

Andrew E Jaffe

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

153 papers	12,818 citations	45 h-index	113 g-index
186 ext. papers	18,343 ext. citations	12.8 avg, IF	6.42 L-index

#	Paper	IF	Citations
153	The sva package for removing batch effects and other unwanted variation in high-throughput experiments. <i>Bioinformatics</i> , 2012 , 28, 882-3	7.2	1996
152	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014 , 30, 1363-9	7.2	1941
151	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015 , 16, 25	18.3	670
150	Accounting for cellular heterogeneity is critical in epigenome-wide association studies. <i>Genome Biology</i> , 2014 , 15, R31	18.3	660
149	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <i>Science</i> , 2018 , 359, 693-697	33.3	547
148	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. <i>Science</i> , 2018 , 362,	33.3	434
147	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. <i>International Journal of Epidemiology</i> , 2012 , 41, 200-9	7.8	430
146	Ballgown bridges the gap between transcriptome assembly and expression analysis. <i>Nature Biotechnology</i> , 2015 , 33, 243-6	44.5	413
145	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018 , 362,	33.3	319
144	Mapping DNA methylation across development, genotype and schizophrenia in the human frontal cortex. <i>Nature Neuroscience</i> , 2016 , 19, 40-7	25.5	299
143	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. <i>Nature Genetics</i> , 2009 , 41, 1191-8	36.3	285
142	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018 , 362,	33.3	277
141	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015 , 18, 1707-12	25.5	226
140	Reproducible RNA-seq analysis using recount2. <i>Nature Biotechnology</i> , 2017 , 35, 319-321	44.5	211
139	Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. <i>Nature Neuroscience</i> , 2018 , 21, 1117-1125	25.5	176
138	Polyester: simulating RNA-seq datasets with differential transcript expression. <i>Bioinformatics</i> , 2015 , 31, 2778-84	7.2	160
137	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. <i>Science</i> , 2017 , 356,	33.3	152

136	Global DNA hypomethylation is associated with in utero exposure to cotinine and perfluorinated alkyl compounds. <i>Epigenetics</i> , 2010 , 5, 539-46	5.7	146
135	Transcriptome and epigenome landscape of human cortical development modeled in organoids. <i>Science</i> , 2018 , 362,	33.3	142
134	Convergence of placenta biology and genetic risk for schizophrenia. <i>Nature Medicine</i> , 2018 , 24, 792-801	50.5	141
133	Genome-wide analysis of promoter methylation associated with gene expression profile in pancreatic adenocarcinoma. <i>Clinical Cancer Research</i> , 2011 , 17, 4341-54	12.9	131
132	A human-specific AS3MT isoform and BORCS7 are molecular risk factors in the 10q24.32 schizophrenia-associated locus. <i>Nature Medicine</i> , 2016 , 22, 649-56	50.5	112
131	Developmental regulation of human cortex transcription and its clinical relevance at single base resolution. <i>Nature Neuroscience</i> , 2015 , 18, 154-161	25.5	110
130	Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. <i>JAMA Psychiatry</i> , 2016 , 73, 506-14	14.5	108
129	A Bayesian framework for multiple trait colocalization from summary association statistics. <i>Bioinformatics</i> , 2018 , 34, 2538-2545	7.2	99
128	Paternal sperm DNA methylation associated with early signs of autism risk in an autism-enriched cohort. <i>International Journal of Epidemiology</i> , 2015 , 44, 1199-210	7.8	91
127	Expression of ZNF804A in human brain and alterations in schizophrenia, bipolar disorder, and major depressive disorder: a novel transcript fetally regulated by the psychosis risk variant rs1344706. <i>JAMA Psychiatry</i> , 2014 , 71, 1112-20	14.5	89
126	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	1.3	78
125	O4.7. PLACENTAL GENE EXPRESSION, OBSTETRICAL HISTORY AND POLYGENIC RISK FOR SCHIZOPHRENIA. <i>Schizophrenia Bulletin</i> , 2018 , 44, S85-S86	1.3	78
124	Mouse-human experimental epigenetic analysis unmask dietary targets and genetic liability for diabetic phenotypes. <i>Cell Metabolism</i> , 2015 , 21, 138-49	24.6	76
123	Prenatal expression patterns of genes associated with neuropsychiatric disorders. <i>American Journal of Psychiatry</i> , 2014 , 171, 758-67	11.9	76
122	Significance analysis and statistical dissection of variably methylated regions. <i>Biostatistics</i> , 2012 , 13, 1663-78	3.7	75
121	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. <i>Nature Neuroscience</i> , 2021 , 24, 425-436	25.5	69
120	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	13.9	68
119	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	13.9	67

