Zhiyu Peng

List of Publications by Year
in descending order

46 papers	3,719 citations	331670 21 h-index	233421 45 g-index
59 all docs	59 docs citations	59 times ranked	6892 citing authors

#	Article	IF	Citations
1	Genome-wide association study dissects the genetic architecture of oil biosynthesis in maize kernels. Nature Genetics, 2013, 45, 43-50.	21.4	764
2	Telomerase activation by genomic rearrangements in high-risk neuroblastoma. Nature, 2015, 526, 700-704.	27.8	478
3	Comprehensive analysis of RNA-Seq data reveals extensive RNA editing in a human transcriptome. Nature Biotechnology, 2012, 30, 253-260.	17.5	461
4	RNA-seq analysis of prostate cancer in the Chinese population identifies recurrent gene fusions, cancer-associated long noncoding RNAs and aberrant alternative splicings. Cell Research, 2012, 22, 806-821.	12.0	352
5	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
6	RNA sequencing reveals the complex regulatory network in the maize kernel. Nature Communications, 2013, 4, 2832.	12.8	252
7	Rapid Targeted Next-Generation Sequencing Platform for Molecular Screening and Clinical Genotyping in Subjects with Hemoglobinopathies. EBioMedicine, 2017, 23, 150-159.	6.1	138
8	SOAPsplice: Genome-Wide ab initio Detection of Splice Junctions from RNA-Seq Data. Frontiers in Genetics, 2011, 2, 46.	2.3	89
9	Lack of evidence for existence of noncanonical RNA editing. Nature Biotechnology, 2013, 31, 19-20.	17.5	87
10	Next-generation sequencing improves thalassemia carrier screening among premarital adults in a high prevalence population: the Dai nationality, China. Genetics in Medicine, 2017, 19, 1022-1031.	2.4	82
11	A platform of high-density INDEL/CAPS markers for map-based cloning in Arabidopsis. Plant Journal, 2010, 63, 880-888.	5.7	72
12	RNA Editome in Rhesus Macaque Shaped by Purifying Selection. PLoS Genetics, 2014, 10, e1004274.	3.5	71
13	Caste-specific RNA editomes in the leaf-cutting ant Acromyrmex echinatior. Nature Communications, 2014, 5, 4943.	12.8	60
14	Genome-wide identification of RNA editing in hepatocellular carcinoma. Genomics, 2015, 105, 76-82.	2.9	40
15	Nationwide population genetic screening improves outcomes of newborn screening for hearing loss in China. Genetics in Medicine, 2019, 21, 2231-2238.	2.4	40
16	Reinterpretation of common pathogenic variants in ClinVar revealed a high proportion of downgrades. Scientific Reports, 2020, 10, 331.	3.3	34
17	AutoPVS1: An automatic classification tool for PVS1 interpretation of null variants. Human Mutation, 2020, 41, 1488-1498.	2.5	34
18	Pilot study of expanded carrier screening for 11 recessive diseases in China: results from 10,476 ethnically diverse couples. European Journal of Human Genetics, 2019, 27, 254-262.	2.8	33

