

Katie Lunnon

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

8,733
citations

93792

39
h-index

64407

83
g-index

109
all docs

109
docs citations

109
times ranked

14929
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenomic features related to microglia are associated with attenuated effect of <i>APOE</i> ϵ 4 on Alzheimer's disease risk in humans. <i>Alzheimer's and Dementia</i> , 2022, 18, 688-699.	0.4	9
2	Increased isoform-specific phosphodiesterase 4D expression is associated with pathology and cognitive impairment in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2021, 97, 56-64.	1.5	15
3	Telomere length and risk of idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease: a mendelian randomisation study. <i>Lancet Respiratory Medicine</i> , 2021, 9, 285-294.	5.2	94
4	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.	3.8	49
5	The histone modification H3K4me3 is altered at the <i>ANK1</i> locus in Alzheimer's disease brain. <i>Future Science OA</i> , 2021, 7, FSO665.	0.9	10
6	Mitochondrial D-Loop Region Methylation and Copy Number in Peripheral Blood DNA of Parkinson's Disease Patients. <i>Genes</i> , 2021, 12, 720.	1.0	14
7	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex. <i>Nature Communications</i> , 2021, 12, 3517.	5.8	72
8	Novel epigenetic clock for fetal brain development predicts prenatal age for cellular stem cell models and derived neurons. <i>Molecular Brain</i> , 2021, 14, 98.	1.3	19
9	Characterization of DNA Methylation Signatures in Induced Pluripotent Stem Cells During Neuronal Differentiation. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 647981.	1.8	7
10	Psychosis-associated DNA methylomic variation in Alzheimer's disease cortex. <i>Neurobiology of Aging</i> , 2020, 89, 83-88.	1.5	13
11	Applying gene editing technology to elucidate the functional consequence of genetic and epigenetic variation in Alzheimer's disease. <i>Brain Pathology</i> , 2020, 30, 992-1004.	2.1	8
12	The Molecular Etiology of Alzheimer's disease. <i>Brain Pathology</i> , 2020, 30, 964-965.	2.1	11
13	An epigenome-wide association study of Alzheimer's disease blood highlights robust DNA hypermethylation in the <i>HOXB6</i> gene. <i>Neurobiology of Aging</i> , 2020, 95, 26-45.	1.5	51
14	Invited Review "A 5-year update on epigenome-wide association studies of DNA modifications in Alzheimer's disease: progress, practicalities and promise. <i>Neuropathology and Applied Neurobiology</i> , 2020, 46, 641-653.	1.8	10
15	Genome-wide transcriptome analysis identifies novel dysregulated genes implicated in Alzheimer's pathology. <i>Alzheimer's and Dementia</i> , 2020, 16, 1213-1223.	0.4	23
16	Exploring Beyond the DNA Sequence: A Review of Epigenomic Studies of DNA and Histone Modifications in Dementia. <i>Current Genetic Medicine Reports</i> , 2020, 8, 79-92.	1.9	12
17	Altered DNA methylation profiles in blood from patients with sporadic Creutzfeldt-Jakob disease. <i>Acta Neuropathologica</i> , 2020, 140, 863-879.	3.9	18
18	Reduced mitochondrial D-loop methylation levels in sporadic amyotrophic lateral sclerosis. <i>Clinical Epigenetics</i> , 2020, 12, 137.	1.8	26

