Leonard Cornelis Schalkwyk

List of Publications by Year
in descending order

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	Characterising sex differences of autosomal DNA methylation in whole blood using the Illumina EPIC array. Clinical Epigenetics, 2022, 14, 62.	4.1	34
2	InterpolatedXY: a two-step strategy to normalize DNA methylation microarray data avoiding sex bias. Bioinformatics, 2022, 38, 3950-3957.	4.1	5
3	A meta-analysis of epigenome-wide association studies in Alzheimerâ€™s disease highlights novel differentially methylated loci across cortex. Nature Communications, 2021, 12, 3517.	12.8	72
4	DNA methylation-based sex classifier to predict sex and identify sex chromosome aneuploidy. BMC Genomics, 2021, 22, 484.	2.8	9
5	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
6	Full-length transcript sequencing of human and mouse cerebral cortex identifies widespread isoform diversity and alternative splicing. Cell Reports, 2021, 37, 110022.	6.4	79
7	The DNA methylome of human sperm is distinct from blood with little evidence for tissue-consistent obesity associations. PLoS Genetics, 2020, 16, e1009035.	3.5	13
8	Recalibrating the epigenetic clock: implications for assessing biological age in the human cortex. Brain, 2020, 143, 3763-3775.	7.6	100
9	Genome-wide DNA methylation profiling identifies convergent molecular signatures associated with idiopathic and syndromic autism in post-mortem human brain tissue. Human Molecular Genetics, 2019, 28, 2201-2211.	2.9	70
10	Systematic underestimation of the epigenetic clock and age acceleration in older subjects. Genome Biology, 2019, 20, 283.	8.8	97
11	RNA sequencing of identical twins discordant for autism reveals blood-based signatures implicating immune and transcriptional dysregulation. Molecular Autism, 2019, 10, 38.	4.9	14
12	DNA methylation aging clocks: challenges and recommendations. Genome Biology, 2019, 20, 249.	8.8	552
13	Bigmelon: tools for analysing large DNA methylation datasets. Bioinformatics, 2019, 35, 981-986.	4.1	49
14	Elevated DNA methylation across a 48â€kb region spanning the HOXA gene cluster is associated with Alzheimer's disease neuropathology. Alzheimer's and Dementia, 2018, 14, 1580-1588.	0.8	138
15	Expression quantitative trait loci in the developing human brain and their enrichment in neuropsychiatric disorders. Genome Biology, 2018, 19, 194.	8.8	126
16	Leveraging DNA-Methylation Quantitative-Trait Loci to Characterize the Relationship between Methylomic Variation, Gene Expression, and Complex Traits. American Journal of Human Genetics, 2018, 103, 654-665.	6.2	126
17	A histone acetylome-wide association study of Alzheimerâ€™s disease identifies disease-associated H3K27ac differences in the entorhinal cortex. Nature Neuroscience, 2018, 21, 1618-1627.	14.8	138
18	Schizophrenia-associated methylomic variation: molecular signatures of disease and polygenic risk burden across multiple brain regions. Human Molecular Genetics, 2017, 26, ddw373.	2.9	74

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19	Mitochondrial genes are altered in blood early in Alzheimer's disease. Neurobiology of Aging, 2017, 53, 36-47.	3.1	132
20	Advanced paternal age effects in neurodevelopmental disordersâ€"review of potential underlying mechanisms. Translational Psychiatry, 2017, 7, e1019-e1019.	4.8	94
21	Genetic polymorphisms and their association with brain and behavioural measures in heterogeneous stock mice. Scientific Reports, 2017, 7, 41204.	3.3	2
22	Paternal Age Alters Social Development in Offspring. Journal of the American Academy of Child and Adolescent Psychiatry, 2017, 56, 383-390.	0.5	20
23	Highly polygenic architecture of antidepressant treatment response: Comparative analysis of SSRI and NRI treatment in an animal model of depression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 235-250.	1.7	10
24	Regional differences in mitochondrial DNA methylation in human post-mortem brain tissue. Clinical Epigenetics, 2017, 9, 47.	4.1	34
25	5-hydroxymethylcytosine is highly dynamic across human fetal brain development. BMC Genomics, 2017, 18, 738.	2.8	63
