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List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

30,879
citations

218381

26
h-index

149479

56
g-index

69
all docs

69
docs citations

69
times ranked

53995
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
3	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	13.7	1,994
4	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. <i>Science</i> , 2012, 337, 64-69.	6.0	1,535
5	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
6	Loss-of-Function Mutations in <i>APOC3</i> , Triglycerides, and Coronary Disease. <i>New England Journal of Medicine</i> , 2014, 371, 22-31.	13.9	936
7	Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. <i>Nature</i> , 2013, 493, 216-220.	13.7	898
8	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	5.8	636
9	Detecting and Estimating Contamination of Human DNA Samples in Sequencing and Array-Based Genotype Data. <i>American Journal of Human Genetics</i> , 2012, 91, 839-848.	2.6	441
10	An efficient and scalable analysis framework for variant extraction and refinement from population-scale DNA sequence data. <i>Genome Research</i> , 2015, 25, 918-925.	2.4	308
11	Microscopic examination of spatial transcriptome using Seq-Scope. <i>Cell</i> , 2021, 184, 3559-3572.e22.	13.5	233
12	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	2.6	193
13	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. <i>Nature Genetics</i> , 2013, 45, 1375-1379.	9.4	158
14	Randomised clinical trial: faecal microbiota transplantation for recurrent <i>Clostridium difficile</i> infection – fresh, or frozen, or lyophilised microbiota from a small pool of healthy donors delivered by colonoscopy. <i>Alimentary Pharmacology and Therapeutics</i> , 2017, 45, 899-908.	1.9	148
15	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. <i>Circulation</i> , 2018, 137, 2741-2756.	1.6	100
16	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. <i>PLoS Genetics</i> , 2015, 11, e1004876.	1.5	95
17	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. <i>ELife</i> , 2015, 4, .	2.8	95
18	Prosaposin is a regulator of progranulin levels and oligomerization. <i>Nature Communications</i> , 2016, 7, 11992.	5.8	68

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19	Data for Genetic Analysis Workshop 18: human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees. BMC Proceedings, 2014, 8, S2.	1.8	65
20	Parliament2: Accurate structural variant calling at scale. GigaScience, 2020, 9, .	3.3	51
21	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
22	Correcting for Sample Contamination in Genotype Calling of DNA Sequence Data. American Journal of Human Genetics, 2015, 97, 284-290.	2.6	39
23	Spatially Adaptive Classification of Land Cover With Remote Sensing Data. IEEE Transactions on Geoscience and Remote Sensing, 2011, 49, 2662-2673.	2.7	37
24	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics, 2013, 29, 2744-2749.	1.8	36
25	An Efficient Active Learning Algorithm with Knowledge Transfer for Hyperspectral Data Analysis. , 2008, , .		31
26	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
27	Semisupervised Learning of Hyperspectral Data With Unknown Land-Cover Classes. IEEE Transactions on Geoscience and Remote Sensing, 2013, 51, 273-282.	2.7	29
28	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
29	Genes and microRNAs associated with mouse cleft palate: A systematic review and bioinformatics analysis. Mechanisms of Development, 2018, 150, 21-27.	1.7	27
30	A self-training approach to cost sensitive uncertainty sampling. Machine Learning, 2009, 76, 257-270.	3.4	26
31	In search of rare variants: Preliminary results from whole genome sequencing of 1,325 individuals with psychophysiological endophenotypes. Psychophysiology, 2014, 51, 1309-1320.	1.2	25
32	Spatially Cost-sensitive Active Learning. , 2009, , .		25
33	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	2.6	25
34	Tracking and Segmentation of Highway Vehicles in Cluttered and Crowded Scenes. , 2008, , .		24
35	Active learning of hyperspectral data with spatially dependent label acquisition costs. , 2009, , .		20
36	MicroRNA-655-3p and microRNA-497-5p inhibit cell proliferation in cultured human lip cells through the regulation of genes related to human cleft lip. BMC Medical Genomics, 2019, 12, 70.	0.7	20

