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	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
2	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
3	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15
4	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. Molecular Psychiatry, 2020, 25, 2455-2467.	4.1	82
5	Exome sequencing in schizophrenia-affected parentâ€“offspring trios reveals risk conferred by protein-coding de novo mutations. Nature Neuroscience, 2020, 23, 185-193.	7.1	125
6	An integrative ENCODE resource for cancer genomics. Nature Communications, 2020, 11, 3696.	5.8	95
7	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
8	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
9	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
10	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594
11	Contribution of Rare Copy Number Variants toÂBipolar Disorder Risk Is Limited to Schizoaffective Cases. Biological Psychiatry, 2019, 86, 110-119.	0.7	45
12	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
13	The ModERN Resource: Genome-Wide Binding Profiles for Hundreds ofDrosophilaandCaenorhabditis elegansTranscription Factors. Genetics, 2018, 208, 937-949.	1.2	164
14	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	0.7	146
15	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.	1.1	1
16	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.	1.1	19
17	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
18	Exome Sequencing of Familial Bipolar Disorder. JAMA Psychiatry, 2016, 73, 590.	6.0	97

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19	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	7.1	427
20	Evidence of Common Genetic Overlap Between Schizophrenia and Cognition. Schizophrenia Bulletin, 2016, 42, 832-842.	2.3	102
21	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. Lancet Psychiatry,the, 2016, 3, 350-357.	3.7	107
22	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
23	Novel Findings from CNVs Implicate Inhibitory and Excitatory Signaling Complexes in Schizophrenia. Neuron, 2015, 86, 1203-1214.	3.8	173
24	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. European Journal of Human Genetics, 2015, 23, 555-557.	1.4	21
25	Validation of Electronic Health Record Phenotyping of Bipolar Disorder Cases and Controls. American Journal of Psychiatry, 2015, 172, 363-372.	4.0	116
26	Analysis of copy number variations at 15 schizophrenia-associated loci. British Journal of Psychiatry, 2014, 204, 108-114.	1.7	380
27	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.	2.6	91
28	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. New England Journal of Medicine, 2014, 371, 2477-2487.	13.9	2,669
29	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.	1.4	82
30	De novo CNVs in bipolar affective disorder and schizophrenia. Human Molecular Genetics, 2014, 23, 6677-6683.	1.4	70
31	The Penetrance of Copy Number Variations for Schizophrenia and Developmental Delay. Biological Psychiatry, 2014, 75, 378-385.	0.7	321
32	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
33	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	1,305
34	Screening for novel risk factors related to peripherally inserted central catheterâ€associated complications. Journal of Hospital Medicine, 2014, 9, 481-489.	0.7	29
35	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
36	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067

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37	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.	1.1	16
38	Implication of a Rare Deletion at Distal 16p11.2 in Schizophrenia. JAMA Psychiatry, 2013, 70, 253.	6.0	69
39	Mosaic copy number variation in schizophrenia. European Journal of Human Genetics, 2013, 21, 1007-1011.	1.4	15
40	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.	0.2	11
41	The genomic psychiatry cohort: Partners in discovery. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 306-312.	1.1	66
42	The IFT-A complex regulates Shh signaling through cilia structure and membrane protein trafficking. Journal of Cell Biology, 2012, 197, 789-800.	2.3	194
43	Polymorphisms in Toll-Like Receptor 4 Underlie Susceptibility to Tumor Induction by the Mouse Polyomavirus. Journal of Virology, 2012, 86, 11541-11547.	1.5	6
44	zCall: a rare variant caller for array-based genotyping. Bioinformatics, 2012, 28, 2543-2545.	1.8	195
45	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
46	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. Nature Genetics, 2012, 44, 631-635.	9.4	239
47	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	9.4	340
48	ENU mutagenesis in mice identifies candidate genes for hypogonadism. Mammalian Genome, 2012, 23, 346-355.	1.0	16
49	A Spontaneous Fatp4/Scl27a4 Splice Site Mutation in a New Murine Model for Congenital Ichthyosis. PLoS ONE, 2012, 7, e50634.	1.1	11
50	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.	1.4	38
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.	1.1	40
52	Cholesterol Metabolism Is Required for Intracellular Hedgehog Signal Transduction In Vivo. PLoS Genetics, 2011, 7, e1002224.	1.5	42
53	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
54	Genome-wide identification of mouse congenital heart disease loci. Human Molecular Genetics, 2010, 19, 3105-3113.	1.4	19

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55	Lethal Skeletal Dysplasia in Mice and Humans Lacking the Golgin GMAP-210. New England Journal of Medicine, 2010, 362, 206-216.	13.9	122
56	Concurrent Lpin1 and Nrcam Mouse Mutations Result in Severe Peripheral Neuropathy with Transitory Hindlimb Paralysis. Journal of Neuroscience, 2009, 29, 12089-12100.	1.7	19
57	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.	0.8	41
58	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.	1.0	6
59	Agouti C57BL/6N embryonic stem cells for mouse genetic resources. Nature Methods, 2009, 6, 493-495.	9.0	340
60	Latent TGF-Î²â€“binding protein 4 modifies muscular dystrophy in mice. Journal of Clinical Investigation, 2009, 119, 3703-3712.	3.9	172
61	Bile duct proliferation in Jag1/fringe heterozygous mice identifies candidate modifiers of the alagille syndrome hepatic phenotype. Hepatology, 2008, 48, 1989-1997.	3.6	69
62	Rescue of the Mouse DDK Syndrome by Parent-of-Origin-Dependent Modifiers1. Biology of Reproduction, 2007, 76, 286-293.	1.2	5
63	Three loci on mouse chromosome 5 and 10 modulate sex determination in XX Ods/+ mice. Genesis, 2007, 45, 452-455.	0.8	2
64	A Mouse Mutation in the 12R-Lipoxygenase, Alox12b, Disrupts Formation of the Epidermal Permeability Barrier. Journal of Investigative Dermatology, 2007, 127, 1893-1897.	0.3	52
65	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.	4.0	8
66	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.	1.0	14
67	Utilization of a whole genome SNP panel for efficient genetic mapping in the mouse. Genome Research, 2006, 16, 436-440.	2.4	89
68	De Novo Exon Duplication in a New Allele of Mouse Glra1 (Spasmodic). Genetics, 2006, 174, 2245-2247.	1.2	14
69	Gene expression changes during mouse skeletal myoblast differentiation revealed by transcriptional profiling. Physiological Genomics, 2002, 10, 103-111.	1.0	97
70	Limbs move beyond the Radical fringe. Nature, 1999, 399, 742-743.	13.7	48
71	Genomic structure, mapping, and expression analysis of the mammalian Lunatic, Manic, and Radical fringe genes. Mammalian Genome, 1999, 10, 535-541.	1.0	24
72	A HUMANIZED ANTI-CD3 ANTIBODY, HuM291, WITH LOW MITOGENIC ACTIVITY, MEDIATES COMPLETE AND REVERSIBLE T-CELL DEPLETION IN CHIMPANZEES. Transplantation, 1999, 68, 545-554.	0.5	42

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73	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.	1.0	22
74	ERG Measurements of the Spectral Sensitivity of Common Chimpanzee (Pan troglodytes). Vision Research, 1996, 36, 2587-2594.	0.7	52