

# Chris Gaiteri

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

4,912  
citations

218677

26  
h-index

233421

45  
g-index

53  
all docs

53  
docs citations

53  
times ranked

8933  
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level. <i>Nature Neuroscience</i> , 2022, 25, 213-225.	14.8	202
2	Inferring protein expression changes from mRNA in Alzheimer's dementia using deep neural networks. <i>Nature Communications</i> , 2022, 13, 655.	12.8	29
3	Cortical proteins may provide motor resilience in older adults. <i>Scientific Reports</i> , 2021, 11, 11311.	3.3	14
4	Stem cell-derived neurons reflect features of protein networks, neuropathology, and cognitive outcome of their aged human donors. <i>Neuron</i> , 2021, 109, 3402-3420.e9.	8.1	75
5	A cortical immune network map identifies distinct microglial transcriptional programs associated with $\beta$ -amyloid and Tau pathologies. <i>Translational Psychiatry</i> , 2021, 11, 50.	4.8	19
6	Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level. <i>Alzheimer's and Dementia</i> , 2021, 17, e055041.	0.8	1
7	Quantitative Systems Pharmacology for Neuroscience Drug Discovery and Development: Current Status, Opportunities, and Challenges. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2020, 9, 5-20.	2.5	29
8	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	5.3	75
9	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020, 32, 107908.	6.4	199
10	Deconvolving the contributions of cell-type heterogeneity on cortical gene expression. <i>PLoS Computational Biology</i> , 2020, 16, e1008120.	3.2	66
11	Identifying the molecular systems that influence cognitive resilience to Alzheimer's disease in genetically diverse mice. <i>Learning and Memory</i> , 2020, 27, 355-371.	1.3	15
12	Deep learning decodes the principles of differential gene expression. <i>Nature Machine Intelligence</i> , 2020, 2, 376-386.	16.0	22
13	Gene expression and DNA methylation are extensively coordinated with MRI-based brain microstructural characteristics. <i>Brain Imaging and Behavior</i> , 2019, 13, 963-972.	2.1	24
14	Microstructural changes in the brain mediate the association of AK4, IGFBP5, HSPB2, and ITPK1 with cognitive decline. <i>Neurobiology of Aging</i> , 2019, 84, 17-25.	3.1	11
15	Using Transcriptomic Hidden Variables to Infer Context-Specific Genotype Effects in the Brain. <i>American Journal of Human Genetics</i> , 2019, 105, 562-572.	6.2	7
16	Genetic risk for Alzheimer's dementia predicts motor deficits through multi-omic systems in older adults. <i>Translational Psychiatry</i> , 2019, 9, 241.	4.8	11
17	Cognition may link cortical IGFBP5 levels with motor function in older adults. <i>PLoS ONE</i> , 2019, 14, e0220968.	2.5	8
18	Association of Cortical $\beta$ -Amyloid Protein in the Absence of Insoluble Deposits With Alzheimer Disease. <i>JAMA Neurology</i> , 2019, 76, 818.	9.0	25