26	Comparative mRNA analysis of behavioral and genetic mouse models of aggression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 427-436.	1.7	9
27	An integrated genetic-epigenetic analysis of schizophrenia: evidence for co-localization of genetic associations and differential DNA methylation. Genome Biology, 2016, 17, 176.	8.8	287
28	Increased DNA methylation near TREM2 is consistently seen in the superior temporal gyrus in Alzheimer's disease brain. Neurobiology of Aging, 2016, 47, 35-40.	3.1	79
29	Genome-wide DNA methylation levels and altered cortisol stress reactivity following childhood trauma in humans. Nature Communications, 2016, 7, 10967.	12.8	175
30	Variation in 5-hydroxymethylcytosine across human cortex and cerebellum. Genome Biology, 2016, 17, 27.	8.8	83
31	ViPAR: a software platform for the Virtual Pooling and Analysis of Research Data. International Journal of Epidemiology, 2016, 45, 408-416.	1.9	42
32	Transcriptome analysis of genes and gene networks involved in aggressive behavior in mouse and zebrafish. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 827-838.	1.7	35
33	Tissue-specific patterns of allelically-skewed DNA methylation. Epigenetics, 2016, 11, 24-35.	2.7	32
34	Methylation QTLs in the developing brain and their enrichment in schizophrenia risk loci. Nature Neuroscience, 2016, 19, 48-54.	14.8	306
35	Effects of advanced paternal age on trajectories of social behavior in offspring. Genes, Brain and Behavior, 2015, 14, 443-453.	2.2	22
36	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	12.8	91

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37	Methylomic trajectories across human fetal brain development. Genome Research, 2015, 25, 338-352.	5.5	250
38	The inflammatory cytokines: molecular biomarkers for major depressive disorder?. Biomarkers in Medicine, 2015, 9, 169-180.	1.4	31
39	Pervasive and opposing effects of Unpredictable Chronic Mild Stress (UCMS) on hippocampal gene expression in BALB/cJ and C57BL/6J mouse strains. BMC Genomics, 2015, 16, 262.	2.8	30
40	Interindividual methylomic variation across blood, cortex, and cerebellum: implications for epigenetic studies of neurological and neuropsychiatric phenotypes. Epigenetics, 2015, 10, 1024-1032.	2.7	393
41	Identification of genes and gene pathways associated with major depressive disorder by integrative brain analysis of rat and human prefrontal cortex transcriptomes. Translational Psychiatry, 2015, 5, e519-e519.	4.8	43
42	Longitudinal changes of telomere length and epigenetic age related to traumatic stress and post-traumatic stress disorder. Psychoneuroendocrinology, 2015, 51, 506-512.	2.7	186
43	Putative Transcriptomic Biomarkers in the Inflammatory Cytokine Pathway Differentiate Major Depressive Disorder Patients from Control Subjects and Bipolar Disorder Patients. PLoS ONE, 2014, 9, e91076.	2.5	39
44	Long-Term Effects of Gestational Nicotine Exposure and Food-Restriction on Gene Expression in the Striatum of Adolescent Rats. PLoS ONE, 2014, 9, e88896.	2.5	5
45	Epigenomic and transcriptomic signatures of a Klinefelter syndrome (47,XXY) karyotype in the brain. Epigenetics, 2014, 9, 587-599.	2.7	53
46	Differential methylation of the TRPA1 promoter in pain sensitivity. Nature Communications, 2014, 5, 2978.	12.8	132
47	Effect of Chronic Valproic Acid Treatment on Hepatic Gene Expression Profile inWfs1Knockout Mouse. PPAR Research, 2014, 2014, 1-11.	2.4	8
48	Methylomic analysis of monozygotic twins discordant for autism spectrum disorder and related behavioural traits. Molecular Psychiatry, 2014, 19, 495-503.	7.9	280
49	Genes and Gene Networks Implicated in Aggression Related Behaviour. Neurogenetics, 2014, 15, 255-266.	1.4	30
50	Moodâ€stabilizers differentially affect housekeeping gene expression in human cells. International Journal of Methods in Psychiatric Research, 2014, 23, 279-288.	2.1	14
51	Methylomic profiling of human brain tissue supports a neurodevelopmental origin for schizophrenia. Genome Biology, 2014, 15, 483.	8.8	141
52	Transcriptomic changes in the frontal cortex associated with paternal age. Molecular Autism, 2014, 5, 24.	4.9	11
