## Yongchao Ge

List of Publications by Year in descending order

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YONCCHAO GE

#	Article	IF	CITATIONS
1	Contribution of Age, Brain Region, Mood Disorder Pathology, and Interindividual Factors on the Methylome of Human Microglia. Biological Psychiatry, 2022, 91, 572-581.	1.3	12
2	Optimization of the Omni-ATAC protocol to chromatin accessibility profiling in snap-frozen rat adipose and muscle tissues. MethodsX, 2022, 9, 101681.	1.6	1
3	Asymptomatic SARS-CoV-2 Infection Is Associated With Higher Levels of Serum IL-17C, Matrix Metalloproteinase 10 andÂFibroblast Growth Factors Than Mild Symptomatic COVID-19. Frontiers in Immunology, 2022, 13, 821730.	4.8	21
4	Transcription factor GATA2 may potentiate follicle-stimulating hormone production in mice via induction of the BMP antagonist gremlin in gonadotrope cells. Journal of Biological Chemistry, 2022, 298, 102072.	3.4	5
5	Lessons Learned From a Prospective Observational Study of U.S. Marine Recruits During a Supervised Quarantine, Spring‒Fall 2020. , 2022, 1, 100003.		0
6	Earlier detection of SARS oVâ€2 infection by blood RNA signature microfluidics assay. Clinical and Translational Discovery, 2022, 2, .	0.5	2
7	The association of childhood trauma with sleep disturbances and risk of suicide in US veterans. Journal of Psychiatric Research, 2021, 136, 54-62.	3.1	8
8	SARS-CoV-2 Seropositivity among US Marine Recruits Attending Basic Training, United States, Spring–Fall 2020. Emerging Infectious Diseases, 2021, 27, 1188-1192.	4.3	13
9	Viable virus shedding during SARS-CoV-2 reinfection. Lancet Respiratory Medicine, the, 2021, 9, e56-e57.	10.7	11
10	Antibody Responses to SARS-CoV-2 Following an Outbreak Among Marine Recruits With Asymptomatic or Mild Infection. Frontiers in Immunology, 2021, 12, 681586.	4.8	6
11	Bisulfite Amplicon Sequencing Can Detect Glia and Neuron Cell-Free DNA in Blood Plasma. Frontiers in Molecular Neuroscience, 2021, 14, 672614.	2.9	12
12	SARS-CoV-2 seropositivity and subsequent infection risk in healthy young adults: a prospective cohort study. Lancet Respiratory Medicine,the, 2021, 9, 712-720.	10.7	136
13	Attenuated activation of pulmonary immune cells in mRNA-1273–vaccinated hamsters after SARS-CoV-2 infection. Journal of Clinical Investigation, 2021, 131, .	8.2	23
14	Differential analysis of chromatin accessibility and gene expression profiles identifies cis-regulatory elements in rat adipose and muscle. Genomics, 2021, 113, 3827-3841.	2.9	11
15	Penetrating Ballistic Brain Injury Produces Acute Alterations in Sleep and Circadian-Related Genes in the Rodent Cortex: A Preliminary Study. Frontiers in Neurology, 2021, 12, 745330.	2.4	4
16	Acute and Chronic Molecular Signatures and Associated Symptoms of Blast Exposure in Military Breachers. Journal of Neurotrauma, 2020, 37, 1221-1232.	3.4	41
17	Skeletal muscle transcriptional networks linked to type I myofiber grouping in Parkinson's disease. Journal of Applied Physiology, 2020, 128, 229-240.	2.5	18
18	SAT-298 Integrative Single-Cell Transcriptomic and Epigenomic Landscape of Mouse Anterior Pituitary Cell Types. Journal of the Endocrine Society, 2020, 4, .	0.2	0

