Janine M Lasalle

List of Publications by Citations

140 papers	7,008 citations	50 h-index	81 g-index
166 ext. papers	8,090 ext. citations	6.9 avg, IF	6 L-index

#	Paper	IF	Citations
140	Epigenetic overlap in autism-spectrum neurodevelopmental disorders: MECP2 deficiency causes reduced expression of UBE3A and GABRB3. *Human Molecular Genetics*, **2005**, 14, 483-92	5.6	339
139	Integrated epigenomic analyses of neuronal MeCP2 reveal a role for long-range interaction with active genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 19416-21	11.5	316
138	Reduced MeCP2 expression is frequent in autism frontal cortex and correlates with aberrant MECP2 promoter methylation. *Epigenetics*, **2006**, 1, e1-11	5.7	267
137	Rett syndrome astrocytes are abnormal and spread MeCP2 deficiency through gap junctions. *Journal of Neuroscience*, **2009**, 29, 5051-61	6.6	220
136	Homologous association of oppositely imprinted chromosomal domains. *Science*, **1996**, 272, 725-8	33.3	215
135	RAB22 and RAB163/mouse BRCA2: proteins that specifically interact with the RAD51 protein. *Proceedings of the National Academy of Sciences of the United States of America*, **1997**, 94, 6927-32	11.5	209
134	The comorbidity of autism with the genomic disorders of chromosome 15q11.2-q13. *Neurobiology of Disease*, **2010**, 38, 181-91	7.5	203
133	The human placenta methylome. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 6037-42	11.5	194
132	15q11-13 GABAA receptor genes are normally biallelically expressed in brain yet are subject to epigenetic dysregulation in autism-spectrum disorders. *Human Molecular Genetics*, **2007**, 16, 691-703	5.6	181
131	Small-Magnitude Effect Sizes in Epigenetic End Points are Important in Children's Environmental Health Studies: The Children's Environmental Health and Disease Prevention Research Center's Epigenetics Working Group. *Environmental Health Perspectives*, **2017**, 125, 511-526	8.4	158
130	The role of MeCP2 in brain development and neurodevelopmental disorders. *Current Psychiatry Reports*, **2010**, 12, 127-34	9.1	131
129	Multiple pathways regulate MeCP2 expression in normal brain development and exhibit defects in autism-spectrum disorders. *Human Molecular Genetics*, **2004**, 13, 629-39	5.6	129
128	Early signaling defects in human T cells anergized by T cell presentation of autoantigen. *Journal of Experimental Medicine*, **1992**, 176, 177-86	16.6	127
127	Does HER2/neu expression provide prognostic information in patients with advanced urothelial carcinoma?. *Cancer*, **2002**, 95, 1009-15	6.4	115
126	A Prader-Willi locus lncRNA cloud modulates diurnal genes and energy expenditure. *Human Molecular Genetics*, **2013**, 22, 4318-28	5.6	112
125	Levels of select PCB and PBDE congeners in human postmortem brain reveal possible environmental involvement in 15q11-q13 duplication autism spectrum disorder. *Environmental and Molecular Mutagenesis*, **2012**, 53, 589-98	3.2	110
124	R-loop formation at Snord116 mediates topotecan inhibition of Ube3a-antisense and allele-specific chromatin decondensation. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 13938-43	11.5	109

