

# Leonard Cornelis Schalkwyk

## List of Publications by Year in descending order

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Version: 2024-02-01

159  
papers

15,383  
citations

19657

61  
h-index

20358

116  
g-index

181  
all docs

181  
docs citations

181  
times ranked

20157  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004, 36, 1133-1137.	21.4	1,034
2	A data-driven approach to preprocessing Illumina 450K methylation array data. <i>BMC Genomics</i> , 2013, 14, 293.	2.8	850
3	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014, 17, 1156-1163.	14.8	800
4	Functional annotation of the human brain methylome identifies tissue-specific epigenetic variation across brain and blood. <i>Genome Biology</i> , 2012, 13, R43.	9.6	585
5	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	8.8	552
6	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014, 17, 1164-1170.	14.8	488
7	Disease-associated epigenetic changes in monozygotic twins discordant for schizophrenia and bipolar disorder. <i>Human Molecular Genetics</i> , 2011, 20, 4786-4796.	2.9	407
8	Interindividual methylomic variation across blood, cortex, and cerebellum: implications for epigenetic studies of neurological and neuropsychiatric phenotypes. <i>Epigenetics</i> , 2015, 10, 1024-1032.	2.7	393
9	The nature and identification of quantitative trait loci: a community's view. <i>Nature Reviews Genetics</i> , 2003, 4, 911-916.	16.3	390
10	Moderation of breastfeeding effects on the IQ by genetic variation in fatty acid metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18860-18865.	7.1	324
11	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. <i>Nature Neuroscience</i> , 2016, 19, 48-54.	14.8	306
12	Genetic analysis of the mouse brain proteome. <i>Nature Genetics</i> , 2002, 30, 385-393.	21.4	293
13	Transformation methods for halophilic archaeobacteria. <i>Canadian Journal of Microbiology</i> , 1989, 35, 148-152.	1.7	290
14	An integrated genetic-epigenetic analysis of schizophrenia: evidence for co-localization of genetic associations and differential DNA methylation. <i>Genome Biology</i> , 2016, 17, 176.	8.8	287
15	Methylomic analysis of monozygotic twins discordant for autism spectrum disorder and related behavioural traits. <i>Molecular Psychiatry</i> , 2014, 19, 495-503.	7.9	280
16	High resolution cosmid and P1 maps spanning the 14 Mb genome of the fission yeast <i>S. pombe</i> . <i>Cell</i> , 1993, 73, 109-120.	28.9	271
17	Methylomic trajectories across human fetal brain development. <i>Genome Research</i> , 2015, 25, 338-352.	5.5	250
18	Allelic Skewing of DNA Methylation Is Widespread across the Genome. <i>American Journal of Human Genetics</i> , 2010, 86, 196-212.	6.2	228

