

Whole-Genome and RNA Sequencing Reveal Variation at the Developing Human Prefrontal Cortex

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Citation Report

#	ARTICLE	IF	CITATIONS
1	De novo missense variants disrupting protein-protein interactions affect risk for autism through gene co-expression and protein networks in neuronal cell types. <i>Molecular Autism</i> , 2020, 11, 76.	4.9	19
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4	Epigenomic and Transcriptomic Dynamics During Human Heart Organogenesis. <i>Circulation Research</i> , 2020, 127, e184-e209.	4.5	27
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6	Regulatory landscape in brain development and disease. <i>Current Opinion in Genetics and Development</i> , 2020, 65, 53-60.	3.3	6
7	From Rare Copy Number Variants to Biological Processes in ADHD. <i>American Journal of Psychiatry</i> , 2020, 177, 855-866.	7.2	26
8	Emerging Methods and Resources for Biological Interrogation of Neuropsychiatric Polygenic Signal. <i>Biological Psychiatry</i> , 2021, 89, 41-53.	1.3	38
9	Transcriptomic Insight Into the Polygenic Mechanisms Underlying Psychiatric Disorders. <i>Biological Psychiatry</i> , 2021, 89, 54-64.	1.3	36
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16	Identification of cell-type-specific marker genes from co-expression patterns in tissue samples. <i>Bioinformatics</i> , 2021, 37, 3228-3234.	4.1	9
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21	Regulatory SNPs: Altered Transcription Factor Binding Sites Implicated in Complex Traits and Diseases. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6454.	4.1	29

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25	An approach to gene-based testing accounting for dependence of tests among nearby genes. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	0
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47	Ferroptosis and Its Potential Role in the Nervous System Diseases. <i>Journal of Inflammation Research</i> , 2022, Volume 15, 1555-1574.	3.5	32
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77	Transcriptional cartography integrates multiscale biology of the human cortex. <i>ELife</i> , 0, 12, .	6.0	1

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