53	Introduction to mammalian genome special issue: genetics of behavior. Mammalian Genome, 2014, 25, 1-2.	2.2	1
54	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. Nature Neuroscience, 2014, 17, 1156-1163.	14.8	800

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55	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. Nature Neuroscience, 2014, 17, 1164-1170.	14.8	488
56	The correlation between reading and mathematics ability at age twelve has a substantial genetic component. Nature Communications, 2014, 5, 4204.	12.8	72
57	The endogenous and reactive depression subtypes revisited: integrative animal and human studies implicate multiple distinct molecular mechanisms underlying major depressive disorder. BMC Medicine, 2014, 12, 73.	5.5	52
58	Cross-region reduction in 5-hydroxymethylcytosine in Alzheimer's disease brain. Neurobiology of Aging, 2014, 35, 1850-1854.	3.1	114
59	O3-04-03: CROSS-TISSUE METHYLOMIC PROFILING IN ALZHEIMER'S DISEASE. , 2014, 10, P215-P215.		0
60	A data-driven approach to preprocessing Illumina 450K methylation array data. BMC Genomics, 2013, 14, 293.	2.8	850
61	TCF4 (e2â€2; ITF2): A schizophreniaâ€associated gene with pleiotropic effects on human disease. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 1-16.	1.7	46
62	Tumor necrosis factor and its targets in the inflammatory cytokine pathway are identified as putative transcriptomic biomarkers for escitalopram response. European Neuropsychopharmacology, 2013, 23, 1105-1114.	0.7	68
63	Advanced paternal age is associated with altered DNA methylation at brain-expressed imprinted loci in inbred mice: implications for neuropsychiatric disease. Molecular Psychiatry, 2013, 18, 635-636.	7.9	31
64	Silencing of the WFS1 gene in HEK cells induces pathways related to neurodegeneration and mitochondrial damage. Physiological Genomics, 2013, 45, 182-190.	2.3	21
65	Integrative mouse and human mRNA studies using WGCNA nominates novel candidate genes involved in the pathogenesis of major depressive disorder. Pharmacogenomics, 2013, 14, 1979-1990.	1.3	55
66	DNA methylation in interleukin-11 predicts clinical response to antidepressants in GENDEP. Translational Psychiatry, 2013, 3, e300-e300.	4.8	71
67	ATP-binding cassette sub-family F member 1 (ABCF1) is identified as a putative therapeutic target of escitalopram in the inflammatory cytokine pathway. Journal of Psychopharmacology, 2013, 27, 609-615.	4.0	20
68	Peripheral blood RNA gene expression profiling in patients with bacterial meningitis. Frontiers in Neuroscience, 2013, 7, 33.	2.8	38
69	Functional annotation of the human brain methylome identifies tissue-specific epigenetic variation across brain and blood. Genome Biology, 2012, 13, R43.	9.6	585
70	Pharmacoproteomic investigation into antidepressant response in two mouse inbred strains. Proteomics, 2012, 12, 2355-2365.	2.2	18
71	Stochastic Choice of Allelic Expression in Human Neural Stem Cells. Stem Cells, 2012, 30, 1938-1947.	3.2	53
72	Genetic variation in hippocampal microRNA expression differences in C57BL/6 J X DBA/2 J (BXD) recombinant inbred mouse strains. BMC Genomics, 2012, 13, 476.	2.8	20

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73	DNA methylation at the Igf2/H19 imprinting control region is associated with cerebellum mass in outbred mice. Molecular Brain, 2012, 5, 42.	2.6	15
74	Depressionâ€Related Behavioral Tests. Current Protocols in Mouse Biology, 2012, 2, 119-127.	1.2	82
75	Maternal separation is associated with strainâ€specific responses to stress and epigenetic alterations to Nr3c1, Avp, and Nr4a1 in mouse. Brain and Behavior, 2012, 2, 455-467.	2.2	123
76	Antidepressant-dependent mRNA changes in mouse associated with hippocampal neurogenesis in a mouse model of depression. Pharmacogenetics and Genomics, 2012, 22, 765-776.	1.5	28
77	Reduced Anxiety and Depression-Like Behaviours in the Circadian Period Mutant Mouse Afterhours. PLoS ONE, 2012, 7, e38263.	2.5	54
78	Convergent Animal and Human Evidence Suggests a Role of PPM1A Gene in Response to Antidepressants. Biological Psychiatry, 2011, 69, 360-365.	1.3	30
