

Andrew E Jaffe

List of Publications by Year in descending order

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Version: 2024-02-01

133
papers

21,493
citations

38738

50
h-index

14758

127
g-index

186
all docs

186
docs citations

186
times ranked

33869
citing authors

#	ARTICLE	IF	CITATIONS
1	The <code>sva</code> package for removing batch effects and other unwanted variation in high-throughput experiments. <i>Bioinformatics</i> , 2012, 28, 882-883.	4.1	3,912
2	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014, 30, 1363-1369.	4.1	3,192
3	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015, 16, 25.	8.8	928
4	Accounting for cellular heterogeneity is critical in epigenome-wide association studies. <i>Genome Biology</i> , 2014, 15, R31.	9.6	880
5	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018, 359, 693-697.	12.6	851
6	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018, 362, .	12.6	805
7	Ballgown bridges the gap between transcriptome assembly and expression analysis. <i>Nature Biotechnology</i> , 2015, 33, 243-246.	17.5	716
8	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	12.6	618
9	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. <i>International Journal of Epidemiology</i> , 2012, 41, 200-209.	1.9	567
10	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	12.6	516
11	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. <i>Nature Neuroscience</i> , 2021, 24, 425-436.	14.8	418
12	Mapping DNA methylation across development, genotype and schizophrenia in the human frontal cortex. <i>Nature Neuroscience</i> , 2016, 19, 40-47.	14.8	417
13	Reproducible RNA-seq analysis using recount2. <i>Nature Biotechnology</i> , 2017, 35, 319-321.	17.5	395
14	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	14.8	371
15	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. <i>Nature Genetics</i> , 2009, 41, 1191-1198.	21.4	324
16	Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. <i>Nature Neuroscience</i> , 2018, 21, 1117-1125.	14.8	300
17	<code>Polyester</code> : simulating RNA-seq datasets with differential transcript expression. <i>Bioinformatics</i> , 2015, 31, 2778-2784.	4.1	250
18	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018, 362, .	12.6	220

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19	Convergence of placenta biology and genetic risk for schizophrenia. <i>Nature Medicine</i> , 2018, 24, 792-801.	30.7	214
20	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. <i>Science</i> , 2017, 356, .	12.6	206
21	A Bayesian framework for multiple trait colocalization from summary association statistics. <i>Bioinformatics</i> , 2018, 34, 2538-2545.	4.1	203
22	Global DNA hypomethylation is associated with in utero exposure to cotinine and perfluorinated alkyl compounds. <i>Epigenetics</i> , 2010, 5, 539-546.	2.7	172
23	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. <i>Neuron</i> , 2019, 103, 203-216.e8.	8.1	158
24	Genome-Wide Analysis of Promoter Methylation Associated with Gene Expression Profile in Pancreatic Adenocarcinoma. <i>Clinical Cancer Research</i> , 2011, 17, 4341-4354.	7.0	154
25	Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. <i>JAMA Psychiatry</i> , 2016, 73, 506.	11.0	151
26	Developmental regulation of human cortex transcription and its clinical relevance at single base resolution. <i>Nature Neuroscience</i> , 2015, 18, 154-161.	14.8	142
27	A human-specific AS3MT isoform and BORCS7 are molecular risk factors in the 10q24.32 schizophrenia-associated locus. <i>Nature Medicine</i> , 2016, 22, 649-656.	30.7	142
28	Paternal sperm DNA methylation associated with early signs of autism risk in an autism-enriched cohort. <i>International Journal of Epidemiology</i> , 2015, 44, 1199-1210.	1.9	121
29	recount3: summaries and queries for large-scale RNA-seq expression and splicing. <i>Genome Biology</i> , 2021, 22, 323.	8.8	103
30	Expression of <i>ZNF804A</i> in Human Brain and Alterations in Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2014, 71, 1112.	11.0	102
31	Mouse-Human Experimental Epigenetic Analysis Unmasks Dietary Targets and Genetic Liability for Diabetic Phenotypes. <i>Cell Metabolism</i> , 2015, 21, 138-149.	16.2	98
32	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.	7.9	98
33	Prenatal Expression Patterns of Genes Associated With Neuropsychiatric Disorders. <i>American Journal of Psychiatry</i> , 2014, 171, 758-767.	7.2	96
34	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. <i>Nature Communications</i> , 2020, 11, 462.	12.8	96
35	qSVA framework for RNA quality correction in differential expression analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7130-7135.	7.1	95
36	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. <i>Neuron</i> , 2021, 109, 3088-3103.e5.	8.1	95

