Janine M Lasalle

List of Publications by Year
in descending order

140	8,797	31974	48312
papers	citations	53 h-index	88 g-index

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

#	Article	IF	Citations
1	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
2	Comethyl: a network-based methylome approach to investigate the multivariate nature of health and disease. Briefings in Bioinformatics, 2022, 23, .	6.5	5
3	Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism. Genome Biology, 2022, 23, 46.	8.8	22
4	The Promise of DNA Methylation in Understanding Multigenerational Factors in Autism Spectrum Disorders. Frontiers in Genetics, 2022, 13, 831221.	2.3	5
5	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
6	X Chromosome Inactivation Timing is Not eXACT: Implications for Autism Spectrum Disorders. Frontiers in Genetics, 2022, 13, 864848.	2.3	1
7	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
8	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
9	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
10	Epigenetics in Prader-Willi Syndrome. Frontiers in Genetics, 2021, 12, 624581.	2.3	16
11	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
12	Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. Communications Biology, 2021, 4, 769.	4.4	65
13	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
14	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
15	Epigenomic Convergence of Neural-Immune Risk Factors in Neurodevelopmental Disorder Cortex. Cerebral Cortex, 2020, 30, 640-655.	2.9	29
16	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
17	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
18	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

#	Article	IF	Citations
19	Integrated analysis of a compendium of RNA-Seq datasets for splicing factors. Scientific Data, 2020, 7, 178.	5.3	2
20	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
21	Editorial: Secondary vs. Idiopathic Autism. Frontiers in Psychiatry, 2020, 11, 297.	2.6	19
22	Genetic variants drive altered epigenetic regulation of endotoxin response in BTBR macrophages. Brain, Behavior, and Immunity, 2020, 89, 20-31.	4.1	4
23	mtDNA depletionâ€like syndrome in Wilson disease. Liver International, 2020, 40, 2776-2787.	3.9	7
24	Cognitive deficits in the Snord116 deletion mouse model for Prader-Willi syndrome. Neurobiology of Learning and Memory, 2019, 165, 106874.	1.9	53
25	Imprinting effects of UBE3A loss on synaptic gene networks and Wnt signaling pathways. Human Molecular Genetics, 2019, 28, 3842-3852.	2.9	9
26	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
27	Genetic and epigenetic influences on the phenotype of Rett syndrome. , 2019, , 183-217.		1
28	Whole genome bisulfite sequencing of Down syndrome brain reveals regional DNA hypermethylation and novel disorder insights. Epigenetics, 2019, 14, 672-684.	2.7	39
29	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
30	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
31	Genetics and epigenetic factors of Wilson disease. Annals of Translational Medicine, 2019, 7, S58-S58.	1.7	33
32	Cord blood buffy coat DNA methylation is comparable to whole cord blood methylation. Epigenetics, 2018, 13, 108-116.	2.7	5
33	Snord116-dependent diurnal rhythm of DNA methylation in mouse cortex. Nature Communications, 2018, 9, 1616.	12.8	53
34	Experience-dependent neuroplasticity of the developing hypothalamus: integrative epigenomic approaches. Epigenetics, 2018, 13, 318-330.	2.7	21
35	Microglia from offspring of dams with allergic asthma exhibit epigenomic alterations in genes dysregulated in autism. Glia, 2018, 66, 505-521.	4.9	54
36	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

#	Article	IF	Citations
37	Epigenetics of Circadian Rhythms in Imprinted Neurodevelopmental Disorders. Progress in Molecular Biology and Translational Science, 2018, 157, 67-92.	1.7	10
38	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
39	MeCP2 isoform e1 mutant mice recapitulate motor and metabolic phenotypes of Rett syndrome. Human Molecular Genetics, 2018, 27, 4077-4093.	2.9	9
40	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
41	UBE3A: An E3 Ubiquitin Ligase With Genome-Wide Impact in Neurodevelopmental Disease. Frontiers in Molecular Neuroscience, 2018, 11, 476.	2.9	41
42	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
43	Dental Pulp Stem Cells Model Early Life and Imprinted DNA Methylation Patterns. Stem Cells, 2017, 35, 981-988.	3.2	28
44	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
45	UBE3A-mediated regulation of imprinted genes and epigenome-wide marks in human neurons. Epigenetics, 2017, 12, 982-990.	2.7	18
46	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
47	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
48	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
49	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
50	Placental methylome analysis from a prospective autism study. Molecular Autism, 2016, 7, 51.	4.9	57
51	The landscape of DNA methylation amid a perfect storm of autism aetiologies. Nature Reviews Neuroscience, 2016, 17, 411-423.	10.2	139
52	Wilson Disease: Epigenetic effects of choline supplementation on phenotype and clinical course in a mouse model. Epigenetics, 2016, 11, 804-818.	2.7	35
53	Self-reported pregnancy exposures and placental DNA methylation in the MARBLES prospective autism sibling study. Environmental Epigenetics, 2016, 2, dvw024.	1.8	25
54	Sequence features accurately predict genome-wide MeCP2 binding in vivo. Nature Communications, 2016, 7, 11025.	12.8	46