79	Peripheral blood RNA expression profiling in illicit methcathinone users reveals effect on immune system. Frontiers in Genetics, 2011, 2, 42.	2.3	3
80	Antidepressants and the resilience to early-life stress in inbred mouse strains. Pharmacogenetics and Genomics, 2011, 21, 779-789.	1.5	28
81	Disease-associated epigenetic changes in monozygotic twins discordant for schizophrenia and bipolar disorder. Human Molecular Genetics, 2011, 20, 4786-4796.	2.9	407
82	Hypothalamic gene expression profile indicates a reduction in G protein signaling in the Wfs1 mutant mice. Physiological Genomics, 2011, 43, 1351-1358.	2.3	7
83	Allelic Skewing of DNA Methylation Is Widespread across the Genome. American Journal of Human Genetics, 2010, 86, 196-212.	6.2	228
84	A Genome-Wide Association Study of Social and Non-Social Autistic-Like Traits in the General Population Using Pooled DNA, 500ÂK SNP Microarrays and Both Community and Diagnosed Autism Replication Samples. Behavior Genetics, 2010, 40, 31-45.	2.1	49
85	Response to comment by Stuart Macgregor. Behavior Genetics, 2010, 40, 48-48.	2.1	0
86	A Three-Stage Genome-Wide Association Study of General Cognitive Ability: Hunting the Small Effects. Behavior Genetics, 2010, 40, 759-767.	2.1	74
87	Utility of the pooling approach as applied to whole genome association scans with high-density Affymetrix microarrays. BMC Research Notes, 2010, 3, 274.	1.4	3
88	A genomeâ€wide association study identifies multiple loci associated with mathematics ability and disability. Genes, Brain and Behavior, 2010, 9, 234-247.	2.2	100
89	A B2 SINE insertion in the Comt1 gene (Comt1^{B2i}) results in an overexpressing, behavior modifying allele present in classical inbred mouse strains. Genes, Brain and Behavior, 2010, 9, 925-932.	2.2	24
90	Gene set enrichment; a problem of pathways. Briefings in Functional Genomics, 2010, 9, 385-390.	2.7	9

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91	Allele-specific methylation in the human genome. Epigenetics, 2010, 5, 578-582.	2.7	129
92	The differential transcriptome and ontology profiles of floating and cumulus granulosa cells in stimulated human antral follicles. Molecular Human Reproduction, 2010, 16, 229-240.	2.8	61
93	Behavioural battery testing: Evaluation and behavioural outcomes in 8 inbred mouse strains. Physiology and Behavior, 2010, 99, 301-316.	2.1	92
94	To what extent is blood a reasonable surrogate for brain in gene expression studies: estimation from mouse hippocampus and spleen. Frontiers in Neuroscience, 2009, 3, 54.	2.8	15
95	Genetics of the hippocampal transcriptome in mouse: a systematic survey and online neurogenomics resource. Frontiers in Neuroscience, 2009, 3, 55.	2.8	84
96	Assessing Individual Differences in Genome-Wide Gene Expression in Human Whole Blood: Reliability Over Four Hours and Stability Over 10 Months. Twin Research and Human Genetics, 2009, 12, 372-380.	0.6	4
97	Wfs1 gene deletion causes growth retardation in mice and interferes with the growth hormone pathway. Physiological Genomics, 2009, 37, 249-259.	2.3	49
98	The SNPMaP package for R: a framework for genome-wide association using DNA pooling on microarrays. Bioinformatics, 2009, 25, 281-283.	4.1	27
99	Interspecies comparisons of functional genetic variations and their implications in neuropsychiatry. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 309-317.	1.7	22
100	Advancing Paternal Age Is Associated with Deficits in Social and Exploratory Behaviors in the Offspring: A Mouse Model. PLoS ONE, 2009, 4, e8456.	2.5	77
101	Using hippocampal microRNA expression differences between mouse inbred strains to characterise miRNA function. Mammalian Genome, 2008, 19, 552-60.	2.2	38
102	Quantitative trait locus association scan of early reading disability and ability using pooled DNA and 100K SNP microarrays in a sample of 5760 children. Molecular Psychiatry, 2008, 13, 729-740.	7.9	101
103	Gene expression profiling reveals upregulation of Tlr4 receptors in Cckb receptor deficient mice. Behavioural Brain Research, 2008, 188, 62-70.	2.2	29
104	Moderation of breastfeeding effects on the IQ by genetic variation in fatty acid metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18860-18865.	7.1	324