123	Quantitative localization of heterogeneous methyl-CpG-binding protein 2 (MeCP2) expression phenotypes in normal and Rett syndrome brain by laser scanning cytometry. *Human Molecular Genetics*, **2001**, 10, 1729-40	5.6	109
122	The landscape of DNA methylation amid a perfect storm of autism aetiologies. *Nature Reviews Neuroscience*, **2016**, 17, 411-23	13.5	103
121	Chromosome 15q11-13 duplication syndrome brain reveals epigenetic alterations in gene expression not predicted from copy number. *Journal of Medical Genetics*, **2009**, 46, 86-93	5.8	94
120	MECP2 promoter methylation and X chromosome inactivation in autism. *Autism Research*, **2008**, 1, 169-78	5.1	91
119	Elevated methyl-CpG-binding protein 2 expression is acquired during postnatal human brain development and is correlated with alternative polyadenylation. *Journal of Molecular Medicine*, **2003**, 81, 61-8	5.5	90
118	Long-lived epigenetic interactions between perinatal PBDE exposure and Mecp2308 mutation. *Human Molecular Genetics*, **2012**, 21, 2399-411	5.6	87
117	Inhibitors of differentiation (ID1, ID2, ID3 and ID4) genes are neuronal targets of MeCP2 that are elevated in Rett syndrome. *Human Molecular Genetics*, **2006**, 15, 2003-14	5.6	86
116	X-Chromosome inactivation ratios affect wild-type MeCP2 expression within mosaic Rett syndrome and Mecp2-/+ mouse brain. *Human Molecular Genetics*, **2004**, 13, 1275-86	5.6	85
115	15q11.2-13.3 chromatin analysis reveals epigenetic regulation of CHRNA7 with deficiencies in Rett and autism brain. *Human Molecular Genetics*, **2011**, 20, 4311-23	5.6	84
114	Evolving role of MeCP2 in Rett syndrome and autism. *Epigenomics*, **2009**, 1, 119-30	4.4	79
113	Epigenetic regulation of UBE3A and roles in human neurodevelopmental disorders. *Epigenomics*, **2015**, 7, 1213-28	4.4	78
112	Homologous pairing of 15q11-13 imprinted domains in brain is developmentally regulated but deficient in Rett and autism samples. *Human Molecular Genetics*, **2005**, 14, 785-97	5.6	74
111	Large-scale methylation domains mark a functional subset of neuronally expressed genes. *Genome Research*, **2011**, 21, 1583-91	9.7	72
110	A genomic point-of-view on environmental factors influencing the human brain methylome. *Epigenetics*, **2011**, 6, 862-9	5.7	71
109	Autism and Cancer Share Risk Genes, Pathways, and Drug Targets. *Trends in Genetics*, **2016**, 32, 139-146	8.5	68
108	Phosphorylation of distinct sites in MeCP2 modifies cofactor associations and the dynamics of transcriptional regulation. *Molecular and Cellular Biology*, **2012**, 32, 2894-903	4.8	68
107	Early Developmental and Evolutionary Origins of Gene Body DNA Methylation Patterns in Mammalian Placentas. *PLoS Genetics*, **2015**, 11, e1005442	6	68
106	MeCP2 modulates gene expression pathways in astrocytes. *Molecular Autism*, **2013**, 4, 3	6.5	67

105	Wilson's disease: changes in methionine metabolism and inflammation affect global DNA methylation in early liver disease. *Hepatology*, **2013**, 57, 555-65	11.2	67
104	Epigenetic layers and players underlying neurodevelopment. *Trends in Neurosciences*, **2013**, 36, 460-70	13.3	66
103	Epigenetic investigation of variably X chromosome inactivated genes in monozygotic female twins discordant for primary biliary cirrhosis. *Epigenetics*, **2011**, 6, 95-102	5.7	64
102	Domain organization of allele-specific replication within the GABRB3 gene cluster requires a biparental 15q11-13 contribution. *Nature Genetics*, **1995**, 9, 386-94	36.3	64
101	Role of DNMT3B in the regulation of early neural and neural crest specifiers. *Epigenetics*, **2012**, 7, 71-82	5.7	63
100	Analysis of protein domains and Rett syndrome mutations indicate that multiple regions influence chromatin-binding dynamics of the chromatin-associated protein MECP2 in vivo. *Journal of Cell Science*, **2008**, 121, 1128-37	5.3	63
99	MECP2 mutations in Rett syndrome adversely affect lymphocyte growth, but do not affect imprinted gene expression in blood or brain. *Human Genetics*, **2002**, 110, 545-52	6.3	62
98	Epigenomic strategies at the interface of genetic and environmental risk factors for autism. *Journal of Human Genetics*, **2013**, 58, 396-401	4.3	61
97	Imprinting regulates mammalian snoRNA-encoding chromatin decondensation and neuronal nucleolar size. *Human Molecular Genetics*, **2009**, 18, 4227-38	5.6	61
96	A survey of seizures and current treatments in 15q duplication syndrome. *Epilepsia*, **2014**, 55, 396-402	6.4	60
95	T cell anergy. *FASEB Journal*, **1994**, 8, 601-8	0.9	60
94	Reciprocal co-regulation of EGR2 and MECP2 is disrupted in Rett syndrome and autism. *Human Molecular Genetics*, **2009**, 18, 525-34	5.6	58
93	Increased copy number for methylated maternal 15q duplications leads to changes in gene and protein expression in human cortical samples. *Molecular Autism*, **2011**, 2, 19	6.5	56
92	Neuron-specific impairment of inter-chromosomal pairing and transcription in a novel model of human 15q-duplication syndrome. *Human Molecular Genetics*, **2011**, 20, 3798-810	5.6	53
91	Mice with an isoform-ablating Mecp2 exon 1 mutation recapitulate the neurologic deficits of Rett syndrome. *Human Molecular Genetics*, **2014**, 23, 2447-58	5.6	50
90	MeCP2 is required for global heterochromatic and nucleolar changes during activity-dependent neuronal maturation. *Neurobiology of Disease*, **2011**, 43, 190-200	7.5	49
89	X chromosome gene methylation in peripheral lymphocytes from monozygotic twins discordant for scleroderma. *Clinical and Experimental Immunology*, **2012**, 169, 253-62	6.2	47
88	Maternal choline modifies fetal liver copper, gene expression, DNA methylation, and neonatal growth in the tx-j mouse model of Wilson disease. *Epigenetics*, **2014**, 9, 286-96	5.7	46