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19	Hypothesis: Artifacts, Including Spurious Chimeric RNAs with a Short Homologous Sequence, Caused by Consecutive Reverse Transcriptions and Endogenous Random Primers. Journal of Cancer, 2015, 6, 555-567.	2.5	32
20	A systems genetics study of swine illustrates mechanisms underlying human phenotypic traits. BMC Genomics, 2015, 16, 88.	2.8	28
21	Concurrent hearing and genetic screening in a general newborn population. Human Genetics, 2020, 139, 521-530.	3.8	24
22	SOAPfusion: a robust and effective computational fusion discovery tool for RNA-seq reads. Bioinformatics, 2013, 29, 2971-2978.	4.1	23
23	A comprehensive assessment of Nextâ€Generation Sequencing variants validation using a secondary technology. Molecular Genetics & Genomic Medicine, 2019, 7, e00748.	1.2	17
24	NGS-based spinal muscular atrophy carrier screening of 10,585 diverse couples in China: a pan-ethnic study. European Journal of Human Genetics, 2021, 29, 194-204.	2.8	17
25	Increased diagnostic yield by reanalysis of data from a hearing loss gene panel. BMC Medical Genomics, 2019, 12, 76.	1.5	16
26	Noninvasive prenatal testing of Î±-thalassemia and Î²-thalassemia through population-based parental haplotyping. Genome Medicine, 2021, 13, 18.	8.2	16
27	Characterizing sensitivity and coverage of clinical WGS as a diagnostic test for genetic disorders. BMC Medical Genomics, 2021, 14, 102.	1.5	16
28	Hemoglobin, 2019, 43, 7-11.	0.8	11
29	VIPâ€HL: Semiâ€automated ACMG/AMP variant interpretation platform for genetic hearing loss. Human Mutation, 2021, 42, 1567-1575.	2.5	10
30	Next generation sequencing is a highly reliable method to analyze exon 7 deletion of survival motor neuron 1 (SMN1) gene. Scientific Reports, 2022, 12, 223.	3.3	9
31	Molecular diagnosis of non-syndromic hearing loss patients using a stepwise approach. Scientific Reports, 2021, 11, 4036.	3.3	7
32	The mutational landscape of MYCN, Lin28b and ALKF1174L driven murine neuroblastoma mimics human disease. Oncotarget, 2018, 9, 8334-8349.	1.8	6
33	AutoCNV: a semiautomatic CNV interpretation system based on the 2019 ACMG/ClinGen Technical Standards for CNVs. BMC Genomics, 2021, 22, 721.	2.8	6
34	Noninvasive prenatal diagnosis of monogenic disorders based on direct haplotype phasing through targeted linked-read sequencing. BMC Medical Genomics, 2021, 14, 244.	1.5	6
35	A multiplex PCR amplicon sequencing assay to screen genetic hearing loss variants in newborns. BMC Medical Genomics, 2021, 14, 61.	1.5	5
36	Comprehensive genetic testing improves the clinical diagnosis and medical management of pediatric patients with isolated hearing loss. BMC Medical Genomics, 2022, 15, .	1.5	4

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37	Clinical and genomic evaluation of a Chinese patient with a novel deletion associated with Phelan-McDermid syndrome. Oncotarget, 2016, 7, 80327-80335.	1.8	3
38	Five novel globin gene mutations identified in five Chinese families by nextâ€generation sequencing. Molecular Genetics & Genomic Medicine, 2021, , e1835.	1.2	2
39	Î²-thalassemia caused by compound heterozygous mutations and cured by bone marrow transplantation: A case report. Molecular Medicine Reports, 2017, 16, 6552-6557.	2.4	1
40	Identification of a novel breast cancerâ€causing mutation in the BRCA1 gene by targeted next generation sequencing: A case report. Oncology Letters, 2018, 16, 3913-3916.	1.8	1
41	Impact of ultrasonography on identifying noninvasive prenatal screening falseâ€negative aneuploidy. Molecular Genetics & Genomic Medicine, 2020, 8, e1213.	1.2	1
42	Applications of Noninvasive Prenatal Testing for Subchromosomal Copy Number Variations Using Cell-Free DNA. Advances in Molecular Pathology, 2021, 4, 17-25.	0.4	1
43	Utility of Whole Genome Sequencing for Population Screening of Deafness-Related Genetic Variants and Cytomegalovirus Infection in Newborns. Frontiers in Genetics, 2022, 13, 883617.	2.3	1
44	The effect of hemolysis on quality control metrics for noninvasive prenatal testing. BMC Medical Genomics, 2022, 15, .	1.5	1
45	Identification of Two Novel Thalassemia Variants, HBA1: c.263delA and HBA2: c.376dupC, in Chinese Individuals. Hemoglobin, 2021, 45, 49-51.	0.8	0
46	Report of Two Novel Thalassemia Variants, HBB: c.181delG and HBA1: c.121_126delAAGACC, in Chinese Individuals. Hemoglobin, 2021, 45, 52-55.	0.8	0