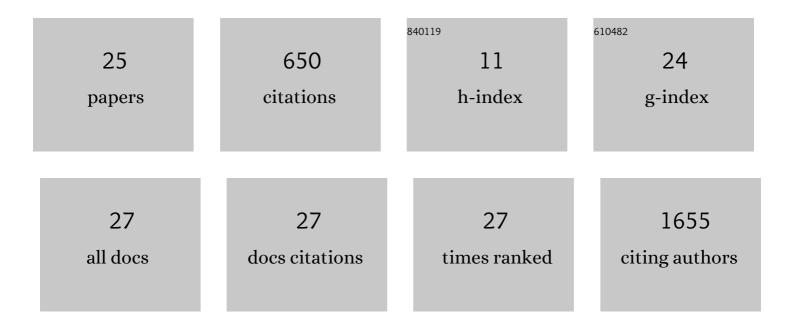
Saara Marttila

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Obesity accelerates epigenetic aging in middle-aged but not in elderly individuals. Clinical Epigenetics, 2017, 9, 20.	1.8	128
2	Ageing-associated changes in the human DNA methylome: genomic locations and effects on gene expression. BMC Genomics, 2015, 16, 179.	1.2	110
3	Characterization of the role of distinct plasma cellâ€free <scp>DNA</scp> species in ageâ€associated inflammation and frailty. Aging Cell, 2013, 12, 388-397.	3.0	102
4	Transcriptional Analysis Reveals Gender-Specific Changes in the Aging of the Human Immune System. PLoS ONE, 2013, 8, e66229.	1.1	53
5	Cytomegalovirus infection accelerates epigenetic aging. Experimental Gerontology, 2015, 72, 227-229.	1.2	35
6	Ageing-associated changes in the expression of IncRNAs in human tissues reflect a transcriptional modulation in ageing pathways. Mechanisms of Ageing and Development, 2020, 185, 111177.	2.2	27
7	Aging-associated patterns in the expression of human endogenous retroviruses. PLoS ONE, 2018, 13, e0207407.	1.1	25
8	Androgen receptor overexpression alters binding dynamics of the receptor to chromatin and chromatin structure. Prostate, 2012, 72, 1223-1232.	1.2	21
9	Identification of a prognostic signature for old-age mortality by integrating genome-wide transcriptomic data with the conventional predictors: the Vitality 90+ Study. BMC Medical Genomics, 2014, 7, 54.	0.7	17
10	Aging-associated increase in indoleamine 2,3-dioxygenase (IDO) activity appears to be unrelated to the transcription of the IDO1 or IDO2 genes in peripheral blood mononuclear cells. Immunity and Ageing, 2011, 8, 9.	1.8	15
11	Cytomegalovirus (CMV)-dependent and -independent changes in the aging of the human immune system: A transcriptomic analysis. Experimental Gerontology, 2013, 48, 305-312.	1.2	15
12	Methylation status of nc886 epiallele reflects periconceptional conditions and is associated with glucose metabolism through nc886 RNAs. Clinical Epigenetics, 2021, 13, 143.	1.8	13
13	Ageing-associated changes in DNA methylation in X and Y chromosomes. Epigenetics and Chromatin, 2021, 14, 33.	1.8	12
14	IL-7 concentration is increased in nonagenarians but is not associated with markers of T cell immunosenescence. Experimental Gerontology, 2011, 46, 1000-1002.	1.2	11
15	Adulthood blood levels of hsa-miR-29b-3p associate with preterm birth and adult metabolic and cognitive health. Scientific Reports, 2021, 11, 9203.	1.6	10
16	Methylomic predictors demonstrate the role of NF-κB in old-age mortality and are unrelated to the aging-associated epigenetic drift. Oncotarget, 2016, 7, 19228-19241.	0.8	9
17	Number of sons contributes to ageing-associated inflammation. Scientific Reports, 2015, 5, 8631.	1.6	8
18	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. Bioscience Reports, 2020, 40, .	1.1	8

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#	Article	IF	CITATIONS
19	Modular genome-wide gene expression architecture shared by early traits of osteoporosis and atherosclerosis in the Young Finns Study. Scientific Reports, 2021, 11, 7111.	1.6	7
20	Increased Paternal Age at Conception Is Associated with Transcriptomic Changes Involved in Mitochondrial Function in Elderly Individuals. PLoS ONE, 2016, 11, e0167028.	1.1	7
21	Molecular mechanisms associated with the strength of the anti-CMV response in nonagenarians. Immunity and Ageing, 2014, 11, 2.	1.8	4
22	Human endogenous retrovirus HERV-K(HML-2) env expression is not associated with markers of immunosenescence. Experimental Gerontology, 2017, 97, 60-63.	1.2	4
23	Length of paternal lifespan is manifested in the DNA methylome of their nonagenarian progeny. Oncotarget, 2015, 6, 30557-30567.	0.8	3
24	Methylation pattern of polymorphically imprinted nc886 is not conserved across mammalia. PLoS ONE, 2022, 17, e0261481.	1.1	3
25	Reproductive history and blood cell DNA methylation later in life: the Young Finns Study. Clinical Epigenetics, 2021, 13, 227.	1.8	2