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	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
2	Investigation of Chromosomal Structural Abnormalities in Patients With Undiagnosed Neurodevelopmental Disorders. Frontiers in Genetics, 2022, 13, 803088.	2.3	1
3	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
4	Deciphering the complexity of simple chromosomal insertions by genome sequencing. Human Genetics, 2021, 140, 361-380.	3.8	15
5	Low-pass genome sequencingâ€“based detection of absence of heterozygosity: validation in clinical cytogenetics. Genetics in Medicine, 2021, 23, 1225-1233.	2.4	16
6	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
7	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
8	LOW-PASS GENOME SEQUENCING IDENTIFIED MACROSCOPIC AND MICROSCOPIC CHROMOSOMAL MOSAICISMS TO EXPLAIN FIRST-TRIMESTER MISCARRIAGE. Fertility and Sterility, 2021, 116, e6.	1.0	0
9	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
10	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
11	Low-pass genome sequencing versus chromosomal microarray analysis: implementation in prenatal diagnosis. Genetics in Medicine, 2020, 22, 500-510.	2.4	64
12	Low-pass genome sequencing: a validated method in clinical cytogenetics. Human Genetics, 2020, 139, 1403-1415.	3.8	31
13	Genome Sequencing Explores Complexity of Chromosomal Abnormalities in Recurrent Miscarriage. American Journal of Human Genetics, 2019, 105, 1102-1111.	6.2	66
14	Prenatal Diagnosis of Fetuses With Increased Nuchal Translucency by Genome Sequencing Analysis. Frontiers in Genetics, 2019, 10, 761.	2.3	52
15	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
16	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
17	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
18	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

#	Article	IF	Citations
19	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
20	Low-pass whole-genome sequencing in clinical cytogenetics: a validated approach. Genetics in Medicine, 2016, 18, 940-948.	2.4	138
21	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
22	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
23	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
24	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
25	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
26	Comprehensive analysis of RNA-Seq data reveals extensive RNA editing in a human transcriptome. Nature Biotechnology, 2012, 30, 253-260.	17.5	461