Yun Zhu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6941343/publications.pdf

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35	1,359	19	36
papers	citations	h-index	g-index
36	36	36	2970 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	Methylation biomarkers of polybrominated diphenyl ethers (PBDEs) and association with breast cancer risk at the time of menopause. Environment International, 2021, 156, 106772.	10.0	5
2	Brain and blood metabolome for Alzheimer's dementia: findings from a targeted metabolomics analysis. Neurobiology of Aging, 2020, 86, 123-133.	3.1	83
3	Shared Causal Paths underlying Alzheimer's dementia and Type 2 Diabetes. Scientific Reports, 2020, 10, 4107.	3.3	37
4	Genome-wide profiling of DNA methylome and transcriptome in peripheral blood monocytes for major depression: A Monozygotic Discordant Twin Study. Translational Psychiatry, 2019, 9, 215.	4.8	49
5	Telomere length and cancer mortality in American Indians: the Strong Heart Study. GeroScience, 2019, 41, 351-361.	4.6	18
6	DNA Methylation of Five Core Circadian Genes Jointly Contributes to Glucose Metabolism: A Gene-Set Analysis in Monozygotic Twins. Frontiers in Genetics, 2019, 10, 329.	2.3	20
7	DNA methylation variability in Alzheimer's disease. Neurobiology of Aging, 2019, 76, 35-44.	3.1	25
8	Urinary metals and leukocyte telomere length in American Indian communities: The Strong Heart and the Strong Heart Family Study. Environmental Pollution, 2019, 246, 311-318.	7.5	23
9	Perinatal Exposure to Western Diet Programs Autonomic Dysfunction in the Male Offspring. Cellular and Molecular Neurobiology, 2018, 38, 233-242.	3.3	15
10	Childhood Trauma, DNA Methylation of Stress-Related Genes, and Depression: Findings From Two Monozygotic Twin Studies. Psychosomatic Medicine, 2018, 80, 599-608.	2.0	74
11	A genomeâ€wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. Alzheimer's and Dementia, 2017, 13, 674-688.	0.8	83
12	A quadratically regularized functional canonical correlation analysis for identifying the global structure of pleiotropy with NGS data. PLoS Computational Biology, 2017, 13, e1005788.	3.2	12
13	Metabolic Profiles of Obesity in American Indians: The Strong Heart Family Study. PLoS ONE, 2016, 11, e0159548.	2.5	16
14	Genome-wide gene–gene interaction analysis for next-generation sequencing. European Journal of Human Genetics, 2016, 24, 421-428.	2.8	23
15	Impact of biological aging on arterial aging in American Indians: findings from the Strong Heart Family Study. Aging, 2016, 8, 1583-1592.	3.1	13
16	Depressive symptoms are associated with leukocyte telomere length in American Indians: findings from the Strong Heart Family Study. Aging, 2016, 8, 2961-2970.	3.1	6
17	Urinary triclosan concentrations are inversely associated with body mass index and waist circumference in the US general population: Experience in NHANES 2003–2010. International Journal of Hygiene and Environmental Health, 2015, 218, 401-406.	4.3	60
18	Pathway analysis with next-generation sequencing data. European Journal of Human Genetics, 2015, 23, 507-515.	2.8	7

#	Article	IF	Citations
19	Joint Association of Nicotinic Acetylcholine Receptor Variants with Abdominal Obesity in American Indians: The Strong Heart Family Study. PLoS ONE, 2014, 9, e102220.	2.5	10
20	Metabolic profiles of biological aging in American Indians: The strong heart family study. Aging, 2014, 6, 176-186.	3.1	22
21	Short Leukocyte Telomere Length Predicts Risk of Diabetes in American Indians: the Strong Heart Family Study. Diabetes, 2014, 63, 354-362.	0.6	133
22	Genetic variants in nicotinic acetylcholine receptor genes jointly contribute to kidney function in American Indians. Journal of Hypertension, 2014, 32, 1042-1049.	0.5	7
23	Smoothed functional principal component analysis for testing association of the entire allelic spectrum of genetic variation. European Journal of Human Genetics, 2013, 21, 217-224.	2.8	21
24	Joint Associations of 61 Genetic Variants in the Nicotinic Acetylcholine Receptor Genes with Subclinical Atherosclerosis in American Indians. Circulation: Cardiovascular Genetics, 2013, 6, 89-96.	5.1	11
25	Effects of shear stresses and antioxidant concentrations on the production of reactive oxygen species in lung cancer cells. Biomicrofluidics, 2013, 7, 064108.	2.4	31
26	QTL mapping of leukocyte telomere length in American Indians: The Strong Heart Family Study. Aging, 2013, 5, 704-716.	3.1	17
27	A Novel Genome-Information Content-Based Statistic for Genome-Wide Association Analysis Designed for Next-Generation Sequencing Data. Journal of Computational Biology, 2012, 19, 731-744.	1.6	3
28	Quantitative trait locus analysis for next-generation sequencing with the functional linear models. Journal of Medical Genetics, 2012, 49, 513-524.	3.2	38
29	Weighted pedigree-based statistics for testing the association of rare variants. BMC Genomics, 2012, 13, 667.	2.8	11
30	A Gene-Family Analysis of 61 Genetic Variants in the Nicotinic Acetylcholine Receptor Genes for Insulin Resistance and Type 2 Diabetes in American Indians. Diabetes, 2012, 61, 1888-1894.	0.6	27
31	Family-Based Association Studies for Next-Generation Sequencing. American Journal of Human Genetics, 2012, 90, 1028-1045.	6.2	48
32	Implication of next-generation sequencing on association studies. BMC Genomics, 2011, 12, 322.	2.8	19
33	Gene and pathway-based second-wave analysis of genome-wide association studies. European Journal of Human Genetics, 2010, 18, 111-117.	2.8	228
34	Genome-wide gene and pathway analysis. European Journal of Human Genetics, 2010, 18, 1045-1053.	2.8	99
35	A Novel Statistic for Genome-Wide Interaction Analysis. PLoS Genetics, 2010, 6, e1001131.	3.5	64