Zhongyang Zhang

List of Publications by Year
in descending order

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32 papers	1,449 citations	430874 18 h-index	454955 30 g-index
36 all docs	36 docs citations	36 times ranked	3612 citing authors

#	Article	IF	Citations
1	Ambient Air Pollutants and Traffic Factors Were Associated with Blood and Urine Biomarkers and Asthma Risk. Environmental Science & Technology, 2022, 56, 7298-7307.	10.0	6
2	Polygenic risk score for alcohol drinking behavior improves prediction of inflammatory bowel disease risk. Human Molecular Genetics, 2021, 30, 514-523.	2.9	2
3	Intestinal Dysbiosis in Young Cystic Fibrosis Rabbits. Journal of Personalized Medicine, 2021, 11, 132.	2.5	6
4	Recipient APOL1 risk alleles associate with death-censored renal allograft survival and rejection episodes. Journal of Clinical Investigation, 2021, 131, .	8.2	33
5	Enabling Clinical Trials for AMR in the Era of Precision Medicine. Transplantation, 2021, 105, 482-483.	1.0	0
6	Non-HLA donorâ€“recipient mismatches in kidney transplantationâ€”A stone left unturned. American Journal of Transplantation, 2020, 20, 19-24.	4.7	13
7	Collagenous Colitis Is Associated With HLA Signature and Shares Genetic Risks With Other Immune-Mediated Diseases. Gastroenterology, 2020, 159, 549-561.e8.	1.3	31
8	Prenatal exposure to ambient air multi-pollutants significantly impairs intrauterine fetal development trajectory. Ecotoxicology and Environmental Safety, 2020, 201, 110726.	6.0	20
9	Contribution of common and rare variants to bipolar disorder susceptibility in extended pedigrees from population isolates. Translational Psychiatry, 2020, 10, 74.	4.8	25
10	Genome-wide non-HLA donor-recipient genetic differences influence renal allograft survival via early allograft fibrosis. Kidney International, 2020, 98, 758-768.	5.2	25
11	Molecular predictors of prevention of recurrence in HCC with sorafenib as adjuvant treatment and prognostic factors in the phase 3 STORM trial. Gut, 2019, 68, 1065-1075.	12.1	195
12	EnsembleCNV: an ensemble machine learning algorithm to identify and genotype copy number variation using SNP array data. Nucleic Acids Research, 2019, 47, e39-e39.	14.5	15
13	Airway microbiome is associated with respiratory functions and responses to ambient particulate matter exposure. Ecotoxicology and Environmental Safety, 2019, 167, 269-277.	6.0	48
14	Bio3Air, an integrative system for monitoring individual-level air pollutant exposure with high time and spatial resolution. Ecotoxicology and Environmental Safety, 2019, 169, 756-763.	6.0	3
15	NPHP1 (Nephrocystin-1) Gene Deletions Cause Adult-Onset ESRD. Journal of the American Society of Nephrology: JASN, 2018, 29, 1772-1779.	6.1	74
16	Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. PLoS Genetics, 2018, 14, e1007799.	3.5	38
17	Understanding the Hidden Complexity of Latin American Population Isolates. American Journal of Human Genetics, 2018, 103, 707-726.	6.2	48
18	Using SAAS-CNV to Detect and Characterize Somatic Copy Number Alterations in Cancer Genomes from Next Generation Sequencing and SNP Array Data. Methods in Molecular Biology, 2018, 1833, 29-47.	0.9	5

#	Article	IF	Citations
19	A Dynamic Pooling Approach to Extract Complete Allele Signal Information in Somatic Copy Number Alternations Detection. , 2018, , .		0
20	Identification of human age-associated gene co-expressions in functional modules using liquid association. Oncotarget, 2018, 9, 1063-1074.	1.8	16
21	Mixed hepatocellular cholangiocarcinoma tumors: Cholangiolocellular carcinoma is a distinct molecular entity. Journal of Hepatology, 2017, 66, 952-961.	3.7	120
22	Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. Nature Communications, 2017, 8, 15608.	12.8	31
23	Trunk mutational events present minimal intra- and inter-tumoral heterogeneity in hepatocellular carcinoma. Journal of Hepatology, 2017, 67, 1222-1231.	3.7	121
24	APOL1 G2 risk alleleâ€”clarifying nomenclature. Kidney International, 2017, 92, 518-519.	5.2	4
25	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211.	0.6	67
26	Development and clinical application of an integrative genomic approach to personalized cancer therapy. Genome Medicine, 2016, 8, 62.	8.2	71
27	Massive parallel sequencing uncovers actionable FGFR2â€“PPHLN1 fusion and ARAF mutations in intrahepatic cholangiocarcinoma. Nature Communications, 2015, 6, 6087.	12.8	240
28	Unique Genomic Profile of Fibrolamellar Hepatocellular Carcinoma. Gastroenterology, 2015, 148, 806-818.e10.	1.3	109
29	SAAS-CNV: A Joint Segmentation Approach on Aggregated and Allele Specific Signals for the Identification of Somatic Copy Number Alterations with Next-Generation Sequencing Data. PLoS Computational Biology, 2015, 11, e1004618.	3.2	40
30	A Novel Targeted Learning Method for Quantitative Trait Loci Mapping. Genetics, 2014, 198, 1369-1376.	2.9	4
31	Reconstructing DNA copy number by joint segmentation of multiple sequences. BMC Bioinformatics, 2012, 13, 205.	2.6	15
32	Reconstructing DNA copy number by penalized estimation and imputation. Annals of Applied Statistics, 2010, 4, 1749-1773.	1.1	22