118	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	15.1	67
117	BrainSeq: Neurogenomics to Drive Novel Target Discovery for Neuropsychiatric Disorders. <i>Neuron</i> , 2015 , 88, 1078-1083	13.9	67
116	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	18.3	65
115	DNA methylation shows genome-wide association of NFIX, RAPGEF2 and MSRB3 with gestational age at birth. <i>International Journal of Epidemiology</i> , 2012 , 41, 188-99	7.8	60
114	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	11.5	58
113	Altered expression of histamine signaling genes in autism spectrum disorder. <i>Translational Psychiatry</i> , 2017 , 7, e1126	8.6	49
112	Prenatal mercury concentration is associated with changes in DNA methylation at TCEANC2 in newborns. <i>International Journal of Epidemiology</i> , 2015 , 44, 1249-62	7.8	48
111	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , 2017 , 14, 216-217	21.6	47
110	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	15.1	47
109	Differential DNA methylation identified in the blood and retina of AMD patients. <i>Epigenetics</i> , 2015 , 10, 698-707	5.7	46
108	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,	4.2	44
107	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	18.3	42
106	Investigation of the prenatal expression patterns of 108 schizophrenia-associated genetic loci. <i>Biological Psychiatry</i> , 2015 , 77, e43-51	7.9	42
105	Investigating the neuroimmunogenic architecture of schizophrenia. <i>Molecular Psychiatry</i> , 2018 , 23, 1251-1260	15.2	41
104	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, 247-50	3.9	41
103	Addressing confounding artifacts in reconstruction of gene co-expression networks. <i>Genome Biology</i> , 2019 , 20, 94	18.3	37
102	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. <i>Nature Communications</i> , 2020 , 11, 462	17.4	37
101	Hypomethylation of the IL17RC promoter in peripheral blood leukocytes is not a hallmark of age-related macular degeneration. <i>Cell Reports</i> , 2013 , 5, 1527-35	10.6	37

100	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	4.5	36
99	A myelin-related transcriptomic profile is shared by Pitt-Hopkins syndrome models and human autism spectrum disorder. <i>Nature Neuroscience</i> , 2020 , 23, 375-385	25.5	34
98	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. <i>Bioinformatics</i> , 2017 , 33, 4033-4040	7.2	33
97	Flexible expressed region analysis for RNA-seq with derfinder. <i>Nucleic Acids Research</i> , 2017 , 45, e9	20.1	32
96	Practical impacts of genomic data "cleaning" on biological discovery using surrogate variable analysis. <i>BMC Bioinformatics</i> , 2015 , 16, 372	3.6	32
95	Paternal age, de novo mutations and schizophrenia. <i>Molecular Psychiatry</i> , 2014 , 19, 274-5	15.1	32
94	Improving the value of public RNA-seq expression data by phenotype prediction. <i>Nucleic Acids Research</i> , 2018 , 46, e54	20.1	31
93	Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimer's disease. <i>Acta Neuropathologica</i> , 2019 , 137, 557-569	14.3	30
92	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	25.5	30
91	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. <i>F1000Research</i> , 2017 , 6, 1558	3.6	30
90	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	15.1	29
89	Revealing the brain's molecular architecture. <i>Science</i> , 2018 , 362, 1262-1263	33.3	29
88	GAD1 alternative transcripts and DNA methylation in human prefrontal cortex and hippocampus in brain development, schizophrenia. <i>Molecular Psychiatry</i> , 2018 , 23, 1496-1505	15.1	28
87	Genetic neuropathology of obsessive psychiatric syndromes. <i>Translational Psychiatry</i> , 2014 , 4, e432	8.6	26
86	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, 2211-7	5.6	26
85	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	5.5	20
84	Use of postmortem human dura mater and scalp for deriving human fibroblast cultures. <i>PLoS ONE</i> , 2012 , 7, e45282	3.7	19
83	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	8.6	19

