Michelle M Clark

List of Publications by Year
in descending order

14 papers	1,792 citations	759233 12 h-index	940533 16 g-index
16 all docs	16 docs citations	16 times ranked	2470 citing authors

#	Article	IF	Citations
1	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
2	Rapid whole-genome sequencing decreases infant morbidity and cost of hospitalization. Npj Genomic Medicine, 2018, 3, 10.	3.8	314
3	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
4	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
5	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
6	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
7	Rapid Whole Genome Sequencing Has Clinical Utility in Children in the PICU*. Pediatric Critical Care Medicine, 2019, 20, 1007-1020.	0.5	105
8	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
9	A Prospective Study of Parental Perceptions of Rapid Whole-Genome and -Exome Sequencing among Seriously Ill Infants. American Journal of Human Genetics, 2020, 107, 953-962.	6.2	65
10	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
11	Measurement of genetic diseases as a cause of mortality in infants receiving whole genome sequencing. Npj Genomic Medicine, 2020, 5, 49.	3.8	29
12	Rapid whole genome sequencing impacts care and resource utilization in infants with congenital heart disease. Npj Genomic Medicine, 2021, 6, 29.	3.8	27
13	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
14	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