Karen Y He

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6552418/publications.pdf

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11	287	1162889 8	1281743 11
papers	citations	h-index	g-index

11	11	11	785
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
2	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
3	Detecting fitness epistasis in recently admixed populations with genome-wide data. BMC Genomics, 2020, 21, 476.	1.2	4
4	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. American Journal of Human Genetics, 2019, 105, 1057-1068.	2.6	10
5	Variant Interpretation for Cancer (VIC): a computational tool for assessing clinical impacts of somatic variants. Genome Medicine, 2019, 11, 53.	3.6	36
6	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. Human Genetics, 2019, 138, 199-210.	1.8	29
7	Big Data Analytics for Genomic Medicine. International Journal of Molecular Sciences, 2017, 18, 412.	1.8	121
8	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	1.5	18
9	Pathogenic Mutations in Cancer-Predisposing Genes: A Survey of 300 Patients with Whole-Genome Sequencing and Lifetime Electronic Health Records. PLoS ONE, 2016, 11, e0167847.	1.1	4
10	SparkText: Biomedical Text Mining on Big Data Framework. PLoS ONE, 2016, 11, e0162721.	1.1	32
11	Multivariate Analysis of Anthropometric Traits Using Summary Statistics of Genome-Wide Association Studies from GIANT Consortium. PLoS ONE, 2016, 11, e0163912.	1.1	19