List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Early downregulation of hsa-miR-144-3p in serum from drug-naÃ⁻ve Parkinson's disease patients. Scientific Reports, 2022, 12, 1330.	3.3	14
2	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive Parkinson's disease patients. Npj Parkinson's Disease, 2022, 8, 14.	5.3	11
3	Accelerated epigenetic aging and inflammatory/immunological profile (ipAGE) in patients with chronic kidney disease. GeroScience, 2022, 44, 817-834.	4.6	13
4	Association of rs3027178 polymorphism in the circadian clock gene PER1 with susceptibility to Alzheimer's disease and longevity in an Italian population. GeroScience, 2022, 44, 881-896.	4.6	6
5	Role of Epigenetic Therapy in the Modulation of Tumor Growth and Migration in Human Castration-Resistant Prostate Cancer Cells with Neuroendocrine Differentiation. Neuroendocrinology, 2022, 112, 580-594.	2.5	2
6	DNA Methylation Analysis of Ribosomal DNA in Adults With Down Syndrome. Frontiers in Genetics, 2022, 13, 792165.	2.3	7
7	Blood circulating miR-28-5p and let-7d-5p associate with premature ageing in Down syndrome. Mechanisms of Ageing and Development, 2022, 206, 111691.	4.6	4
8	A geroscience approach for Parkinson's disease: Conceptual framework and design of PROPAG-AGEING project. Mechanisms of Ageing and Development, 2021, 194, 111426.	4.6	14
9	A Meta-Analysis of Brain DNA Methylation Across Sex, Age, and Alzheimer's Disease Points for Accelerated Epigenetic Aging in Neurodegeneration. Frontiers in Aging Neuroscience, 2021, 13, 639428.	3.4	45
10	Ageing affects subtelomeric DNA methylation in blood cells from a large European population enrolled in the MARK-AGE study. GeroScience, 2021, 43, 1283-1302.	4.6	4
11	Whole-genome sequencing analysis of semi-supercentenarians. ELife, 2021, 10, .	6.0	37
12	Increased PARylation impacts the DNA methylation process in type 2 diabetes mellitus. Clinical Epigenetics, 2021, 13, 114.	4.1	11
13	Circulating miRâ€19aâ€3p and miRâ€19bâ€3p characterize the human aging process and their isomiRs associate with healthy status at extreme ages. Aging Cell, 2021, 20, e13409.	6.7	12
14	No association between frailty index and epigenetic clocks in Italian semi-supercentenarians. Mechanisms of Ageing and Development, 2021, 197, 111514.	4.6	8
15	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. Npj Parkinson's Disease, 2021, 7, 78.	5.3	2
16	Multimodal evaluation of the melanopsin retinal ganglion cells system in relation to circadian rhythms in Alzheimer's disease and aging. Journal of the Neurological Sciences, 2021, 429, 118980.	0.6	0
17	Ribosomal DNA instability: An evolutionary conserved fuel for inflammaging. Ageing Research Reviews, 2020, 58, 101018.	10.9	18
18	Gene duplication, rather than epigenetic changes, drives FGF4 overexpression in KIT/PDGFRA/SDH/RAS-P WT GIST. Scientific Reports, 2020, 10, 19829.	3.3	10

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19	Down syndrome, accelerated aging and immunosenescence. Seminars in Immunopathology, 2020, 42, 635-645.	6.1	35
20	The Human Body as a Super Network: Digital Methods to Analyze the Propagation of Aging. Frontiers in Aging Neuroscience, 2020, 12, 136.	3.4	24
21	Analysis of Epigenetic Age Predictors in Pain-Related Conditions. Frontiers in Public Health, 2020, 8, 172.	2.7	8
22	Small extracellular vesicles deliver miRâ€21 and miRâ€217 as proâ€senescence effectors to endothelial cells. Journal of Extracellular Vesicles, 2020, 9, 1725285.	12.2	104
23	Aging and Caloric Restriction Modulate the DNA Methylation Profile of the Ribosomal RNA Locus in Human and Rat Liver. Nutrients, 2020, 12, 277.	4.1	12
24	One-year Mediterranean diet promotes epigenetic rejuvenation with country- and sex-specific effects: a pilot study from the NU-AGE project. GeroScience, 2020, 42, 687-701.	4.6	76
25	Lamin A involvement in ageing processes. Ageing Research Reviews, 2020, 62, 101073.	10.9	41
26	Age-related DNA methylation changes are sex-specific: a comprehensive assessment. Aging, 2020, 12, 24057-24080.	3.1	55
27	Network markers of DNA methylation in neurodegenerative diseases. , 2020, , .		1
28	Molecular Aging of Human Liver: An Epigenetic/Transcriptomic Signature. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 1-8.	3.6	23
29	Regulatory T cells from patients with end-stage organ disease can be isolated, expanded and cryopreserved according good manufacturing practice improving their function. Journal of Translational Medicine, 2019, 17, 250.	4.4	4
30	Age-Related DNA Methylation Changes: Potential Impact on Skeletal Muscle Aging in Humans. Frontiers in Physiology, 2019, 10, 996.	2.8	35