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19	DNA methylation differences associated with peripheral biomarkers in the EMIFâ€AD cohort. <i>Alzheimer's and Dementia</i> , 2020, 16, e045853.	0.4	0
20	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020, 143, 3763-3775.	3.7	100
21	Epigenomic features related to microglia are associated with attenuated effect of APOE Îµ4 on Alzheimerâ€™s disease risk in humans. <i>Alzheimer's and Dementia</i> , 2020, 16, e043533.	0.4	2
22	Epigenetic regulation in the pathophysiology of Lewy body dementia. <i>Progress in Neurobiology</i> , 2020, 192, 101822.	2.8	10
23	Transcriptional Signatures of Tau and Amyloid Neuropathology. <i>Cell Reports</i> , 2020, 30, 2040-2054.e5.	2.9	45
24	T40. Alzheimerâ€™s Disease DNA (Hydroxy)Methylome in the Brain and Blood: Evidence for OXT Methylation as a Preclinical Marker. <i>Biological Psychiatry</i> , 2019, 85, S144.	0.7	1
25	Alzheimerâ€™s Disease Associated Genes Ankyrin and Tau Cause Shortened Lifespan and Memory Loss in <i>Drosophila</i> . <i>Frontiers in Cellular Neuroscience</i> , 2019, 13, 260.	1.8	32
26	Epigenetic processes in Alzheimer's disease. , 2019, , 153-180.		5
27	Parallel profiling of DNA methylation and hydroxymethylation highlights neuropathology-associated epigenetic variation in Alzheimerâ€™s disease. <i>Clinical Epigenetics</i> , 2019, 11, 52.	1.8	84
28	Alzheimerâ€™s disease-associated (hydroxy)methylomic changes in the brain and blood. <i>Clinical Epigenetics</i> , 2019, 11, 164.	1.8	88
29	A cross-brain regions study of ANK1 DNA methylation in different neurodegenerative diseases. <i>Neurobiology of Aging</i> , 2019, 74, 70-76.	1.5	58
30	S67â€...Evidence that telomere length is causal for idiopathic pulmonary fibrosis but not chronic obstructive pulmonary disease: a UK biobank mendelian randomisation study. , 2019, , .		0
31	Peripheral DNA methylation, cognitive decline and brain aging: pilot findings from the Whitehall II imaging study. <i>Epigenomics</i> , 2018, 10, 585-595.	1.0	50
32	Elevated DNA methylation across a 48â€kb region spanning the <i>HOXA</i> gene cluster is associated with Alzheimer's disease neuropathology. <i>Alzheimer's and Dementia</i> , 2018, 14, 1580-1588.	0.4	138
33	Mendelian adult-onset leukodystrophy genes in Alzheimer's disease: critical influence of CSF1R and NOTCH3. <i>Neurobiology of Aging</i> , 2018, 66, 179.e17-179.e29.	1.5	32
34	Longitudinal analyses of the DNA methylome in deployed military servicemen identify susceptibility loci for post-traumatic stress disorder. <i>Molecular Psychiatry</i> , 2018, 23, 1145-1156.	4.1	98
35	A histone acetylome-wide association study of Alzheimerâ€™s disease identifies disease-associated H3K27ac differences in the entorhinal cortex. <i>Nature Neuroscience</i> , 2018, 21, 1618-1627.	7.1	138
36	Which Risk Factors Causally Influence Dementia? A Systematic Review of Mendelian Randomization Studies. <i>Journal of Alzheimer's Disease</i> , 2018, 64, 181-193.	1.2	46