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37	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. <i>Genome Biology</i> , 2016, 17, 266.	8.8	94
38	Significance analysis and statistical dissection of variably methylated regions. <i>Biostatistics</i> , 2012, 13, 166-178.	1.5	92
39	BrainSeq: Neurogenomics to Drive Novel Target Discovery for Neuropsychiatric Disorders. <i>Neuron</i> , 2015, 88, 1078-1083.	8.1	92
40	Altered expression of histamine signaling genes in autism spectrum disorder. <i>Translational Psychiatry</i> , 2017, 7, e1126-e1126.	4.8	89
41	A myelin-related transcriptomic profile is shared by Pittâ€“Hopkins syndrome models and human autism spectrum disorder. <i>Nature Neuroscience</i> , 2020, 23, 375-385.	14.8	89
42	Psychiatric Risk Gene Transcription Factor 4 Regulates Intrinsic Excitability of Prefrontal Neurons via Repression of SCN10a and KCNQ1. <i>Neuron</i> , 2016, 90, 43-55.	8.1	88
43	Identification and prioritization of gene sets associated with schizophrenia risk by co-expression network analysis in human brain. <i>Molecular Psychiatry</i> , 2020, 25, 791-804.	7.9	86
44	Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimerâ€™s disease. <i>Acta Neuropathologica</i> , 2019, 137, 557-569.	7.7	73
45	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. <i>Nature Neuroscience</i> , 2021, 24, 176-185.	14.8	73
46	DNA methylation shows genome-wide association of <i>NFIX</i> , <i>RAPGEF2</i> and <i>MSRB3</i> with gestational age at birth. <i>International Journal of Epidemiology</i> , 2012, 41, 188-199.	1.9	71
47	Addressing confounding artifacts in reconstruction of gene co-expression networks. <i>Genome Biology</i> , 2019, 20, 94.	8.8	68
48	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. <i>Genome Biology</i> , 2019, 20, 196.	8.8	67
49	Profiling gene expression in the human dentate gyrus granule cell layer reveals insights into schizophrenia and its genetic risk. <i>Nature Neuroscience</i> , 2020, 23, 510-519.	14.8	67
50	DNA Methylation Profiling of Human Prefrontal Cortex Neurons in Heroin Users Shows Significant Difference between Genomic Contexts of Hyper- and Hypomethylation and a Younger Epigenetic Age. <i>Genes</i> , 2017, 8, 152.	2.4	66
51	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods. <i>BMC Genomics</i> , 2019, 20, 513.	2.8	65
52	Differential DNA methylation identified in the blood and retina of AMD patients. <i>Epigenetics</i> , 2015, 10, 698-707.	2.7	62
53	Prenatal mercury concentration is associated with changes in DNA methylation at <i>TCEANC2</i> in newborns. <i>International Journal of Epidemiology</i> , 2015, 44, 1249-1262.	1.9	60
54	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , 2017, 14, 216-217.	19.0	59

