Andrew E Jaffe

List of Publications by Year in Descending Order

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	Induction of Bdnf from promoter I following electroconvulsive seizures contributes to structural plasticity in neurons of the piriform cortex.. *Brain Stimulation*, **2022**, 15, 427-433	5.1	1
152	Genetics and Brain Transcriptomics of Completed Suicide.. *American Journal of Psychiatry*, **2022**, 179, 226-241	11.9	0
151	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways.. *Nature Neuroscience*, **2022**, 25, 381-389	25.5	2
150	Differential expression of NPAS4 in the dorsolateral prefrontal cortex following opioid overdose **2022**, 3, 100040		
149	Epigenome-wide association analyses of active injection drug use.. *Drug and Alcohol Dependence*, **2022**, 235, 109431	4.9	0
148	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. *BMC Genomics*, **2022**, 23,	4.5	2
147	Older molecular brain age in severe mental illness. *Molecular Psychiatry*, **2021**, 26, 3646-3656	15.1	8
146	recount3: summaries and queries for large-scale RNA-seq expression and splicing. *Genome Biology*, **2021**, 22, 323	18.3	3
145	Single molecule in situ hybridization reveals distinct localizations of schizophrenia risk-related transcripts SNX19 and AS3MT in human brain. *Molecular Psychiatry*, **2021**, 26, 3536-3547	15.1	2
144	Epigenome-wide study of brain DNA methylation following acute opioid intoxication. *Drug and Alcohol Dependence*, **2021**, 221, 108658	4.9	3
143	SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses. *BMC Bioinformatics*, **2021**, 22, 224	3.6	3
142	Altered adipokines in obese adolescents: a cross-sectional and longitudinal analysis across the spectrum of glycemia. *American Journal of Physiology - Endocrinology and Metabolism*, **2021**, 320, E1044-E1052	6	
141	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968	17.4	2
140	Cortical cellular diversity and development in schizophrenia. *Molecular Psychiatry*, **2021**, 26, 203-217	15.1	3
139	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. *Epigenetics*, **2021**, 16, 1-13	5.7	9
138	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers. *Neuropsychopharmacology*, **2021**, 46, 554-560	8.7	3
137	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. *Nature Neuroscience*, **2021**, 24, 176-185	25.5	19

136	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. *Nature Neuroscience*, **2021**, 24, 425-436	25.5	69
135	Cerebral cortex and blood transcriptome changes in mouse neonates prenatally exposed to air pollution particulate matter. *Journal of Neurodevelopmental Disorders*, **2021**, 13, 30	4.6	0
134	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. *Biological Psychiatry*, **2021**, 90, 399-408	7.9	3
133	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. *Nature Communications*, **2021**, 12, 5251	17.4	3
132	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. *Neuron*, **2021**, 109, 3088-3103.e5	13.9	8
131	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. *Nature Neuroscience*, **2021**, 24, 186-196	25.5	9
130	Curating the Evidence About COVID-19 for Frontline Public Health and Clinical Care: The Novel Coronavirus Research Compendium.. *Public Health Reports*, **2021**, 333549211058732	2.5	0
129	Early developmental exposure to air pollution increases the risk of Alzheimers disease and amyloid production: Studies in mouse and Caenorhabditis elegans. *Alzheimers and Dementia*, **2020**, 16, e043846	1.2	
128	dotdotdot: an automated approach to quantify multiplex single molecule fluorescent in situ hybridization (smFISH) images in complex tissues. *Nucleic Acids Research*, **2020**, 48, e66	20.1	15
127	Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders. *Science Advances*, **2020**, 6,	14.3	15
126	Profiling gene expression in the human dentate gyrus granule cell layer reveals insights into schizophrenia and its genetic risk. *Nature Neuroscience*, **2020**, 23, 510-519	25.5	30
125	Adult mouse hippocampal transcriptome changes associated with long-term behavioral and metabolic effects of gestational air pollution toxicity. *Translational Psychiatry*, **2020**, 10, 218	8.6	12
124	Recounting the FANTOM CAGE-Associated Transcriptome. *Genome Research*, **2020**, 30, 1073-1081	9.7	13
123	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. *Nature Communications*, **2020**, 11, 462	17.4	37
122	Molecularly Defined Hippocampal Inputs Regulate Population Dynamics in the Prelimbic Cortex to Suppress Context Fear Memory Retrieval. *Biological Psychiatry*, **2020**, 88, 554-565	7.9	5
121	Epigenome-wide association scan identifies methylation sites associated with HIV infection. *Epigenomics*, **2020**, 12, 1917-1927	4.4	1
120	TrkB Signaling Influences Gene Expression in Cortistatin-Expressing Interneurons. *ENeuro*, **2020**, 7,	3.9	1
119	Cannabinoid receptor CNR1 expression and DNA methylation in human prefrontal cortex, hippocampus and caudate in brain development and schizophrenia. *Translational Psychiatry*, **2020**, 10, 158	8.6	19

