

Maria Giulia Bacalini

List of Publications by Year in descending order

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88
papers

4,158
citations

117625

34
h-index

128289

60
g-index

93
all docs

93
docs citations

93
times ranked

6619
citing authors

#	ARTICLE	IF	CITATIONS
1	Accelerated epigenetic aging in Down syndrome. <i>Aging Cell</i> , 2015, 14, 491-495.	6.7	446
2	Methylation of <i>ELOVL2</i> gene as a new epigenetic marker of age. <i>Aging Cell</i> , 2012, 11, 1132-1134.	6.7	362
3	Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring. <i>Aging</i> , 2015, 7, 1159-1170.	3.1	276
4	Immune system, cell senescence, aging and longevity--inflamm-aging reappraised. <i>Current Pharmaceutical Design</i> , 2013, 19, 1675-9.	1.9	144
5	ADP-ribose polymers localized on Ctcf/Parp1/Dnmt1 complex prevent methylation of Ctcf target sites. <i>Biochemical Journal</i> , 2012, 441, 645-652.	3.7	110
6	Small extracellular vesicles deliver miR-21 and miR-217 as pro-senescence effectors to endothelial cells. <i>Journal of Extracellular Vesicles</i> , 2020, 9, 1725285.	12.2	104
7	Immune System, Cell Senescence, Aging and Longevity - Inflamm-Aging Reappraised. <i>Current Pharmaceutical Design</i> , 2013, 19, 1675-1679.	1.9	101
8	Parp1 Localizes within the Dnmt1 Promoter and Protects Its Unmethylated State by Its Enzymatic Activity. <i>PLoS ONE</i> , 2009, 4, e4717.	2.5	97
9	Identification of a DNA methylation signature in blood cells from persons with Down Syndrome. <i>Aging</i> , 2014, 7, 82-96.	3.1	92
10	From lifetime to evolution: timescales of human gut microbiota adaptation. <i>Frontiers in Microbiology</i> , 2014, 5, 587.	3.5	91
11	Acceleration of leukocytes' epigenetic age as an early tumor and sex-specific marker of breast and colorectal cancer. <i>Oncotarget</i> , 2017, 8, 23237-23245.	1.8	90
12	N-Glycomic Changes in Serum Proteins in Type 2 Diabetes Mellitus Correlate with Complications and with Metabolic Syndrome Parameters. <i>PLoS ONE</i> , 2015, 10, e0119983.	2.5	81
13	Present and future of anti-ageing epigenetic diets. <i>Mechanisms of Ageing and Development</i> , 2014, 136-137, 101-115.	4.6	76
14	One-year Mediterranean diet promotes epigenetic rejuvenation with country- and sex-specific effects: a pilot study from the NU-AGE project. <i>GeroScience</i> , 2020, 42, 687-701.	4.6	76
15	Metformin improves putative longevity effectors in peripheral mononuclear cells from subjects with prediabetes. A randomized controlled trial. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2015, 25, 686-693.	2.6	71
16	The Impact of Caloric Restriction on the Epigenetic Signatures of Aging. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2022.	4.1	71
17	Stochastic epigenetic mutations (DNA methylation) increase exponentially in human aging and correlate with X chromosome inactivation skewing in females. <i>Aging</i> , 2015, 7, 568-578.	3.1	68
18	Systemic Age-Associated DNA Hypermethylation of ELOVL2 Gene: In Vivo and In Vitro Evidences of a Cell Replication Process. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017, 72, 1015-1023.	3.6	66

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19	The epigenetic landscape of age-related diseases: the geroscience perspective. Biogerontology, 2017, 18, 549-559.	3.9	62
20	Validation of suitable internal control genes for expression studies in aging. Mechanisms of Ageing and Development, 2010, 131, 89-95.	4.6	60
21	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
22	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
23	Inferring chronological age from DNA methylation patterns of human teeth. American Journal of Physical Anthropology, 2016, 159, 585-595.	2.1	60
24	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
25	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
26	Age-related DNA methylation changes are sex-specific: a comprehensive assessment. Aging, 2020, 12, 24057-24080.	3.1	55
27	Accelerated bio-cognitive aging in Down syndrome: State of the art and possible deceleration strategies. Aging Cell, 2019, 18, e12903.	6.7	47
28	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
29	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
30	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
31	Lamin A involvement in ageing processes. Ageing Research Reviews, 2020, 62, 101073.	10.9	41
32	Responders and non-responders to influenza vaccination: A DNA methylation approach on blood cells. Experimental Gerontology, 2018, 105, 94-100.	2.8	39
33	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
34	Whole-genome sequencing analysis of semi-supercentenarians. ELife, 2021, 10, .	6.0	37
35	The methylation of nuclear and mitochondrial DNA in ageing phenotypes and longevity. Mechanisms of Ageing and Development, 2017, 165, 156-161.	4.6	36
36	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

