Jennifer Brody

List of Publications by Year
in descending order

12	2,741	759233 12	1199594 12
papers	citations	h-index	g-index

14	14	14	11454
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
2	Association of dietary folate and vitamin B-12 intake with genome-wide DNA methylation in blood: a large-scale epigenome-wide association analysis in 5841 individuals. American Journal of Clinical Nutrition, 2019, 110, 437-450.	4.7	46
3	FastSKAT: Sequence kernel association tests for very large sets of markers. Genetic Epidemiology, 2018, 42, 516-527.	1.3	26
4	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	11.0	78
5	Assessing the causal relationship between obesity and venous thromboembolism through a Mendelian Randomization study. Human Genetics, 2017, 136, 897-902.	3.8	46
6	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
7	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
8	Sequencing of 2 Subclinical Atherosclerosis Candidate Regions in 3669 Individuals. Circulation: Cardiovascular Genetics, 2014, 7, 359-364.	5.1	18
9	Sequence Kernel Association Test for Survival Traits. Genetic Epidemiology, 2014, 38, 191-197.	1.3	58
10	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
11	Common variation in fatty acid metabolic genes and risk of incident sudden cardiac arrest. Heart Rhythm, 2014, 11, 471-477.	0.7	16
12	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544