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List of Publications by Year in descending order

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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	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
2	muCNV: genotyping structural variants for population-level sequencing. Bioinformatics, 2021, 37, 2055-2057.	1.8	7
3	Microscopic examination of spatial transcriptome using Seq-Scope. Cell, 2021, 184, 3559-3572.e22.	13.5	233
4	Identifying Individualized Risk Profiles for Radiotherapy-Induced Lymphopenia Among Patients With Esophageal Cancer Using Machine Learning. JCO Clinical Cancer Informatics, 2021, 5, 1044-1053.	1.0	7
5	The impact of the Th17:Treg axis on the IgA-Biome across the glycemic spectrum. PLoS ONE, 2021, 16, e0258812.	1.1	4
6	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
7	Dexamethasone Suppresses Palatal Cell Proliferation through miR-130a-3p. International Journal of Molecular Sciences, 2021, 22, 12453.	1.8	7
8	A novel deep learning model using dosimetric and clinical information for grade 4 radiotherapy-induced lymphopenia prediction. Physics in Medicine and Biology, 2020, 65, 035014.	1.6	17
9	Metabolomic profiles associated with subtypes of prediabetes among Mexican Americans in Starr County, Texas, USA. Diabetologia, 2020, 63, 287-295.	2.9	9
10	Impact of Diabetes on the Gut and Salivary IgA Microbiomes. Infection and Immunity, 2020, 88, .	1.0	11
11	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
12	Parliament2: Accurate structural variant calling at scale. GigaScience, 2020, 9, .	3.3	51
13	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
14	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
15	A cleft lip and palate gene,Irf6, is involved in osteoblast differentiation of craniofacial bone. Developmental Dynamics, 2019, 248, 221-232.	0.8	20
16	MicroRNA-124-3p suppresses mouse lip mesenchymal cell proliferation through the regulation of genes associated with cleft lip in the mouse. BMC Genomics, 2019, 20, 852.	1.2	16
17	Genes and microRNAs associated with mouse cleft palate: A systematic review and bioinformatics analysis. Mechanisms of Development, 2018, 150, 21-27.	1.7	27
18	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

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19	Gene datasets associated with mouse cleft palate. Data in Brief, 2018, 18, 655-673.	0.5	7
20	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. Circulation, 2018, 137, 2741-2756.	1.6	100
21	Randomised clinical trial: faecal microbiota transplantation for recurrent Clostridum difficile infection â€“ fresh, or frozen, or lyophilised microbiota from a small pool of healthy donors delivered by colonoscopy. Alimentary Pharmacology and Therapeutics, 2017, 45, 899-908.	1.9	148
22	Whole Exome Sequencing to Identify Genetic Variants Associated with Raised Atherosclerotic Lesions in Young Persons. Scientific Reports, 2017, 7, 4091.	1.6	15
23	A Low-Frequency Inactivating AKT2 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
24	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
25	Lyophilized Fecal Microbiota Transplantation Capsules for Recurrent Clostridium difficile Infection. Open Forum Infectious Diseases, 2017, 4, S381-S381.	0.4	2
26	Optimal sequencing strategies for identifying disease-associated singletons. PLoS Genetics, 2017, 13, e1006811.	1.5	19
27	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
28	Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992.	5.8	68
29	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.8	17
30	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.8	1
31	Correcting for Sample Contamination in Genotype Calling of DNA Sequence Data. American Journal of Human Genetics, 2015, 97, 284-290.	2.6	39
32	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
33	An efficient and scalable analysis framework for variant extraction and refinement from population-scale DNA sequence data. Genome Research, 2015, 25, 918-925.	2.4	308
34	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	1.4	8
35	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
36	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994

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37	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, .	2.8	95
38	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
39	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
40	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
41	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	13.9	936
42	Semisupervised Learning of Hyperspectral Data With Unknown Land-Cover Classes. IEEE Transactions on Geoscience and Remote Sensing, 2013, 51, 273-282.	2.7	29
43	Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. Nature, 2013, 493, 216-220.	13.7	898
44	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature Genetics, 2013, 45, 1375-1379.	9.4	158
45	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics, 2013, 29, 2744-2749.	1.8	36
46	Bias Selection Using Task-Targeted Random Subspaces for Robust Application of Graph-Based Semi-supervised Learning. , 2012, , .		0
47	Detecting and Estimating Contamination of Human DNA Samples in Sequencing and Array-Based Genotype Data. American Journal of Human Genetics, 2012, 91, 839-848.	2.6	441
48	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
49	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69.	6.0	1,535
50	Spatially Adaptive Classification of Land Cover With Remote Sensing Data. IEEE Transactions on Geoscience and Remote Sensing, 2011, 49, 2662-2673.	2.7	37
51	Spatially adaptive semiâ€supervised learning with Gaussian processes for hyperspectral data analysis. Statistical Analysis and Data Mining, 2011, 4, 358-371.	1.4	10
52	GX-Means: A model-based divide and merge algorithm for geospatial image clustering. Procedia Computer Science, 2011, 4, 186-195.	1.2	7
53	Nearest-Manifold Classification with Gaussian Processes. , 2010, , .		3
54	Spatially Adaptive Classification and Active Learning of Multispectral Data with Gaussian Processes. , 2009, , .		8

#	Article	IF	Citations
55	Spatially adaptive classification of hyperspectral data with Gaussian processes. , 2009, , .		6
56	A self-training approach to cost sensitive uncertainty sampling. Machine Learning, 2009, 76, 257-270.	3.4	26
57	Active learning of hyperspectral data with spatially dependent label acquisition costs. , 2009, , .		20
58	Multi-class Boosting with Class Hierarchies. Lecture Notes in Computer Science, 2009, , 32-41.	1.0	9
59	Spatially Cost-sensitive Active Learning. , 2009, , .		25
60	Hybrid Hierarchical Classifiers for Hyperspectral Data Analysis. Lecture Notes in Computer Science, 2009, , 42-51.	1.0	1
61	A Self-training Approach to Cost Sensitive Uncertainty Sampling. Lecture Notes in Computer Science, 2009, , 10-10.	1.0	4
62	An Efficient Active Learning Algorithm with Knowledge Transfer for Hyperspectral Data Analysis. , 2008, , .		31
63	Tracking and Segmentation of Highway Vehicles in Cluttered and Crowded Scenes. , 2008, , .		24
64	Home media center and media clients for multi-room audio and video applications. , 0, , .		11