Judong Shen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/550394/publications.pdf

Version: 2024-02-01

		759055	580701
27	2,247	12	25
papers	citations	h-index	g-index

27	27	27	6648
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Fast and Accurate Approximation to the Distributions of Quadratic Forms of Gaussian Variables. Journal of Computational and Graphical Statistics, 2022, 31, 304-311.	0.9	3
2	Germline HLA landscape does not predict efficacy of pembrolizumab monotherapy across solid tumor types. Immunity, 2022, 55, 56-64.e4.	6.6	19
3	GWAS of longitudinal trajectories at biobank scale. American Journal of Human Genetics, 2022, 109, 433-445.	2.6	13
4	A statistical perspective on baseline adjustment in pharmacogenomic genome-wide association studies of quantitative change. Npj Genomic Medicine, 2022, 7, .	1.7	3
5	Global Landscape of Clostridioides Difficile Phylogeography, Antibiotic Susceptibility, and Toxin Polymorphisms by Post-Hoc Whole-Genome Sequencing from the MODIFY I/II Studies. Infectious Diseases and Therapy, 2021, 10, 853-870.	1.8	17
6	CauchyCP: A powerful test under non-proportional hazards using Cauchy combination of change-point Cox regressions. Statistical Methods in Medical Research, 2021, 30, 096228022110370.	0.7	1
7	VCSEL: Prioritizing SNP-set by penalized variance component selection. Annals of Applied Statistics, 2021, 15, 1652-1672.	0.5	2
8	Effect of Endogenous Clostridioides difficile Toxin Antibodies on Recurrence of C. difficile Infection. Clinical Infectious Diseases, 2020, 71, 81-86.	2.9	17
9	Bezlotoxumab for prevention of Clostridium difficile infection recurrence: Distinguishing relapse from reinfection with whole genome sequencing. Anaerobe, 2020, 61, 102137.	1.0	6
10	Multi-trait analysis of rare-variant association summary statistics using MTAR. Nature Communications, 2020, 11, 2850.	5.8	19
11	Genetic Association Reveals Protection against Recurrence of Clostridium difficile Infection with Bezlotoxumab Treatment. MSphere, 2020, 5, .	1.3	13
12	Composite Kernel Association Test (CKAT) for SNP-set joint assessment of genotype and genotype-by-treatment interaction in Pharmacogenetics studies. Bioinformatics, 2020, 36, 3162-3168.	1.8	3
13	STOPGAP: a database for systematic target opportunity assessment by genetic association predictions. Bioinformatics, 2017, 33, 2784-2786.	1.8	32
14	No evidence of large genetic effects on steroid response in asthma patients. Journal of Allergy and Clinical Immunology, 2017, 139, 797-803.e7.	1.5	35
15	Genome Wide Analysis Reveals Host Genetic Variants that Associate with Reduction in Clostridium difficile Infection Recurrence (rCDI) in Patients Treated with Bezlotoxumab. Open Forum Infectious Diseases, 2017, 4, S380-S380.	0.4	0
16	Endogenous Serum IgG Antibodies to Clostridium difficile Toxin B Are Associated with Protection against C.Âdifficile Infection Recurrence. Open Forum Infectious Diseases, 2017, 4, S388-S388.	0.4	0
17	The support of human genetic evidence for approved drug indications. Nature Genetics, 2015, 47, 856-860.	9.4	1,112
18	Rare variant testing across methods and thresholds using the multi-kernel sequence kernel association test (MK-SKAT). Statistics and Its Interface, 2015, 8, 495-505.	0.2	11

#	Article	IF	Citations
19	Pharmacogenetic investigation of dabrafenib efficacy in a meta-analysis of three melanoma studies.. Journal of Clinical Oncology, 2014, 32, e20018-e20018.	0.8	1
20	Multi-Population Classical HLA Type Imputation. PLoS Computational Biology, 2013, 9, e1002877.	1.5	157
21	Deep Resequencing Unveils Genetic Architecture of ADIPOQ and Identifies a Novel Low-Frequency Variant Strongly Associated With Adiponectin Variation. Diabetes, 2012, 61, 1297-1301.	0.3	29
22	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	6.0	626
23	Deep sequencing of theLRRK2gene in 14,002 individuals reveals evidence of purifying selection and independent origin of the p.Arg1628Pro mutation in Europe. Human Mutation, 2012, 33, 1087-1098.	1.1	24
24	Support Vector Fuzzy Adaptive Network in the Modeling of Material Removal Rate in Rotary Ultrasonic Machining. Journal of Manufacturing Science and Engineering, Transactions of the ASME, 2008, 130, .	1.3	6
25	Support vector fuzzy adaptive network in regression analysis. Computers and Mathematics With Applications, 2007, 54, 1353-1366.	1.4	10
26	Modelling and analysis of waviness reduction in soft-pad grinding of wire-sawn silicon wafers by support vector regression. International Journal of Production Research, 2006, 44, 2605-2623.	4.9	10
27	Determination of cluster number in clustering microarray data. Applied Mathematics and Computation, 2005, 169, 1172-1185.	1.4	78