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19	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
20	Longitudinal changes of telomere length and epigenetic age related to traumatic stress and post-traumatic stress disorder. <i>Psychoneuroendocrinology</i> , 2015, 51, 506-512.	2.7	186
21	Towards high resolution maps of the mouse and human genomes—a facility for ordering markers to 0.1 cM resolution. <i>Human Molecular Genetics</i> , 1994, 3, 621-627.	2.9	185
22	Genome-wide DNA methylation levels and altered cortisol stress reactivity following childhood trauma in humans. <i>Nature Communications</i> , 2016, 7, 10967.	12.8	175
23	Loss of adenylyl cyclase I activity disrupts patterning of mouse somatosensory cortex. <i>Nature Genetics</i> , 1998, 19, 289-291.	21.4	156
24	Assessing Reliability, Heritability and General Cognitive Ability in a Battery of Cognitive Tasks for Laboratory Mice. <i>Behavior Genetics</i> , 2005, 35, 675-692.	2.1	146
25	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. <i>Genome Biology</i> , 2014, 15, 483.	8.8	141
26	Elevated DNA methylation across a 48 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.	0.8	138
27	A histone acetylome-wide association study of Alzheimer's disease identifies disease-associated H3K27ac differences in the entorhinal cortex. <i>Nature Neuroscience</i> , 2018, 21, 1618-1627.	14.8	138
28	Differential methylation of the TRPA1 promoter in pain sensitivity. <i>Nature Communications</i> , 2014, 5, 2978.	12.8	132
29	Mitochondrial genes are altered in blood early in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2017, 53, 36-47.	3.1	132
30	Allele-specific methylation in the human genome. <i>Epigenetics</i> , 2010, 5, 578-582.	2.7	129
31	Expression quantitative trait loci in the developing human brain and their enrichment in neuropsychiatric disorders. <i>Genome Biology</i> , 2018, 19, 194.	8.8	126
32	Leveraging DNA-Methylation Quantitative-Trait Loci to Characterize the Relationship between Methylomic Variation, Gene Expression, and Complex Traits. <i>American Journal of Human Genetics</i> , 2018, 103, 654-665.	6.2	126
33	Maternal separation is associated with strain-specific responses to stress and epigenetic alterations to <i>Nr3c1</i> , <i>Avp</i> , and <i>Nr4a1</i> in mouse. <i>Brain and Behavior</i> , 2012, 2, 455-467.	2.2	123
34	Genetics of behavioural domains across the neuropsychiatric spectrum; of mice and men. <i>Molecular Psychiatry</i> , 2007, 12, 324-330.	7.9	117
35	Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. <i>Neurobiology of Aging</i> , 2014, 35, 1850-1854.	3.1	114
36	Quantitative trait locus association scan of early reading disability and ability using pooled DNA and 100K SNP microarrays in a sample of 5760 children. <i>Molecular Psychiatry</i> , 2008, 13, 729-740.	7.9	101

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37	A genome-wide association study identifies multiple loci associated with mathematics ability and disability. <i>Genes, Brain and Behavior</i> , 2010, 9, 234-247.	2.2	100
38	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. <i>Brain</i> , 2020, 143, 3763-3775.	7.6	100
39	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. <i>Genome Biology</i> , 2019, 20, 283.	8.8	97
40	Advanced paternal age effects in neurodevelopmental disorders—review of potential underlying mechanisms. <i>Translational Psychiatry</i> , 2017, 7, e1019-e1019.	4.8	94
41	Performance deficit of $\hat{1}\pm 7$ nicotinic receptor knockout mice in a delayed matching-to-place task suggests a mild impairment of working/episodic-like memory. <i>Genes, Brain and Behavior</i> , 2006, 5, 433-440.	2.2	92
42	Genotyping pooled DNA using 100K SNP microarrays: a step towards genomewide association scans. <i>Nucleic Acids Research</i> , 2006, 34, e27-e27.	14.5	92
43	Behavioural battery testing: Evaluation and behavioural outcomes in 8 inbred mouse strains. <i>Physiology and Behavior</i> , 2010, 99, 301-316.	2.1	92
44	SNPs, microarrays and pooled DNA: identification of four loci associated with mild mental impairment in a sample of 6000 children. <i>Human Molecular Genetics</i> , 2005, 14, 1315-1325.	2.9	91
45	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	12.8	91
46	Detailed physical map and set of overlapping clones covering the genome of the archaeobacterium <i>Haloferax volcanii</i> DS2. <i>Journal of Molecular Biology</i> , 1991, 222, 509-524.	4.2	90
47	Genotyping Pooled DNA on Microarrays: A Systematic Genome Screen of Thousands of SNPs in Large Samples to Detect QTLs for Complex Traits. <i>Behavior Genetics</i> , 2004, 34, 549-555.	2.1	89
48	The mouse homeobox gene <i>Not</i> is required for caudal notochord development and affected by the truncate mutation. <i>Genes and Development</i> , 2004, 18, 1725-1736.	5.9	84
49	Genetics of the hippocampal transcriptome in mouse: a systematic survey and online neurogenomics resource. <i>Frontiers in Neuroscience</i> , 2009, 3, 55.	2.8	84
50	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. <i>Genome Biology</i> , 2016, 17, 27.	8.8	83
51	Depression-Related Behavioral Tests. <i>Current Protocols in Mouse Biology</i> , 2012, 2, 119-127.	1.2	82
52	Increased DNA methylation near <i>TREM2</i> is consistently seen in the superior temporal gyrus in Alzheimer's disease brain. <i>Neurobiology of Aging</i> , 2016, 47, 35-40.	3.1	79
53	Full-length transcript sequencing of human and mouse cerebral cortex identifies widespread isoform diversity and alternative splicing. <i>Cell Reports</i> , 2021, 37, 110022.	6.4	79
54	Hippocampal gene expression profiling across eight mouse inbred strains: towards understanding the molecular basis for behaviour. <i>European Journal of Neuroscience</i> , 2004, 19, 2576-2582.	2.6	77

