Michelle M Clark

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/875035/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Rapid whole genome sequencing impacts care and resource utilization in infants with congenital heart disease. Npj Genomic Medicine, 2021, 6, 29.	3.8	27
2	Measurement of genetic diseases as a cause of mortality in infants receiving whole genome sequencing. Npj Genomic Medicine, 2020, 5, 49.	3.8	29
3	Partially automated whole-genome sequencing reanalysis of previously undiagnosed pediatric patients can efficiently yield new diagnoses. Npj Genomic Medicine, 2020, 5, 33.	3.8	36
4	An RCT of Rapid Genomic Sequencing among Seriously Ill Infants Results in High Clinical Utility, Changes in Management, and Low Perceived Harm. American Journal of Human Genetics, 2020, 107, 942-952.	6.2	110
5	A Prospective Study of Parental Perceptions of Rapid Whole-Genome and -Exome Sequencing among Seriously III Infants. American Journal of Human Genetics, 2020, 107, 953-962.	6.2	65
6	A Randomized, Controlled Trial of the Analytic and Diagnostic Performance of Singleton and Trio, Rapid Genome and Exome Sequencing in Ill Infants. American Journal of Human Genetics, 2019, 105, 719-733.	6.2	238
7	Diagnosis of genetic diseases in seriously ill children by rapid whole-genome sequencing and automated phenotyping and interpretation. Science Translational Medicine, 2019, 11, .	12.4	203
8	Rapid Whole Genome Sequencing Has Clinical Utility in Children in the PICU*. Pediatric Critical Care Medicine, 2019, 20, 1007-1020.	0.5	105
9	Rapid whole-genome sequencing decreases infant morbidity and cost of hospitalization. Npj Genomic Medicine, 2018, 3, 10.	3.8	314
10	The NSIGHT1-randomized controlled trial: rapid whole-genome sequencing for accelerated etiologic diagnosis in critically ill infants. Npj Genomic Medicine, 2018, 3, 6.	3.8	156
11	Meta-analysis of the diagnostic and clinical utility of genome and exome sequencing and chromosomal microarray in children with suspected genetic diseases. Npj Genomic Medicine, 2018, 3, 16.	3.8	420
12	The concerted impact of domestication and transposon insertions on methylation patterns between dogs and grey wolves. Molecular Ecology, 2016, 25, 1838-1855.	3.9	73
13	The Quantitative-MFG Test: A Linear Mixed Effect Model to Detect Maternal-Offspring Gene Interactions. Annals of Human Genetics, 2016, 80, 63-80.	0.8	3
14	Human Birth Weight and Reproductive Immunology: Testing for Interactions between Maternal and Offspring <i>KIR</i> and <i>HLA-C</i> Genes. Human Heredity, 2016, 81, 181-193.	0.8	10