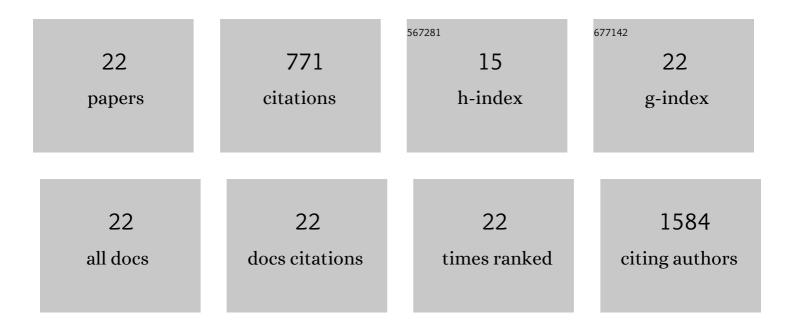
Meeshanthini V Dogan

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The effect of smoking on DNA methylation of peripheral blood mononuclear cells from African American women. BMC Genomics, 2014, 15, 151.	2.8	193
2	Integrated genetic and epigenetic prediction of coronary heart disease in the Framingham Heart Study. PLoS ONE, 2018, 13, e0190549.	2.5	83
3	Methylomic Aging as a Window onto the Influence of Lifestyle: Tobacco and Alcohol Use Alter the Rate of Biological Aging. Journal of the American Geriatrics Society, 2015, 63, 2519-2525.	2.6	76
4	Current and Future Prospects for Epigenetic Biomarkers of Substance Use Disorders. Genes, 2015, 6, 991-1022.	2.4	70
5	AHRR methylation predicts smoking status and smoking intensity in both saliva and blood DNA. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 51-60.	1.7	55
6	Genetically contextual effects of smoking on genome wide DNA methylation. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 595-607.	1.7	34
7	Alcohol and tobacco consumption alter hypothalamic pituitary adrenal axis DNA methylation. Psychoneuroendocrinology, 2016, 66, 176-184.	2.7	33
8	Differential impact of cumulative SES risk on methylation of protein–protein interaction pathways as a function of SLC6A4 genetic variation in African American young adults. Biological Psychology, 2014, 96, 28-34.	2.2	31
9	Blood-Based Biomarkers for Predicting the Risk for Five-Year Incident Coronary Heart Disease in the Framingham Heart Study via Machine Learning. Genes, 2018, 9, 641.	2.4	29
10	Ethnicity and Smoking-Associated DNA Methylation Changes at HIV Co-Receptor GPR15. Frontiers in Psychiatry, 2015, 6, 132.	2.6	26
11	Higher levels of protective parenting are associated with better young adult health: exploration of mediation through epigenetic influences on pro-inflammatory processes. Frontiers in Psychology, 2015, 6, 676.	2.1	25
12	Array-Based Epigenetic Aging Indices May Be Racially Biased. Genes, 2020, 11, 685.	2.4	22
13	MTHFR methylation moderates the impact of smoking on DNA methylation at AHRR for African American young adults. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 608-618.	1.7	20
14	A Direct Comparison of the Relationship of Epigenetic Aging and Epigenetic Substance Consumption Markers to Mortality in the Framingham Heart Study. Genes, 2019, 10, 51.	2.4	16
15	A Four Marker Digital PCR Toolkit for Detecting Heavy Alcohol Consumption and the Effectiveness of Its Treatment. Journal of Insurance Medicine (New York, N Y), 2019, 48, 90-102.	0.2	16
16	A pilot investigation of the impact of smoking cessation on biological age. American Journal on Addictions, 2017, 26, 129-135.	1.4	14
17	External validation of integrated genetic-epigenetic biomarkers for predicting incident coronary heart disease. Epigenomics, 2021, 13, 1095-1112.	2.1	10
18	AHRR Methylation is a Significant Predictor of Mortality Risk in Framingham Heart Study. Journal of Insurance Medicine (New York, N Y), 2019, 48, 79-89.	0.2	10

#	Article	IF	CITATIONS
19	The Reversion of DNA Methylation at Coronary Heart Disease Risk Loci in Response to Prevention Therapy. Processes, 2021, 9, 699.	2.8	3
20	A simple, rapid, interpretable, actionable and implementable digital PCR based mortality index. Epigenetics, 2020, 16, 1-15.	2.7	2
21	Cost–utility analysis of an integrated genetic/epigenetic test for assessing risk for coronary heart disease. Epigenomics, 2021, 13, 531-547.	2.1	2
22	<i>MTHFR</i> regulatory effects on methylation of CG05575921 in response to smoking: Effects are also discernable using <i>MTHFR</i> expression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 529-534.	1.7	1