31	DNA methylation of shelf, shore and open sea CpG positions distinguish high microsatellite instability from low or stable microsatellite status colon cancer stem cells. Epigenomics, 2019, 11, 587-604.	2.1	29
32	The Impact of Caloric Restriction on the Epigenetic Signatures of Aging. International Journal of Molecular Sciences, 2019, 20, 2022.	4.1	71
33	Down Syndrome, Ageing and Epigenetics. Sub-Cellular Biochemistry, 2019, 91, 161-193.	2.4	10
34	Accelerated bioâ€cognitive aging in Down syndrome: State of the art and possible deceleration strategies. Aging Cell, 2019, 18, e12903.	6.7	47
35	The peculiar aging of human liver: A geroscience perspective within transplant context. Ageing Research Reviews, 2019, 51, 24-34.	10.9	35
36	Genomic stability, anti-inflammatory phenotype, and up-regulation of the RNAseH2 in cells from centenarians. Cell Death and Differentiation, 2019, 26, 1845-1858.	11.2	37

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37	Responders and non-responders to influenza vaccination: A DNA methylation approach on blood cells. Experimental Gerontology, 2018, 105, 94-100.	2.8	39
38	DNA Hydroxymethylation Levels Are Altered in Blood Cells From Down Syndrome Persons Enrolled in the MARK-AGE Project. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2018, 73, 737-744.	3.6	16
39	The epigenetics of inflammaging: The contribution of age-related heterochromatin loss and locus-specific remodelling and the modulation by environmental stimuli. Seminars in Immunology, 2018, 40, 49-60.	5.6	29
40	Evaluation of Lymphocyte Response to the Induced Oxidative Stress in a Cohort of Ageing Subjects, including Semisupercentenarians and Their Offspring. Mediators of Inflammation, 2018, 2018, 1-14.	3.0	11
41	Age-Related Epigenetic Derangement upon Reprogramming and Differentiation of Cells from the Elderly. Genes, 2018, 9, 39.	2.4	11
42	Epigenetic DNA methylation changes in episodic and chronic migraine. Neurological Sciences, 2018, 39, 67-68.	1.9	24
43	Impact of demography and population dynamics on the genetic architecture of human longevity. Aging, 2018, 10, 1947-1963.	3.1	16
44	The methylation of nuclear and mitochondrial DNA in ageing phenotypes and longevity. Mechanisms of Ageing and Development, 2017, 165, 156-161.	4.6	36
45	Assessing the combined effect of extremely low-frequency magnetic field exposure and oxidative stress on LINE-1 promoter methylation in human neural cells. Radiation and Environmental Biophysics, 2017, 56, 193-200.	1.4	16
46	The epigenetic landscape of age-related diseases: the geroscience perspective. Biogerontology, 2017, 18, 549-559.	3.9	62
47	Systemic Age-Associated DNA Hypermethylation of ELOVL2 Gene: In Vivo and In Vitro Evidences of a Cell Replication Process. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2017, 72, 1015-1023.	3.6	66
48	Genome-wide DNA methylation analysis in blood cells from patients with Werner syndrome. Clinical Epigenetics, 2017, 9, 92.	4.1	33
49	Aberrant methylation patterns in colorectal cancer: a meta-analysis. Oncotarget, 2017, 8, 12820-12830.	1.8	15
50	Acceleration of leukocytes' epigenetic age as an early tumor and sex-specific marker of breast and colorectal cancer. Oncotarget, 2017, 8, 23237-23245.	1.8	90
51	Epigenetic up-regulation of ribosome biogenesis and more aggressive phenotype triggered by the lack of the histone demethylase JHDM1B in mammary epithelial cells. Oncotarget, 2017, 8, 37091-37103.	1.8	19
52	Epigenome-wide association study in hepatocellular carcinoma: Identification of stochastic epigenetic mutations through an innovative statistical approach. Oncotarget, 2017, 8, 41890-41902.	1.8	47
53	Abstract A15: Epigenetic up-regulation of ribosome biogenesis and more aggressive phenotype triggered by the lack of the histone demethylase JHDM1B in mammary epithelial cells. , 2017, , .		0
54	Epigenetic Variability across Human Populations: A Focus on DNA Methylation Profiles of the <i>KRTCAP3 </i> , <i>MAD1L1 </i> and <i>BRSK2 </i> Genes. Genome Biology and Evolution, 2016, 8, 2760-2773.	2.5	31

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55	Age-dependent expression of <i>DNMT1</i> and <i>DNMT3B</i> in PBMCs from a large European population enrolled in the MARK-AGE study. Aging Cell, 2016, 15, 755-765.	6.7	60
56	Inferring chronological age from <scp>DNA</scp> methylation patterns of human teeth. American Journal of Physical Anthropology, 2016, 159, 585-595.	2.1	60
57	Systems medicine of inflammaging. Briefings in Bioinformatics, 2016, 17, 527-540.	6.5	35