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19	SARS-CoV-2 Transmission among Marine Recruits during Quarantine. New England Journal of Medicine, 2020, 383, 2407-2416.	27.0	94
20	Blast-Related Mild TBI Alters Anxiety-Like Behavior and Transcriptional Signatures in the Rat Amygdala. Frontiers in Behavioral Neuroscience, 2020, 14, 160.	2.0	20
21	DNA Methylation Patterns of Chronic Explosive Breaching in U.S. Military Warfighters. Frontiers in Neurology, 2020, 11, 1010.	2.4	4
22	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. Cell, 2020, 181, 1464-1474.	28.9	147
23	Biosignatures of Stress in Suicide Neuropathology. Biological Psychiatry, 2020, 87, S145-S146.	1.3	1
24	Rehabilitative Impact of Exercise Training on Human Skeletal Muscle Transcriptional Programs in Parkinson's Disease. Frontiers in Physiology, 2020, 11, 653.	2.8	15
25	Sedentary and Trained Older Men Have Distinct Circulating Exosomal microRNA Profiles at Baseline and in Response to Acute Exercise. Frontiers in Physiology, 2020, 11, 605.	2.8	52
26	0012 Molecular Correlates of Operational Blast and Associated Sleep Disturbances. Sleep, 2019, 42, A5-A5.	1.1	0
27	Cytogenetic, Genomic, and Functional Characterization of Pituitary Gonadotrope Cell Lines. Journal of the Endocrine Society, 2019, 3, 902-920.	0.2	13
28	Brain Imagingâ€Guided Analysis Reveals DNA Methylation Profiles Correlated with Insular Surface Area and Alcohol Use Disorder. Alcoholism: Clinical and Experimental Research, 2019, 43, 628-639.	2.4	3
29	Single-cell stabilization method identifies gonadotrope transcriptional dynamics and pituitary cell type heterogeneity. Nucleic Acids Research, 2018, 46, 11370-11380.	14.5	21
30	Ex vivo human HSC expansion requires coordination of cellular reprogramming with mitochondrial remodeling and p53 activation. Blood Advances, 2018, 2, 2766-2779.	5.2	48
31	Regulatory Architecture of the LβT2 Gonadotrope Cell Underlying the Response to Gonadotropin-Releasing Hormone. Frontiers in Endocrinology, 2018, 9, 34.	3.5	15
32	Biopsy transcriptome expression profiling: proper validation is key – Authors' reply. Lancet, The, 2017, 389, 601.	13.7	2
33	In utero exposure to maternal smoking is associated with DNA methylation alterations and reduced neuronal content in the developing fetal brain. Epigenetics and Chromatin, 2017, 10, 4.	3.9	74
34	Antipsychotic-induced Hdac2 transcription via NF-κB leads to synaptic and cognitive side effects. Nature Neuroscience, 2017, 20, 1247-1259.	14.8	79
35	Alterations of miRNAs reveal a dysregulated molecular regulatory network in Parkinson's disease striatum. Neuroscience Letters, 2016, 629, 99-104.	2.1	54
36	Biopsy transcriptome expression profiling to identify kidney transplants at risk of chronic injury: a multicentre, prospective study. Lancet, The, 2016, 388, 983-993.	13.7	148

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37	Perfluoroalkyl substance serum concentrations and immune response to FluMist vaccination among healthy adults. Environmental Research, 2016, 149, 171-178.	7.5	31
38	Allosteric signaling through an mGlu2 and 5-HT <sub>2A</sub> heteromeric receptor complex and its potential contribution to schizophrenia. Science Signaling, 2016, 9, ra5.	3.6	91
39	Neuronal DNA Methylation Profiling of Blast-Related Traumatic Brain Injury. Journal of Neurotrauma, 2015, 32, 1200-1209.	3.4	60
40	Decrease of mRNA Editing after Spinal Cord Injury is Caused by Down-regulation of ADAR2 that is Triggered by Inflammatory Response. Scientific Reports, 2015, 5, 12615.	3.3	27
41	Lowâ€variance RNAs identify Parkinson's disease molecular signature in blood. Movement Disorders, 2015, 30, 813-821.	3.9	18
42	Single-cell analysis shows that paracrine signaling by first responder cells shapes the interferon-Î <sup>2</sup> response to viral infection. Science Signaling, 2015, 8, ra16.	3.6	73
43	Age-related sperm DNA methylation changes are transmitted to offspring and associated with abnormal behavior and dysregulated gene expression. Molecular Psychiatry, 2015, 20, 995-1001.	7.9	144
44	Human Cytomegalovirus Modulates Monocyte-Mediated Innate Immune Responses during Short-Term Experimental Latency <i>In Vitro</i> . Journal of Virology, 2014, 88, 9391-9405.	3.4	41
45	Increased DNA methylation in the suicide brain. Dialogues in Clinical Neuroscience, 2014, 16, 430-438.	3.7	74
46	Critical assessment of automated flow cytometry data analysis techniques. Nature Methods, 2013, 10, 228-238.	19.0	509
47	Localized Mucosal Response to Intranasal Live Attenuated Influenza Vaccine in Adults. Journal of Infectious Diseases, 2013, 207, 115-124.	4.0	97
48	Control of the False Discovery Proportion for Independently Tested Null Hypotheses. Journal of Probability and Statistics, 2012, 2012, 1-19.	0.7	6
49	MethylomeDB: a database of DNA methylation profiles of the brain. Nucleic Acids Research, 2012, 40, D1245-D1249.	14.5	62
50	Involvement of Histone Demethylase LSD1 in Short-Time-Scale Gene Expression Changes during Cell Cycle Progression in Embryonic Stem Cells. Molecular and Cellular Biology, 2012, 32, 4861-4876.	2.3	32
51	flowPeaks: a fast unsupervised clustering for flow cytometry data via <i>K</i> -means and density peak finding. Bioinformatics, 2012, 28, 2052-2058.	4.1	123
52	Compensatory redistribution of neuroligins and Nâ€cadherin following deletion of synaptic β1â€integrin. Journal of Comparative Neurology, 2012, 520, 2041-2052.	1.6	54
53	Wdr5 Mediates Self-Renewal and Reprogramming via the Embryonic Stem Cell Core Transcriptional Network. Cell, 2011, 145, 183-197.	28.9	521
54	Nonsense mutations of the bHLH transcription factor TWIST2 found in Setleis Syndrome patients cause dysregulation of periostin. International Journal of Biochemistry and Cell Biology, 2011, 43, 1523-1531.	2.8	18

