Andrew E Jaffe

List of Publications by Year
in descending order

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Version: 2024-02-01

133 papers	21,493 citations	38720 50 h-index	14736 127 g-index
186 all docs	186 docs citations	186 times ranked	33869 citing authors

#	Article	IF	Citations
1	Electrophysiological measures from human iPSC-derived neurons are associated with schizophrenia clinical status and predict individual cognitive performance. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	29
2	Molecular phenotypes associated with antipsychotic drugs in the human caudate nucleus. Molecular Psychiatry, 2022, 27, 2061-2067.	4.1	10
3	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.	0.7	4
4	Genetics and Brain Transcriptomics of Completed Suicide. American Journal of Psychiatry, 2022, 179, 226-241.	4.0	17
5	Amygdala and anterior cingulate transcriptomes from individuals with bipolar disorder reveal downregulated neuroimmune and synaptic pathways. Nature Neuroscience, 2022, 25, 381-389.	7.1	27
6	Differential expression of NPAS4 in the dorsolateral prefrontal cortex following opioid overdose. , 2022, 3, 100040.		5
7	Epigenome-wide association analyses of active injection drug use. Drug and Alcohol Dependence, 2022, 235, 109431.	1.6	5
8	Curating the Evidence About COVID-19 for Frontline Public Health and Clinical Care: The Novel Coronavirus Research Compendium. Public Health Reports, 2022, 137, 197-202.	1.3	2
9	spatialLIBD: an R/Bioconductor package to visualize spatially-resolved transcriptomics data. BMC Genomics, 2022, 23, .	1.2	50
10	Decoding Shared Versus Divergent Transcriptomic Signatures Across Cortico-Amygdala Circuitry in PTSD and Depressive Disorders. American Journal of Psychiatry, 2022, 179, 673-686.	4.0	21
11	Older molecular brain age in severe mental illness. Molecular Psychiatry, 2021, 26, 3646-3656.	4.1	23
12	Cortical cellular diversity and development in schizophrenia. Molecular Psychiatry, 2021, 26, 203-217.	4.1	11
13	Characterizing the dynamic and functional DNA methylation landscape in the developing human cortex. Epigenetics, 2021, 16, 1-13.	1.3	19
14	Genome-wide DNA methylation differences in nucleus accumbens of smokers vs. nonsmokers. Neuropsychopharmacology, 2021, 46, 554-560.	2.8	19
15	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.	7.1	73
16	Transcriptome-scale spatial gene expression in the human dorsolateral prefrontal cortex. Nature Neuroscience, 2021, 24, 425-436.	7.1	418
17	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.	4.1	5
18	Epigenome-wide study of brain DNA methylation following acute opioid intoxication. Drug and Alcohol Dependence, 2021, 221, 108658.	1.6	15

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19	SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses. BMC Bioinformatics, 2021, 22, 224.	1.2	14
20	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.	1.8	5
21	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
22	Cerebral cortex and blood transcriptome changes in mouse neonates prenatally exposed to air pollution particulate matter. Journal of Neurodevelopmental Disorders, 2021, 13, 30.	1.5	9
23	Developmental Profile of Psychiatric Risk Associated With Voltage-Gated Cation Channel Activity. Biological Psychiatry, 2021, 90, 399-408.	0.7	10
24	Genome-wide sequencing-based identification of methylation quantitative trait loci and their role in schizophrenia risk. Nature Communications, 2021, 12, 5251.	5.8	37
25	Single-nucleus transcriptome analysis reveals cell-type-specific molecular signatures across reward circuitry in the human brain. Neuron, 2021, 109, 3088-3103.e5.	3.8	95
26	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. Nature Neuroscience, 2021, 24, 186-196.	7.1	22
27	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	3.8	103
28	Identification and prioritization of gene sets associated with schizophrenia risk by co-expression network analysis in human brain. Molecular Psychiatry, 2020, 25, 791-804.	4.1	86
29	Schizophrenia risk variants influence multiple classes of transcripts of sorting nexin 19 (SNX19). Molecular Psychiatry, 2020, 25, 831-843.	4.1	36
30	Developmental effects of maternal smoking during pregnancy on the human frontal cortex transcriptome. Molecular Psychiatry, 2020, 25, 3267-3277.	4.1	16
31	Spatial transcriptomics: putting genome-wide expression on the map. Neuropsychopharmacology, 2020, 45, 232-233.	2.8	17
32	KCNH2-3.1 mediates aberrant complement activation and impaired hippocampal-medial prefrontal circuitry associated with working memory deficits. Molecular Psychiatry, 2020, 25, 206-229.	4.1	13
33	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.	2.4	29
34	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.	4.0	29
35	Early developmental exposure to air pollution increases the risk of Alzheimers disease and amyloid production: Studies in mouse and Caenorhabditis elegans. Alzheimer's and Dementia, 2020, 16, e043846.	0.4	0
36	dotdotdot: an automated approach to quantify multiplex single molecule fluorescent in situ hybridization (smFISH) images in complex tissues. Nucleic Acids Research, 2020, 48, e66-e66.	6.5	46