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55	Investigating the neuroimmunogenic architecture of schizophrenia. <i>Molecular Psychiatry</i> , 2018, 23, 1251-1260.	7.9	59
56	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. <i>Bioinformatics</i> , 2017, 33, 4033-4040.	4.1	57
57	Flexible expressed region analysis for RNA-seq with <code>derfinder</code> . <i>Nucleic Acids Research</i> , 2017, 45, e9-e9.	14.5	54
58	GAD1 alternative transcripts and DNA methylation in human prefrontal cortex and hippocampus in brain development, schizophrenia. <i>Molecular Psychiatry</i> , 2018, 23, 1496-1505.	7.9	52
59	Olfactory cells via nasal biopsy reflect the developing brain in gene expression profiles: Utility and limitation of the surrogate tissues in research for brain disorders. <i>Neuroscience Research</i> , 2013, 77, 247-250.	1.9	51
60	Practical impacts of genomic data "cleaning" on biological discovery using surrogate variable analysis. <i>BMC Bioinformatics</i> , 2015, 16, 372.	2.6	51
61	Investigation of the Prenatal Expression Patterns of 108 Schizophrenia-Associated Genetic Loci. <i>Biological Psychiatry</i> , 2015, 77, e43-e51.	1.3	51
62	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. <i>F1000Research</i> , 2017, 6, 1558.	1.6	50
63	spatialLBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. <i>BMC Genomics</i> , 2022, 23, .	2.8	50
64	Improving the value of public RNA-seq expression data by phenotype prediction. <i>Nucleic Acids Research</i> , 2018, 46, e54-e54.	14.5	49
65	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021, 12, 3968.	12.8	48
66	dotdotdot: an automated approach to quantify multiplex single molecule fluorescent in situ hybridization (smFISH) images in complex tissues. <i>Nucleic Acids Research</i> , 2020, 48, e66-e66.	14.5	46
67	Revealing the brain's molecular architecture. <i>Science</i> , 2018, 362, 1262-1263.	12.6	45
68	Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders. <i>Science Advances</i> , 2020, 6, .	10.3	44
69	The schizophrenia- and autism-associated gene, transcription factor 4 regulates the columnar distribution of layer 2/3 prefrontal pyramidal neurons in an activity-dependent manner. <i>Molecular Psychiatry</i> , 2018, 23, 304-315.	7.9	43
70	Hypomethylation of the IL17RC Promoter in Peripheral Blood Leukocytes Is Not A Hallmark of Age-Related Macular Degeneration. <i>Cell Reports</i> , 2013, 5, 1527-1535.	6.4	42
71	Cannabinoid receptor CNR1 expression and DNA methylation in human prefrontal cortex, hippocampus and caudate in brain development and schizophrenia. <i>Translational Psychiatry</i> , 2020, 10, 158.	4.8	42
72	BDNF-TrkB signaling in oxytocin neurons contributes to maternal behavior. <i>ELife</i> , 2018, 7, .	6.0	38

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73	Paternal age, de novo mutations and schizophrenia. <i>Molecular Psychiatry</i> , 2014, 19, 274-275.	7.9	37
74	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. <i>Nature Communications</i> , 2021, 12, 5251.	12.8	37
75	C1q/TNF-Related Protein-9 (CTRP9) Levels Are Associated With Obesity and Decrease Following Weight Loss Surgery. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 2211-2217.	3.6	36
76	Schizophrenia risk variants influence multiple classes of transcripts of sorting nexin 19 (SNX19). <i>Molecular Psychiatry</i> , 2020, 25, 831-843.	7.9	36
77	Genetic neuropathology of obsessive psychiatric syndromes. <i>Translational Psychiatry</i> , 2014, 4, e432-e432.	4.8	35
78	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020, 30, 1073-1081.	5.5	35
79	Genetic vulnerability to DUSP22 promoter hypermethylation is involved in the relation between in utero famine exposure and schizophrenia. <i>NPJ Schizophrenia</i> , 2018, 4, 16.	3.6	34
80	Characterizing the nuclear and cytoplasmic transcriptomes in developing and mature human cortex uncovers new insight into psychiatric disease gene regulation. <i>Genome Research</i> , 2020, 30, 1-11.	5.5	29
81	Association of Missense Mutation in FOLH1 With Decreased NAAG Levels and Impaired Working Memory Circuitry and Cognition. <i>American Journal of Psychiatry</i> , 2020, 177, 1129-1139.	7.2	29
82	Electrophysiological measures from human iPSC-derived neurons are associated with schizophrenia clinical status and predict individual cognitive performance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	29
83	Use of Postmortem Human Dura Mater and Scalp for Deriving Human Fibroblast Cultures. <i>PLoS ONE</i> , 2012, 7, e45282.	2.5	28
84	Prefrontal Coexpression of Schizophrenia Risk Genes Is Associated With Treatment Response in Patients. <i>Biological Psychiatry</i> , 2019, 86, 45-55.	1.3	27
85	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways. <i>Nature Neuroscience</i> , 2022, 25, 381-389.	14.8	27
86	Genetic risk mechanisms of posttraumatic stress disorder in the human brain. <i>Journal of Neuroscience Research</i> , 2018, 96, 21-30.	2.9	24
87	Cytokine, Chemokine, and Cytokine Receptor Changes Are Associated With Metabolic Improvements After Bariatric Surgery. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 947-956.	3.6	23
88	Adult mouse hippocampal transcriptome changes associated with long-term behavioral and metabolic effects of gestational air pollution toxicity. <i>Translational Psychiatry</i> , 2020, 10, 218.	4.8	23
89	Older molecular brain age in severe mental illness. <i>Molecular Psychiatry</i> , 2021, 26, 3646-3656.	7.9	23
90	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. <i>Nature Neuroscience</i> , 2021, 24, 186-196.	14.8	22

