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	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
2	Genome-wide association analyses using electronic health records identify new loci influencing blood pressure variation. Nature Genetics, 2017, 49, 54-64.	21.4	281
3	Trans-ethnic meta-analysis of genome-wide association studies for Hirschsprung disease. Human Molecular Genetics, 2016, 25, ddw333.	2.9	38
4	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
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	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	3.5	18
7	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
8	Nuclear genome-wide associations with mitochondrial heteroplasmy. Science Advances, 2021, 7, .	10.3	16
9	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
10	Rare coding TTN variants are associated with electrocardiographic QT interval in the general population. Scientific Reports, 2016, 6, 28356.	3.3	6
11	Contributions of rare coding variants in hypotension syndrome genes to population blood pressure variation. Medicine (United States), 2018, 97, e11865.	1.0	6
12	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
13	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