Devika Ganesamoorthy

List of Publications by Year
in descending order

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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	Whole genome deep sequencing analysis of cell-free DNA in samples with low tumour content. BMC Cancer, 2022, 22, 85.	2.6	9
2	Nanopore sequencing as a scalable, cost-effective platform for analyzing polyclonal vector integration sites following clinical T cell therapy. , 2020, 8, e000299.		5
3	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. Clinical Cancer Research, 2019, 25, 1749-1755.	7.0	18
4	Octapeptin C4 and polymyxin resistance occur via distinct pathways in an epidemic XDRKlebsiella pneumoniaeST258 isolate. Journal of Antimicrobial Chemotherapy, 2019, 74, 582-593.	3.0	16
5	Simulating the dynamics of targeted capture sequencing with CapSim. Bioinformatics, 2018, 34, 873-874.	4.1	14
6	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant Klebsiella pneumoniae. Microbial Genomics, 2018, 4, .	2.0	39
7	npInv: accurate detection and genotyping of inversions using long read sub-alignment. BMC Bioinformatics, 2018, 19, 261.	2.6	29
8	GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. BMC Bioinformatics, 2018, 19, 267.	2.6	2
9	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. Nature Communications, 2017, 8, 14515.	12.8	104
10	sCNAphase: using haplotype resolved read depth to genotype somatic copy number alterations from low cellularity aneuploid tumors. Nucleic Acids Research, 2017, 45, e34-e34.	14.5	7
11	Complete Genome Sequence of Klebsiella quasipneumoniae subsp. similipneumoniae Strain ATCC 700603. Genome Announcements, 2016, 4, .	0.8	44
12	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinIONTM sequencing. GigaScience, 2016, 5, 32.	6.4	79
13	Realtime analysis and visualization of MinION sequencing data with npReader. Bioinformatics, 2016, 32, 764-766.	4.1	25
14	Investigating and Correcting Plasma DNA Sequencing Coverage Bias to Enhance Aneuploidy Discovery. PLoS ONE, 2014, 9, e86993.	2.5	24
15	Highâ€resolution microarray in the assessment of fetal anomalies detected by ultrasound. Australian and New Zealand Journal of Obstetrics and Gynaecology, 2014, 54, 46-52.	1.0	14
16	Use of Copy Number Deletion Polymorphisms to Assess DNA Chimerism. Clinical Chemistry, 2014, 60, 1105-1114.	3.2	20
17	Meeting the challenge of interpreting highâ€resolution single nucleotide polymorphism array data in prenatal diagnosis: does increased diagnostic power outweigh the dilemma of rare variants?. BJOG: an International Journal of Obstetrics and Gynaecology, 2013, 120, 594-606.	2.3	34
18	Molecular and clinical characterization of 25 individuals with exonic deletions of NRXN1 and comprehensive review of the literature. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 388-403.	1.7	93

#	Article	IF	Citations
19	Application of a new molecular technique for the genetic evaluation of products of conception. Prenatal Diagnosis, 2013, 33, 32-41.	2.3	17
20	Phenotypic variability of distal 22q11.2 copy number abnormalities. American Journal of Medical Genetics, Part A, 2011, 155, 1623-1633.	1.2	59
21	Extending the scope of diagnostic chromosome analysis: Detection of single gene defects using high-resolution SNP microarrays. Human Mutation, 2011, 32, 1500-1506.	2.5	41
22	Pathogenic aberrations revealed exclusively by single nucleotide polymorphism (SNP) genotyping data in 5000 samples tested by molecular karyotyping. Journal of Medical Genetics, 2011, 48, 831-839.	3.2	71
23	A Genotype-First Approach for the Molecular and Clinical Characterization of Uncommon De Novo Microdeletion of 20q13.33. PLoS ONE, 2010, 5, e12462.	2.5	19
24	Methylation of novel markers of fragile X alleles is inversely correlated with FMRP expression and FMR1 activation ratio. Human Molecular Genetics, 2010, 19, 1618-1632.	2.9	92
25	Further molecular and clinical delineation of co-locating 17p13.3 microdeletions and microduplications that show distinctive phenotypes. Journal of Medical Genetics, 2010, 47, 299-311.	3.2	137
26	Development of a Multiplex Ligation-Dependent Probe Amplification Assay for Diagnosis and Estimation of the Frequency of Spinocerebellar Ataxia Type 15. Clinical Chemistry, 2009, 55, 1415-1418.	3.2	39
27	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. Journal of Medical Genetics, 2008, 46, 123-131.	3.2	61
28	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. F1000Research, 0, 9, 1084.	1.6	0