118	A myelin-related transcriptomic profile is shared by Pitt-Hopkins syndrome models and human autism spectrum disorder. *Nature Neuroscience*, **2020**, 23, 375-385	25.5	34
117	Characterizing the nuclear and cytoplasmic transcriptomes in developing and mature human cortex uncovers new insight into psychiatric disease gene regulation. *Genome Research*, **2020**, 30, 1-11	9.7	12
116	Association of Missense Mutation in FOLH1 With Decreased NAAG Levels and Impaired Working Memory Circuitry and Cognition. *American Journal of Psychiatry*, **2020**, 177, 1129-1139	11.9	13
115	Identification and prioritization of gene sets associated with schizophrenia risk by co-expression network analysis in human brain. *Molecular Psychiatry*, **2020**, 25, 791-804	15.1	47
114	Schizophrenia risk variants influence multiple classes of transcripts of sorting nexin 19 (SNX19). *Molecular Psychiatry*, **2020**, 25, 831-843	15.1	17
113	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. *Molecular Psychiatry*, **2020**, 25, 3267-3277	15.1	4
112	KCNH2-3.1 mediates aberrant complement activation and impaired hippocampal-medial prefrontal circuitry associated with working memory deficits. *Molecular Psychiatry*, **2020**, 25, 206-229	15.1	4
111	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. *Genome Biology*, **2019**, 20, 196	18.3	42
110	Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimer's disease. *Acta Neuropathologica*, **2019**, 137, 557-569	14.3	30
109	Comparison of quantitative trait loci methods: Total expression and allelic imbalance method in brain RNA-seq. *PLoS ONE*, **2019**, 14, e0217765	3.7	
108	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods. *BMC Genomics*, **2019**, 20, 513	4.5	36
107	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. *Neuron*, **2019**, 103, 203-216.e8	13.9	67
106	Addressing confounding artifacts in reconstruction of gene co-expression networks. *Genome Biology*, **2019**, 20, 94	18.3	37
105	Prefrontal Coexpression of Schizophrenia Risk Genes Is Associated With Treatment Response in Patients. *Biological Psychiatry*, **2019**, 86, 45-55	7.9	14
104	Cytokine, Chemokine, and Cytokine Receptor Changes Are Associated With Metabolic Improvements After Bariatric Surgery. *Journal of Clinical Endocrinology and Metabolism*, **2019**, 104, 947-956	5.6	13
103	African-American and Caucasian participation in postmortem human brain donation for neuropsychiatric research. *PLoS ONE*, **2019**, 14, e0222565	3.7	1
102	Association of a Noncoding RNA Postmortem With Suicide by Violent Means and In Vivo With Aggressive Phenotypes. *Biological Psychiatry*, **2019**, 85, 417-424	7.9	9
101	Improving the value of public RNA-seq expression data by phenotype prediction. *Nucleic Acids Research*, **2018**, 46, e54	20.1	31

