Goo Jun

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7607883/publications.pdf

Version: 2024-02-01

64 papers	30,879 citations	218677 26 h-index	149698 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. Nature, 2015, 526, 68-74.	27.8	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
3	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
4	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69.	12.6	1,535
5	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
6	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	27.0	936
7	Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. Nature, 2013, 493, 216-220.	27.8	898
8	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
9	Detecting and Estimating Contamination of Human DNA Samples in Sequencing and Array-Based Genotype Data. American Journal of Human Genetics, 2012, 91, 839-848.	6.2	441
10	An efficient and scalable analysis framework for variant extraction and refinement from population-scale DNA sequence data. Genome Research, 2015, 25, 918-925.	5.5	308
11	Microscopic examination of spatial transcriptome using Seq-Scope. Cell, 2021, 184, 3559-3572.e22.	28.9	233
12	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
13	Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. Nature Genetics, 2013, 45, 1375-1379.	21.4	158
14	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.	3.7	148
15	Proteomic Architecture of Human Coronary and Aortic Atherosclerosis. Circulation, 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. PLoS Genetics, 2015, 11, e1004876.	3.5	95
17	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, .	6.0	95
18	Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992.	12.8	68

#	Article	IF	Citations
19	Data for Genetic Analysis Workshop 18: human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees. BMC Proceedings, 2014, 8, S2.	1.6	65
20	Parliament2: Accurate structural variant calling at scale. GigaScience, 2020, 9, .	6.4	51
21	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.	0.6	47
22	Correcting for Sample Contamination in Genotype Calling of DNA Sequence Data. American Journal of Human Genetics, 2015, 97, 284-290.	6.2	39
23	Spatially Adaptive Classification of Land Cover With Remote Sensing Data. IEEE Transactions on Geoscience and Remote Sensing, 2011, 49, 2662-2673.	6.3	37
24	Imputation of coding variants in African Americans: better performance using data from the exome sequencing project. Bioinformatics, 2013, 29, 2744-2749.	4.1	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.	5.3	31
27	Semisupervised Learning of Hyperspectral Data With Unknown Land-Cover Classes. IEEE Transactions on Geoscience and Remote Sensing, 2013, 51, 273-282.	6.3	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.	7.1	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.	5.4	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.	2.4	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.	6.2	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.	1.5	20

#	Article	IF	Citations
37	A cleft lip and palate gene,Irf6, is involved in osteoblast differentiation of craniofacial bone. Developmental Dynamics, 2019, 248, 221-232.	1.8	20
38	Optimal sequencing strategies for identifying disease-associated singletons. PLoS Genetics, 2017, 13, e1006811.	3.5	19
39	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.6	17
40	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.	3.0	17
41	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.	2.8	16
42	Whole Exome Sequencing to Identify Genetic Variants Associated with Raised Atherosclerotic Lesions in Young Persons. Scientific Reports, 2017, 7, 4091.	3.3	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. Infection and Immunity, 2020, 88, .	2.2	11
45	Spatially adaptive semiâ€supervised learning with Gaussian processes for hyperspectral data analysis. Statistical Analysis and Data Mining, 2011, 4, 358-371.	2.8	10
46	Metabolomic profiles associated with subtypes of prediabetes among Mexican Americans in Starr County, Texas, USA. Diabetologia, 2020, 63, 287-295.	6.3	9
47	Multi-class Boosting with Class Hierarchies. Lecture Notes in Computer Science, 2009, , 32-41.	1.3	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. Human Molecular Genetics, 2015, 24, 1504-1512.	2.9	8
50	GX-Means: A model-based divide and merge algorithm for geospatial image clustering. Procedia Computer Science, 2011, 4, 186-195.	2.0	7
51	Gene datasets associated with mouse cleft palate. Data in Brief, 2018, 18, 655-673.	1.0	7
52	muCNV: genotyping structural variants for population-level sequencing. Bioinformatics, 2021, 37, 2055-2057.	4.1	7
53	Identifying Individualized Risk Profiles for Radiotherapy-Induced Lymphopenia Among Patients With Esophageal Cancer Using Machine Learning. JCO Clinical Cancer Informatics, 2021, 5, 1044-1053.	2.1	7
54	Dexamethasone Suppresses Palatal Cell Proliferation through miR-130a-3p. International Journal of Molecular Sciences, 2021, 22, 12453.	4.1	7

#	Article	IF	Citations
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.	3.6	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.	2.4	4
58	The impact of the Th17:Treg axis on the IgA-Biome across the glycemic spectrum. PLoS ONE, 2021, 16, e0258812.	2.5	4
59	A Self-training Approach to Cost Sensitive Uncertainty Sampling. Lecture Notes in Computer Science, 2009, , 10-10.	1.3	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.	0.9	2
62	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.6	1
63	Hybrid Hierarchical Classifiers for Hyperspectral Data Analysis. Lecture Notes in Computer Science, 2009, , 42-51.	1.3	1
64	Bias Selection Using Task-Targeted Random Subspaces for Robust Application of Graph-Based Semi-supervised Learning. , 2012, , .		0