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37	Neuroepigenetics of Aging and Age-Related Neurodegenerative Disorders. <i>Progress in Molecular Biology and Translational Science</i> , 2018, 158, 49-82.	0.9	27
38	Mitochondrial genes are altered in blood early in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2017, 53, 36-47.	1.5	132
39	Genetic architecture of epigenetic and neuronal ageing rates in human brain regions. <i>Nature Communications</i> , 2017, 8, 15353.	5.8	92
40	DNA Modifications and Alzheimer's Disease. <i>Advances in Experimental Medicine and Biology</i> , 2017, 978, 303-319.	0.8	14
41	Using induced pluripotent stem cells to explore genetic and epigenetic variation associated with Alzheimer's disease. <i>Epigenomics</i> , 2017, 9, 1455-1468.	1.0	13
42	Epigenetics and DNA methylomic profiling in Alzheimer's disease and other neurodegenerative diseases. <i>Journal of Neurochemistry</i> , 2017, 143, 158-170.	2.1	65
43	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. <i>Clinical Epigenetics</i> , 2017, 9, 47.	1.8	34
44	Epigenetic dysregulation of brainstem nuclei in the pathogenesis of Alzheimer's disease: looking in the correct place at the right time?. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 509-523.	2.4	14
45	ANK1 is up-regulated in laser captured microglia in Alzheimer's brain; the importance of addressing cellular heterogeneity. <i>PLoS ONE</i> , 2017, 12, e0177814.	1.1	34
46	Genetic variants near MLST8 and DHX57 affect the epigenetic age of the cerebellum. <i>Nature Communications</i> , 2016, 7, 10561.	5.8	69
47	ICP072: Gene Expression Of ABCA7 Dysregulated in Peripheral Blood is Associated With Decreased Metabolic Activity in Hippocampus. <i>Alzheimer's and Dementia</i> , 2016, 12, P56.	0.4	0
48	ICP074: Genome-Wide Meta-Analysis of Transcriptome Profiling Identifies Novel Dysregulated Genes Implicated in Alzheimer's Disease. <i>Alzheimer's and Dementia</i> , 2016, 12, P58.	0.4	0
49	P3087: Gene Expression of <i>ABCA7</i> Dysregulated in Peripheral Blood is Associated With Decreased Metabolic Activity in Hippocampus. <i>Alzheimer's and Dementia</i> , 2016, 12, P851.	0.4	0
50	O2-06-02: Genome-Wide Meta-Analysis of Transcriptome Profiling Identifies Novel Dysregulated Genes Implicated in Alzheimer's Disease. , 2016, 12, P238-P239.		0
51	O20605: Hydroxymethylomic Profiling Implicates Cortical Deregulation of <i>ANK1</i> and <i>APP</i> in the Alzheimer's Disease Brain. <i>Alzheimer's and Dementia</i> , 2016, 12, P240.	0.4	0
52	Increased DNA methylation near TREM2 is consistently seen in the superior temporal gyrus in Alzheimer's disease brain. <i>Neurobiology of Aging</i> , 2016, 47, 35-40.	1.5	79
53	Elucidating novel dysfunctional pathways in Alzheimer's disease by integrating loci identified in genetic and epigenetic studies. <i>Neuroepigenetics</i> , 2016, 6, 32-50.	2.8	17
54	ABCA7 p.G215S as potential protective factor for Alzheimer's disease. <i>Neurobiology of Aging</i> , 2016, 46, 235.e1-235.e9.	1.5	37

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55	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016, 17, 27.	3.8	83
56	Tissue-specific patterns of allelically-skewed DNA methylation. <i>Epigenetics</i> , 2016, 11, 24-35.	1.3	32
57	Genome-wide analysis of genetic correlation in dementia with Lewy bodies, Parkinson's and Alzheimer's diseases. <i>Neurobiology of Aging</i> , 2016, 38, 214.e7-214.e10.	1.5	78
58	Epigenetic regulation of mitochondrial function in neurodegenerative disease: New insights from advances in genomic technologies. <i>Neuroscience Letters</i> , 2016, 625, 47-55.	1.0	34
59	Influence of Coding Variability in APP- β Metabolism Genes in Sporadic Alzheimer's Disease. <i>PLoS ONE</i> , 2016, 11, e0150079.	1.1	34
60	No Evidence to Suggest that the Use of Acetylcholinesterase Inhibitors Confounds the Results of Two Blood-Based Biomarker Studies in Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2015, 47, 741-750.	1.2	2
61	A comparison of mitochondrial DNA isolation methods in frozen post-mortem human brain tissue—applications for studies of mitochondrial genetics in brain disorders. <i>BioTechniques</i> , 2015, 59, 241-246.	0.8	17
62	A Pathway Based Classification Method for Analyzing Gene Expression for Alzheimer's Disease Diagnosis. <i>Journal of Alzheimer's Disease</i> , 2015, 49, 659-669.	1.2	43
63	O3-05-01: Systems-level evidence for epigenetic dysfunction in Alzheimer's disease. , 2015, 11, P228-P228.		0
64	Blood methylomic signatures of presymptomatic dementia in elderly subjects with type 2 diabetes mellitus. <i>Neurobiology of Aging</i> , 2015, 36, 1600.e1-1600.e4.	1.5	21
65	Interindividual methylomic variation across blood, cortex, and cerebellum: implications for epigenetic studies of neurological and neuropsychiatric phenotypes. <i>Epigenetics</i> , 2015, 10, 1024-1032.	1.3	393
66	A novel multi-tissue RNA diagnostic of healthy ageing relates to cognitive health status. <i>Genome Biology</i> , 2015, 16, 185.	3.8	189
67	Clusterin regulates β -amyloid toxicity via Dickkopf-1-driven induction of the wnt/PCP/JNK pathway. <i>Molecular Psychiatry</i> , 2014, 19, 88-98.	4.1	197
68	The mitochondrial epigenome: a role in Alzheimer's disease?. <i>Epigenomics</i> , 2014, 6, 665-675.	1.0	36
69	TEMPORARY REMOVAL: Blood methylomic signatures of presymptomatic dementia in elderly subjects with type 2 diabetes mellitus. <i>Neurobiology of Aging</i> , 2014, , .	1.5	1
70	Exome sequencing identifies 2 novel presenilin 1 mutations (p.L166V and p.S230R) in British early-onset Alzheimer's disease. <i>Neurobiology of Aging</i> , 2014, 35, 2422.e13-2422.e16.	1.5	28
71	Epigenetic regulation of adult neural stem cells: implications for Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2014, 9, 25.	4.4	55
72	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014, 17, 1156-1163.	7.1	800

