

# Neelroop N Parikshak

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8151671/publications.pdf>

Version: 2024-02-01

41  
papers

11,181  
citations

126858

33  
h-index

315616

38  
g-index

47  
all docs

47  
docs citations

47  
times ranked

18379  
citing authors

#	ARTICLE	IF	CITATIONS
1	De novo mutations revealed by whole-exome sequencing are strongly associated with autism. Nature, 2012, 485, 237-241.	13.7	1,863
2	Integrative Functional Genomic Analyses Implicate Specific Molecular Pathways and Circuits in Autism. Cell, 2013, 155, 1008-1021.	13.5	948
3	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. Science, 2018, 359, 693-697.	6.0	851
4	Psychiatric genome-wide association study analyses implicate neuronal, immune and histone pathways. Nature Neuroscience, 2015, 18, 199-209.	7.1	701
5	Genome-wide changes in lncRNA, splicing, and regional gene expression patterns in autism. Nature, 2016, 540, 423-427.	13.7	603
6	Brain structure and obesity. Human Brain Mapping, 2010, 31, 353-364.	1.9	555
7	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. Cell, 2014, 159, 1511-1523.	13.5	546
8	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
9	Chromosome conformation elucidates regulatory relationships in developing human brain. Nature, 2016, 538, 523-527.	13.7	507
10	Systems biology and gene networks in neurodevelopmental and neurodegenerative disorders. Nature Reviews Genetics, 2015, 16, 441-458.	7.7	378
11	The PsychENCODE project. Nature Neuroscience, 2015, 18, 1707-1712.	7.1	371
12	Tensor-based morphometry as a neuroimaging biomarker for Alzheimer's disease: An MRI study of 676 AD, MCI, and normal subjects. NeuroImage, 2008, 43, 458-469.	2.1	317
13	Histone Acetylome-wide Association Study of Autism Spectrum Disorder. Cell, 2016, 167, 1385-1397.e11.	13.5	237
14	Gene expression in human brain implicates sexually dimorphic pathways in autism spectrum disorders. Nature Communications, 2016, 7, 10717.	5.8	227
15	Automated mapping of hippocampal atrophy in 1-year repeat MRI data from 490 subjects with Alzheimer's disease, mild cognitive impairment, and elderly controls. NeuroImage, 2009, 45, S3-S15.	2.1	211
16	Cytoplasmic Rbfox1 Regulates the Expression of Synaptic and Autism-Related Genes. Neuron, 2016, 89, 113-128.	3.8	205
17	RBFOX1 regulates both splicing and transcriptional networks in human neuronal development. Human Molecular Genetics, 2012, 21, 4171-4186.	1.4	192
18	The road to precision psychiatry: translating genetics into disease mechanisms. Nature Neuroscience, 2016, 19, 1397-1407.	7.1	189

#	ARTICLE	IF	CITATIONS
19	A Quantitative Framework to Evaluate Modeling of Cortical Development by Neural Stem Cells. <i>Neuron</i> , 2014, 83, 69-86.	3.8	184
20	Validation of a fully automated 3D hippocampal segmentation method using subjects with Alzheimer's disease mild cognitive impairment, and elderly controls. <i>NeuroImage</i> , 2008, 43, 59-68.	2.1	181
21	Automated 3D mapping of hippocampal atrophy and its clinical correlates in 400 subjects with Alzheimer's disease, mild cognitive impairment, and elderly controls. <i>Human Brain Mapping</i> , 2009, 30, 2766-2788.	1.9	178
22	Genome-wide, integrative analysis implicates microRNA dysregulation in autism spectrum disorder. <i>Nature Neuroscience</i> , 2016, 19, 1463-1476.	7.1	163
23	Alzheimer's Disease Neuroimaging Initiative: A one-year follow up study using tensor-based morphometry correlating degenerative rates, biomarkers and cognition. <i>NeuroImage</i> , 2009, 45, 645-655.	2.1	159
24	Sex-chromosome dosage effects on gene expression in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7398-7403.	3.3	139
25	Autism-like phenotype and risk gene mRNA deadenylation by CPEB4 mis-splicing. <i>Nature</i> , 2018, 560, 441-446.	13.7	113
26	Mapping correlations between ventricular expansion and CSF amyloid and tau biomarkers in 240 subjects with Alzheimer's disease, mild cognitive impairment and elderly controls. <i>NeuroImage</i> , 2009, 46, 394-410.	2.1	102
27	Tropism of SARS-CoV-2 for human cortical astrocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	77
28	Genome-wide DNA methylation profiling identifies convergent molecular signatures associated with idiopathic and syndromic autism in post-mortem human brain tissue. <i>Human Molecular Genetics</i> , 2019, 28, 2201-2211.	1.4	70
29	Apolipoprotein E Genotype is Associated with Temporal and Hippocampal Atrophy Rates in Healthy Elderly Adults: A Tensor-Based Morphometry Study <sup>1</sup> . <i>Journal of Alzheimer's Disease</i> , 2011, 23, 433-442.	1.2	65
30	Rare Inherited Variation in Autism: Beginning to See the Forest and a Few Trees. <i>Neuron</i> , 2013, 77, 209-211.	3.8	56
31	Spatiotemporal dynamics of the postnatal developing primate brain transcriptome. <i>Human Molecular Genetics</i> , 2015, 24, 4327-4339.	1.4	53
32	Strong correlation of downregulated genes related to synaptic transmission and mitochondria in post-mortem autism cerebral cortex. <i>Journal of Neurodevelopmental Disorders</i> , 2018, 10, 18.	1.5	51
33	Measurement of cortical thickness from MRI by minimum line integrals on soft-tissue. <i>Human Brain Mapping</i> , 2009, 30, 3188-3199.	1.9	45
34	Specific responses of human hippocampal neurons are associated with better memory. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10503-10508.	3.3	44
35	Integrative network analysis reveals biological pathways associated with Williams syndrome. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2019, 60, 585-598.	3.1	24
36	Shared Molecular Neuropathology Across Major Psychiatric Disorders Parallels Polygenic Overlap. <i>Focus (American Psychiatric Publishing)</i> , 2019, 17, 66-72.	0.4	20

#	ARTICLE	IF	CITATIONS
37	Mapping hippocampal degeneration in 400 subjects with a novel automated segmentation approach. , 2008, , .		9
38	Segmentation-free measurement of cortical thickness from MRI. , 2008, 2008, 1625-1628.		3
39	O4-12-02: Protein co-expression network analysis in Alzheimer's disease. , 2015, 11, P299-P299.		0
40	Gene Networks in Neuropsychiatric Disease. , 2016, , 161-178.		0
41	Neuroscience and the Genomic Revolution: An Overview. , 2013, , 1018-1027.		0