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55	Advancing Paternal Age Is Associated with Deficits in Social and Exploratory Behaviors in the Offspring: A Mouse Model. <i>PLoS ONE</i> , 2009, 4, e8456.	2.5	77
56	Molecular and biochemical characterisation of DNA-dependent protein kinase-defective rodent mutant <i>irs-20</i> . <i>Nucleic Acids Research</i> , 1998, 26, 1965-1973.	14.5	74
57	A Three-Stage Genome-Wide Association Study of General Cognitive Ability: Hunting the Small Effects. <i>Behavior Genetics</i> , 2010, 40, 759-767.	2.1	74
58	Schizophrenia-associated methylomic variation: molecular signatures of disease and polygenic risk burden across multiple brain regions. <i>Human Molecular Genetics</i> , 2017, 26, ddw373.	2.9	74
59	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. <i>Nature Communications</i> , 2014, 5, 4204.	12.8	72
60	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.	12.8	72
61	DNA methylation in interleukin-11 predicts clinical response to antidepressants in GENDEP. <i>Translational Psychiatry</i> , 2013, 3, e300-e300.	4.8	71
62	Genome-wide DNA methylation profiling identifies convergent molecular signatures associated with idiopathic and syndromic autism in post-mortem human brain tissue. <i>Human Molecular Genetics</i> , 2019, 28, 2201-2211.	2.9	70
63	Tumor necrosis factor and its targets in the inflammatory cytokine pathway are identified as putative transcriptomic biomarkers for escitalopram response. <i>European Neuropsychopharmacology</i> , 2013, 23, 1105-1114.	0.7	68
64	<i>Tetraodon fluviatilis</i> , a New Puffer Fish Model for Genome Studies. <i>Genomics</i> , 1997, 41, 177-184.	2.9	66
65	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. <i>BMC Genomics</i> , 2017, 18, 738.	2.8	63
66	The differential transcriptome and ontology profiles of floating and cumulus granulosa cells in stimulated human antral follicles. <i>Molecular Human Reproduction</i> , 2010, 16, 229-240.	2.8	61
67	Genotyping DNA pools on microarrays: Tackling the QTL problem of large samples and large numbers of SNPs. <i>BMC Genomics</i> , 2005, 6, 52.	2.8	60
68	The role of nicotinic receptor $\alpha 7$ subunits in nicotine discrimination. <i>Neuropharmacology</i> , 2004, 46, 363-371.	4.1	56
69	Integrative mouse and human mRNA studies using WGCNA nominates novel candidate genes involved in the pathogenesis of major depressive disorder. <i>Pharmacogenomics</i> , 2013, 14, 1979-1990.	1.3	55
70	Reduced Anxiety and Depression-Like Behaviours in the Circadian Period Mutant Mouse <i>Afterhours</i> . <i>PLoS ONE</i> , 2012, 7, e38263.	2.5	54
71	A 5Å genome coverage bovine BAC library: production, characterization, and distribution. <i>Mammalian Genome</i> , 1999, 10, 706-709.	2.2	53
72	Stochastic Choice of Allelic Expression in Human Neural Stem Cells. <i>Stem Cells</i> , 2012, 30, 1938-1947.	3.2	53

