Mutation in the 12R-Lipoxygenase, Alox12b, Disrupts Formation of the Epidermal Permeability Barrier. <i>Journal of Investigative Dermatology</i> , 2007, 127, 1893-1897.	0.3	52
46	Limbs move beyond the Radical fringe. <i>Nature</i> , 1999, 399, 742-743.	13.7	48
47	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
48	Cholesterol Metabolism Is Required for Intracellular Hedgehog Signal Transduction In Vivo. <i>PLoS Genetics</i> , 2011, 7, e1002224.	1.5	42
49	A HUMANIZED ANTI-CD3 ANTIBODY, HuM291, WITH LOW MITOGENIC ACTIVITY, MEDIATES COMPLETE AND REVERSIBLE T-CELL DEPLETION IN CHIMPANZEES. <i>Transplantation</i> , 1999, 68, 545-554.	0.5	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. <i>Developmental Dynamics</i> , 2009, 238, 1803-1812.	0.8	41
51	A forward genetic screen with a thalamocortical axon reporter mouse yields novel neurodevelopment mutants and a distinct emx2 mutant phenotype. <i>Neural Development</i> , 2011, 6, 3.	1.1	40
52	Analysis of genetic deletions and duplications in the University College London bipolar disorder case control sample. <i>European Journal of Human Genetics</i> , 2011, 19, 588-592.	1.4	38
53	Screening for novel risk factors related to peripherally inserted central catheter-associated complications. <i>Journal of Hospital Medicine</i> , 2014, 9, 481-489.	0.7	29
54	Genomic structure, mapping, and expression analysis of the mammalian Lunatic, Manic, and Radical fringe genes. <i>Mammalian Genome</i> , 1999, 10, 535-541.	1.0	24

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55	High resolution mapping and positional cloning of ENU-induced mutations in the Rw region of mouse chromosome 5. <i>BMC Genetics</i> , 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)1Ald heterozygotes. <i>Mammalian Genome</i> , 1997, 8, 94-97.	1.0	22
57	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
58	Concurrent Lpin1 and Nrcam Mouse Mutations Result in Severe Peripheral Neuropathy with Transitory Hindlimb Paralysis. <i>Journal of Neuroscience</i> , 2009, 29, 12089-12100.	1.7	19
59	Genome-wide identification of mouse congenital heart disease loci. <i>Human Molecular Genetics</i> , 2010, 19, 3105-3113.	1.4	19
60	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
61	ENU mutagenesis in mice identifies candidate genes for hypogonadism. <i>Mammalian Genome</i> , 2012, 23, 346-355.	1.0	16
62	A genome wide survey supports the involvement of large copy number variants in schizophrenia with and without intellectual disability. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 847-854.	1.1	16
63	Mosaic copy number variation in schizophrenia. <i>European Journal of Human Genetics</i> , 2013, 21, 1007-1011.	1.4	15
64	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	4.1	15
65	Description and genetic mapping of Polypodia: an X-linked dominant mouse mutant with ectopic caudal limbs and other malformations. <i>Mammalian Genome</i> , 2006, 17, 903-913.	1.0	14
66	De Novo Exon Duplication in a New Allele of Mouse Glra1 (Spasmodic). <i>Genetics</i> , 2006, 174, 2245-2247.	1.2	14
67	Residents Examine Factors Associated With 30-Day, Same-Cause Hospital Readmissions on an Internal Medicine Service. <i>American Journal of Medical Quality</i> , 2013, 28, 492-501.	0.2	11
68	A Spontaneous Fatp4/Sc127a4 Splice Site Mutation in a New Murine Model for Congenital Ichthyosis. <i>PLoS ONE</i> , 2012, 7, e50634.	1.1	11
69	A mouse model of Waardenburg syndrome type IV resulting from an ENU-induced mutation in endothelin 3. <i>Pigment Cell & Melanoma Research</i> , 2007, 20, 210-215.	4.0	8
70	An N-ethyl-N-nitrosourea mutagenesis recessive screen identifies two candidate regions for murine cardiomyopathy that map to chromosomes 1 and 15. <i>Mammalian Genome</i> , 2009, 20, 296-304.	1.0	6
71	Polymorphisms in Toll-Like Receptor 4 Underlie Susceptibility to Tumor Induction by the Mouse Polyomavirus. <i>Journal of Virology</i> , 2012, 86, 11541-11547.	1.5	6
72	Rescue of the Mouse DDK Syndrome by Parent-of-Origin-Dependent Modifiers1. <i>Biology of Reproduction</i> , 2007, 76, 286-293.	1.2	5

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73	Three loci on mouse chromosome 5 and 10 modulate sex determination in XX <i>Odsⁱ/+</i> mice. <i>Genesis</i> , 2007, 45, 452-455.	0.8	2
74	Genome-wide significant locus for Research Diagnostic Criteria Schizoaffective Disorder Bipolar type. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 767-771.	1.1	1