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73	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014, 17, 1164-1170.	7.1	488
74	Plasma proteins predict conversion to dementia from prodromal disease. <i>Alzheimer's and Dementia</i> , 2014, 10, 799.	0.4	180
75	Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. <i>Neurobiology of Aging</i> , 2014, 35, 1850-1854.	1.5	114
76	Alzheimer's disease susceptibility variants in the MS4A6A gene are associated with altered levels of MS4A6A expression in blood. <i>Neurobiology of Aging</i> , 2014, 35, 279-290.	1.5	56
77	O3-04-03: CROSS-TISSUE METHYLOMIC PROFILING IN ALZHEIMER'S DISEASE. , 2014, 10, P215-P215.		0
78	A data-driven approach to preprocessing Illumina 450K methylation array data. <i>BMC Genomics</i> , 2013, 14, 293.	1.2	850
79	Epigenetic studies in Alzheimer's disease: Current findings, caveats, and considerations for future studies. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 789-799.	1.1	68
80	A Blood Gene Expression Marker of Early Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2013, 33, 737-753.	1.2	91
81	Inflammatory Proteins in Plasma Are Associated with Severity of Alzheimer's Disease. <i>PLoS ONE</i> , 2013, 8, e64971.	1.1	122
82	Mitochondrial Dysfunction and Immune Activation are Detectable in Early Alzheimer's Disease Blood. <i>Journal of Alzheimer's Disease</i> , 2012, 30, 685-710.	1.2	141
83	Functional annotation of the human brain methylome identifies tissue-specific epigenetic variation across brain and blood. <i>Genome Biology</i> , 2012, 13, R43.	13.9	585
84	Plasma Based Markers of [11C] PiB-PET Brain Amyloid Burden. <i>PLoS ONE</i> , 2012, 7, e44260.	1.1	89
85	Identification of cis-regulatory variation influencing protein abundance levels in human plasma. <i>Human Molecular Genetics</i> , 2012, 21, 3719-3726.	1.4	94
86	Systemic Inflammation Modulates Fc Receptor Expression on Microglia during Chronic Neurodegeneration. <i>Journal of Immunology</i> , 2011, 186, 7215-7224.	0.4	109
87	Genome-wide association with MRI atrophy measures as a quantitative trait locus for Alzheimer's disease. <i>Molecular Psychiatry</i> , 2011, 16, 1130-1138.	4.1	133
88	Association of Plasma Clusterin Concentration With Severity, Pathology, and Progression in Alzheimer Disease. <i>Archives of General Psychiatry</i> , 2010, 67, 739.	13.8	353
89	Alpha-synuclein deficiency in the C57BL/6J.OlaHsd strain does not modify disease progression in the ME7-model of prion disease. <i>Neuroscience</i> , 2010, 165, 662-674.	1.1	18
90	Systemic Inflammation Induces Acute Behavioral and Cognitive Changes and Accelerates Neurodegenerative Disease. <i>Biological Psychiatry</i> , 2009, 65, 304-312.	0.7	475

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91	Central and Systemic Endotoxin Challenges Exacerbate the Local Inflammatory Response and Increase Neuronal Death during Chronic Neurodegeneration. <i>Journal of Neuroscience</i> , 2005, 25, 9275-9284.	1.7	659