58	Analysis of the machinery and intermediates of the 5hmC-mediated DNA demethylation pathway in aging on samples from the MARK-AGE Study. Aging, 2016, 8, 1896-1922.	3.1	36
59	Accelerated epigenetic aging in Down syndrome. Aging Cell, 2015, 14, 491-495.	6.7	446
60	Genomics and epigenomics. Journal of Headache and Pain, 2015, 16, A7.	6.0	2
61	N-Glycomic Changes in Serum Proteins in Type 2 Diabetes Mellitus Correlate with Complications and with Metabolic Syndrome Parameters. PLoS ONE, 2015, 10, e0119983.	2.5	81
62	Statistical strategies and stochastic predictive models for the MARK-AGE data. Mechanisms of Ageing and Development, 2015, 151, 45-53.	4.6	3
63	Metformin improves putative longevity effectors in peripheral mononuclear cells from subjects with prediabetes. A randomized controlled trial. Nutrition, Metabolism and Cardiovascular Diseases, 2015, 25, 686-693.	2.6	71
64	The epigenetic side of human adaptation: hypotheses, evidences and theories. Annals of Human Biology, 2015, 42, 1-9.	1.0	31
65	A meta-analysis on age-associated changes in blood DNA methylation: results from an original analysis pipeline for Infinium 450k data. Aging, 2015, 7, 97-109.	3.1	46
66	Stochastic epigenetic mutations (DNA methylation) increase exponentially in human aging and correlate with X chromosome inactivation skewing in females. Aging, 2015, 7, 568-578.	3.1	68
67	Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring. Aging, 2015, 7, 1159-1170.	3.1	276
68	From lifetime to evolution: timescales of human gut microbiota adaptation. Frontiers in Microbiology, 2014, 5, 587.	3.5	91
69	Identification of a DNA methylation signature in blood cells from persons with Down Syndrome. Aging, 2014, 7, 82-96.	3.1	92
70	The Three Genetics (Nuclear DNA, Mitochondrial DNA, and Gut Microbiome) of Longevity in Humans Considered as Metaorganisms. BioMed Research International, 2014, 2014, 1-14.	1.9	25
71	Present and future of anti-ageing epigenetic diets. Mechanisms of Ageing and Development, 2014, 136-137, 101-115.	4.6	76
72	The nucleolar size is associated to the methylation status of ribosomal DNA in breast carcinomas. BMC Cancer, 2014, 14, 361.	2.6	22

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73	TET2 gene expression and 5-hydroxymethylcytosine level in multiple sclerosis peripheral blood cells. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1130-1136.	3.8	55
74	Poly(ADP-ribosyl)ation is involved in the epigenetic control of TET1 gene transcription. Oncotarget, 2014, 5, 10356-10367.	1.8	36
75	ADP-ribose polymer depletion leads to nuclear Ctcf re-localization and chromatin rearrangement. Biochemical Journal, 2013, 449, 623-630.	3.7	27
76	Centenarians as super-controls to assess the biological relevance of genetic risk factors for common age-related diseases: A proof of principle on type 2 diabetes. Aging, 2013, 5, 373-385.	3.1	57
77	Immune System, Cell Senescence, Aging and Longevity - Inflamm-Aging Reappraised. Current Pharmaceutical Design, 2013, 19, 1675-1679.	1.9	101
78	Genes of Human Longevity: An Endless Quest?. Current Vascular Pharmacology, 2013, 12, 707-717.	1.7	22
79	Immune system, cell senescence, aging and longevityinflamm-aging reappraised. Current Pharmaceutical Design, 2013, 19, 1675-9.	1.9	144
80	ADP-ribose polymers localized on Ctcf–Parp1–Dnmt1 complex prevent methylation of Ctcf target sites. Biochemical Journal, 2012, 441, 645-652.	3.7	110
81	Methylation of <scp><i>ELOVL</i></scp> <i>2</i> gene as a new epigenetic marker of age. Aging Cell, 2012, 11, 1132-1134.	6.7	362
82	Poly(ADP-ribosyl)ation Acts in the DNA Demethylation of Mouse Primordial Germ Cells Also with DNA Damage-Independent Roles. PLoS ONE, 2012, 7, e46927.	2.5	60
83	A subset of chronic lymphocytic leukemia patients display reduced levels of PARP1 expression coupled with a defective irradiation-induced apoptosis. Experimental Hematology, 2012, 40, 197-206.e1.	0.4	15
84	Space/Population and Time/Age in DNA methylation variability in humans: a study on IGF2/H19 locus in different Italian populations and in mono- and di-zygotic twins of different age. Aging, 2012, 4, 509-520.	3.1	33
85	Poly(ADP-ribosyl)ation affects stabilization of Che-1 protein in response to DNA damage. DNA Repair, 2011, 10, 380-389.	2.8	18
86	Validation of suitable internal control genes for expression studies in aging. Mechanisms of Ageing and Development, 2010, 131, 89-95.	4.6	60
87	Parp1 Localizes within the Dnmt1 Promoter and Protects Its Unmethylated State by Its Enzymatic Activity. PLoS ONE, 2009, 4, e4717.	2.5	97
88	Origin and evolution of the c.844_845ins68/c.833T>C mutations within the cystathionine βâ€synthase gene in great apes. FEBS Letters, 2008, 582, 423-426.	2.8	5