Zirui Dong

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4132163/publications.pdf

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26 papers	2,443 citations	623734 14 h-index	580821 25 g-index
29 all docs	29 docs citations	29 times ranked	4807 citing authors

#	Article	IF	Citations
1	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883
2	Comprehensive analysis of RNA-Seq data reveals extensive RNA editing in a human transcriptome. Nature Biotechnology, 2012, 30, 253-260.	17.5	461
3	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
4	An investigation of biomarkers derived from legacy microarray data for their utility in the RNA-seq era. Genome Biology, 2014, 15, 523.	8.8	147
5	Low-pass whole-genome sequencing in clinical cytogenetics: a validated approach. Genetics in Medicine, 2016, 18, 940-948.	2.4	138
6	Genome Sequencing Explores Complexity of Chromosomal Abnormalities in Recurrent Miscarriage. American Journal of Human Genetics, 2019, 105, 1102-1111.	6.2	66
7	A Robust Approach for Blind Detection of Balanced Chromosomal Rearrangements with Whole-Genome Low-Coverage Sequencing. Human Mutation, 2014, 35, 625-636.	2.5	65
8	Low-pass genome sequencing versus chromosomal microarray analysis: implementation in prenatal diagnosis. Genetics in Medicine, 2020, 22, 500-510.	2.4	64
9	Identification of balanced chromosomal rearrangements previously unknown among participants in the 1000 Genomes Project: implications for interpretation of structural variation in genomes and the future of clinical cytogenetics. Genetics in Medicine, 2018, 20, 697-707.	2.4	52
10	Prenatal Diagnosis of Fetuses With Increased Nuchal Translucency by Genome Sequencing Analysis. Frontiers in Genetics, 2019, 10, 761.	2.3	52
11	Low-pass genome sequencing: a validated method in clinical cytogenetics. Human Genetics, 2020, 139, 1403-1415.	3.8	31
12	Genetic Study on Small Insertions and Deletions in Psoriasis Reveals a Role in Complex Human Diseases. Journal of Investigative Dermatology, 2019, 139, 2302-2312.e14.	0.7	22
13	Copyâ€Number Variants Detection by Lowâ€Pass Wholeâ€Genome Sequencing. Current Protocols in Human Genetics, 2017, 94, 8.17.1-8.17.16.	3.5	19
14	Development of coupling controlled polymerizations by adapter-ligation in mate-pair sequencing for detection of various genomic variants in one single assay. DNA Research, 2019, 26, 313-325.	3.4	17
15	Low-pass genome sequencingâ€“based detection of absence of heterozygosity: validation in clinical cytogenetics. Genetics in Medicine, 2021, 23, 1225-1233.	2.4	16
16	Performance of Cell-Free DNA Screening for Fetal Common Aneuploidies and Sex Chromosomal Abnormalities: A Prospective Study from a Less Developed Autonomous Region in Mainland China. Genes, 2021, 12, 478.	2.4	16
17	Deciphering the complexity of simple chromosomal insertions by genome sequencing. Human Genetics, 2021, 140, 361-380.	3.8	15
18	Intragenic and extragenic disruptions of FOXL2 mapped by whole genome low-coverage sequencing in two BPES families with chromosome reciprocal translocation. Genomics, 2014, 104, 170-176.	2.9	14

#	Article	IF	Citations
19	Investigation of the genetic etiology in male infertility with apparently balanced chromosomal structural rearrangements by genome sequencing. Asian Journal of Andrology, 2022, 24, 248.	1.6	11
20	Balanced Chromosomal Rearrangement Detection by Lowâ€Pass Wholeâ€Genome Sequencing. Current Protocols in Human Genetics, 2018, 96, 8.18.1-8.18.16.	3.5	10
21	Trio-Based Low-Pass Genome Sequencing Reveals Characteristics and Significance of Rare Copy Number Variants in Prenatal Diagnosis. Frontiers in Genetics, 2021, 12, 742325.	2.3	9
22	SVInterpreter: A Comprehensive Topologically Associated Domain-Based Clinical Outcome Prediction Tool for Balanced and Unbalanced Structural Variants. Frontiers in Genetics, 2021, 12, 757170.	2.3	5
23	Genome sequencing reveals the role of rare genomic variants in Chinese patients with symptomatic intracranial atherosclerotic disease. Stroke and Vascular Neurology, 2021, , svn-2021-001157.	3.3	2
24	The Burden and Benefits of Knowledge: Ethical Considerations Surrounding Population-Based Newborn Genome Screening for Hearing. International Journal of Neonatal Screening, 2022, 8, 36.	3.2	2
25	Investigation of Chromosomal Structural Abnormalities in Patients With Undiagnosed Neurodevelopmental Disorders. Frontiers in Genetics, 2022, 13, 803088.	2.3	1
26	LOW-PASS GENOME SEQUENCING IDENTIFIED MACROSCOPIC AND MICROSCOPIC CHROMOSOMAL MOSAICISMS TO EXPLAIN FIRST-TRIMESTER MISCARRIAGE. Fertility and Sterility, 2021, 116, e6.	1.0	0