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List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

7,431
citations

304743

22
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345221

36
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docs citations

43
times ranked

14247
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. <i>Human Reproduction</i> , 2022, 37, 366-383.	0.9	19
2	DeepNull models non-linear covariate effects to improve phenotypic prediction and association power. <i>Nature Communications</i> , 2022, 13, 241.	12.8	17
3	Genetic analysis of endometriosis and depression identifies shared loci and implicates causal links with gastric mucosa abnormality. <i>Human Genetics</i> , 2021, 140, 529-552.	3.8	36
4	Disease risk scores for skin cancers. <i>Nature Communications</i> , 2021, 12, 160.	12.8	46
5	Genomewide Association Studies of <i>LRRK2</i> Modifiers of Parkinson's Disease. <i>Annals of Neurology</i> , 2021, 90, 76-88.	5.3	30
6	Large-scale machine-learning-based phenotyping significantly improves genomic discovery for optic nerve head morphology. <i>American Journal of Human Genetics</i> , 2021, 108, 1217-1230.	6.2	35
7	Insights into the genetic basis of retinal detachment. <i>Human Molecular Genetics</i> , 2020, 29, 689-702.	2.9	26
8	Genome-wide association studies of antidepressant class response and treatment-resistant depression. <i>Translational Psychiatry</i> , 2020, 10, 360.	4.8	33
9	The effect of <i>LRRK2</i> loss-of-function variants in humans. <i>Nature Medicine</i> , 2020, 26, 869-877.	30.7	79
10	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2019, 18, 1091-1102.	10.2	1,414
11	The Parkinson's phenotype traits associated with Parkinson's disease in a broadly phenotyped cohort. <i>Npj Parkinson's Disease</i> , 2019, 5, 4.	5.3	34
12	Correspondence between cerebral glucose metabolism and BOLD reveals relative power and cost in human brain. <i>Nature Communications</i> , 2019, 10, 690.	12.8	62
13	Association of Whole-Genome and <i>NETRIN1</i> Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019, 4, 91-100.	1.5	16
14	Common Variant Burden Contributes to the Familial Aggregation of Migraine in 1,589 Families. <i>Neuron</i> , 2018, 98, 743-753.e4.	8.1	63
15	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. <i>Lancet Neurology</i> , The, 2017, 16, 898-907.	10.2	191
16	Replication and characterization of <i>CADM2</i> and <i>MSRA</i> genes on human behavior. <i>Heliyon</i> , 2017, 3, e00349.	3.2	80
17	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. <i>American Journal of Human Genetics</i> , 2017, 101, 913-924.	6.2	29
18	Does conservation account for splicing patterns?. <i>BMC Genomics</i> , 2016, 17, 787.	2.8	15

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19	Whole-genome sequencing expands diagnostic utility and improves clinical management in paediatric medicine. <i>Npj Genomic Medicine</i> , 2016, 1, .	3.8	295
20	Genome-wide characteristics of de novo mutations in autism. <i>Npj Genomic Medicine</i> , 2016, 1, 160271-1602710.	3.8	200
21	Machine Learning in Genomic Medicine: A Review of Computational Problems and Data Sets. <i>Proceedings of the IEEE</i> , 2016, 104, 176-197.	21.3	186
22	Whole-Genome Sequencing Suggests Schizophrenia Risk Mechanisms in Humans with 22q11.2 Deletion Syndrome. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2453-2461.	1.8	43
23	Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning. <i>Nature Biotechnology</i> , 2015, 33, 831-838.	17.5	2,206
24	The human splicing code reveals new insights into the genetic determinants of disease. <i>Science</i> , 2015, 347, 1254806.	12.6	1,053
25	Brain-expressed exons under purifying selection are enriched for de novo mutations in autism spectrum disorder. <i>Nature Genetics</i> , 2014, 46, 742-747.	21.4	149
26	Widespread intron retention in mammals functionally tunes transcriptomes. <i>Genome Research</i> , 2014, 24, 1774-1786.	5.5	554
27	Protein Structure Idealization: How accurately is it possible to model protein structures with dihedral angles?. <i>Algorithms for Molecular Biology</i> , 2013, 8, 5.	1.2	2
28	Network cleanup. <i>Nature Biotechnology</i> , 2013, 31, 714-715.	17.5	26
29	Determining Protein Structures from NOESY Distance Constraints by Semidefinite Programming. <i>Journal of Computational Biology</i> , 2013, 20, 296-310.	1.6	25
30	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. <i>Nature</i> , 2013, 498, 241-245.	27.8	326
31	Protein Structure by Semidefinite Facial Reduction. <i>Lecture Notes in Computer Science</i> , 2012, , 1-11.	1.3	2
32	How Accurately Can We Model Protein Structures with Dihedral Angles?. <i>Lecture Notes in Computer Science</i> , 2012, , 274-287.	1.3	0
33	Guided Locally Linear Embedding. <i>Pattern Recognition Letters</i> , 2011, 32, 1029-1035.	4.2	15
34	ERROR TOLERANT NMR BACKBONE RESONANCE ASSIGNMENT AND AUTOMATED STRUCTURE GENERATION. <i>Journal of Bioinformatics and Computational Biology</i> , 2011, 09, 15-41.	0.8	18
35	PROTEIN SECONDARY STRUCTURE PREDICTION USING NMR CHEMICAL SHIFT DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 867-884.	0.8	19
36	PICKY: a novel SVD-based NMR spectra peak picking method. <i>Bioinformatics</i> , 2009, 25, i268-i275.	4.1	61