

Nazanin Mirza-Schreiber

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

2,113
citations

471509

17
h-index

580821

25
g-index

29
all docs

29
docs citations

29
times ranked

5447
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Cis</i> -epistasis at the <i>LPA</i> locus and risk of cardiovascular diseases. <i>Cardiovascular Research</i> , 2022, 118, 1088-1102.	3.8	14
2	GWAS meta-analysis followed by Mendelian randomization revealed potential control mechanisms for circulating β -Klotho levels. <i>Human Molecular Genetics</i> , 2022, 31, 792-802.	2.9	5
3	Blood DNA methylation provides an accurate biomarker of <i>KMT2B</i> -related dystonia and predicts onset. <i>Brain</i> , 2022, 145, 644-654.	7.6	18
4	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. <i>Molecular Psychiatry</i> , 2021, 26, 3004-3017.	7.9	56
5	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	12.8	61
6	The genetic architecture of the human cerebral cortex. <i>Science</i> , 2020, 367, .	12.6	450
7	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. <i>Translational Psychiatry</i> , 2019, 9, 77.	4.8	82
8	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	21.4	192
9	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	12.8	250
10	Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. <i>Nature Communications</i> , 2017, 8, 1511.	12.8	60
11	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016, 19, 1569-1582.	14.8	213
12	GWAS for executive function and processing speed suggests involvement of the <i>CADM2</i> gene. <i>Molecular Psychiatry</i> , 2016, 21, 189-197.	7.9	134
13	Solid Organ Transplantation in Patients with Inflammatory Bowel Diseases (IBD): Analysis of Transplantation Outcome and IBD Activity in a Large Single Center Cohort. <i>PLoS ONE</i> , 2015, 10, e0135807.	2.5	33
14	Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders. <i>Neuron</i> , 2015, 86, 1189-1202.	8.1	102
15	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Biological Psychiatry</i> , 2015, 77, 749-763.	1.3	67
16	Integrating gene expression and epidemiological data for the discovery of genetic interactions associated with cancer risk. <i>Carcinogenesis</i> , 2014, 35, 578-585.	2.8	1
17	Restless Legs Syndrome-associated intronic common variant in <i>Meis1</i> alters enhancer function in the developing telencephalon. <i>Genome Research</i> , 2014, 24, 592-603.	5.5	102
18	The Challenges of Genome-Wide Interaction Studies: Lessons to Learn from the Analysis of HDL Blood Levels. <i>PLoS ONE</i> , 2014, 9, e109290.	2.5	13

#	ARTICLE	IF	CITATIONS
19	Cost-effective GPU-Grid for Genome-wide Epistasis Calculations. <i>Methods of Information in Medicine</i> , 2013, 52, 91-95.	1.2	7
20	A Genome-Wide Association Study Suggests Novel Loci Associated with a Schizophrenia-Related Brain-Based Phenotype. <i>PLoS ONE</i> , 2013, 8, e64872.	2.5	21
21	Replication and meta-analysis of TMEM132D gene variants in panic disorder. <i>Translational Psychiatry</i> , 2012, 2, e156-e156.	4.8	74
22	GLIDE: GPU-Based Linear Regression for Detection of Epistasis. <i>Human Heredity</i> , 2012, 73, 220-236.	0.8	32
23	ANK3 and CACNA1C “Missing genetic link for bipolar disorder and major depressive disorder in two German case-control samples. <i>Journal of Psychiatric Research</i> , 2012, 46, 973-979.	3.1	19
24	PTPN2 Gene Variants Are Associated with Susceptibility to Both Crohn's Disease and Ulcerative Colitis Supporting a Common Genetic Disease Background. <i>PLoS ONE</i> , 2012, 7, e33682.	2.5	57
25	Epistasis detection on quantitative phenotypes by exhaustive enumeration using GPUs. <i>Bioinformatics</i> , 2011, 27, i214-i221.	4.1	19