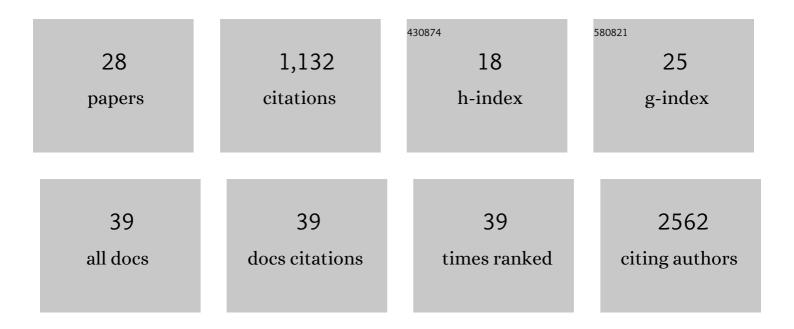
Devika Ganesamoorthy

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	Scaffolding and completing genome assemblies in real-time with nanopore sequencing. Nature Communications, 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. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 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. Human Molecular Genetics, 2010, 19, 1618-1632.	2.9	92
5	Streaming algorithms for identification of pathogens and antibiotic resistance potential from real-time MinIONTM sequencing. GigaScience, 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. Journal of Medical Genetics, 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. Journal of Medical Genetics, 2008, 46, 123-131.	3.2	61
8	Phenotypic variability of distal 22q11.2 copy number abnormalities. American Journal of Medical Genetics, Part A, 2011, 155, 1623-1633.	1.2	59
9	Complete Genome Sequence of Klebsiella quasipneumoniae subsp. <i>similipneumoniae</i> Strain ATCC 700603. Genome Announcements, 2016, 4, .	0.8	44
10	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
11	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
12	Multifactorial chromosomal variants regulate polymyxin resistance in extensively drug-resistant Klebsiella pneumoniae. Microbial Genomics, 2018, 4, .	2.0	39
13	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
14	nplnv: accurate detection and genotyping of inversions using long read sub-alignment. BMC Bioinformatics, 2018, 19, 261.	2.6	29
15	Realtime analysis and visualization of MinION sequencing data with npReader. Bioinformatics, 2016, 32, 764-766.	4.1	25
16	Investigating and Correcting Plasma DNA Sequencing Coverage Bias to Enhance Aneuploidy Discovery. PLoS ONE, 2014, 9, e86993.	2.5	24
17	Use of Copy Number Deletion Polymorphisms to Assess DNA Chimerism. Clinical Chemistry, 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. PLoS ONE, 2010, 5, e12462.	2.5	19

#	Article	IF	CITATIONS
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. Clinical Cancer Research, 2019, 25, 1749-1755.	7.0	18
20	Application of a new molecular technique for the genetic evaluation of products of conception. Prenatal Diagnosis, 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. Journal of Antimicrobial Chemotherapy, 2019, 74, 582-593.	3.0	16
22	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
23	Simulating the dynamics of targeted capture sequencing with CapSim. Bioinformatics, 2018, 34, 873-874.	4.1	14
24	Whole genome deep sequencing analysis of cell-free DNA in samples with low tumour content. BMC Cancer, 2022, 22, 85.	2.6	9
25	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
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. BMC Bioinformatics, 2018, 19, 267.	2.6	2
28	High-throughput multiplexed tandem repeat genotyping using targeted long-read sequencing. F1000Research, 0, 9, 1084.	1.6	0