Janine M Lasalle

List of Publications by Year
in descending order

140	8,797	31976	48315
papers	citations	53 h-index	88 g-index

166	166	166	9694
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Epigenetic overlap in autism-spectrum neurodevelopmental disorders: MECP2 deficiency causes reduced expression of UBE3A and GABRB3. Human Molecular Genetics, 2005, 14, 483-492.	2.9	377
2	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, 19416-19421.	7.1	345
3	Reduced MeCP2 Expression is Frequent in Autism Frontal Cortex and Correlates with Aberrant MECP2 Promoter Methylation. Epigenetics, 2006, 1, 172-182.	2.7	306
4	The human placenta methylome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6037-6042.	7.1	256
5	Rett Syndrome Astrocytes Are Abnormal and Spread MeCP2 Deficiency through Gap Junctions. Journal of Neuroscience, 2009, 29, 5051-5061.	3.6	247
6	Small-Magnitude Effect Sizes in Epigenetic End Points are Important in Childrenâ€™s Environmental Health Studies: The Childrenâ€™s Environmental Health and Disease Prevention Research Centerâ€™s Epigenetics Working Group. Environmental Health Perspectives, 2017, 125, 511-526.	6.0	243
7	Homologous Association of Oppositely Imprinted Chromosomal Domains. Science, 1996, 272, 725-728.	12.6	242
8	The comorbidity of autism with the genomic disorders of chromosome 15q11.2-q13. Neurobiology of Disease, 2010, 38, 181-191.	4.4	241
9	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, 6927-6932.	7.1	231
10	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.	2.9	218
11	The Role of MeCP2 in Brain Development and Neurodevelopmental Disorders. Current Psychiatry Reports, 2010, 12, 127-134.	4.5	161
12	Multiple pathways regulate MeCP2 expression in normal brain development and exhibit defects in autism-spectrum disorders. Human Molecular Genetics, 2004, 13, 629-639.	2.9	140
13	The landscape of DNA methylation amid a perfect storm of autism aetiologies. Nature Reviews Neuroscience, 2016, 17, 411-423.	10.2	139
14	Levels of select PCB and PBDE congeners in human postmortem brain reveal possible environmental involvement in 15q11â€q13 duplication autism spectrum disorder. Environmental and Molecular Mutagenesis, 2012, 53, 589-598.	2.2	138
15	Early signaling defects in human T cells anergized by T cell presentation of autoantigen.. Journal of Experimental Medicine, 1992, 176, 177-186.	8.5	132
16	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, 13938-13943.	7.1	131
17	A Praderâ€“Willi locus lncRNA cloud modulates diurnal genes and energy expenditure. Human Molecular Genetics, 2013, 22, 4318-4328.	2.9	129
18	Does HER2/neu expression provide prognostic information in patients with advanced urothelial carcinoma?. Cancer, 2002, 95, 1009-1015.	4.1	128