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37	Incomplete annotation has a disproportionate impact on our understanding of Mendelian and complex neurogenetic disorders. Science Advances, 2020, 6, .	4.7	44
38	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.	7.1	67
39	Adult mouse hippocampal transcriptome changes associated with long-term behavioral and metabolic effects of gestational air pollution toxicity. Translational Psychiatry, 2020, 10, 218.	2.4	23
40	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	2.4	35
41	Dissecting transcriptomic signatures of neuronal differentiation and maturation using iPSCs. Nature Communications, 2020, 11, 462.	5.8	96
42	Molecularly Defined Hippocampal Inputs Regulate Population Dynamics in the Prelimbic Cortex to Suppress Context Fear Memory Retrieval. Biological Psychiatry, 2020, 88, 554-565.	0.7	17
43	Cannabinoid receptor CNR1 expression and DNA methylation in human prefrontal cortex, hippocampus and caudate in brain development and schizophrenia. Translational Psychiatry, 2020, 10, 158.	2.4	42
44	A myelin-related transcriptomic profile is shared by Pittâ€“Hopkins syndrome models and human autism spectrum disorder. Nature Neuroscience, 2020, 23, 375-385.	7.1	89
45	TrkB Signaling Influences Gene Expression in Cortistatin-Expressing Interneurons. ENeuro, 2020, 7, ENEURO.0310-19.2019.	0.9	10
46	Epigenome-wide association scan identifies methylation sites associated with HIV infection. Epigenomics, 2020, 12, 1917-1927.	1.0	7
47	Divergent neuronal DNA methylation patterns across human cortical development reveal critical periods and a unique role of CpH methylation. Genome Biology, 2019, 20, 196.	3.8	67
48	Integrated DNA methylation and gene expression profiling across multiple brain regions implicate novel genes in Alzheimerâ€™s disease. Acta Neuropathologica, 2019, 137, 557-569.	3.9	73
49	Comparison of quantitative trait loci methods: Total expression and allelic imbalance method in brain RNA-seq. PLoS ONE, 2019, 14, e0217765.	1.1	0
50	Comprehensive assessment of multiple biases in small RNA sequencing reveals significant differences in the performance of widely used methods. BMC Genomics, 2019, 20, 513.	1.2	65
51	Regional Heterogeneity in Gene Expression, Regulation, and Coherence in the Frontal Cortex and Hippocampus across Development and Schizophrenia. Neuron, 2019, 103, 203-216.e8.	3.8	158
52	Addressing confounding artifacts in reconstruction of gene co-expression networks. Genome Biology, 2019, 20, 94.	3.8	68
53	Prefrontal Coexpression of Schizophrenia Risk Genes Is Associated With Treatment Response in Patients. Biological Psychiatry, 2019, 86, 45-55.	0.7	27
54	Cytokine, Chemokine, and Cytokine Receptor Changes Are Associated With Metabolic Improvements After Bariatric Surgery. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 947-956.	1.8	23