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73	Epigenomic and transcriptomic signatures of a Klinefelter syndrome (47,XXY) karyotype in the brain. <i>Epigenetics</i> , 2014, 9, 587-599.	2.7	53
74	The endogenous and reactive depression subtypes revisited: integrative animal and human studies implicate multiple distinct molecular mechanisms underlying major depressive disorder. <i>BMC Medicine</i> , 2014, 12, 73.	5.5	52
75	Microarrays. <i>Developmental Science</i> , 2007, 10, 19-23.	2.4	51
76	Wfs1 gene deletion causes growth retardation in mice and interferes with the growth hormone pathway. <i>Physiological Genomics</i> , 2009, 37, 249-259.	2.3	49
77	A Genome-Wide Association Study of Social and Non-Social Autistic-Like Traits in the General Population Using Pooled DNA, 500K SNP Microarrays and Both Community and Diagnosed Autism Replication Samples. <i>Behavior Genetics</i> , 2010, 40, 31-45.	2.1	49
78	BigMELON: tools for analysing large DNA methylation datasets. <i>Bioinformatics</i> , 2019, 35, 981-986.	4.1	49
79	Genome mapping in halobacteria. <i>Canadian Journal of Microbiology</i> , 1989, 35, 21-29.	1.7	48
80	Association analysis of mild mental impairment using DNA pooling to screen 432 brain-expressed single-nucleotide polymorphisms. <i>Molecular Psychiatry</i> , 2005, 10, 384-392.	7.9	46
81	TCF4 (ITF2): A schizophrenia-associated gene with pleiotropic effects on human disease. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 1-16.	1.7	46
82	Interpretation of knockout experiments: the congenic footprint. <i>Genes, Brain and Behavior</i> , 2007, 6, 299-303.	2.2	45
83	Applicability of DNA pools on 500 K SNP microarrays for cost-effective initial screens in genomewide association studies. <i>BMC Genomics</i> , 2007, 8, 214.	2.8	43
84	Identification of genes and gene pathways associated with major depressive disorder by integrative brain analysis of rat and human prefrontal cortex transcriptomes. <i>Translational Psychiatry</i> , 2015, 5, e519-e519.	4.8	43
85	ISH51: a large, degenerate family of insertion sequence-like elements in the genome of the archaeobacterium, <i>Halobacterium volcanii</i> . <i>Nucleic Acids Research</i> , 1986, 14, 6983-7000.	14.5	42
86	Construction and Characterization of a 10-Genome Equivalent Yeast Artificial Chromosome Library for the Laboratory Rat, <i>Rattus norvegicus</i> . <i>Genomics</i> , 1997, 39, 385-392.	2.9	42
87	ViPAR: a software platform for the Virtual Pooling and Analysis of Research Data. <i>International Journal of Epidemiology</i> , 2016, 45, 408-416.	1.9	42
88	A central resource for accurate allele frequency estimation from pooled DNA genotyped on DNA microarrays. <i>Nucleic Acids Research</i> , 2005, 33, e25-e25.	14.5	39
89	Putative Transcriptomic Biomarkers in the Inflammatory Cytokine Pathway Differentiate Major Depressive Disorder Patients from Control Subjects and Bipolar Disorder Patients. <i>PLoS ONE</i> , 2014, 9, e91076.	2.5	39
90	Using hippocampal microRNA expression differences between mouse inbred strains to characterise miRNA function. <i>Mammalian Genome</i> , 2008, 19, 552-60.	2.2	38