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19	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, 1729-1740.	2.9	124
20	Autism and Cancer Share Risk Genes, Pathways, and Drug Targets. Trends in Genetics, 2016, 32, 139-146.	6.7	123
21	Chromosome 15q11-13 duplication syndrome brain reveals epigenetic alterations in gene expression not predicted from copy number. Journal of Medical Genetics, 2008, 46, 86-93.	3.2	116
22	MECP2 promoter methylation and X chromosome inactivation in autism. Autism Research, 2008, 1, 169-178.	3.8	107
23	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, 61-68.	3.9	104
24	Long-lived epigenetic interactions between perinatal PBDE exposure and Mecp2308 mutation. Human Molecular Genetics, 2012, 21, 2399-2411.	2.9	104
25	Epigenetic regulation of UBE3A and roles in human neurodevelopmental disorders. Epigenomics, 2015, 7, 1213-1228.	2.1	100
26	X-Chromosome inactivation ratios affect wild-type MeCP2 expression within mosaic Rett syndrome and Mecp2-/+ mouse brain. Human Molecular Genetics, 2004, 13, 1275-1286.	2.9	98
27	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, 2003-2014.	2.9	98
28	15q11.2â€“13.3 chromatin analysis reveals epigenetic regulation of CHRNA7 with deficiencies in Rett and autism brain. Human Molecular Genetics, 2011, 20, 4311-4323.	2.9	93
29	Early Developmental and Evolutionary Origins of Gene Body DNA Methylation Patterns in Mammalian Placentas. PLoS Genetics, 2015, 11, e1005442.	3.5	93
30	Evolving role of MeCP2 in Rett syndrome and autism. Epigenomics, 2009, 1, 119-130.	2.1	89
31	Phosphorylation of Distinct Sites in MeCP2 Modifies Cofactor Associations and the Dynamics of Transcriptional Regulation. Molecular and Cellular Biology, 2012, 32, 2894-2903.	2.3	87
32	Large-scale methylation domains mark a functional subset of neuronally expressed genes. Genome Research, 2011, 21, 1583-1591.	5.5	86
33	Epigenomic strategies at the interface of genetic and environmental risk factors for autism. Journal of Human Genetics, 2013, 58, 396-401.	2.3	82
34	Wilson's disease: Changes in methionine metabolism and inflammation affect global DNA methylation in early liver disease. Hepatology, 2013, 57, 555-565.	7.3	82
35	A survey of seizures and current treatments in 15q duplication syndrome. Epilepsia, 2014, 55, 396-402.	5.1	80
36	A genomic point-of-view on environmental factors influencing the human brain methylome. Epigenetics, 2011, 6, 862-869.	2.7	79

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37	Homologous pairing of 15q11â€“13 imprinted domains in brain is developmentally regulated but deficient in Rett and autism samples. Human Molecular Genetics, 2005, 14, 785-797.	2.9	77
38	Reciprocal co-regulation of EGR2 and MECP2 is disrupted in Rett syndrome and autism. Human Molecular Genetics, 2009, 18, 525-534.	2.9	77
39	Epigenetic layers and players underlying neurodevelopment. Trends in Neurosciences, 2013, 36, 460-470.	8.6	77
40	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.	6.0	77
41	Epigenetic investigation of variably X chromosome inactivated genes in monozygotic female twins discordant for primary biliary cirrhosis. Epigenetics, 2011, 6, 95-102.	2.7	74
42	MeCP2 modulates gene expression pathways in astrocytes. Molecular Autism, 2013, 4, 3.	4.9	74
43	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, 1128-1137.	2.0	73
44	Role of DNMT3B in the regulation of early neural and neural crest specifiers. Epigenetics, 2012, 7, 71-82.	2.7	72
45	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.	6.4	69
46	Domain organization of alleleâ€“specific replication within the GABRB3 gene cluster requires a biparental 15q11â€“13 contribution. Nature Genetics, 1995, 9, 386-394.	21.4	68
47	Imprinting regulates mammalian snoRNA-encoding chromatin decondensation and neuronal nucleolar size. Human Molecular Genetics, 2009, 18, 4227-4238.	2.9	67
48	MeCP2 is required for global heterochromatic and nucleolar changes during activity-dependent neuronal maturation. Neurobiology of Disease, 2011, 43, 190-200.	4.4	66
49	MECP2 mutations in Rett syndrome adversely affect lymphocyte growth, but do not affect imprinted gene expression in blood or brain. Human Genetics, 2002, 110, 545-552.	3.8	65
50	Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. Communications Biology, 2021, 4, 769.	4.4	65
51	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.	4.9	64
52	T cell anergy. FASEB Journal, 1994, 8, 601-608.	0.5	63
53	Mice with an isoform-ablating Mecp2 exon 1 mutation recapitulate the neurologic deficits of Rett syndrome. Human Molecular Genetics, 2014, 23, 2447-2458.	2.9	63
54	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.	2.9	59

