John F Fullard

List of Publications by Year
in descending order

46 papers	5,205 citations	236925 25 h-index	265206 42 g-index
61 all docs	61 docs citations	61 times ranked	9413 citing authors

#	Article	IF	Citations
1	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	14.8	952
2	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	12.6	618
3	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	12.6	516
4	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. Scientific Reports, 2018, 8, 8868.	3.3	335
5	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	5.3	320
6	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. Science, 2016, 353, 827-830.	12.6	241
7	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	6.4	225
8	An atlas of chromatin accessibility in the adult human brain. Genome Research, 2018, 28, 1243-1252.	5.5	170
9	Non-cell-autonomous disruption of nuclear architecture as a potential cause of COVID-19-induced anosmia. Cell, 2022, 185, 1052-1064.e12.	28.9	154
10	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	5.3	149
11	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. Nature Communications, 2018, 9, 3121.	12.8	141
12	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	6.2	128
13	Integration of Alzheimerâ€™s disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. Nature Communications, 2021, 12, 1610.	12.8	118
14	The Role of the Platelet Glycoprotein IIb / IIIa in Thrombosis and Haemostasis. Current Pharmaceutical Design, 2004, 10, 1567-1576.	1.9	107
15	Common genetic variation influencing human white matter microstructure. Science, 2021, 372, .	12.6	106
16	Single-nucleus transcriptome analysis of human brain immune response in patients with severe COVID-19. Genome Medicine, 2021, 13, 118.	8.2	81
17	Striatal H3K27 Acetylation Linked to Glutamatergic Gene Dysregulation in Human Heroin Abusers Holds Promise as Therapeutic Target. Biological Psychiatry, 2017, 81, 585-594.	1.3	77
18	Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. Human Molecular Genetics, 2017, 26, 1942-1951.	2.9	69

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19	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. Nature Communications, 2019, 10, 3834.	12.8	68
20	A complete temporal transcription factor series in the fly visual system. Nature, 2022, 604, 316-322.	27.8	60
21	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581.	12.8	53
22	Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits. Nature Genetics, 2022, 54, 161-169.	21.4	49
23	Revealing the brain's molecular architecture. Science, 2018, 362, 1262-1263.	12.6	45
24	The Relationship of Common Risk Variants and Polygenic Risk for Schizophrenia to Sensorimotor Gating. Biological Psychiatry, 2016, 79, 988-996.	1.3	44
25	Clearance of apoptotic corpses. Apoptosis: an International Journal on Programmed Cell Death, 2009, 14, 1029-1037.	4.9	40
26	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. Molecular Psychiatry, 2019, 24, 1685-1695.	7.9	40
27	Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. Biological Psychiatry, 2022, 91, 92-101.	1.3	38
28	Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517.	21.4	37
29	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. Nature Neuroscience, 2022, 25, 474-483.	14.8	25
30	Role of the Sc C Terminus in Transcriptional Activation and E(spl) Repressor Recruitment. Journal of Biological Chemistry, 2005, 280, 1299-1305.	3.4	24
31	Understanding the genetic liability to schizophrenia through the neuroepigenome. Schizophrenia Research, 2016, 177, 115-124.	2.0	22
32	Chromatin accessibility mapping of the striatum identifies tyrosine kinase FYN as a therapeutic target for heroin use disorder. Nature Communications, 2020, 11, 4634.	12.8	21
33	A bidirectional competitive interaction between circHomer1 and Homer1b within the orbitofrontal cortex regulates reversal learning. Cell Reports, 2022, 38, 110282.	6.4	17
34	Assessment of somatic single-nucleotide variation in brain tissue of cases with schizophrenia. Translational Psychiatry, 2019, 9, 21.	4.8	16
35	A Val193Met mutation in GPIIIa results in a GPIIb/IIIa receptor with a constitutively high affinity for a small ligand. British Journal of Haematology, 2001, 115, 131-139.	2.5	11
36	Dissecting Hes-centred transcriptional networks in neural stem cell maintenance and tumorigenesis in Drosophila. Development (Cambridge), 2020, 147, .	2.5	9

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37	Unbiased identification of novel transcription factors in striatal compartmentation and striosome maturation. ELife, 2021, 10, .	6.0	9
38	The Neuroepigenome: Implications of Chemical and Physical Modifications of Genomic DNA in Schizophrenia. Biological Psychiatry, 2022, 92, 443-449.	1.3	6
39	Impact of schizophrenia GWAS loci converge onto distinct pathways in cortical interneurons vs glutamatergic neurons during development. Molecular Psychiatry, 2022, 27, 4218-4233.	7.9	6
40	Genetic Variation in Long-Range Enhancers. Current Topics in Behavioral Neurosciences, 2019, 42, 35-50.	1.7	2
41	237. Large-Scale Gene-Trait Association Study IdentifiesÂNovel Genes Across Multiple Traits. Biological Psychiatry, 2019, 85, S98.	1.3	0
42	Large-Scale Integrative Brain Transcriptome and Epigenome Imputation for PTSD Identifies Implicated Genes and Pathways. Biological Psychiatry, 2020, 87, S52.	1.3	0
43	Genetic studies of Alzheimer's disease risk implicate clearance of lipid rich debris in myeloid cells. Alzheimer's and Dementia, 2020, 16, e040601.	0.8	0
44	Integration of Alzheimerâ€™s disease genetics and myeloid genomics reveals novel disease risk mechanisms. Alzheimer's and Dementia, 2020, 16, e043897.	0.8	0
45	ATAC-seq and psychiatric disorders. , 2021, , 143-162.		0
46	Characterization of a ligand-attenuated binding site on glycoprotein IIb/IIIa. Thrombosis and Haemostasis, 2002, 88, 811-6.	3.4	0