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91	Decoding Shared Versus Divergent Transcriptomic Signatures Across Cortico-Amygdala Circuitry in PTSD and Depressive Disorders. <i>American Journal of Psychiatry</i> , 2022, 179, 673-686.	7.2	21
92	Postmortem human brain genomics in neuropsychiatric disorders—how far can we go?. <i>Current Opinion in Neurobiology</i> , 2016, 36, 107-111.	4.2	20
93	Strong Components of Epigenetic Memory in Cultured Human Fibroblasts Related to Site of Origin and Donor Age. <i>PLoS Genetics</i> , 2016, 12, e1005819.	3.5	20
94	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. <i>Epigenetics</i> , 2021, 16, 1-13.	2.7	19
95	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers. <i>Neuropsychopharmacology</i> , 2021, 46, 554-560.	5.4	19
96	Spatial transcriptomics: putting genome-wide expression on the map. <i>Neuropsychopharmacology</i> , 2020, 45, 232-233.	5.4	17
97	Molecularly Defined Hippocampal Inputs Regulate Population Dynamics in the Prelimbic Cortex to Suppress Context Fear Memory Retrieval. <i>Biological Psychiatry</i> , 2020, 88, 554-565.	1.3	17
98	Genetics and Brain Transcriptomics of Completed Suicide. <i>American Journal of Psychiatry</i> , 2022, 179, 226-241.	7.2	17
99	Schizophrenia-Associated hERG channel Kv11.1-3.1 Exhibits a Unique Trafficking Deficit that is Rescued Through Proteasome Inhibition for High Throughput Screening. <i>Scientific Reports</i> , 2016, 6, 19976.	3.3	16
100	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. <i>Molecular Psychiatry</i> , 2020, 25, 3267-3277.	7.9	16
101	Epigenome-wide study of brain DNA methylation following acute opioid intoxication. <i>Drug and Alcohol Dependence</i> , 2021, 221, 108658.	3.2	15
102	SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses. <i>BMC Bioinformatics</i> , 2021, 22, 224.	2.6	14
103	Association of a Noncoding RNA Postmortem With Suicide by Violent Means and In Vivo With Aggressive Phenotypes. <i>Biological Psychiatry</i> , 2019, 85, 417-424.	1.3	13
104	KCNH2-3.1 mediates aberrant complement activation and impaired hippocampal-medial prefrontal circuitry associated with working memory deficits. <i>Molecular Psychiatry</i> , 2020, 25, 206-229.	7.9	13
105	TE-array—a high throughput tool to study transposon transcription. <i>BMC Genomics</i> , 2013, 14, 869.	2.8	12
106	Multiple testing of local maxima for detection of peaks in ChIP-Seq data. <i>Annals of Applied Statistics</i> , 2013, 7, 471-494.	1.1	12
107	Genome-Wide and Gene-Specific Epigenomic Platforms for Hepatocellular Carcinoma Biomarker Development Trials. <i>Gastroenterology Research and Practice</i> , 2014, 2014, 1-9.	1.5	12
108	Cortical cellular diversity and development in schizophrenia. <i>Molecular Psychiatry</i> , 2021, 26, 203-217.	7.9	11