87	Genome-wide analysis of DNA methylation, copy number variation, and gene expression in monozygotic twins discordant for primary biliary cirrhosis. *Frontiers in Immunology*, **2014**, 5, 128	8.4	46
86	Cumulative Impact of Polychlorinated Biphenyl and Large Chromosomal Duplications on DNA Methylation, Chromatin, and Expression of Autism Candidate Genes. *Cell Reports*, **2016**, 17, 3035-3048	10.6	46
85	A Prospective Study of Environmental Exposures and Early Biomarkers in Autism Spectrum Disorder: Design, Protocols, and Preliminary Data from the MARBLES Study. *Environmental Health Perspectives*, **2018**, 126, 117004	8.4	44
84	The Odyssey of MeCP2 and parental imprinting. *Epigenetics*, **2007**, 2, 5-10	5.7	42
83	Snord116-dependent diurnal rhythm of DNA methylation in mouse cortex. *Nature Communications*, **2018**, 9, 1616	17.4	39
82	Gender influences monoallelic expression of ATP10A in human brain. *Human Genetics*, **2008**, 124, 235-42	6.3	39
81	Loss of MeCP2 in the rat models regression, impaired sociability and transcriptional deficits of Rett syndrome. *Human Molecular Genetics*, **2016**, 25, 3284-3302	5.6	38
80	Chimeric MicroRNA-1291 Biosynthesized Efficiently in Escherichia coli Is Effective to Reduce Target Gene Expression in Human Carcinoma Cells and Improve Chemosensitivity. *Drug Metabolism and Disposition*, **2015**, 43, 1129-36	4	37
79	Sequence features accurately predict genome-wide MeCP2 binding in vivo. *Nature Communications*, **2016**, 7, 11025	17.4	37
78	Immunologic and neurodevelopmental susceptibilities of autism. *NeuroToxicology*, **2008**, 29, 532-45	4.4	37
77	Autism genes keep turning up chromatin. *OA Autism*, **2013**, 1, 14		37
76	Neuronal overexpression of Ube3a isoform 2 causes behavioral impairments and neuroanatomical pathology relevant to 15q11.2-q13.3 duplication syndrome. *Human Molecular Genetics*, **2017**, 26, 3995-4010	5.6	35
75	Placental methylome analysis from a prospective autism study. *Molecular Autism*, **2016**, 7, 51	6.5	35
74	Cognitive deficits in the Snord116 deletion mouse model for Prader-Willi syndrome. *Neurobiology of Learning and Memory*, **2019**, 165, 106874	3.1	34
73	Microglia from offspring of dams with allergic asthma exhibit epigenomic alterations in genes dysregulated in autism. *Glia*, **2018**, 66, 505-521	9	34
72	Multiple forms of atypical rearrangements generating supernumerary derivative chromosome 15. *BMC Genetics*, **2008**, 9, 2	2.6	33
71	Expression profiling of clonal lymphocyte cell cultures from Rett syndrome patients. *BMC Medical Genetics*, **2006**, 7, 61	2.1	33
70	Dynamic changes in Histone H3 lysine 9 acetylation localization patterns during neuronal maturation require MeCP2. *Epigenetics*, **2006**, 1, 24-31	5.7	32