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19	Physical activity, common brain pathologies, and cognition in community-dwelling older adults. <i>Neurology</i> , 2019, 92, e811-e822.	1.1	61
20	<i>APOE</i> genotypes as a risk factor for age-dependent accumulation of cerebrovascular disease in older adults. <i>Alzheimer's and Dementia</i> , 2019, 15, 258-266.	0.8	17
21	Association Between Quantitative Gait and Balance Measures and Total Daily Physical Activity in Community-Dwelling Older Adults. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 636-642.	3.6	33
22	A multi-omic atlas of the human frontal cortex for aging and Alzheimer's disease research. <i>Scientific Data</i> , 2018, 5, 180142.	5.3	357
23	The Molecular and Neuropathological Consequences of Genetic Risk for Alzheimer's Dementia. <i>Frontiers in Neuroscience</i> , 2018, 12, 699.	2.8	47
24	Seasonal plasticity of cognition and related biological measures in adults with and without Alzheimer disease: Analysis of multiple cohorts. <i>PLoS Medicine</i> , 2018, 15, e1002647.	8.4	42
25	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease. <i>Nature Neuroscience</i> , 2018, 21, 811-819.	14.8	422
26	Multi-omic Directed Networks Describe Features of Gene Regulation in Aged Brains and Expand the Set of Genes Driving Cognitive Decline. <i>Frontiers in Genetics</i> , 2018, 9, 294.	2.3	30
27	Polygenic analysis of inflammatory disease variants and effects on microglia in the aging brain. <i>Molecular Neurodegeneration</i> , 2018, 13, 38.	10.8	44
28	<i>APOE</i> $\epsilon$ 4 genotype, incident AD and MCI, cognitive decline, and AD pathology in older adults. <i>Neurology</i> , 2018, 90, e2127-e2134.	1.1	42
29	Targeted brain proteomics uncover multiple pathways to Alzheimer's dementia. <i>Annals of Neurology</i> , 2018, 84, 78-88.	5.3	102
30	<i>TOMM40</i> $\epsilon$ 523 variant and cognitive decline in older persons with <i>APOE</i> $\epsilon$ 3/3 genotype. <i>Neurology</i> , 2017, 88, 661-668.	1.1	45
31	Association Between Brain Gene Expression, DNA Methylation, and Alteration of Ex Vivo Magnetic Resonance Imaging Transverse Relaxation in Late-Life Cognitive Decline. <i>JAMA Neurology</i> , 2017, 74, 1473.	9.0	21
32	An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome. <i>Nature Neuroscience</i> , 2017, 20, 1418-1426.	14.8	377
33	<i>APOE</i> $\epsilon$ 4- <i>TOMM40</i> $\epsilon$ 523 haplotypes and the risk of Alzheimer's disease in older Caucasian and African Americans. <i>PLoS ONE</i> , 2017, 12, e0180356.	2.5	39
34	Supporting novel biomedical research via multilayer collaboration networks. <i>Applied Network Science</i> , 2016, 1, 11.	1.5	3
35	Genetic variants in Alzheimer disease – molecular and brain network approaches. <i>Nature Reviews Neurology</i> , 2016, 12, 413-427.	10.1	97
36	Identifying robust communities and multi-community nodes by combining top-down and bottom-up approaches to clustering. <i>Scientific Reports</i> , 2015, 5, 16361.	3.3	74

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37	Bayesian Network Reconstruction Using Systems Genetics Data: Comparison of MCMC Methods. <i>Genetics</i> , 2015, 199, 973-989.	2.9	27
38	Beyond modules and hubs: the potential of gene coexpression networks for investigating molecular mechanisms of complex brain disorders. <i>Genes, Brain and Behavior</i> , 2014, 13, 13-24.	2.2	229
39	Variants in triggering receptor expressed on myeloid cells 2 are associated with both behavioral variant frontotemporal lobar degeneration and Alzheimer's disease. <i>Neurobiology of Aging</i> , 2013, 34, 2077.e11-2077.e18.	3.1	124
40	Integrated Systems Approach Identifies Genetic Nodes and Networks in Late-Onset Alzheimer's Disease. <i>Cell</i> , 2013, 153, 707-720.	28.9	1,505
41	The Interaction of Intrinsic Dynamics and Network Topology in Determining Network Burst Synchrony. <i>Frontiers in Computational Neuroscience</i> , 2011, 5, 10.	2.1	35
42	Differentially Expressed Genes in Major Depression Reside on the Periphery of Resilient Gene Coexpression Networks. <i>Frontiers in Neuroscience</i> , 2011, 5, 95.	2.8	33
43	Network analysis of positional candidate genes of schizophrenia highlights more than myelin-related pathways. <i>Molecular Psychiatry</i> , 2010, 15, 786-788.	7.9	7
44	Altered Gene Synchrony Suggests a Combined Hormone-Mediated Dysregulated State in Major Depression. <i>PLoS ONE</i> , 2010, 5, e9970.	2.5	38
45	A Molecular Signature of Depression in the Amygdala. <i>American Journal of Psychiatry</i> , 2009, 166, 1011-1024.	7.2	177