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109	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. <i>Biological Psychiatry</i> , 2021, 90, 399-408.	1.3	10
110	TrkB Signaling Influences Gene Expression in Cortistatin-Expressing Interneurons. <i>ENeuro</i> , 2020, 7, ENEURO.0310-19.2019.	1.9	10
111	Molecular phenotypes associated with antipsychotic drugs in the human caudate nucleus. <i>Molecular Psychiatry</i> , 2022, 27, 2061-2067.	7.9	10
112	Identification of functional genetic variation in exome sequence analysis. <i>BMC Proceedings</i> , 2011, 5, S13.	1.6	9
113	Genetic and epigenetic analysis of schizophrenia in blood—a no-brainer?. <i>Genome Medicine</i> , 2016, 8, 96.	8.2	9
114	Cerebral cortex and blood transcriptome changes in mouse neonates prenatally exposed to air pollution particulate matter. <i>Journal of Neurodevelopmental Disorders</i> , 2021, 13, 30.	3.1	9
115	Gene set bagging for estimating the probability a statistically significant result will replicate. <i>BMC Bioinformatics</i> , 2013, 14, 360.	2.6	7
116	Epigenome-wide association scan identifies methylation sites associated with HIV infection. <i>Epigenomics</i> , 2020, 12, 1917-1927.	2.1	7
117	Assessment of genetic risk for distribution of total interstitial white matter neurons in dorsolateral prefrontal cortex: role in schizophrenia. <i>Schizophrenia Research</i> , 2016, 176, 141-143.	2.0	6
118	African-American and Caucasian participation in postmortem human brain donation for neuropsychiatric research. <i>PLoS ONE</i> , 2019, 14, e0222565.	2.5	5
119	Single molecule in situ hybridization reveals distinct localizations of schizophrenia risk-related transcripts SNX19 and AS3MT in human brain. <i>Molecular Psychiatry</i> , 2021, 26, 3536-3547.	7.9	5
120	Altered adipokines in obese adolescents: a cross-sectional and longitudinal analysis across the spectrum of glycemia. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2021, 320, E1044-E1052.	3.5	5
121	regionReport: Interactive reports for region-based analyses. <i>F1000Research</i> , 2015, 4, 105.	1.6	5
122	Differential expression of NPAS4 in the dorsolateral prefrontal cortex following opioid overdose. , 2022, 3, 100040.		5
123	Epigenome-wide association analyses of active injection drug use. <i>Drug and Alcohol Dependence</i> , 2022, 235, 109431.	3.2	5
124	Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. <i>Frontiers in Immunology</i> , 2018, 9, 2679.	4.8	4
125	Strategies for cellular deconvolution in human brain RNA sequencing data. <i>F1000Research</i> , 0, 10, 750.	1.6	4
126	regionReport: Interactive reports for region-level and feature-level genomic analyses. <i>F1000Research</i> , 2015, 4, 105.	1.6	4

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127	Induction of Bdnf from promoter I following electroconvulsive seizures contributes to structural plasticity in neurons of the piriform cortex. <i>Brain Stimulation</i> , 2022, 15, 427-433.	1.6	4
128	Curating the Evidence About COVID-19 for Frontline Public Health and Clinical Care: The Novel Coronavirus Research Compendium. <i>Public Health Reports</i> , 2022, 137, 197-202.	2.5	2
129	O4.1. GENETIC VULNERABILITY TO DUSP22 PROMOTOR HYPERMETHYLATION IS INVOLVED IN THE RELATION BETWEEN IN UTERO FAMINE EXPOSURE AND SCHIZOPHRENIA. <i>Schizophrenia Bulletin</i> , 2018, 44, S82-S82.	4.3	0
130	O4.7. PLACENTAL GENE EXPRESSION, OBSTETRICAL HISTORY AND POLYGENIC RISK FOR SCHIZOPHRENIA. <i>Schizophrenia Bulletin</i> , 2018, 44, S85-S86.	4.3	0
131	Comparison of quantitative trait loci methods: Total expression and allelic imbalance method in brain RNA-seq. <i>PLoS ONE</i> , 2019, 14, e0217765.	2.5	0
132	Early developmental exposure to air pollution increases the risk of Alzheimers disease and amyloid production: Studies in mouse and <i>Caenorhabditis elegans</i> . <i>Alzheimer's and Dementia</i> , 2020, 16, e043846.	0.8	0
133	Measurement, Summary, and Methodological Variation in RNA-sequencing. , 2014, , 115-128.		0