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55	African-American and Caucasian participation in postmortem human brain donation for neuropsychiatric research. PLoS ONE, 2019, 14, e0222565.	1.1	5
56	Association of a Noncoding RNA Postmortem With Suicide by Violent Means and InÂVivo With Aggressive Phenotypes. Biological Psychiatry, 2019, 85, 417-424.	0.7	13
57	Improving the value of public RNA-seq expression data by phenotype prediction. Nucleic Acids Research, 2018, 46, e54-e54.	6.5	49
58	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
59	A Bayesian framework for multiple trait colocalization from summary association statistics. Bioinformatics, 2018, 34, 2538-2545.	1.8	203
60	Genetic risk mechanisms of posttraumatic stress disorder in the human brain. Journal of Neuroscience Research, 2018, 96, 21-30.	1.3	24
61	Investigating the neuroimmunogenic architecture of schizophrenia. Molecular Psychiatry, 2018, 23, 1251-1260.	4.1	59
62	GAD1 alternative transcripts and DNA methylation in human prefrontal cortex and hippocampus in brain development, schizophrenia. Molecular Psychiatry, 2018, 23, 1496-1505.	4.1	52
63	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.	4.1	43
64	Longitudinal analyses of the DNA methylome in deployed military servicemen identify susceptibility loci for post-traumatic stress disorder. Molecular Psychiatry, 2018, 23, 1145-1156.	4.1	98
65	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.	2.3	0
66	O4.7. PLACENTAL GENE EXPRESSION, OBSTETRICAL HISTORY AND POLYGENIC RISK FOR SCHIZOPHRENIA. Schizophrenia Bulletin, 2018, 44, S85-S86.	2.3	0
67	Revealing the brain's molecular architecture. Science, 2018, 362, 1262-1263.	6.0	45
68	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
69	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
70	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805
71	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
72	Non-coding Class Switch Recombination-Related Transcription in Human Normal and Pathological Immune Responses. Frontiers in Immunology, 2018, 9, 2679.	2.2	4

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73	Convergence of placenta biology and genetic risk for schizophrenia. Nature Medicine, 2018, 24, 792-801.	15.2	214
74	Developmental and genetic regulation of the human cortex transcriptome illuminate schizophrenia pathogenesis. Nature Neuroscience, 2018, 21, 1117-1125.	7.1	300
75	Genetic vulnerability to DUSP22 promoter hypermethylation is involved in the relation between in utero famine exposure and schizophrenia. NPJ Schizophrenia, 2018, 4, 16.	2.0	34
76	BDNF-TrkB signaling in oxytocin neurons contributes to maternal behavior. ELife, 2018, 7, .	2.8	38
77	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. Bioinformatics, 2017, 33, 4033-4040.	1.8	57
78	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. Nature Methods, 2017, 14, 216-217.	9.0	59
79	Reproducible RNA-seq analysis using recount2. Nature Biotechnology, 2017, 35, 319-321.	9.4	395
80	Altered expression of histamine signaling genes in autism spectrum disorder. Translational Psychiatry, 2017, 7, e1126-e1126.	2.4	89
81	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. Science, 2017, 356, .	6.0	206
82	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.	3.3	95
83	Flexible expressed region analysis for RNA-seq with<tt>derfinder</tt>. Nucleic Acids Research, 2017, 45, e9-e9.	6.5	54
84	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, 152.	1.0	66
85	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. F1000Research, 2017, 6, 1558.	0.8	50
86	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.	3.8	94
87	Association of DNA Methylation Differences With Schizophrenia in an Epigenome-Wide Association Study. JAMA Psychiatry, 2016, 73, 506.	6.0	151
88	A human-specific AS3MT isoform and BORCS7 are molecular risk factors in the 10q24.32 schizophrenia-associated locus. Nature Medicine, 2016, 22, 649-656.	15.2	142
89	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, 2211-2217.	1.8	36
90	Genetic and epigenetic analysis of schizophrenia in bloodâ€"a no-brainer?. Genome Medicine, 2016, 8, 96.	3.6	9

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91	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.	1.6	16
92	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.	1.1	6
93	Psychiatric Risk Gene Transcription Factor 4 Regulates Intrinsic Excitability of Prefrontal Neurons via Repression of SCN10a and KCNQ1. Neuron, 2016, 90, 43-55.	3.8	88
94	Postmortem human brain genomics in neuropsychiatric disordersâ€"how far can we go?. Current Opinion in Neurobiology, 2016, 36, 107-111.	2.0	20
95	Mapping DNA methylation across development, genotype and schizophrenia in the human frontal cortex. Nature Neuroscience, 2016, 19, 40-47.	7.1	417
96	Strong Components of Epigenetic Memory in Cultured Human Fibroblasts Related to Site of Origin and Donor Age. PLoS Genetics, 2016, 12, e1005819.	1.5	20
97	Practical impacts of genomic data â€œcleaningâ€•on biological discovery using surrogate variable analysis. BMC Bioinformatics, 2015, 16, 372.	1.2	51
98	BrainSeq: Neurogenomics to Drive Novel Target Discovery for Neuropsychiatric Disorders. Neuron, 2015, 88, 1078-1083.	3.8	92
99	Investigation of the Prenatal Expression Patterns of 108 Schizophrenia-Associated Genetic Loci. Biological Psychiatry, 2015, 77, e43-e51.	0.7	51
100	Mouse-Human Experimental Epigenetic Analysis Unmasks Dietary Targets and Genetic Liability for Diabetic Phenotypes. Cell Metabolism, 2015, 21, 138-149.	7.2	98
101	Ballgown bridges the gap between transcriptome assembly and expression analysis. Nature Biotechnology, 2015, 33, 243-246.	9.4	716
102	Prenatal mercury concentration is associated with changes in DNA methylation atTCEANC2in newborns. International Journal of Epidemiology, 2015, 44, 1249-1262.	0.9	60
103	Differential DNA methylation identified in the blood and retina of AMD patients. Epigenetics, 2015, 10, 698-707.	1.3	62
104	Polyester: simulating RNA-seq datasets with differential transcript expression. Bioinformatics, 2015, 31, 2778-2784.	1.8	250
105	Paternal sperm DNA methylation associated with early signs of autism risk in an autism-enriched cohort. International Journal of Epidemiology, 2015, 44, 1199-1210.	0.9	121
106	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	3.8	928
107	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
108	Developmental regulation of human cortex transcription and its clinical relevance at single base resolution. Nature Neuroscience, 2015, 18, 154-161.	7.1	142