100	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. *Science*, **2018**, 359, 693-697	33.3	547
99	A Bayesian framework for multiple trait colocalization from summary association statistics. *Bioinformatics*, **2018**, 34, 2538-2545	7.2	99
98	Genetic risk mechanisms of posttraumatic stress disorder in the human brain. *Journal of Neuroscience Research*, **2018**, 96, 21-30	4.4	16
97	Investigating the neuroimmunogenic architecture of schizophrenia. *Molecular Psychiatry*, **2018**, 23, 1251-1260	15.1	41
96	GAD1 alternative transcripts and DNA methylation in human prefrontal cortex and hippocampus in brain development, schizophrenia. *Molecular Psychiatry*, **2018**, 23, 1496-1505	15.1	28
95	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. *Molecular Psychiatry*, **2018**, 23, 304-315	15.1	29
94	Longitudinal analyses of the DNA methylome in deployed military servicemen identify susceptibility loci for post-traumatic stress disorder. *Molecular Psychiatry*, **2018**, 23, 1145-1156	15.1	67
93	Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. *Nature Neuroscience*, **2018**, 21, 1117-1125	25.5	176
92	Genetic vulnerability to DUSP22 promoter hypermethylation is involved in the relation between in utero famine exposure and schizophrenia. *NPJ Schizophrenia*, **2018**, 4, 16	5.5	20
91	BDNF-TrkB signaling in oxytocin neurons contributes to maternal behavior. *ELife*, **2018**, 7,	8.9	18
90	O4.1. GENETIC VULNERABILITY TO DUSP22 PROMOTOR HYPERMETHYLATION IS INVOLVED IN THE RELATION BETWEEN IN UTERO FAMINE EXPOSURE AND SCHIZOPHRENIA. *Schizophrenia Bulletin*, **2018**, 44, S82-S82	1.3	78
89	O4.7. PLACENTAL GENE EXPRESSION, OBSTETRICAL HISTORY AND POLYGENIC RISK FOR SCHIZOPHRENIA. *Schizophrenia Bulletin*, **2018**, 44, S85-S86	1.3	78
88	Revealing the brainS molecular architecture. *Science*, **2018**, 362, 1262-1263	33.3	29
87	Transcriptome and epigenome landscape of human cortical development modeled in organoids. *Science*, **2018**, 362,	33.3	142
86	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
85	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. *Science*, **2018**, 362,	33.3	434
84	Comprehensive functional genomic resource and integrative model for the human brain. *Science*, **2018**, 362,	33.3	319
83	Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. *Frontiers in Immunology*, **2018**, 9, 2679	8.4	2

82	Convergence of placenta biology and genetic risk for schizophrenia. *Nature Medicine*, **2018**, 24, 792-801	50.5	141
81	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. *Nature Methods*, **2017**, 14, 216-217	21.6	47
80	Reproducible RNA-seq analysis using recount2. *Nature Biotechnology*, **2017**, 35, 319-321	44.5	211
79	Altered expression of histamine signaling genes in autism spectrum disorder. *Translational Psychiatry*, **2017**, 7, e1126	8.6	49
78	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. *Science*, **2017**, 356,	33.3	152
77	qSVA framework for RNA quality correction in differential expression analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 7130-7135	11.5	58
76	Flexible expressed region analysis for RNA-seq with derfinder. *Nucleic Acids Research*, **2017**, 45, e9	20.1	32
75	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. *Genes*, **2017**, 8,	4.2	44
74	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. *F1000Research*, **2017**, 6, 1558	3.6	30
73	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. *Bioinformatics*, **2017**, 33, 4033-4040	7.2	33
72	Schizophrenia-Associated hERG channel Kv11.1-3.1 Exhibits a Unique Trafficking Deficit that is Rescued Through Proteasome Inhibition for High Throughput Screening. *Scientific Reports*, **2016**, 6, 19976	4.9	12
71	Assessment of genetic risk for distribution of total interstitial white matter neurons in dorsolateral prefrontal cortex: role in schizophrenia. *Schizophrenia Research*, **2016**, 176, 141-143	3.6	6
70	Psychiatric Risk Gene Transcription Factor 4 Regulates Intrinsic Excitability of Prefrontal Neurons via Repression of SCN10a and KCNQ1. *Neuron*, **2016**, 90, 43-55	13.9	68
69	Postmortem human brain genomics in neuropsychiatric disorders--how far can we go?. *Current Opinion in Neurobiology*, **2016**, 36, 107-11	7.6	18
68	Mapping DNA methylation across development, genotype and schizophrenia in the human frontal cortex. *Nature Neuroscience*, **2016**, 19, 40-7	25.5	299
67	Strong Components of Epigenetic Memory in Cultured Human Fibroblasts Related to Site of Origin and Donor Age. *PLoS Genetics*, **2016**, 12, e1005819	6	15
66	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. *Genome Biology*, **2016**, 17, 266	18.3	65
65	Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. *JAMA Psychiatry*, **2016**, 73, 506-14	14.5	108

