Alexander Nord

List of Publications by Year
in descending order

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36 papers	4,125 citations	236833 25 h-index	360920 35 g-index
48 all docs	48 docs citations	48 times ranked	8899 citing authors

#	Article	IF	Citations
1	Mutations in 12 genes for inherited ovarian, fallopian tube, and peritoneal carcinoma identified by massively parallel sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18032-18037.	3.3	814
2	Detection of inherited mutations for breast and ovarian cancer using genomic capture and massively parallel sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12629-12633.	3.3	426
3	Rapid and Pervasive Changes in Genome-wide Enhancer Usage during Mammalian Development. Cell, 2013, 155, 1521-1531.	13.5	342
4	A High-Resolution Enhancer Atlas of the Developing Telencephalon. Cell, 2013, 152, 895-908.	13.5	241
5	Germline Chd8 haploinsufficiency alters brain development in mouse. Nature Neuroscience, 2017, 20, 1062-1073.	7.1	210
6	Fine Tuning of Craniofacial Morphology by Distant-Acting Enhancers. Science, 2013, 342, 1241006.	6.0	209
7	ColoSeq Provides Comprehensive Lynch and Polyposis Syndrome Mutational Analysis Using Massively Parallel Sequencing. Journal of Molecular Diagnostics, 2012, 14, 357-366.	1.2	179
8	Accurate and exact CNV identification from targeted high-throughput sequence data. BMC Genomics, 2011, 12, 184.	1.2	177
9	Genomic Perspectives of Transcriptional Regulation in Forebrain Development. Neuron, 2015, 85, 27-47.	3.8	136
10	Transcriptional Networks Controlled by NKX2-1 in the Development of Forebrain GABAergic Neurons. Neuron, 2016, 91, 1260-1275.	3.8	120
11	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
12	Reduced transcript expression of genes affected by inherited and de novo CNVs in autism. European Journal of Human Genetics, 2011, 19, 727-731.	1.4	109
13	Spectrum of DNA variants for non-syndromic deafness in a large cohort from multiple continents. Human Genetics, 2016, 135, 953-961.	1.8	102
14	Transcriptional Regulation of Enhancers Active in Protodomains of the Developing Cerebral Cortex. Neuron, 2014, 82, 989-1003.	3.8	99
15	Neonatal Tbr1 Dosage Controls Cortical Layer 6 Connectivity. Neuron, 2018, 100, 831-845.e7.	3.8	83
16	Neurobiological functions of transcriptional enhancers. Nature Neuroscience, 2020, 23, 5-14.	7.1	83
17	Targeted capture and sequencing for detection of mutations causing early onset epileptic encephalopathy. Epilepsia, 2013, 54, 1262-1269.	2.6	76
18	Dlx1andDlx2Promote Interneuron GABA Synthesis, Synaptogenesis, and Dendritogenesis. Cerebral Cortex, 2018, 28, 3797-3815.	1.6	72

#	Article	IF	Citations
19	Function-based identification of mammalian enhancers using site-specific integration. Nature Methods, 2014, 11, 566-571.	9.0	71
20	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. Cell Reports, 2019, 28, 2048-2063.e8.	2.9	68
21	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. Genome Research, 2014, 24, 920-929.	2.4	63
22	Subpallial Enhancer Transgenic Lines: a Data and Tool Resource to Study Transcriptional Regulation of GABAergic Cell Fate. Neuron, 2016, 92, 59-74.	3.8	62
23	Autism risk gene POGZ promotes chromatin accessibility and expression of clustered synaptic genes. Cell Reports, 2021, 37, 110089.	2.9	38
24	Common CHD8 Genomic Targets Contrast With Model-Specific Transcriptional Impacts of CHD8 Haploinsufficiency. Frontiers in Molecular Neuroscience, 2018, 11, 481.	1.4	34
25	Congenital Heart Defects in Patients with Deletions Upstream ofSOX9. Human Mutation, 2013, 34, 1628-1631.	1.1	33
26	Genomic Views of Transcriptional Enhancers: Essential Determinants of Cellular Identity and Activity-Dependent Responses in the CNS. Journal of Neuroscience, 2015, 35, 13819-13826.	1.7	33
27	Transcriptional network orchestrating regional patterning of cortical progenitors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
28	Parallel functional testing identifies enhancers active in early postnatal mouse brain. ELife, 2021, 10, .	2.8	19
29	Genomic analysis of transcriptional networks directing progression of cell states during MGE development. Neural Development, 2018, 13, 21.	1.1	17
30	Sequential perturbations to mouse corticogenesis following in utero maternal immune activation. ELife, 2021, 10, .	2.8	17
31	Deletion of a non-canonical regulatory sequence causes loss of Scn1a expression and epileptic phenotypes in mice. Genome Medicine, 2021, 13, 69.	3.6	15
32	Single cell enhancer activity distinguishes GABAergic and cholinergic lineages in embryonic mouse basal ganglia. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2108760119.	3.3	15
33	Learning about mammalian gene regulation from functional enhancer assays in the mouse. Genomics, 2015, 106, 178-184.	1.3	4
34	InÂvivo targeted DamID identifies CHD8 genomic targets in fetal mouse brain. IScience, 2021, 24, 103234.	1.9	4
35	Transcriptional Pathology Evolves over Time in Rat Hippocampus after Lateral Fluid Percussion Traumatic Brain Injury. Neurotrauma Reports, 2021, 2, 512-525.	0.5	4
36	AAV Deployment of Enhancer-Based Expression Constructs In Vivo in Mouse Brain. Journal of Visualized Experiments, 2022, , .	0.2	1