Judong Shen

List of Publications by Year
in descending order

27 papers	2,247 citations	759055 12 h-index	580701 25 g-index
27 all docs	27 docs citations	27 times ranked	6648 citing authors

#	Article	IF	Citations
1	The support of human genetic evidence for approved drug indications. Nature Genetics, 2015, 47, 856-860.	9.4	1,112
2	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	6.0	626
3	Multi-Population Classical HLA Type Imputation. PLoS Computational Biology, 2013, 9, e1002877.	1.5	157
4	Determination of cluster number in clustering microarray data. Applied Mathematics and Computation, 2005, 169, 1172-1185.	1.4	78
5	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
6	STOPGAP: a database for systematic target opportunity assessment by genetic association predictions. Bioinformatics, 2017, 33, 2784-2786.	1.8	32
7	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
8	Deep sequencing of the *LRRK2* gene 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
9	Multi-trait analysis of rare-variant association summary statistics using MTAR. Nature Communications, 2020, 11, 2850.	5.8	19
10	Germline HLA landscape does not predict efficacy of pembrolizumab monotherapy across solid tumor types. Immunity, 2022, 55, 56-64.e4.	6.6	19
11	Effect of Endogenous Clostridioides difficile Toxin Antibodies on Recurrence of C. difficile Infection. Clinical Infectious Diseases, 2020, 71, 81-86.	2.9	17
12	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
13	Genetic Association Reveals Protection against Recurrence of *Clostridium difficile* Infection with Bezlotoxumab Treatment. MSphere, 2020, 5, .	1.3	13
14	GWAS of longitudinal trajectories at biobank scale. American Journal of Human Genetics, 2022, 109, 433-445.	2.6	13
15	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
16	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
17	Support vector fuzzy adaptive network in regression analysis. Computers and Mathematics With Applications, 2007, 54, 1353-1366.	1.4	10
18	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

#	ARTICLE	IF	CITATIONS
19	Bezlotoxumab for prevention of Clostridium difficile infection recurrence: Distinguishing relapse from reinfection with whole genome sequencing. Anaerobe, 2020, 61, 102137.	1.0	6
20	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
21	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
22	A statistical perspective on baseline adjustment in pharmacogenomic genome-wide association studies of quantitative change. Npj Genomic Medicine, 2022, 7, .	1.7	3
23	VCSEL: Prioritizing SNP-set by penalized variance component selection. Annals of Applied Statistics, 2021, 15, 1652-1672.	0.5	2
24	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
25	Pharmacogenetic investigation of dabrafenib efficacy in a meta-analysis of three melanoma studies.. Journal of Clinical Oncology, 2014, 32, e20018-e20018.	0.8	1
26	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
27	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