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37	A cleft lip and palate gene, <i>Irf6</i> , is involved in osteoblast differentiation of craniofacial bone. <i>Developmental Dynamics</i> , 2019, 248, 221-232.	0.8	20
38	Optimal sequencing strategies for identifying disease-associated singletons. <i>PLoS Genetics</i> , 2017, 13, e1006811.	1.5	19
39	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. <i>BMC Proceedings</i> , 2016, 10, 71-77.	1.8	17
40	A novel deep learning model using dosimetric and clinical information for grade 4 radiotherapy-induced lymphopenia prediction. <i>Physics in Medicine and Biology</i> , 2020, 65, 035014.	1.6	17
41	MicroRNA-124-3p suppresses mouse lip mesenchymal cell proliferation through the regulation of genes associated with cleft lip in the mouse. <i>BMC Genomics</i> , 2019, 20, 852.	1.2	16
42	Whole Exome Sequencing to Identify Genetic Variants Associated with Raised Atherosclerotic Lesions in Young Persons. <i>Scientific Reports</i> , 2017, 7, 4091.	1.6	15
43	Home media center and media clients for multi-room audio and video applications. , 0, , .		11
44	Impact of Diabetes on the Gut and Salivary IgA Microbiomes. <i>Infection and Immunity</i> , 2020, 88, .	1.0	11
45	Spatially adaptive semi-supervised learning with Gaussian processes for hyperspectral data analysis. <i>Statistical Analysis and Data Mining</i> , 2011, 4, 358-371.	1.4	10
46	Metabolomic profiles associated with subtypes of prediabetes among Mexican Americans in Starr County, Texas, USA. <i>Diabetologia</i> , 2020, 63, 287-295.	2.9	9
47	Multi-class Boosting with Class Hierarchies. <i>Lecture Notes in Computer Science</i> , 2009, , 32-41.	1.0	9
48	Spatially Adaptive Classification and Active Learning of Multispectral Data with Gaussian Processes. , 2009, , .		8
49	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. <i>Human Molecular Genetics</i> , 2015, 24, 1504-1512.	1.4	8
50	GX-Means: A model-based divide and merge algorithm for geospatial image clustering. <i>Procedia Computer Science</i> , 2011, 4, 186-195.	1.2	7
51	Gene datasets associated with mouse cleft palate. <i>Data in Brief</i> , 2018, 18, 655-673.	0.5	7
52	muCNV: genotyping structural variants for population-level sequencing. <i>Bioinformatics</i> , 2021, 37, 2055-2057.	1.8	7
53	Identifying Individualized Risk Profiles for Radiotherapy-Induced Lymphopenia Among Patients With Esophageal Cancer Using Machine Learning. <i>JCO Clinical Cancer Informatics</i> , 2021, 5, 1044-1053.	1.0	7
54	Dexamethasone Suppresses Palatal Cell Proliferation through miR-130a-3p. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12453.	1.8	7

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55	Spatially adaptive classification of hyperspectral data with Gaussian processes. , 2009, , .		6
56	Identification of Functional Genetic Determinants of Cardiac Troponin T and I in a Multiethnic Population and Causal Associations With Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003460.	1.6	5
57	Secondary Genome-Wide Association Study Using Novel Analytical Strategies Disentangle Genetic Components of Cleft Lip and/or Cleft Palate in 1q32.2. Genes, 2020, 11, 1280.	1.0	4
58	The impact of the Th17:Treg axis on the IgA-Biome across the glycemic spectrum. PLoS ONE, 2021, 16, e0258812.	1.1	4
59	A Self-training Approach to Cost Sensitive Uncertainty Sampling. Lecture Notes in Computer Science, 2009, , 10-10.	1.0	4
60	Nearest-Manifold Classification with Gaussian Processes. , 2010, , .		3
61	Lyophilized Fecal Microbiota Transplantation Capsules for Recurrent Clostridium difficile Infection. Open Forum Infectious Diseases, 2017, 4, S381-S381.	0.4	2
62	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.8	1
63	Hybrid Hierarchical Classifiers for Hyperspectral Data Analysis. Lecture Notes in Computer Science, 2009, , 42-51.	1.0	1
64	Bias Selection Using Task-Targeted Random Subspaces for Robust Application of Graph-Based Semi-supervised Learning. , 2012, , .		0