#	Article	IF	Citations
55	Autism and Cancer Share Risk Genes, Pathways, and Drug Targets. Trends in Genetics, 2016, 32, 139-146.	6.7	123
56	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
57	Epigenetic mechanisms in diurnal cycles of metabolism and neurodevelopment. Human Molecular Genetics, 2015, 24, R1-R9.	2.9	32
58	Epigenetic regulation of UBE3A and roles in human neurodevelopmental disorders. Epigenomics, 2015, 7, 1213-1228.	2.1	100
59	Early Developmental and Evolutionary Origins of Gene Body DNA Methylation Patterns in Mammalian Placentas. PLoS Genetics, 2015, 11, e1005442.	3.5	93
60	Epigenetic Mechanisms in Rett Syndrome. , 2015, , 199-216.		2
61	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
62	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
63	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
64	A survey of seizures and current treatments in 15q duplication syndrome. Epilepsia, 2014, 55, 396-402.	5.1	80
65	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
66	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
67	MeCP2 regulates activity-dependent transcriptional responses in olfactory sensory neurons. Human Molecular Genetics, 2014, 23, 6366-6374.	2.9	17
68	The Potential Brain Drain from Environmental Exposures on the Methylome and Genome Across Generations. , 2014, , 375-406.		0
69	Abstract 1513: Use of complex oligonucleotide libraries for concurrent high-resolution fluorescence imaging of both DNA and RNA in various sample types. , 2014, , .		0
70	MeCP2 modulates gene expression pathways in astrocytes. Molecular Autism, 2013, 4, 3.	4.9	74
71	Epigenomic strategies at the interface of genetic and environmental risk factors for autism. Journal of Human Genetics, 2013, 58, 396-401.	2.3	82
72	Epigenetic layers and players underlying neurodevelopment. Trends in Neurosciences, 2013, 36, 460-470.	8.6	77

#	Article	IF	Citations
73	How has the study of the human placenta aided our understanding of partially methylated genes?. Epigenomics, 2013, 5, 645-654.	2.1	25
74	A Praderâ€“Willi locus lncRNA cloud modulates diurnal genes and energy expenditure. Human Molecular Genetics, 2013, 22, 4318-4328.	2.9	129
75	MeCP2 and Autism Spectrum Disorders. , 2013, , 421-436.		0
76	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
77	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
78	The human placenta methylome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6037-6042.	7.1	256
79	Imprinting in the CNS and Neurodevelopmental Disorders. , 2013, , 267-279.		0
80	Epigenetics at the Interface of Genetics and Environmental Factors in Autism. Epigenetics and Human Health, 2013, , 97-114.	0.2	2
81	Autism genes keep turning up chromatin. OA Autism, 2013, 1, 14.	0.7	59
82	Recurrent CNVs in the Etiology of Epigenetic Neurodevelopmental Disorders. , 2013, , 147-178.		0
83	Role of DNMT3B in the regulation of early neural and neural crest specifiers. Epigenetics, 2012, 7, 71-82.	2.7	72
84	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
85	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
86	Epigenetic Epidemiology of Autism and Other Neurodevelopmental Disorders. , 2012, , 321-342.		2
87	Long-lived epigenetic interactions between perinatal PBDE exposure and Mecp2308 mutation. Human Molecular Genetics, 2012, 21, 2399-2411.	2.9	104
88	X chromosome gene methylation in peripheral lymphocytes from monozygotic twins discordant for scleroderma. Clinical and Experimental Immunology, 2012, 169, 253-262.	2.6	52
89	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
90	Neuronal chromatin dynamics of imprinting in development and disease. Journal of Cellular Biochemistry, 2011, 112, 365-373.	2.6	18