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91	Peripheral blood RNA gene expression profiling in patients with bacterial meningitis. <i>Frontiers in Neuroscience</i> , 2013, 7, 33.	2.8	38
92	Efficient high-resolution genetic mapping of mouse interspersed repetitive sequence PCR products, toward integrated genetic and physical mapping of the mouse genome.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 5302-5306.	7.1	36
93	Application of microarrays to the analysis of the inactivation status of human X-linked genes expressed in lymphocytes. <i>European Journal of Human Genetics</i> , 2004, 12, 639-646.	2.8	35
94	Transcriptome analysis of genes and gene networks involved in aggressive behavior in mouse and zebrafish. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 827-838.	1.7	35
95	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. <i>Clinical Epigenetics</i> , 2017, 9, 47.	4.1	34
96	Characterising sex differences of autosomal DNA methylation in whole blood using the Illumina EPIC array. <i>Clinical Epigenetics</i> , 2022, 14, 62.	4.1	34
97	Tissue-specific patterns of allelically-skewed DNA methylation. <i>Epigenetics</i> , 2016, 11, 24-35.	2.7	32
98	Advanced paternal age is associated with altered DNA methylation at brain-expressed imprinted loci in inbred mice: implications for neuropsychiatric disease. <i>Molecular Psychiatry</i> , 2013, 18, 635-636.	7.9	31
99	The inflammatory cytokines: molecular biomarkers for major depressive disorder?. <i>Biomarkers in Medicine</i> , 2015, 9, 169-180.	1.4	31
100	Panel of Microsatellite Markers for Whole-Genome Scans and Radiation Hybrid Mapping and a Mouse Family Tree. <i>Genome Research</i> , 1999, 9, 878-887.	5.5	30
101	Convergent Animal and Human Evidence Suggests a Role of PPM1A Gene in Response to Antidepressants. <i>Biological Psychiatry</i> , 2011, 69, 360-365.	1.3	30
102	Genes and Gene Networks Implicated in Aggression Related Behaviour. <i>Neurogenetics</i> , 2014, 15, 255-266.	1.4	30
103	Pervasive and opposing effects of Unpredictable Chronic Mild Stress (UCMS) on hippocampal gene expression in BALB/cj and C57BL/6j mouse strains. <i>BMC Genomics</i> , 2015, 16, 262.	2.8	30
104	Gene expression profiling reveals upregulation of Tlr4 receptors in Cckb receptor deficient mice. <i>Behavioural Brain Research</i> , 2008, 188, 62-70.	2.2	29
105	Genetic and environmental (inter)actions in male mouse lines selected for aggressive and nonaggressive behavior. <i>Genes, Brain and Behavior</i> , 2004, 3, 101-109.	2.2	28
106	Antidepressants and the resilience to early-life stress in inbred mouse strains. <i>Pharmacogenetics and Genomics</i> , 2011, 21, 779-789.	1.5	28
107	Antidepressant-dependent mRNA changes in mouse associated with hippocampal neurogenesis in a mouse model of depression. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 765-776.	1.5	28
108	Quantitative traits for the tail suspension test: automation, optimization, and BXD RI mapping. <i>Mammalian Genome</i> , 2007, 18, 482-491.	2.2	27