64	A human-specific AS3MT isoform and BORCS7 are molecular risk factors in the 10q24.32 schizophrenia-associated locus. *Nature Medicine*, **2016**, 22, 649-56	50.5	112
63	C1q/TNF-Related Protein-9 (CTRP9) Levels Are Associated With Obesity and Decrease Following Weight Loss Surgery. *Journal of Clinical Endocrinology and Metabolism*, **2016**, 101, 2211-7	5.6	26
62	Genetic and epigenetic analysis of schizophrenia in blood-a no-brainer?. *Genome Medicine*, **2016**, 8, 96	14.4	8
61	Ballgown bridges the gap between transcriptome assembly and expression analysis. *Nature Biotechnology*, **2015**, 33, 243-6	44.5	413
60	Prenatal mercury concentration is associated with changes in DNA methylation at TCEANC2 in newborns. *International Journal of Epidemiology*, **2015**, 44, 1249-62	7.8	48
59	Differential DNA methylation identified in the blood and retina of AMD patients. *Epigenetics*, **2015**, 10, 698-707	5.7	46
58	Polyester: simulating RNA-seq datasets with differential transcript expression. *Bioinformatics*, **2015** , 31, 2778-84	7.2	160
57	Paternal sperm DNA methylation associated with early signs of autism risk in an autism-enriched cohort. *International Journal of Epidemiology*, **2015**, 44, 1199-210	7.8	91
56	DNA methylation age of blood predicts all-cause mortality in later life. *Genome Biology*, **2015**, 16, 25	18.3	670
55	The PsychENCODE project. *Nature Neuroscience*, **2015**, 18, 1707-12	25.5	226
54	Developmental regulation of human cortex transcription and its clinical relevance at single base resolution. *Nature Neuroscience*, **2015**, 18, 154-161	25.5	110
53	Practical impacts of genomic data "cleaning" on biological discovery using surrogate variable analysis. *BMC Bioinformatics*, **2015**, 16, 372	3.6	32
52	BrainSeq: Neurogenomics to Drive Novel Target Discovery for Neuropsychiatric Disorders. *Neuron*, **2015**, 88, 1078-1083	13.9	67
51	Investigation of the prenatal expression patterns of 108 schizophrenia-associated genetic loci. *Biological Psychiatry*, **2015**, 77, e43-51	7.9	42
50	Mouse-human experimental epigenetic analysis unmasks dietary targets and genetic liability for diabetic phenotypes. *Cell Metabolism*, **2015**, 21, 138-49	24.6	76
49	regionReport: Interactive reports for region-based analyses. *F1000Research*, **2015**, 4, 105	3.6	4
48	regionReport: Interactive reports for region-level and feature-level genomic analyses. *F1000Research*, **2015**, 4, 105	3.6	4
47	Genetic neuropathology of obsessive psychiatric syndromes. *Translational Psychiatry*, **2014**, 4, e432	8.6	26