105	P.1.31 Gene expression analyses of mouse fibroblast cell line L929 after antidepressant treatment. European Neuropsychopharmacology, 2007, 17, S27-S28.	0.7	0
106	Genetics of behavioural domains across the neuropsychiatric spectrum; of mice and men. Molecular Psychiatry, 2007, 12, 324-330.	7.9	117
107	Microarrays. Developmental Science, 2007, 10, 19-23.	2.4	51
108	Interpretation of knockout experiments: the congenic footprint. Genes, Brain and Behavior, 2007, 6, 299-303.	2.2	45

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109	Applicability of DNA pools on 500 K SNP microarrays for cost-effective initial screens in genomewide association studies. BMC Genomics, 2007, 8, 214.	2.8	43
110	Quantitative traits for the tail suspension test: automation, optimization, and BXD RI mapping. Mammalian Genome, 2007, 18, 482-491.	2.2	27
111	S.16.02 Depression: the GENDEP study. European Neuropsychopharmacology, 2006, 16, S187.	0.7	0
112	Performance deficit of Î±7 nicotinic receptor knockout mice in a delayed matching-to-place task suggests a mild impairment of working/episodic-like memory. Genes, Brain and Behavior, 2006, 5, 433-440.	2.2	92
113	Genotyping pooled DNA using 100K SNP microarrays: a step towards genomewide association scans. Nucleic Acids Research, 2006, 34, e27-e27.	14.5	92
114	Association analysis of mild mental impairment using DNA pooling to screen 432 brain-expressed single-nucleotide polymorphisms. Molecular Psychiatry, 2005, 10, 384-392.	7.9	46
115	Genotyping DNA pools on microarrays: Tackling the QTL problem of large samples and large numbers of SNPs. BMC Genomics, 2005, 6, 52.	2.8	60
116	Assessing Reliability, Heritability and General Cognitive Ability in a Battery of Cognitive Tasks for Laboratory Mice. Behavior Genetics, 2005, 35, 675-692.	2.1	146
117	A central resource for accurate allele frequency estimation from pooled DNA genotyped on DNA microarrays. Nucleic Acids Research, 2005, 33, e25-e25.	14.5	39
118	SNPs, microarrays and pooled DNA: identification of four loci associated with mild mental impairment in a sample of 6000 children. Human Molecular Genetics, 2005, 14, 1315-1325.	2.9	91
119	The mouse homeobox gene Not is required for caudal notochord development and affected by the truncate mutation. Genes and Development, 2004, 18, 1725-1736.	5.9	84
120	Genetic and environmental (inter)actions in male mouse lines selected for aggressive and nonaggressive behavior. Genes, Brain and Behavior, 2004, 3, 101-109.	2.2	28
121	Hippocampal gene expression profiling across eight mouse inbred strains: towards understanding the molecular basis for behaviour. European Journal of Neuroscience, 2004, 19, 2576-2582.	2.6	77
122	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	21.4	1,034
123	Application of microarrays to the analysis of the inactivation status of human X-linked genes expressed in lymphocytes. European Journal of Human Genetics, 2004, 12, 639-646.	2.8	35
124	Genotyping Pooled DNA on Microarrays: A Systematic Genome Screen of Thousands of SNPs in Large Samples to Detect QTLs for Complex Traits. Behavior Genetics, 2004, 34, 549-555.	2.1	89
125	Behavioral Characterization of Wild Derived Male Mice (Mus musculus musculus) of the PWD/Ph Inbred Strain: High Exploration Compared to C57BL/6J. Behavior Genetics, 2004, 34, 621-630.	2.1	25
126	The role of nicotinic receptor Î±7 subunits in nicotine discrimination. Neuropharmacology, 2004, 46, 363-371.	4.1	56

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127	Introduction to the Special Issue: Aggression Across Species. Behavior Genetics, 2003, 33, 457-460.	2.1	0
128	The nature and identification of quantitative trait loci: a community's view. Nature Reviews Genetics, 2003, 4, 911-916.	16.3	390
129	Home-cage activity in heterogeneous stock (HS) mice as a model of baseline activity. Genes, Brain and Behavior, 2002, 1, 166-173.	2.2	14
130	Genetic analysis of the mouse brain proteome. Nature Genetics, 2002, 30, 385-393.	21.4	293
131	Advanced Integrated Mouse YAC Map Including BAC Framework. Genome Research, 2001, 11, 2142-2150.	5.5	7