#	Article	IF	Citations
91	MeCP2 is required for global heterochromatic and nucleolar changes during activity-dependent neuronal maturation. Neurobiology of Disease, 2011, 43, 190-200.	4.4	66
92	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
93	A genomic point-of-view on environmental factors influencing the human brain methylome. Epigenetics, 2011, 6, 862-869.	2.7	79
94	Large-scale methylation domains mark a functional subset of neuronally expressed genes. Genome Research, 2011, 21, 1583-1591.	5.5	86
95	Investigation of modifier genes within copy number variations in Rett syndrome. Journal of Human Genetics, 2011, 56, 508-515.	2.3	25
96	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
97	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
98	The Role of MeCP2 in Brain Development and Neurodevelopmental Disorders. Current Psychiatry Reports, 2010, 12, 127-134.	4.5	161
99	The comorbidity of autism with the genomic disorders of chromosome 15q11.2-q13. Neurobiology of Disease, 2010, 38, 181-191.	4.4	241
100	Epigenetic Dysregulation of 15q11-13 GABAA Receptor Genes in Autism. , 2010, , 113-127.		1
101	Rett Syndrome Astrocytes Are Abnormal and Spread MeCP2 Deficiency through Gap Junctions. Journal of Neuroscience, 2009, 29, 5051-5061.	3.6	247
102	Reciprocal co-regulation of EGR2 and MECP2 is disrupted in Rett syndrome and autism. Human Molecular Genetics, 2009, 18, 525-534.	2.9	77
103	Evolving role of MeCP2 in Rett syndrome and autism. Epigenomics, 2009, 1, 119-130.	2.1	89
104	A novel hypomorphic MECP2 point mutation is associated with a neuropsychiatric phenotype. Human Genetics, 2009, 124, 615-623.	3.8	23
105	Imprinting regulates mammalian snoRNA-encoding chromatin decondensation and neuronal nucleolar size. Human Molecular Genetics, 2009, 18, 4227-4238.	2.9	67
106	Gender influences monoallelic expression of ATP10A in human brain. Human Genetics, 2008, 124, 235-242.	3.8	49
107	Multiple forms of atypical rearrangements generating supernumerary derivative chromosome 15. BMC Genetics, 2008, 9, 2.	2.7	34
108	MECP2 promoter methylation and X chromosome inactivation in autism. Autism Research, 2008, 1, 169-178.	3.8	107

#	Article	IF	Citations
109	Immunologic and neurodevelopmental susceptibilities of autism. NeuroToxicology, 2008, 29, 532-545.	3.0	46
110	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
111	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
112	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
113	The Odyssey of MeCP2 and Parental Imprinting. Epigenetics, 2007, 2, 5-10.	2.7	49
114	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
115	Expression profiling of clonal lymphocyte cell cultures from Rett syndrome patients. BMC Medical Genetics, 2006, 7, 61.	2.1	34
116	Dynamic Changes in Histone H3 Lysine 9 Acetylation Localization Patterns During Neuronal Maturation Require MeCP2. Epigenetics, 2006, 1, 25-32.	2.7	37
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, 2003-2014.	2.9	98
118	Reduced MeCP2 Expression is Frequent in Autism Frontal Cortex and Correlates with Aberrant MECP2 Promoter Methylation. Epigenetics, 2006, 1, 172-182.	2.7	306
119	Rett Syndrome: A Rosetta Stone for Understanding the Molecular Pathogenesis of Autism. International Review of Neurobiology, 2005, 71, 131-165.	2.0	19
120	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
121	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
122	Paradoxical Role of Methyl-CpG-Binding Protein 2 in Rett Syndrome. Current Topics in Developmental Biology, 2004, 59, 61-86.	2.2	14
123	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
124	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
125	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
126	Flow Cytometry and FISH to Investigate Allele-Specific Replication Timing and Homologous Association of Imprinted Chromosomes. , 2002, 181, 181-192.		2

#	Article	IF	Citations
127	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
128	Does HER2/neu expression provide prognostic information in patients with advanced urothelial carcinoma?. Cancer, 2002, 95, 1009-1015.	4.1	128
129	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
130	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
131	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
132	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
133	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
134	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
135	Homologous Association of Oppositely Imprinted Chromosomal Domains. Science, 1996, 272, 725-728.	12.6	242
136	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
137	T cell anergy. FASEB Journal, 1994, 8, 601-608.	0.5	63
138	Biological activity of recombinant human myelin basic protein. Journal of Neuroimmunology, 1993, 44, 157-162.	2.3	11
139	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
140	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