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37	Poly(ADP-ribosyl)ation is involved in the epigenetic control of TET1 gene transcription. <i>Oncotarget</i> , 2014, 5, 10356-10367.	1.8	36
38	Systems medicine of inflammaging. <i>Briefings in Bioinformatics</i> , 2016, 17, 527-540.	6.5	35
39	Age-Related DNA Methylation Changes: Potential Impact on Skeletal Muscle Aging in Humans. <i>Frontiers in Physiology</i> , 2019, 10, 996.	2.8	35
40	The peculiar aging of human liver: A geroscience perspective within transplant context. <i>Ageing Research Reviews</i> , 2019, 51, 24-34.	10.9	35
41	Down syndrome, accelerated aging and immunosenescence. <i>Seminars in Immunopathology</i> , 2020, 42, 635-645.	6.1	35
42	Genome-wide DNA methylation analysis in blood cells from patients with Werner syndrome. <i>Clinical Epigenetics</i> , 2017, 9, 92.	4.1	33
43	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. <i>Aging</i> , 2012, 4, 509-520.	3.1	33
44	The epigenetic side of human adaptation: hypotheses, evidences and theories. <i>Annals of Human Biology</i> , 2015, 42, 1-9.	1.0	31
45	Epigenetic Variability across Human Populations: A Focus on DNA Methylation Profiles of the <i>KRTCAP3</i> , <i>MAD1L1</i> and <i>BRSK2</i> Genes. <i>Genome Biology and Evolution</i> , 2016, 8, 2760-2773.	2.5	31
46	The epigenetics of inflammaging: The contribution of age-related heterochromatin loss and locus-specific remodelling and the modulation by environmental stimuli. <i>Seminars in Immunology</i> , 2018, 40, 49-60.	5.6	29
47	DNA methylation of shelf, shore and open sea CpG positions distinguish high microsatellite instability from low or stable microsatellite status colon cancer stem cells. <i>Epigenomics</i> , 2019, 11, 587-604.	2.1	29
48	ADP-ribose polymer depletion leads to nuclear Ctf re-localization and chromatin rearrangement. <i>Biochemical Journal</i> , 2013, 449, 623-630.	3.7	27
49	The Three Genetics (Nuclear DNA, Mitochondrial DNA, and Gut Microbiome) of Longevity in Humans Considered as Metaorganisms. <i>BioMed Research International</i> , 2014, 2014, 1-14.	1.9	25
50	Epigenetic DNA methylation changes in episodic and chronic migraine. <i>Neurological Sciences</i> , 2018, 39, 67-68.	1.9	24
51	The Human Body as a Super Network: Digital Methods to Analyze the Propagation of Aging. <i>Frontiers in Aging Neuroscience</i> , 2020, 12, 136.	3.4	24
52	Molecular Aging of Human Liver: An Epigenetic/Transcriptomic Signature. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, 1-8.	3.6	23
53	The nucleolar size is associated to the methylation status of ribosomal DNA in breast carcinomas. <i>BMC Cancer</i> , 2014, 14, 361.	2.6	22
54	Genes of Human Longevity: An Endless Quest?. <i>Current Vascular Pharmacology</i> , 2013, 12, 707-717.	1.7	22

