Priyanka Nandakumar

List of Publications by Year
in descending order

13	1,417	933447 10	1058476 14
papers	citations	h-index	g-index

15	15	15	3799
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Nuclear genome-wide associations with mitochondrial heteroplasmy. Science Advances, 2021, 7, .	10.3	16
2	Multiple, independent, common variants at RET, SEMA3 and NRG1 gut enhancers specify Hirschsprung disease risk in European ancestry subjects. Journal of Pediatric Surgery, 2021, 56, 2286-2294.	1.6	3
3	Gene- and tissue-level interactions in normal gastrointestinal development and Hirschsprung disease. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26697-26708.	7.1	16
4	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	2.8	5
5	Genome-wide association study of Hirschsprung disease detects a novel low-frequency variant at the RET locus. European Journal of Human Genetics, 2018, 26, 561-569.	2.8	24
6	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
7	Contributions of rare coding variants in hypotension syndrome genes to population blood pressure variation. Medicine (United States), 2018, 97, e11865.	1.0	6
8	Rare coding variants associated with blood pressure variation in 15â€Š914 individuals of African ancestry. Journal of Hypertension, 2017, 35, 1381-1389.	0.5	15
9	Genome-wide association analyses using electronic health records identify new loci influencing blood pressure variation. Nature Genetics, 2017, 49, 54-64.	21.4	281
10	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	3.5	18
11	MicroRNAs in the miR-17 and miR-15 families are downregulated in chronic kidney disease with hypertension. PLoS ONE, 2017, 12, e0176734.	2.5	38
12	Trans-ethnic meta-analysis of genome-wide association studies for Hirschsprung disease. Human Molecular Genetics, 2016, 25, ddw333.	2.9	38
13	Rare coding TTN variants are associated with electrocardiographic QT interval in the general population. Scientific Reports, 2016, 6, 28356.	3.3	6