69	The coexpression of CD45RA and CD45RO isoforms on T cells during the S/G2/M stages of cell cycle. *Cellular Immunology*, **1991**, 138, 197-206	4.4	30
68	Epigenetic mechanisms in diurnal cycles of metabolism and neurodevelopment. *Human Molecular Genetics*, **2015**, 24, R1-9	5.6	28
67	Placental DNA methylation levels at CYP2E1 and IRS2 are associated with child outcome in a prospective autism study. *Human Molecular Genetics*, **2019**, 28, 2659-2674	5.6	25
66	Early motor phenotype detection in a female mouse model of Rett syndrome is improved by cross-fostering. *Human Molecular Genetics*, **2017**, 26, 1839-1854	5.6	23
65	Epigenomic signatures in liver and blood of Wilson disease patients include hypermethylation of liver-specific enhancers. *Epigenetics and Chromatin*, **2019**, 12, 10	5.8	23
64	Characterization of timed changes in hepatic copper concentrations, methionine metabolism, gene expression, and global DNA methylation in the Jackson toxic milk mouse model of Wilson disease. *International Journal of Molecular Sciences*, **2014**, 15, 8004-23	6.3	23
63	Investigation of modifier genes within copy number variations in Rett syndrome. *Journal of Human Genetics*, **2011**, 56, 508-15	4.3	23
62	Genetics and epigenetic factors of Wilson disease. *Annals of Translational Medicine*, **2019**, 7, S58	3.2	23
61	Wilson Disease: Epigenetic effects of choline supplementation on phenotype and clinical course in a mouse model. *Epigenetics*, **2016**, 11, 804-818	5.7	23
60	A novel hypomorphic MECP2 point mutation is associated with a neuropsychiatric phenotype. *Human Genetics*, **2009**, 124, 615-23	6.3	22
59	UBE3A: An E3 Ubiquitin Ligase With Genome-Wide Impact in Neurodevelopmental Disease. *Frontiers in Molecular Neuroscience*, **2018**, 11, 476	6.1	21
58	Dental Pulp Stem Cells Model Early Life and Imprinted DNA Methylation Patterns. *Stem Cells*, **2017**, 35, 981-988	5.8	20
57	Methylation and gene expression responses to ethanol feeding and betaine supplementation in the cystathionine beta synthase-deficient mouse. *Alcoholism: Clinical and Experimental Research*, **2014**, 38, 1540-9	3.7	20
56	How has the study of the human placenta aided our understanding of partially methylated genes?. *Epigenomics*, **2013**, 5, 645-54	4.4	20
55	Clonal heterogeneity at allelic methylation sites diagnostic for Prader-Willi and Angelman syndromes. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 1675-80	11.5	19
54	Whole genome bisulfite sequencing of Down syndrome brain reveals regional DNA hypermethylation and novel disorder insights. *Epigenetics*, **2019**, 14, 672-684	5.7	18
53	Rett syndrome: a Rosetta stone for understanding the molecular pathogenesis of autism. *International Review of Neurobiology*, **2005**, 71, 131-65	4.4	18
52	Neuronal chromatin dynamics of imprinting in development and disease. *Journal of Cellular Biochemistry*, **2011**, 112, 365-73	4.7	17