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55	Epigenetic up-regulation of ribosome biogenesis and more aggressive phenotype triggered by the lack of the histone demethylase JHDM1B in mammary epithelial cells. <i>Oncotarget</i> , 2017, 8, 37091-37103.	1.8	19
56	Poly(ADP-ribosyl)ation affects stabilization of Che-1 protein in response to DNA damage. <i>DNA Repair</i> , 2011, 10, 380-389.	2.8	18
57	Ribosomal DNA instability: An evolutionary conserved fuel for inflammaging. <i>Ageing Research Reviews</i> , 2020, 58, 101018.	10.9	18
58	Assessing the combined effect of extremely low-frequency magnetic field exposure and oxidative stress on LINE-1 promoter methylation in human neural cells. <i>Radiation and Environmental Biophysics</i> , 2017, 56, 193-200.	1.4	16
59	DNA Hydroxymethylation Levels Are Altered in Blood Cells From Down Syndrome Persons Enrolled in the MARK-AGE Project. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 737-744.	3.6	16
60	Impact of demography and population dynamics on the genetic architecture of human longevity. <i>Aging</i> , 2018, 10, 1947-1963.	3.1	16
61	A subset of chronic lymphocytic leukemia patients display reduced levels of PARP1 expression coupled with a defective irradiation-induced apoptosis. <i>Experimental Hematology</i> , 2012, 40, 197-206.e1.	0.4	15
62	Aberrant methylation patterns in colorectal cancer: a meta-analysis. <i>Oncotarget</i> , 2017, 8, 12820-12830.	1.8	15
63	A geroscience approach for Parkinson's disease: Conceptual framework and design of PROPAG-AGEING project. <i>Mechanisms of Ageing and Development</i> , 2021, 194, 111426.	4.6	14
64	Early downregulation of hsa-miR-144-3p in serum from drug-naïve Parkinson's disease patients. <i>Scientific Reports</i> , 2022, 12, 1330.	3.3	14
65	Accelerated epigenetic aging and inflammatory/immunological profile (ipAGE) in patients with chronic kidney disease. <i>GeroScience</i> , 2022, 44, 817-834.	4.6	13
66	Aging and Caloric Restriction Modulate the DNA Methylation Profile of the Ribosomal RNA Locus in Human and Rat Liver. <i>Nutrients</i> , 2020, 12, 277.	4.1	12
67	Circulating miR-19a-3p and miR-19b-3p characterize the human aging process and their isomiRs associate with healthy status at extreme ages. <i>Aging Cell</i> , 2021, 20, e13409.	6.7	12
68	Evaluation of Lymphocyte Response to the Induced Oxidative Stress in a Cohort of Ageing Subjects, including Semisupercentenarians and Their Offspring. <i>Mediators of Inflammation</i> , 2018, 2018, 1-14.	3.0	11
69	Age-Related Epigenetic Derangement upon Reprogramming and Differentiation of Cells from the Elderly. <i>Genes</i> , 2018, 9, 39.	2.4	11
70	Increased PARylation impacts the DNA methylation process in type 2 diabetes mellitus. <i>Clinical Epigenetics</i> , 2021, 13, 114.	4.1	11
71	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naïve Parkinson's disease patients. <i>Npj Parkinson's Disease</i> , 2022, 8, 14.	5.3	11
72	Down Syndrome, Ageing and Epigenetics. <i>Sub-Cellular Biochemistry</i> , 2019, 91, 161-193.	2.4	10

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73	Gene duplication, rather than epigenetic changes, drives FGF4 overexpression in KIT/PDGFR α /SDH/RAS-P WT GIST. Scientific Reports, 2020, 10, 19829.	3.3	10
74	Analysis of Epigenetic Age Predictors in Pain-Related Conditions. Frontiers in Public Health, 2020, 8, 172.	2.7	8
75	No association between frailty index and epigenetic clocks in Italian semi-supercentenarians. Mechanisms of Ageing and Development, 2021, 197, 111514.	4.6	8
76	DNA Methylation Analysis of Ribosomal DNA in Adults With Down Syndrome. Frontiers in Genetics, 2022, 13, 792165.	2.3	7
77	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
78	Origin and evolution of the c.844_845ins68/c.833T>C mutations within the cystathionine β -synthase gene in great apes. FEBS Letters, 2008, 582, 423-426.	2.8	5
79	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
80	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
81	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
82	Statistical strategies and stochastic predictive models for the MARK-AGE data. Mechanisms of Ageing and Development, 2015, 151, 45-53.	4.6	3
83	Genomics and epigenomics. Journal of Headache and Pain, 2015, 16, A7.	6.0	2
84	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. Npj Parkinson's Disease, 2021, 7, 78.	5.3	2
85	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
86	Network markers of DNA methylation in neurodegenerative diseases. , 2020, , .		1
87	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
88	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