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109	The SNPMap package for R: a framework for genome-wide association using DNA pooling on microarrays. <i>Bioinformatics</i> , 2009, 25, 281-283.	4.1	27
110	A bovine YAC library containing four- to five-fold genome equivalents. <i>Mammalian Genome</i> , 1999, 10, 837-838.	2.2	25
111	Behavioral Characterization of Wild Derived Male Mice ( <i>Mus musculus musculus</i> ) of the PWD/Ph Inbred Strain: High Exploration Compared to C57BL/6J. <i>Behavior Genetics</i> , 2004, 34, 621-630.	2.1	25
112	A B2 SINE insertion in the <i>Comt1</i> gene ( <i>Comt1<sup>B2</sup></i> ) results in an overexpressing, behavior modifying allele present in classical inbred mouse strains. <i>Genes, Brain and Behavior</i> , 2010, 9, 925-932.	2.2	24
113	Interspecies comparisons of functional genetic variations and their implications in neuropsychiatry. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2009, 150B, 309-317.	1.7	22
114	Effects of advanced paternal age on trajectories of social behavior in offspring. <i>Genes, Brain and Behavior</i> , 2015, 14, 443-453.	2.2	22
115	Silencing of the <i>WFS1</i> gene in HEK cells induces pathways related to neurodegeneration and mitochondrial damage. <i>Physiological Genomics</i> , 2013, 45, 182-190.	2.3	21
116	Genetic variation in hippocampal microRNA expression differences in C57BL/6 J X DBA/2 J (BXD) recombinant inbred mouse strains. <i>BMC Genomics</i> , 2012, 13, 476.	2.8	20
117	ATP-binding cassette sub-family F member 1 (ABCF1) is identified as a putative therapeutic target of escitalopram in the inflammatory cytokine pathway. <i>Journal of Psychopharmacology</i> , 2013, 27, 609-615.	4.0	20
118	Paternal Age Alters Social Development in Offspring. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2017, 56, 383-390.	0.5	20
119	Techniques in mammalian genome mapping. <i>Current Opinion in Biotechnology</i> , 1995, 6, 37-43.	6.6	19
120	Toward the construction of integrated physical and genetic maps of the mouse genome using interspersed repetitive sequence PCR (IRS-PCR) genomics.. <i>Genome Research</i> , 1996, 6, 290-299.	5.5	18
121	Construction and characterisation of a gridded chicken cosmid library with four-fold genomic coverage. <i>Animal Genetics</i> , 1998, 29, 295-301.	1.7	18
122	Pharmacoproteomic investigation into antidepressant response in two mouse inbred strains. <i>Proteomics</i> , 2012, 12, 2355-2365.	2.2	18
123	A yeast artificial chromosome (YAC) library containing 10 haploid chicken genome equivalents. <i>Mammalian Genome</i> , 1997, 8, 274-276.	2.2	16
124	High-Throughput Scanning of the Rat Genome Using Interspersed Repetitive Sequence-PCR Markers. <i>Genomics</i> , 2000, 69, 287-294.	2.9	16
125	IRS-PCR-based genetic mapping of the huntingtin interacting protein gene (HIP1) on mouse Chromosome 5. <i>Mammalian Genome</i> , 1998, 9, 26-31.	2.2	15
126	To what extent is blood a reasonable surrogate for brain in gene expression studies: estimation from mouse hippocampus and spleen. <i>Frontiers in Neuroscience</i> , 2009, 3, 54.	2.8	15



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127	DNA methylation at the Igf2/H19 imprinting control region is associated with cerebellum mass in outbred mice. <i>Molecular Brain</i> , 2012, 5, 42.	2.6	15
128	Home-cage activity in heterogeneous stock (HS) mice as a model of baseline activity. <i>Genes, Brain and Behavior</i> , 2002, 1, 166-173.	2.2	14
129	Mood stabilizers differentially affect housekeeping gene expression in human cells. <i>International Journal of Methods in Psychiatric Research</i> , 2014, 23, 279-288.	2.1	14
130	RNA sequencing of identical twins discordant for autism reveals blood-based signatures implicating immune and transcriptional dysregulation. <i>Molecular Autism</i> , 2019, 10, 38.	4.9	14
131	The DNA methylome of human sperm is distinct from blood with little evidence for tissue-consistent obesity associations. <i>PLoS Genetics</i> , 2020, 16, e1009035.	3.5	13
132	Transcriptomic changes in the frontal cortex associated with paternal age. <i>Molecular Autism</i> , 2014, 5, 24.	4.9	11
133	ETn insertion in the mouse <i>Adcy1</i> gene: transcriptional and phylogenetic analyses. <i>Mammalian Genome</i> , 2000, 11, 97-103.	2.2	10
134	Highly polygenic architecture of antidepressant treatment response: Comparative analysis of SSRI and NRI treatment in an animal model of depression. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 235-250.	1.7	10
135	Gene set enrichment; a problem of pathways. <i>Briefings in Functional Genomics</i> , 2010, 9, 385-390.	2.7	9
136	Comparative mRNA analysis of behavioral and genetic mouse models of aggression. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 427-436.	1.7	9
137	DNA methylation-based sex classifier to predict sex and identify sex chromosome aneuploidy. <i>BMC Genomics</i> , 2021, 22, 484.	2.8	9
138	Chapter 15 Halobacterial genes and genomes. <i>New Comprehensive Biochemistry</i> , 1993, , 467-496.	0.1	8
139	Technology development at the interface of proteome research and genomics: Mapping nonpolymorphic proteins on the physical map of mouse chromosomes. <i>Electrophoresis</i> , 1999, 20, 1027-1032.	2.4	8
140	Effect of Chronic Valproic Acid Treatment on Hepatic Gene Expression Profile in <i>Wfs1</i> Knockout Mouse. <i>PPAR Research</i> , 2014, 2014, 1-11.	2.4	8
141	Advanced Integrated Mouse YAC Map Including BAC Framework. <i>Genome Research</i> , 2001, 11, 2142-2150.	5.5	7
142	Hypothalamic gene expression profile indicates a reduction in G protein signaling in the <i>Wfs1</i> mutant mice. <i>Physiological Genomics</i> , 2011, 43, 1351-1358.	2.3	7
143	Refined radiation hybrid map of mouse Chromosome 17. <i>Mammalian Genome</i> , 1998, 9, 807-811.	2.2	6
144	Long-Term Effects of Gestational Nicotine Exposure and Food-Restriction on Gene Expression in the Striatum of Adolescent Rats. <i>PLoS ONE</i> , 2014, 9, e88896.	2.5	5