51	Cord blood DNA methylome in newborns later diagnosed with autism spectrum disorder reflects early dysregulation of neurodevelopmental and X-linked genes. *Genome Medicine*, **2020**, 12, 88	14.4	17
50	Experience-dependent neuroplasticity of the developing hypothalamus: integrative epigenomic approaches. *Epigenetics*, **2018**, 13, 318-330	5.7	16
49	Self-reported pregnancy exposures and placental DNA methylation in the MARBLES prospective autism sibling study. *Environmental Epigenetics*, **2016**, 2,	2.4	15
48	UBE3A-mediated regulation of imprinted genes and epigenome-wide marks in human neurons. *Epigenetics*, **2017**, 12, 982-990	5.7	14
47	Paradoxical role of methyl-CpG-binding protein 2 in Rett syndrome. *Current Topics in Developmental Biology*, **2004**, 59, 61-86	5.3	14
46	Epigenomic Convergence of Neural-Immune Risk Factors in Neurodevelopmental Disorder Cortex. *Cerebral Cortex*, **2020**, 30, 640-655	5.1	14
45	MeCP2 regulates activity-dependent transcriptional responses in olfactory sensory neurons. *Human Molecular Genetics*, **2014**, 23, 6366-74	5.6	13
44	Prader-Willi locus Snord116 RNA processing requires an active endogenous allele and neuron-specific splicing by Rbfox3/NeuN. *Human Molecular Genetics*, **2018**, 27, 4051-4060	5.6	12
43	Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. *Communications Biology*, **2021**, 4, 769	6.7	12
42	A comparison of existing global DNA methylation assays to low-coverage whole-genome bisulfite sequencing for epidemiological studies. *Epigenetics*, **2017**, 12, 206-214	5.7	11
41	Epigenetic changes of the thioredoxin system in the tx-j mouse model and in patients with Wilson disease. *Human Molecular Genetics*, **2018**, 27, 3854-3869	5.6	11
40	Clonal maintenance of imprinted expression of SNRPN and IPW in normal lymphocytes: correlation with allele-specific methylation of SNRPN intron 1 but not intron 7. *Human Genetics*, **2001**, 108, 116-22	6.3	10
39	Biological activity of recombinant human myelin basic protein. *Journal of Neuroimmunology*, **1993**, 44, 157-62	3.5	10
38	A genome-wide association study implicates the BMP7 locus as a risk factor for nonsyndromic metopic craniosynostosis. *Human Genetics*, **2020**, 139, 1077-1090	6.3	9
37	Low-pass whole genome bisulfite sequencing of neonatal dried blood spots identifies a role for RUNX1 in Down syndrome DNA methylation profiles. *Human Molecular Genetics*, **2021**, 29, 3465-3476	5.6	9
36	A meta-analysis of two high-risk prospective cohort studies reveals autism-specific transcriptional changes to chromatin, autoimmune, and environmental response genes in umbilical cord blood. *Molecular Autism*, **2019**, 10, 36	6.5	8
35	MeCP2 isoform e1 mutant mice recapitulate motor and metabolic phenotypes of Rett syndrome. *Human Molecular Genetics*, **2018**, 27, 4077-4093	5.6	6
34	Imprinting effects of UBE3A loss on synaptic gene networks and Wnt signaling pathways. *Human Molecular Genetics*, **2019**, 28, 3842-3852	5.6	6