46	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. *Bioinformatics*, **2014**, 30, 1363-9	7.2	1941
45	Paternal age, de novo mutations and schizophrenia. *Molecular Psychiatry*, **2014**, 19, 274-5	15.1	32
44	Prenatal expression patterns of genes associated with neuropsychiatric disorders. *American Journal of Psychiatry*, **2014**, 171, 758-67	11.9	76
43	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. *JAMA Psychiatry*, **2014**, 71, 1112-20	14.5	89
42	Genome-wide and gene-specific epigenomic platforms for hepatocellular carcinoma biomarker development trials. *Gastroenterology Research and Practice*, **2014**, 2014, 597164	2	12
41	Accounting for cellular heterogeneity is critical in epigenome-wide association studies. *Genome Biology*, **2014**, 15, R31	18.3	660
40	Measurement, Summary, and Methodological Variation in RNA-sequencing **2014**, 115-128		
39	Hypomethylation of the IL17RC promoter in peripheral blood leukocytes is not a hallmark of age-related macular degeneration. *Cell Reports*, **2013**, 5, 1527-35	10.6	37
38	TE-array--a high throughput tool to study transposon transcription. *BMC Genomics*, **2013**, 14, 869	4.5	11
37	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. *Neuroscience Research*, **2013**, 77, 247-50	2.9	41
36	MULTIPLE TESTING OF LOCAL MAXIMA FOR DETECTION OF PEAKS IN CHIP-SEQ DATA. *Annals of Applied Statistics*, **2013**, 7, 471-494	2.1	11
35	Gene set bagging for estimating the probability a statistically significant result will replicate. *BMC Bioinformatics*, **2013**, 14, 360	3.6	6
34	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. *International Journal of Epidemiology*, **2012**, 41, 200-9	7.8	430
33	Use of postmortem human dura mater and scalp for deriving human fibroblast cultures. *PLoS ONE*, **2012**, 7, e45282	3.7	19
32	Significance analysis and statistical dissection of variably methylated regions. *Biostatistics*, **2012**, 13, 166-78	3.7	75
31	The sva package for removing batch effects and other unwanted variation in high-throughput experiments. *Bioinformatics*, **2012**, 28, 882-3	7.2	1996
30	DNA methylation shows genome-wide association of NFIX, RAPGEF2 and MSRB3 with gestational age at birth. *International Journal of Epidemiology*, **2012**, 41, 188-99	7.8	60
29	Identification of functional genetic variation in exome sequence analysis. *BMC Proceedings*, **2011**, 5 Suppl 9, S13	2.3	7

28	Genome-wide analysis of promoter methylation associated with gene expression profile in pancreatic adenocarcinoma. *Clinical Cancer Research*, **2011**, 17, 4341-54	12.9	131
27	Global DNA hypomethylation is associated with in utero exposure to cotinine and perfluorinated alkyl compounds. *Epigenetics*, **2010**, 5, 539-46	5.7	146
26	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. *Nature Genetics*, **2009**, 41, 1191-8	36.3	285
25	Epigenome-Wide Study of Brain DNA Methylation Among Opioid Users and Controls		1
24	Cell type-specific genetic regulation of expression in the granule cell layer of the human dentate gyrus		1
23	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers		1
22	Differential Expression of NPAS4 in the Dorsolateral Prefrontal Cortex Following Acute Opioid Intoxication		1
21	A framework for RNA quality correction in differential expression analysis		2
20	Developmental and genetic regulation of the human cortex transcriptome in schizophrenia		7
19	Defects of myelination are common pathophysiology in syndromic and idiopathic autism spectrum disorder		1
18	A Bayesian Framework for Multiple Trait Colocalization from Summary Association Statistics		5
17	Strategies for cellular deconvolution in human brain RNA sequencing data		3
16	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex		16
15	Widespread methylation quantitative trait loci and their role in schizophrenia risk		1
14	Single-nucleus transcriptome analysis reveals cell type-specific molecular signatures across reward circuitry in the human brain		4
13	Addressing confounding artifacts in reconstruction of gene co-expression networks		2
12	Identification and prioritization of gene sets associated with schizophrenia risk by co-expression network analysis in human brain		3
11	Integrating brain methylome with GWAS for psychiatric risk gene discovery		5

10	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods		1
9	Characterizing the nuclear and cytoplasmic transcriptomes in developing and mature human cortex uncovers new insight into psychiatric disease gene regulation		2
8	recount-brain: a curated repository of human brain RNA-seq datasets metadata		3
7	dotdotdot: an automated approach to quantify multiplex single molecule fluorescent in situ hybridization (smFISH) images in complex tissues		4
6	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex		1
5	Flexible expressed region analysis for RNA-seq with derfinder		6
4	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data		2
3	Decoding shared versus divergent transcriptomic signatures across cortico-amygdala circuitry in PTSD and depressive disorders		2
2	Strategies for cellular deconvolution in human brain RNA sequencing data. *F1000Research*,10, 750	3.6	0
1	Brain expressed FKBP5 delineates a therapeutic subtype of severe mental illness		1