132	New tools for the high throughput characterization of rat genomic DNA samples. Journal of Experimental Animal Science, 2000, 41, 35-37.	0.5	1
133	ETn insertion in the mouse Adcy1 gene: transcriptional and phylogenetic analyses. Mammalian Genome, 2000, 11, 97-103.	2.2	10
134	High-Throughput Scanning of the Rat Genome Using Interspersed Repetitive Sequence-PCR Markers. Genomics, 2000, 69, 287-294.	2.9	16
135	Panel of Microsatellite Markers for Whole-Genome Scans and Radiation Hybrid Mapping and a Mouse Family Tree. Genome Research, 1999, 9, 878-887.	5.5	30
136	A 5Ã— genome coverage bovine BAC library: production, characterization, and distribution. Mammalian Genome, 1999, 10, 706-709.	2.2	53
137	A bovine YAC library containing four- to five-fold genome equivalents. Mammalian Genome, 1999, 10, 837-838.	2.2	25
138	Technology development at the interface of proteome research and genomics: Mapping nonpolymorphic proteins on the physical map of mouse chromosomes. Electrophoresis, 1999, 20, 1027-1032.	2.4	8
139	Technology development at the interface of proteome research and genomics: Mapping nonpolymorphic proteins on the physical map of mouse chromosomes. Electrophoresis, 1999, 20, 1027-1032.	2.4	0
140	Refined radiation hybrid map of mouse Chromosome 17. Mammalian Genome, 1998, 9, 807-811.	2.2	6
141	Loss of adenylyl cyclase I activity disrupts patterning of mouse somatosensory cortex. Nature Genetics, 1998, 19, 289-291.	21.4	156
142	IRS-PCR-based genetic mapping of the huntingtin interacting protein gene (HIP1) on mouse Chromosome 5. Mammalian Genome, 1998, 9, 26-31.	2.2	15
143	Complex probes for high-throughput parallel genetic mapping of genomic mouse BAC clones. Mammalian Genome, 1998, 9, 611-616.	2.2	4
144	Construction and characterisation of a gridded chicken cosmid library with four-fold genomic coverage. Animal Genetics, 1998, 29, 295-301.	1.7	18

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145	Molecular and biochemical characterisation of DNA-dependent protein kinase-defective rodent mutant irs-20. Nucleic Acids Research, 1998, 26, 1965-1973.	14.5	74
146	Construction and Characterization of a 10-Genome Equivalent Yeast Artificial Chromosome Library for the Laboratory Rat,Rattus norvegicus. Genomics, 1997, 39, 385-392.	2.9	42
147	Tetraodon fluviatilis,a New Puffer Fish Model for Genome Studies. Genomics, 1997, 41, 177-184.	2.9	66
148	A yeast artificial chromosome (YAC) library containing 10 haploid chicken genome equivalents. Mammalian Genome, 1997, 8, 274-276.	2.2	16
149	Toward the construction of integrated physical and genetic maps of the mouse genome using interspersed repetitive sequence PCR (IRS-PCR) genomics.. Genome Research, 1996, 6, 290-299.	5.5	18
150	Efficient high-resolution genetic mapping of mouse interspersed repetitive sequence PCR products, toward integrated genetic and physical mapping of the mouse genome.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5302-5306.	7.1	36
151	Techniques in mammalian genome mapping. Current Opinion in Biotechnology, 1995, 6, 37-43.	6.6	19
152	Towards high resolution maps of the mouse and human genomesâ€”a facility for ordering markers to 0.1 cM resolution. Human Molecular Genetics, 1994, 3, 621-627.	2.9	185
153	High resolution cosmid and P1 maps spanning the 14 Mb genome of the fission yeast S. pombe. Cell, 1993, 73, 109-120.	28.9	271
154	Insertion sequences on plasmid pHV1 of Haloferax volcanii. Canadian Journal of Microbiology, 1993, 39, 201-206.	1.7	4
155	Chapter 15 Halobacterial genes and genomes. New Comprehensive Biochemistry, 1993, , 467-496.	0.1	8
156	Detailed physical map and set of overlapping clones covering the genome of the archaebacterium Haloferax volcanii DS2. Journal of Molecular Biology, 1991, 222, 509-524.	4.2	90
157	Genome mapping in halobacteria. Canadian Journal of Microbiology, 1989, 35, 21-29.	1.7	48
158	Transformation methods for halophilic archaebacteria. Canadian Journal of Microbiology, 1989, 35, 148-152.	1.7	290
159	ISH51: a large, degenerate family of insertion sequence-like elements in the genome of the archaehacterium,Halobacterium volcanii. Nucleic Acids Research, 1986, 14, 6983-7000.	14.5	42