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List of Publications by Year in descending order

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30 papers	4,615 citations	331259 21 h-index	476904 29 g-index
45 all docs	45 docs citations	45 times ranked	8617 citing authors

#	Article	IF	Citations
1	Sex Differences in the Human Brain Transcriptome of Cases With Schizophrenia. Biological Psychiatry, 2022, 91, 92-101.	0.7	38
2	Multi-ancestry eQTL meta-analysis of human brain identifies candidate causal variants for brain-related traits. Nature Genetics, 2022, 54, 161-169.	9.4	49
3	Chromatin domain alterations linked to 3D genome organization in a large cohort of schizophrenia and bipolar disorder brains. Nature Neuroscience, 2022, 25, 474-483.	7.1	25
4	Common variants contribute to intrinsic human brain functional networks. Nature Genetics, 2022, 54, 508-517.	9.4	37
5	Impact of schizophrenia GWAS loci converge onto distinct pathways in cortical interneurons vs glutamatergic neurons during development. Molecular Psychiatry, 2022, 27, 4218-4233.	4.1	6
6	ATAC-seq and psychiatric disorders. , 2021, , 143-162.		0
7	Integration of Alzheimerâ€™s disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. Nature Communications, 2021, 12, 1610.	5.8	118
8	Common genetic variation influencing human white matter microstructure. Science, 2021, 372, .	6.0	106
9	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. Nature Communications, 2021, 12, 3968.	5.8	48
10	Unbiased identification of novel transcription factors in striatal compartmentation and striosome maturation. ELife, 2021, 10, .	2.8	9
11	Common schizophrenia risk variants are enriched in open chromatin regions of human glutamatergic neurons. Nature Communications, 2020, 11, 5581.	5.8	53
12	decorate: differential epigenetic correlation test. Bioinformatics, 2020, 36, 2856-2861.	1.8	11
13	A chromosomal connectome for psychiatric and metabolic risk variants in adult dopaminergic neurons. Genome Medicine, 2020, 12, 19.	3.6	31
14	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. Scientific Data, 2019, 6, 180.	2.4	149
15	Functional interpretation of genetic variants using deep learning predicts impact on chromatin accessibility and histone modification. Nucleic Acids Research, 2019, 47, 10597-10611.	6.5	39
16	Transcriptome and epigenome landscape of human cortical development modeled in organoids. Science, 2018, 362, .	6.0	220
17	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
18	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. Science, 2018, 362, .	6.0	805

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19	Comprehensive functional genomic resource and integrative model for the human brain. Science, 2018, 362, .	6.0	618
20	An atlas of chromatin accessibility in the adult human brain. Genome Research, 2018, 28, 1243-1252.	2.4	170
21	The Mount Sinai cohort of large-scale genomic, transcriptomic and proteomic data in Alzheimer's disease. Scientific Data, 2018, 5, 180185.	2.4	320
22	NewProt â€“ a protein engineering portal. Protein Engineering, Design and Selection, 2017, 30, 441-447.	1.0	11
23	FireProt: web server for automated design of thermostable proteins. Nucleic Acids Research, 2017, 45, W393-W399.	6.5	104
24	HotSpot Wizard 2.0: automated design of site-specific mutations and smart libraries in protein engineering. Nucleic Acids Research, 2016, 44, W479-W487.	6.5	76
25	PredictSNP2: A Unified Platform for Accurately Evaluating SNP Effects by Exploiting the Different Characteristics of Variants in Distinct Genomic Regions. PLoS Computational Biology, 2016, 12, e1004962.	1.5	149
26	FireProt: Energy- and Evolution-Based Computational Design of Thermostable Multiple-Point Mutants. PLoS Computational Biology, 2015, 11, e1004556.	1.5	144
27	PredictSNP: Robust and Accurate Consensus Classifier for Prediction of Disease-Related Mutations. PLoS Computational Biology, 2014, 10, e1003440.	1.5	593
28	Maximizing the Efficiency of Multienzyme Process by Stoichiometry Optimization. ChemBioChem, 2014, 15, 1891-1895.	1.3	31
29	Computer-Assisted Engineering of the Synthetic Pathway for Biodegradation of a Toxic Persistent Pollutant. ACS Synthetic Biology, 2014, 3, 172-181.	1.9	39
30	Computational Tools for Designing Smart Libraries. Methods in Molecular Biology, 2014, 1179, 291-314.	0.4	21