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55	Autism genes keep turning up chromatin. OA Autism, 2013, 1, 14.	0.7	59
56	Neuron-specific impairment of inter-chromosomal pairing and transcription in a novel model of human 15q-duplication syndrome. Human Molecular Genetics, 2011, 20, 3798-3810.	2.9	58
57	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.	4.8	57
58	Placental methylome analysis from a prospective autism study. Molecular Autism, 2016, 7, 51.	4.9	57
59	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.	2.9	57
60	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, 286-296.	2.7	54
61	Microglia from offspring of dams with allergic asthma exhibit epigenomic alterations in genes dysregulated in autism. Glia, 2018, 66, 505-521.	4.9	54
62	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, 1129-1136.	3.3	53
63	Snord116-dependent diurnal rhythm of DNA methylation in mouse cortex. Nature Communications, 2018, 9, 1616.	12.8	53
64	Cognitive deficits in the Snord116 deletion mouse model for Prader-Willi syndrome. Neurobiology of Learning and Memory, 2019, 165, 106874.	1.9	53
65	X chromosome gene methylation in peripheral lymphocytes from monozygotic twins discordant for scleroderma. Clinical and Experimental Immunology, 2012, 169, 253-262.	2.6	52
66	Loss of MeCP2 in the rat models regression, impaired sociability and transcriptional deficits of Rett syndrome. Human Molecular Genetics, 2016, 25, 3284-3302.	2.9	52
67	The Odyssey of MeCP2 and Parental Imprinting. Epigenetics, 2007, 2, 5-10.	2.7	49
68	Gender influences monoallelic expression of ATP10A in human brain. Human Genetics, 2008, 124, 235-242.	3.8	49
69	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.	8.2	47
70	Immunologic and neurodevelopmental susceptibilities of autism. NeuroToxicology, 2008, 29, 532-545.	3.0	46
71	Sequence features accurately predict genome-wide MeCP2 binding in vivo. Nature Communications, 2016, 7, 11025.	12.8	46
72	UBE3A: An E3 Ubiquitin Ligase With Genome-Wide Impact in Neurodevelopmental Disease. Frontiers in Molecular Neuroscience, 2018, 11, 476.	2.9	41

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73	Whole genome bisulfite sequencing of Down syndrome brain reveals regional DNA hypermethylation and novel disorder insights. Epigenetics, 2019, 14, 672-684.	2.7	39
74	Dynamic Changes in Histone H3 Lysine 9 Acetylation Localization Patterns During Neuronal Maturation Require MeCP2. Epigenetics, 2006, 1, 25-32.	2.7	37
75	Wilson Disease: Epigenetic effects of choline supplementation on phenotype and clinical course in a mouse model. Epigenetics, 2016, 11, 804-818.	2.7	35
76	Expression profiling of clonal lymphocyte cell cultures from Rett syndrome patients. BMC Medical Genetics, 2006, 7, 61.	2.1	34
77	Multiple forms of atypical rearrangements generating supernumerary derivative chromosome 15. BMC Genetics, 2008, 9, 2.	2.7	34
78	Genetics and epigenetic factors of Wilson disease. Annals of Translational Medicine, 2019, 7, S58-S58.	1.7	33
79	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.	3.0	32
80	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, 8004-8023.	4.1	32
81	Epigenetic mechanisms in diurnal cycles of metabolism and neurodevelopment. Human Molecular Genetics, 2015, 24, R1-R9.	2.9	32
82	Early motor phenotype detection in a female mouse model of Rett syndrome is improved by cross-fostering. Human Molecular Genetics, 2017, 26, 1839-1854.	2.9	32
83	Epigenomic signatures in liver and blood of Wilson disease patients include hypermethylation of liver-specific enhancers. Epigenetics and Chromatin, 2019, 12, 10.	3.9	32
84	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.	2.9	32
85	Epigenomic Convergence of Neural-Immune Risk Factors in Neurodevelopmental Disorder Cortex. Cerebral Cortex, 2020, 30, 640-655.	2.9	29
86	Dental Pulp Stem Cells Model Early Life and Imprinted DNA Methylation Patterns. Stem Cells, 2017, 35, 981-988.	3.2	28
87	Placenta and fetal brain share a neurodevelopmental disorder DNA methylation profile in a mouse model of prenatal PCB exposure. Cell Reports, 2022, 38, 110442.	6.4	27
88	Investigation of modifier genes within copy number variations in Rett syndrome. Journal of Human Genetics, 2011, 56, 508-515.	2.3	25
89	How has the study of the human placenta aided our understanding of partially methylated genes?. Epigenomics, 2013, 5, 645-654.	2.1	25
90	Self-reported pregnancy exposures and placental DNA methylation in the MARBLES prospective autism sibling study. Environmental Epigenetics, 2016, 2, dvw024.	1.8	25