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145	InterpolatedXY: a two-step strategy to normalize DNA methylation microarray data avoiding sex bias. <i>Bioinformatics</i> , 2022, 38, 3950-3957.	4.1	5
146	Insertion sequences on plasmid pHV1 of <i>Haloferax volcanii</i> . <i>Canadian Journal of Microbiology</i> , 1993, 39, 201-206.	1.7	4
147	Complex probes for high-throughput parallel genetic mapping of genomic mouse BAC clones. <i>Mammalian Genome</i> , 1998, 9, 611-616.	2.2	4
148	Assessing Individual Differences in Genome-Wide Gene Expression in Human Whole Blood: Reliability Over Four Hours and Stability Over 10 Months. <i>Twin Research and Human Genetics</i> , 2009, 12, 372-380.	0.6	4
149	Utility of the pooling approach as applied to whole genome association scans with high-density Affymetrix microarrays. <i>BMC Research Notes</i> , 2010, 3, 274.	1.4	3
150	Peripheral blood RNA expression profiling in illicit methcathinone users reveals effect on immune system. <i>Frontiers in Genetics</i> , 2011, 2, 42.	2.3	3
151	Genetic polymorphisms and their association with brain and behavioural measures in heterogeneous stock mice. <i>Scientific Reports</i> , 2017, 7, 41204.	3.3	2
152	New tools for the high throughput characterization of rat genomic DNA samples. <i>Journal of Experimental Animal Science</i> , 2000, 41, 35-37.	0.5	1
153	Introduction to mammalian genome special issue: genetics of behavior. <i>Mammalian Genome</i> , 2014, 25, 1-2.	2.2	1
154	Introduction to the Special Issue: Aggression Across Species. <i>Behavior Genetics</i> , 2003, 33, 457-460.	2.1	0
155	S.16.02 Depression: the GENDEP study. <i>European Neuropsychopharmacology</i> , 2006, 16, S187.	0.7	0
156	P.1.31 Gene expression analyses of mouse fibroblast cell line L929 after antidepressant treatment. <i>European Neuropsychopharmacology</i> , 2007, 17, S27-S28.	0.7	0
157	Response to comment by Stuart Macgregor. <i>Behavior Genetics</i> , 2010, 40, 48-48.	2.1	0
158	O3-04-03: CROSS-TISSUE METHYLOMIC PROFILING IN ALZHEIMER'S DISEASE. , 2014, 10, P215-P215.		0
159	Technology development at the interface of proteome research and genomics: Mapping nonpolymorphic proteins on the physical map of mouse chromosomes. <i>Electrophoresis</i> , 1999, 20, 1027-1032.	2.4	0