

Devika Ganesamoorthy

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,132
citations

430874

18
h-index

580821

25
g-index

39
all docs

39
docs citations

39
times ranked

2562
citing authors

#	ARTICLE	IF	CITATIONS
1	Further molecular and clinical delineation of co-locating 17p13.3 microdeletions and microduplications that show distinctive phenotypes. <i>Journal of Medical Genetics</i> , 2010, 47, 299-311.	3.2	137
2	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. <i>Nature Communications</i> , 2017, 8, 14515.	12.8	104
3	Molecular and clinical characterization of 25 individuals with exonic deletions of <i>NRXN1</i> and comprehensive review of the literature. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013, 162, 388-403.	1.7	93
4	Methylation of novel markers of fragile X alleles is inversely correlated with FMRP expression and FMR1 activation ratio. <i>Human Molecular Genetics</i> , 2010, 19, 1618-1632.	2.9	92
5	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinIONTM sequencing. <i>GigaScience</i> , 2016, 5, 32.	6.4	79
6	Pathogenic aberrations revealed exclusively by single nucleotide polymorphism (SNP) genotyping data in 5000 samples tested by molecular karyotyping. <i>Journal of Medical Genetics</i> , 2011, 48, 831-839.	3.2	71
7	Detection of cryptic pathogenic copy number variations and constitutional loss of heterozygosity using high resolution SNP microarray analysis in 117 patients referred for cytogenetic analysis and impact on clinical practice. <i>Journal of Medical Genetics</i> , 2008, 46, 123-131.	3.2	61
8	Phenotypic variability of distal 22q11.2 copy number abnormalities. <i>American Journal of Medical Genetics, Part A</i> , 2011, 155, 1623-1633.	1.2	59
9	Complete Genome Sequence of <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> Strain ATCC 700603. <i>Genome Announcements</i> , 2016, 4, .	0.8	44
10	Extending the scope of diagnostic chromosome analysis: Detection of single gene defects using high-resolution SNP microarrays. <i>Human Mutation</i> , 2011, 32, 1500-1506.	2.5	41
11	Development of a Multiplex Ligation-Dependent Probe Amplification Assay for Diagnosis and Estimation of the Frequency of Spinocerebellar Ataxia Type 15. <i>Clinical Chemistry</i> , 2009, 55, 1415-1418.	3.2	39
12	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant <i>Klebsiella pneumoniae</i> . <i>Microbial Genomics</i> , 2018, 4, .	2.0	39
13	Meeting the challenge of interpreting high-resolution single nucleotide polymorphism array data in prenatal diagnosis: does increased diagnostic power outweigh the dilemma of rare variants?. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2013, 120, 594-606.	2.3	34
14	nplnv: accurate detection and genotyping of inversions using long read sub-alignment. <i>BMC Bioinformatics</i> , 2018, 19, 261.	2.6	29
15	Realtime analysis and visualization of MinION sequencing data with npReader. <i>Bioinformatics</i> , 2016, 32, 764-766.	4.1	25
16	Investigating and Correcting Plasma DNA Sequencing Coverage Bias to Enhance Aneuploidy Discovery. <i>PLoS ONE</i> , 2014, 9, e86993.	2.5	24
17	Use of Copy Number Deletion Polymorphisms to Assess DNA Chimerism. <i>Clinical Chemistry</i> , 2014, 60, 1105-1114.	3.2	20
18	A Genotype-First Approach for the Molecular and Clinical Characterization of Uncommon De Novo Microdeletion of 20q13.33. <i>PLoS ONE</i> , 2010, 5, e12462.	2.5	19

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19	Phase I Trial of Inducible Caspase 9 T Cells in Adult Stem Cell Transplant Demonstrates Massive Clonotypic Proliferative Potential and Long-term Persistence of Transgenic T Cells. <i>Clinical Cancer Research</i> , 2019, 25, 1749-1755.	7.0	18
20	Application of a new molecular technique for the genetic evaluation of products of conception. <i>Prenatal Diagnosis</i> , 2013, 33, 32-41.	2.3	17
21	Octapeptin C4 and polymyxin resistance occur via distinct pathways in an epidemic XDR <i>Klebsiella pneumoniae</i> ST258 isolate. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 582-593.	3.0	16
22	High-resolution microarray in the assessment of fetal anomalies detected by ultrasound. <i>Australian and New Zealand Journal of Obstetrics and Gynaecology</i> , 2014, 54, 46-52.	1.0	14
23	Simulating the dynamics of targeted capture sequencing with CapSim. <i>Bioinformatics</i> , 2018, 34, 873-874.	4.1	14
24	Whole genome deep sequencing analysis of cell-free DNA in samples with low tumour content. <i>BMC Cancer</i> , 2022, 22, 85.	2.6	9
25	sCNPhase: using haplotype resolved read depth to genotype somatic copy number alterations from low cellularity aneuploid tumors. <i>Nucleic Acids Research</i> , 2017, 45, e34-e34.	14.5	7
26	Nanopore sequencing as a scalable, cost-effective platform for analyzing polyclonal vector integration sites following clinical T cell therapy. , 2020, 8, e000299.		5
27	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. <i>BMC Bioinformatics</i> , 2018, 19, 267.	2.6	2
28	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. <i>F1000Research</i> , 0, 9, 1084.	1.6	0