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91	A comparison of existing global DNA methylation assays to low-coverage whole-genome bisulfite sequencing for epidemiological studies. Epigenetics, 2017, 12, 206-214.	2.7	24
92	A genome-wide association study implicates the BMP7 locus as a risk factor for nonsyndromic metopic craniosynostosis. Human Genetics, 2020, 139, 1077-1090.	3.8	24
93	A novel hypomorphic MECP2 point mutation is associated with a neuropsychiatric phenotype. Human Genetics, 2009, 124, 615-623.	3.8	23
94	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, 1540-1549.	2.4	22
95	Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism. Genome Biology, 2022, 23, 46.	8.8	22
96	Experience-dependent neuroplasticity of the developing hypothalamus: integrative epigenomic approaches. Epigenetics, 2018, 13, 318-330.	2.7	21
97	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, 1675-1680.	7.1	20
98	Rett Syndrome: A Rosetta Stone for Understanding the Molecular Pathogenesis of Autism. International Review of Neurobiology, 2005, 71, 131-165.	2.0	19
99	Praderâ€“Willi locus Snord116 RNA processing requires an active endogenous allele and neuron-specific splicing by Rbfox3/NeuN. Human Molecular Genetics, 2018, 27, 4051-4060.	2.9	19
100	Editorial: Secondary vs. Idiopathic Autism. Frontiers in Psychiatry, 2020, 11, 297.	2.6	19
101	Neuronal chromatin dynamics of imprinting in development and disease. Journal of Cellular Biochemistry, 2011, 112, 365-373.	2.6	18
102	UBE3A-mediated regulation of imprinted genes and epigenome-wide marks in human neurons. Epigenetics, 2017, 12, 982-990.	2.7	18
103	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.	2.9	18
104	MeCP2 regulates activity-dependent transcriptional responses in olfactory sensory neurons. Human Molecular Genetics, 2014, 23, 6366-6374.	2.9	17
105	Epigenetics in Prader-Willi Syndrome. Frontiers in Genetics, 2021, 12, 624581.	2.3	16
106	Paradoxical Role of Methyl-CpG-Binding Protein 2 in Rett Syndrome. Current Topics in Developmental Biology, 2004, 59, 61-86.	2.2	14
107	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.	4.9	14
108	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.	3.9	12