33	Automated quantitation of cell-mediated HIV type 1 infection of human syncytiotrophoblast cells by fluorescence in situ hybridization and laser scanning cytometry. *AIDS Research and Human Retroviruses*, **2001**, 17, 507-16	1.6	6
32	Stable DNMT3L overexpression in SH-SY5Y neurons recreates a facet of the genome-wide Down syndrome DNA methylation signature. *Epigenetics and Chromatin*, **2021**, 14, 13	5.8	5
31	Epigenetics in Prader-Willi Syndrome. *Frontiers in Genetics*, **2021**, 12, 624581	4.5	5
30	Epigenetics of Circadian Rhythms in Imprinted Neurodevelopmental Disorders. *Progress in Molecular Biology and Translational Science*, **2018**, 157, 67-92	4	5
29	Placenta and fetal brain share a neurodevelopmental disorder DNA methylation profile in a mouse model of prenatal PCB exposure.. *Cell Reports*, **2022**, 38, 110442	10.6	4
28	Cord blood buffy coat DNA methylation is comparable to whole cord blood methylation. *Epigenetics*, **2018**, 13, 108-116	5.7	3
27	Expression Changes in Epigenetic Gene Pathways Associated With One-Carbon Nutritional Metabolites in Maternal Blood From Pregnancies Resulting in Autism and Non-Typical Neurodevelopment. *Autism Research*, **2021**, 14, 11-28	5.1	3
26	Integrated analysis of a compendium of RNA-Seq datasets for splicing factors. *Scientific Data*, **2020**, 7, 178	8.2	2
25	Epigenetic Epidemiology of Autism and Other Neurodevelopmental Disorders **2012**, 321-342		2
24	Flow cytometry and FISH to investigate allele-specific replication timing and homologous association of imprinted chromosomes. *Methods in Molecular Biology*, **2001**, 181, 181-92	1.4	2
23	Epigenomic convergence of genetic and immune risk factors in neurodevelopmental disorder cortex		2
22	Epigenetics at the Interface of Genetics and Environmental Factors in Autism. *Epigenetics and Human Health*, **2013**, 97-114		2
21	Genetic variants drive altered epigenetic regulation of endotoxin response in BTBR macrophages. *Brain, Behavior, and Immunity*, **2020**, 89, 20-31	16.6	2
20	A meta-analysis of two high-risk prospective cohort studies reveals autism-specific transcriptional changes to chromatin, autoimmune, and environmental response genes in umbilical cord blood		2
19	Placental DNA methylation levels at CYP2E1 and IRS2 are associated with child outcome in a prospective autism study		2
18	Microglia from offspring of dams with allergic asthma exhibit epigenomic alterations in genes dysregulated in autism		2
17	mtDNA depletion-like syndrome in Wilson disease. *Liver International*, **2020**, 40, 2776-2787	7.9	1
16	Comethyl: a network-based methylome approach to investigate the multivariate nature of health and disease.. *Briefings in Bioinformatics*, **2022**,	13.4	1

List of Publications

15	Cord blood DNA methylome in newborns later diagnosed with autism spectrum disorder reflects early dysregulation of neurodevelopmental and X-linked genes		1
14	Wilson Disease: Intersecting DNA Methylation and Histone Acetylation Regulation of Gene Expression in a Mouse Model of Hepatic Copper Accumulation. *Cellular and Molecular Gastroenterology and Hepatology*, **2021**, 12, 1457-1477	7.9	1
13	Epigenetic Dysregulation of 15q11-13 GABAA Receptor Genes in Autism **2010**, 113-127		1
12	Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism.. *Genome Biology*, **2022**, 23, 46	18.3	1
11	The Promise of DNA Methylation in Understanding Multigenerational Factors in Autism Spectrum Disorders.. *Frontiers in Genetics*, **2022**, 13, 831221	4.5	1
10	Sex disparate gut microbiome and metabolome perturbations precede disease progression in a mouse model of Rett syndrome.. *Communications Biology*, **2021**, 4, 1408	6.7	0
9	Long-term effects of wildfire smoke exposure during early life on the nasal epigenome in rhesus macaques.. *Environment International*, **2022**, 158, 106993	12.9	0
8	Genetic and epigenetic influences on the phenotype of Rett syndrome **2019**, 183-217		
7	MeCP2 and Autism Spectrum Disorders **2013**, 421-436		
6	Imprinting in the CNS and Neurodevelopmental Disorders **2013**, 267-279		
5	18 Combined detection of low level her-2/neu expression and gene amplification in prostate cancer by immunofluorescence and fluorescence in situ hybridization. *Handbook of Immunohistochemistry and in Situ Hybridization of Human Carcinomas*, **2002**, 2, 457-461		
4	The Potential Brain Drain from Environmental Exposures on the Methylome and Genome Across Generations **2014**, 375-406		
3	Neurodevelopmental Toxicology and Autism Spectrum Disorders439-476		
2	Recurrent CNVs in the Etiology of Epigenetic Neurodevelopmental Disorders **2013**, 147-178		
1	X Chromosome Inactivation Timing is Not e: Implications for Autism Spectrum Disorders.. *Frontiers in Genetics*, **2022**, 13, 864848	4.5	