82	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	25.5	19
81	Postmortem human brain genomics in neuropsychiatric disorders--how far can we go?. <i>Current Opinion in Neurobiology</i> , 2016 , 36, 107-11	7.6	18
80	BDNF-TrkB signaling in oxytocin neurons contributes to maternal behavior. <i>ELife</i> , 2018 , 7,	8.9	18
79	Schizophrenia risk variants influence multiple classes of transcripts of sorting nexin 19 (SNX19). <i>Molecular Psychiatry</i> , 2020 , 25, 831-843	15.1	17
78	Genetic risk mechanisms of posttraumatic stress disorder in the human brain. <i>Journal of Neuroscience Research</i> , 2018 , 96, 21-30	4.4	16
77	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex		16
76	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	20.1	15
75	Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders. <i>Science Advances</i> , 2020 , 6,	14.3	15
74	Strong Components of Epigenetic Memory in Cultured Human Fibroblasts Related to Site of Origin and Donor Age. <i>PLoS Genetics</i> , 2016 , 12, e1005819	6	15
73	Prefrontal Coexpression of Schizophrenia Risk Genes Is Associated With Treatment Response in Patients. <i>Biological Psychiatry</i> , 2019 , 86, 45-55	7.9	14
72	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	5.6	13
71	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020 , 30, 1073-1081	9.7	13
70	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	11.9	13
69	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	8.6	12
68	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	4.9	12
67	Genome-wide and gene-specific epigenomic platforms for hepatocellular carcinoma biomarker development trials. <i>Gastroenterology Research and Practice</i> , 2014 , 2014, 597164	2	12
66	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	9.7	12
65	TE-array--a high throughput tool to study transposon transcription. <i>BMC Genomics</i> , 2013 , 14, 869	4.5	11

64	MULTIPLE TESTING OF LOCAL MAXIMA FOR DETECTION OF PEAKS IN CHIP-SEQ DATA. <i>Annals of Applied Statistics</i> , 2013 , 7, 471-494	2.1	11
63	Association of a Noncoding RNA Postmortem With Suicide by Violent Means and InVivo With Aggressive Phenotypes. <i>Biological Psychiatry</i> , 2019 , 85, 417-424	7.9	9
62	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. <i>Epigenetics</i> , 2021 , 16, 1-13	5.7	9
61	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. <i>Nature Neuroscience</i> , 2021 , 24, 186-196	25.5	9
60	Older molecular brain age in severe mental illness. <i>Molecular Psychiatry</i> , 2021 , 26, 3646-3656	15.1	8
59	Genetic and epigenetic analysis of schizophrenia in blood-a no-brainer?. <i>Genome Medicine</i> , 2016 , 8, 96	14.4	8
58	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	13.9	8
57	Identification of functional genetic variation in exome sequence analysis. <i>BMC Proceedings</i> , 2011 , 5 Suppl 9, S13	2.3	7
56	Developmental and genetic regulation of the human cortex transcriptome in schizophrenia		7
55	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	3.6	6
54	Gene set bagging for estimating the probability a statistically significant result will replicate. <i>BMC Bioinformatics</i> , 2013 , 14, 360	3.6	6
53	Flexible expressed region analysis for RNA-seq with derfinder		6
52	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	7.9	5
51	A Bayesian Framework for Multiple Trait Colocalization from Summary Association Statistics		5
50	Integrating brain methylome with GWAS for psychiatric risk gene discovery		5
49	regionReport: Interactive reports for region-based analyses. <i>F1000Research</i> , 2015 , 4, 105	3.6	4
48	regionReport: Interactive reports for region-level and feature-level genomic analyses. <i>F1000Research</i> , 2015 , 4, 105	3.6	4
47	Single-nucleus transcriptome analysis reveals cell type-specific molecular signatures across reward circuitry in the human brain		4

