

# John F Fullard

## List of Publications by Year in descending order

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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	Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. <i>Biological Psychiatry</i> , 2022, 91, 92-101.	1.3	38
2	Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits. <i>Nature Genetics</i> , 2022, 54, 161-169.	21.4	49
3	A bidirectional competitive interaction between circHomer1 and Homer1b within the orbitofrontal cortex regulates reversal learning. <i>Cell Reports</i> , 2022, 38, 110282.	6.4	17
4	Non-cell-autonomous disruption of nuclear architecture as a potential cause of COVID-19-induced anosmia. <i>Cell</i> , 2022, 185, 1052-1064.e12.	28.9	154
5	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. <i>Nature Neuroscience</i> , 2022, 25, 474-483.	14.8	25
6	Common variants contribute to intrinsic human brain functional networks. <i>Nature Genetics</i> , 2022, 54, 508-517.	21.4	37
7	A complete temporal transcription factor series in the fly visual system. <i>Nature</i> , 2022, 604, 316-322.	27.8	60
8	The Neuroepigenome: Implications of Chemical and Physical Modifications of Genomic DNA in Schizophrenia. <i>Biological Psychiatry</i> , 2022, 92, 443-449.	1.3	6
9	Impact of schizophrenia GWAS loci converge onto distinct pathways in cortical interneurons vs glutamatergic neurons during development. <i>Molecular Psychiatry</i> , 2022, 27, 4218-4233.	7.9	6
10	ATAC-seq and psychiatric disorders. , 2021, , 143-162.		0
11	Integration of Alzheimer's disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. <i>Nature Communications</i> , 2021, 12, 1610.	12.8	118
12	Common genetic variation influencing human white matter microstructure. <i>Science</i> , 2021, 372, .	12.6	106
13	Single-nucleus transcriptome analysis of human brain immune response in patients with severe COVID-19. <i>Genome Medicine</i> , 2021, 13, 118.	8.2	81
14	Unbiased identification of novel transcription factors in striatal compartmentation and striosome maturation. <i>ELife</i> , 2021, 10, .	6.0	9
15	Large-Scale Integrative Brain Transcriptome and Epigenome Imputation for PTSD Identifies Implicated Genes and Pathways. <i>Biological Psychiatry</i> , 2020, 87, S52.	1.3	0
16	Dissecting Hes-centred transcriptional networks in neural stem cell maintenance and tumorigenesis in <i>Drosophila</i> . <i>Development (Cambridge)</i> , 2020, 147, .	2.5	9
17	Chromatin accessibility mapping of the striatum identifies tyrosine kinase FYN as a therapeutic target for heroin use disorder. <i>Nature Communications</i> , 2020, 11, 4634.	12.8	21
18	Genetic studies of Alzheimer's disease risk implicate clearance of lipid rich debris in myeloid cells. <i>Alzheimer's and Dementia</i> , 2020, 16, e040601.	0.8	0

#	ARTICLE	IF	CITATIONS
19	Integration of Alzheimer's disease genetics and myeloid genomics reveals novel disease risk mechanisms. <i>Alzheimer's and Dementia</i> , 2020, 16, e043897.	0.8	0
20	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. <i>Nature Communications</i> , 2020, 11, 5581.	12.8	53
21	Differential activity of transcribed enhancers in the prefrontal cortex of 537 cases with schizophrenia and controls. <i>Molecular Psychiatry</i> , 2019, 24, 1685-1695.	7.9	40
22	Genetic Variation in Long-Range Enhancers. <i>Current Topics in Behavioral Neurosciences</i> , 2019, 42, 35-50.	1.7	2
23	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. <i>Nature Communications</i> , 2019, 10, 3834.	12.8	68
24	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. <i>Scientific Data</i> , 2019, 6, 180.	5.3	149
25	237. Large-Scale Gene-Trait Association Study Identifies Novel Genes Across Multiple Traits. <i>Biological Psychiatry</i> , 2019, 85, S98.	1.3	0
26	Assessment of somatic single-nucleotide variation in brain tissue of cases with schizophrenia. <i>Translational Psychiatry</i> , 2019, 9, 21.	4.8	16
27	Revealing the brain's molecular architecture. <i>Science</i> , 2018, 362, 1262-1263.	12.6	45
28	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	12.6	516
29	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	12.6	618
30	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	6.2	128
31	An atlas of chromatin accessibility in the adult human brain. <i>Genome Research</i> , 2018, 28, 1243-1252.	5.5	170
32	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 3121.	12.8	141
33	Brain Cell Type Specific Gene Expression and Co-expression Network Architectures. <i>Scientific Reports</i> , 2018, 8, 8868.	3.3	335
34	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. <i>Scientific Data</i> , 2018, 5, 180185.	5.3	320
35	Open chromatin profiling of human postmortem brain infers functional roles for non-coding schizophrenia loci. <i>Human Molecular Genetics</i> , 2017, 26, 1942-1951.	2.9	69
36	Striatal H3K27 Acetylation Linked to Glutamatergic Gene Dysregulation in Human Heroin Abusers Holds Promise as Therapeutic Target. <i>Biological Psychiatry</i> , 2017, 81, 585-594.	1.3	77

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37	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	14.8	952
38	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830.	12.6	241
39	Understanding the genetic liability to schizophrenia through the neuroepigenome. <i>Schizophrenia Research</i> , 2016, 177, 115-124.	2.0	22
40	The Relationship of Common Risk Variants and Polygenic Risk for Schizophrenia to Sensorimotor Gating. <i>Biological Psychiatry</i> , 2016, 79, 988-996.	1.3	44
41	A Role for Noncoding Variation in Schizophrenia. <i>Cell Reports</i> , 2014, 9, 1417-1429.	6.4	225
42	Clearance of apoptotic corpses. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2009, 14, 1029-1037.	4.9	40
43	Role of the Sc C Terminus in Transcriptional Activation and E(spl) Repressor Recruitment. <i>Journal of Biological Chemistry</i> , 2005, 280, 1299-1305.	3.4	24
44	The Role of the Platelet Glycoprotein IIb / IIIa in Thrombosis and Haemostasis. <i>Current Pharmaceutical Design</i> , 2004, 10, 1567-1576.	1.9	107
45	Characterization of a ligand-attenuated binding site on glycoprotein IIb/IIIa. <i>Thrombosis and Haemostasis</i> , 2002, 88, 811-6.	3.4	0
46	A Val193Met mutation in GPIIIa results in a GPIIb/IIIa receptor with a constitutively high affinity for a small ligand. <i>British Journal of Haematology</i> , 2001, 115, 131-139.	2.5	11