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109	regionReport: Interactive reports for region-based analyses. F1000Research, 2015, 4, 105.	0.8	5
110	regionReport: Interactive reports for region-level and feature-level genomic analyses. F1000Research, 2015, 4, 105.	0.8	4
111	Paternal age, de novo mutations and schizophrenia. Molecular Psychiatry, 2014, 19, 274-275.	4.1	37
112	Prenatal Expression Patterns of Genes Associated With Neuropsychiatric Disorders. American Journal of Psychiatry, 2014, 171, 758-767.	4.0	96
113	Expression ofZNF804Ain Human Brain and Alterations in Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. JAMA Psychiatry, 2014, 71, 1112.	6.0	102
114	Genome-Wide and Gene-Specific Epigenomic Platforms for Hepatocellular Carcinoma Biomarker Development Trials. Gastroenterology Research and Practice, 2014, 2014, 1-9.	0.7	12
115	Accounting for cellular heterogeneity is critical in epigenome-wide association studies. Genome Biology, 2014, 15, R31.	13.9	880
116	Genetic neuropathology of obsessive psychiatric syndromes. Translational Psychiatry, 2014, 4, e432-e432.	2.4	35
117	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. Bioinformatics, 2014, 30, 1363-1369.	1.8	3,192
118	Measurement, Summary, and Methodological Variation in RNA-sequencing. , 2014, , 115-128.		0
119	Hypomethylation of the IL17RC Promoter in Peripheral Blood Leukocytes Is Not A Hallmark of Age-Related Macular Degeneration. Cell Reports, 2013, 5, 1527-1535.	2.9	42
120	TE-arrayâ€"a high throughput tool to study transposon transcription. BMC Genomics, 2013, 14, 869.	1.2	12
121	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, 247-250.	1.0	51
122	Multiple testing of local maxima for detection of peaks in ChIP-Seq data. Annals of Applied Statistics, 2013, 7, 471-494.	0.5	12
123	Gene set bagging for estimating the probability a statistically significant result will replicate. BMC Bioinformatics, 2013, 14, 360.	1.2	7
124	Significance analysis and statistical dissection of variably methylated regions. Biostatistics, 2012, 13, 166-178.	0.9	92
125	The <tt>sva</tt> package for removing batch effects and other unwanted variation in high-throughput experiments. Bioinformatics, 2012, 28, 882-883.	1.8	3,912
126	DNA methylation shows genome-wide association ofNFIX,RAPGEF2andMSRB3with gestational age at birth. International Journal of Epidemiology, 2012, 41, 188-199.	0.9	71

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127	Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. International Journal of Epidemiology, 2012, 41, 200-209.	0.9	567
128	Use of Postmortem Human Dura Mater and Scalp for Deriving Human Fibroblast Cultures. PLoS ONE, 2012, 7, e45282.	1.1	28
129	Identification of functional genetic variation in exome sequence analysis. BMC Proceedings, 2011, 5, S13.	1.8	9
130	Genome-Wide Analysis of Promoter Methylation Associated with Gene Expression Profile in Pancreatic Adenocarcinoma. Clinical Cancer Research, 2011, 17, 4341-4354.	3.2	154
131	Global DNA hypomethylation is associated with in utero exposure to cotinine and perfluorinated alkyl compounds. Epigenetics, 2010, 5, 539-546.	1.3	172
132	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	9.4	324
133	Strategies for cellular deconvolution in human brain RNA sequencing data. F1000Research, 0, 10, 750.	0.8	4