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55	Retinal Gene Expression Changes Related to IOP Exposure and Axonal Loss in DBA/2J Mice. , 2011, 52, 7807.		24
56	Gene Expression Changes in Steroid-Induced IOP Elevation in Bovine Trabecular Meshwork. , 2011, 52, 8636.		28
57	Role of CpG context and content in evolutionary signatures of brain DNA methylation. Epigenetics, 2011, 6, 1308-1318.	2.7	30
58	Methyl-Analyzer—whole genome DNA methylation profiling. Bioinformatics, 2011, 27, 2296-2297.	4.1	8
59	Peripheral Blood Cytokine Profiling During Pregnancy and Postâ€partum Periods. American Journal of Reproductive Immunology, 2010, 64, 411-426.	1.2	112
60	Patient-specific induced pluripotent stem-cell-derived models of LEOPARD syndrome. Nature, 2010, 465, 808-812.	27.8	672
61	Gene Expression Changes in Areas of Focal Loss of Retinal Ganglion Cells in the Retina of DBA/2J Mice. , 2010, 51, 2024.		47
62	Coregulation mapping based on individual phenotypic variation in response to virus infection. Immunome Research, 2010, 6, 2.	0.1	4
63	Multiple testing and its applications to microarrays. Statistical Methods in Medical Research, 2009, 18, 543-563.	1.5	22
64	Requirement for Protein Synthesis at Developing Synapses. Journal of Neuroscience, 2009, 29, 9778-9793.	3.6	32
65	Development of a novel peptide microarray for large-scale epitope mapping of food allergens. Journal of Allergy and Clinical Immunology, 2009, 124, 315-322.e3.	2.9	115
66	ERM proteins regulate growth cone responses to Sema3A. Journal of Comparative Neurology, 2008, 510, 351-366.	1.6	30
67	A Comprehensive Evaluation of Human Plasmacytoid Dendritic Cells Using Small Volumes of Human Blood. Journal of Interferon and Cytokine Research, 2008, 28, 501-508.	1.2	Ο
68	SOME STEP-DOWN PROCEDURES CONTROLLING THE FALSE DISCOVERY RATE UNDER DEPENDENCE. Statistica Sinica, 2008, 18, 881-904.	0.3	33
69	Evolutionary History of Mammalian Transposons Determined by Genome-Wide Defragmentation. PLoS Computational Biology, 2007, 3, e137.	3.2	124
70	Hallucinogens Recruit Specific Cortical 5-HT2A Receptor-Mediated Signaling Pathways to Affect Behavior. Neuron, 2007, 53, 439-452.	8.1	692
71	Noise Propagation and Scaling in Regulation of Gonadotrope Biosynthesis. Biophysical Journal, 2007, 93, 4474-4480.	0.5	23
72	A Holm-type procedure controlling the false discovery rate. Statistics and Probability Letters, 2007, 77, 1756-1762.	0.7	3

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73	Effective Use of Microarrays in Neuroendocrine Research. Journal of Neuroendocrinology, 2007, 19, 145-161.	2.6	4
74	Mixed Analog/Digital Gonadotrope Biosynthetic Response to Gonadotropin-releasing Hormone. Journal of Biological Chemistry, 2006, 281, 30967-30978.	3.4	46
75	Bioconductor: open software development for computational biology and bioinformatics. Genome Biology, 2004, 5, R80.	9.6	10,796
76	Resampling-based multiple testing for microarray data analysis. Test, 2003, 12, 1-77.	1.1	416
77	Molecular Analysis of Gene Expression in the Developing Pontocerebellar Projection System. Neuron, 2002, 36, 417-434.	8.1	84