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109	Biological activity of recombinant human myelin basic protein. Journal of Neuroimmunology, 1993, 44, 157-162.	2.3	11
110	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.	4.5	11
111	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, 116-122.	3.8	10
112	Epigenetics of Circadian Rhythms in Imprinted Neurodevelopmental Disorders. Progress in Molecular Biology and Translational Science, 2018, 157, 67-92.	1.7	10
113	MeCP2 isoform e1 mutant mice recapitulate motor and metabolic phenotypes of Rett syndrome. Human Molecular Genetics, 2018, 27, 4077-4093.	2.9	9
114	Imprinting effects of UBE3A loss on synaptic gene networks and Wnt signaling pathways. Human Molecular Genetics, 2019, 28, 3842-3852.	2.9	9
115	Long-term effects of wildfire smoke exposure during early life on the nasal epigenome in rhesus macaques. Environment International, 2022, 158, 106993.	10.0	9
116	Expression Changes in Epigenetic Gene Pathways Associated With Oneâ€Carbon Nutritional Metabolites in Maternal Blood From Pregnancies Resulting in Autism and Nonâ€Typical Neurodevelopment. Autism Research, 2021, 14, 11-28.	3.8	8
117	Automated Quantitation of Cell-Mediated HIV Type 1 Infection of Human Syncytiotrophoblast Cells by Fluorescencein SituHybridization and Laser Scanning Cytometry. AIDS Research and Human Retroviruses, 2001, 17, 507-516.	1.1	7
118	mtDNA depletionâ€like syndrome in Wilson disease. Liver International, 2020, 40, 2776-2787.	3.9	7
119	Sex disparate gut microbiome and metabolome perturbations precede disease progression in a mouse model of Rett syndrome. Communications Biology, 2021, 4, 1408.	4.4	7
120	Cord blood buffy coat DNA methylation is comparable to whole cord blood methylation. Epigenetics, 2018, 13, 108-116.	2.7	5
121	Comethyl: a network-based methylome approach to investigate the multivariate nature of health and disease. Briefings in Bioinformatics, 2022, 23, .	6.5	5
122	The Promise of DNA Methylation in Understanding Multigenerational Factors in Autism Spectrum Disorders. Frontiers in Genetics, 2022, 13, 831221.	2.3	5
123	Genetic variants drive altered epigenetic regulation of endotoxin response in BTBR macrophages. Brain, Behavior, and Immunity, 2020, 89, 20-31.	4.1	4
124	Flow Cytometry and FISH to Investigate Allele-Specific Replication Timing and Homologous Association of Imprinted Chromosomes. , 2002, 181, 181-192.		2
125	Epigenetic Epidemiology of Autism and Other Neurodevelopmental Disorders. , 2012, , 321-342.		2
126	Integrated analysis of a compendium of RNA-Seq datasets for splicing factors. Scientific Data, 2020, 7, 178.	5.3	2

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127	Epigenetics at the Interface of Genetics and Environmental Factors in Autism. Epigenetics and Human Health, 2013, , 97-114.	0.2	2
128	Epigenetic Mechanisms in Rett Syndrome. , 2015, , 199-216.		2
129	Placenta keeps the score of maternal cannabis use and child anxiety. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	2
130	Genetic and epigenetic influences on the phenotype of Rett syndrome. , 2019, , 183-217.		1
131	Epigenetic Dysregulation of 15q11-13 GABAA Receptor Genes in Autism. , 2010, , 113-127.		1
132	X Chromosome Inactivation Timing is Not eXACT: Implications for Autism Spectrum Disorders. Frontiers in Genetics, 2022, 13, 864848.	2.3	1
133	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.	0.0	0
134	MeCP2 and Autism Spectrum Disorders. , 2013, , 421-436.		0
135	Imprinting in the CNS and Neurodevelopmental Disorders. , 2013, , 267-279.		0
136	19.1 NEUROIMMUNE, EPIGENETIC, AND METABOLIC INTERACTIONS DURING SYMPTOM PROGRESSION IN A MOUSE MODEL OF RETT SYNDROME. Journal of the American Academy of Child and Adolescent Psychiatry, 2020, 59, S294.	0.5	0
137	19.3 DEVELOPMENTAL EXPOSURE TO NEAR-ROADWAY POLLUTION PRODUCES BEHAVIORAL AND HISTOLOGICAL PHENOTYPES RELEVANT TO NEURODEVELOPMENTAL DISORDERS. Journal of the American Academy of Child and Adolescent Psychiatry, 2020, 59, S294-S295.	0.5	0
138	Recurrent CNVs in the Etiology of Epigenetic Neurodevelopmental Disorders. , 2013, , 147-178.		0
139	The Potential Brain Drain from Environmental Exposures on the Methylome and Genome Across Generations. , 2014, , 375-406.		0
140	Abstract 1513: Use of complex oligonucleotide libraries for concurrent high-resolution fluorescence imaging of both DNA and RNA in various sample types. , 2014, , .		0