46	dotdotdot: an automated approach to quantify multiplex single molecule fluorescent in situ hybridization (smFISH) images in complex tissues		4
45	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. <i>Molecular Psychiatry</i> , 2020 , 25, 3267-3277	15.1	4
44	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	15.1	4
43	recount3: summaries and queries for large-scale RNA-seq expression and splicing. <i>Genome Biology</i> , 2021 , 22, 323	18.3	3
42	Strategies for cellular deconvolution in human brain RNA sequencing data		3
41	Identification and prioritization of gene sets associated with schizophrenia risk by co-expression network analysis in human brain		3
40	recount-brain: a curated repository of human brain RNA-seq datasets metadata		3
39	Epigenome-wide study of brain DNA methylation following acute opioid intoxication. <i>Drug and Alcohol Dependence</i> , 2021 , 221, 108658	4.9	3
38	SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses. <i>BMC Bioinformatics</i> , 2021 , 22, 224	3.6	3
37	Cortical cellular diversity and development in schizophrenia. <i>Molecular Psychiatry</i> , 2021 , 26, 203-217	15.1	3
36	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers. <i>Neuropsychopharmacology</i> , 2021 , 46, 554-560	8.7	3
35	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. <i>Biological Psychiatry</i> , 2021 , 90, 399-408	7.9	3
34	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. <i>Nature Communications</i> , 2021 , 12, 5251	17.4	3
33	A framework for RNA quality correction in differential expression analysis		2
32	Addressing confounding artifacts in reconstruction of gene co-expression networks		2
31	Characterizing the nuclear and cytoplasmic transcriptomes in developing and mature human cortex uncovers new insight into psychiatric disease gene regulation		2
30	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	15.1	2
29	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data		2

28	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. <i>Nature Communications</i> , 2021 , 12, 3968	17.4	2
27	Decoding shared versus divergent transcriptomic signatures across cortico-amygdala circuitry in PTSD and depressive disorders		2
26	Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. <i>Frontiers in Immunology</i> , 2018 , 9, 2679	8.4	2
25	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways.. <i>Nature Neuroscience</i> , 2022 , 25, 381-389	25.5	2
24	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. <i>BMC Genomics</i> , 2022 , 23,	4.5	2
23	Epigenome-Wide Study of Brain DNA Methylation Among Opioid Users and Controls		1
22	Epigenome-wide association scan identifies methylation sites associated with HIV infection. <i>Epigenomics</i> , 2020 , 12, 1917-1927	4.4	1
21	Cell type-specific genetic regulation of expression in the granule cell layer of the human dentate gyrus		1
20	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers		1
19	Differential Expression of NPAS4 in the Dorsolateral Prefrontal Cortex Following Acute Opioid Intoxication		1
18	TrkB Signaling Influences Gene Expression in Cortistatin-Expressing Interneurons. <i>ENeuro</i> , 2020 , 7,	3.9	1
17	Defects of myelination are common pathophysiology in syndromic and idiopathic autism spectrum disorder		1
16	Widespread methylation quantitative trait loci and their role in schizophrenia risk		1
15	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods		1
14	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex		1
13	African-American and Caucasian participation in postmortem human brain donation for neuropsychiatric research. <i>PLoS ONE</i> , 2019 , 14, e0222565	3.7	1
12	Brain expressed FKBP5 delineates a therapeutic subtype of severe mental illness		1
11	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	5.1	1

10	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	4.6	o
9	Strategies for cellular deconvolution in human brain RNA sequencing data. <i>F1000Research</i> , 10, 750	3.6	o
8	Genetics and Brain Transcriptomics of Completed Suicide.. <i>American Journal of Psychiatry</i> , 2022 , 179, 226-241	11.9	o
7	Epigenome-wide association analyses of active injection drug use.. <i>Drug and Alcohol Dependence</i> , 2022 , 235, 109431	4.9	o
6	Curating the Evidence About COVID-19 for Frontline Public Health and Clinical Care: The Novel Coronavirus Research Compendium.. <i>Public Health Reports</i> , 2021 , 333549211058732	2.5	o
5	Comparison of quantitative trait loci methods: Total expression and allelic imbalance method in brain RNA-seq. <i>PLoS ONE</i> , 2019 , 14, e0217765	3.7	
4	Early developmental exposure to air pollution increases the risk of Alzheimers disease and amyloid production: Studies in mouse and Caenorhabditis elegans. <i>Alzheimers and Dementia</i> , 2020 , 16, e043846 ^{1.2}		
3	Measurement, Summary, and Methodological Variation in RNA-sequencing 2014 , 115-128		
2	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		
1	Differential expression of NPAS4 in the dorsolateral prefrontal cortex following opioid overdose 2022 , 3, 100040		