

Maria Giulia Bacalini

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

4,158
citations

117453

34
h-index

128067

60
g-index

93
all docs

93
docs citations

93
times ranked

6619
citing authors

#	ARTICLE	IF	CITATIONS
1	Early downregulation of hsa-miR-144-3p in serum from drug-naïve Parkinson's disease patients. <i>Scientific Reports</i> , 2022, 12, 1330.	1.6	14
2	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive Parkinson's disease patients. <i>Npj Parkinson's Disease</i> , 2022, 8, 14.	2.5	11
3	Accelerated epigenetic aging and inflammatory/immunological profile (ipAGE) in patients with chronic kidney disease. <i>GeroScience</i> , 2022, 44, 817-834.	2.1	13
4	Association of rs3027178 polymorphism in the circadian clock gene PER1 with susceptibility to Alzheimer's disease and longevity in an Italian population. <i>GeroScience</i> , 2022, 44, 881-896.	2.1	6
5	Role of Epigenetic Therapy in the Modulation of Tumor Growth and Migration in Human Castration-Resistant Prostate Cancer Cells with Neuroendocrine Differentiation. <i>Neuroendocrinology</i> , 2022, 112, 580-594.	1.2	2
6	DNA Methylation Analysis of Ribosomal DNA in Adults With Down Syndrome. <i>Frontiers in Genetics</i> , 2022, 13, 792165.	1.1	7
7	Blood circulating miR-28-5p and let-7d-5p associate with premature ageing in Down syndrome. <i>Mechanisms of Ageing and Development</i> , 2022, 206, 111691.	2.2	4
8	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.	2.2	14
9	A Meta-Analysis of Brain DNA Methylation Across Sex, Age, and Alzheimer's Disease Points for Accelerated Epigenetic Aging in Neurodegeneration. <i>Frontiers in Aging Neuroscience</i> , 2021, 13, 639428.	1.7	45
10	Ageing affects subtelomeric DNA methylation in blood cells from a large European population enrolled in the MARK-AGE study. <i>GeroScience</i> , 2021, 43, 1283-1302.	2.1	4
11	Whole-genome sequencing analysis of semi-supercentenarians. <i>ELife</i> , 2021, 10, .	2.8	37
12	Increased PARylation impacts the DNA methylation process in type 2 diabetes mellitus. <i>Clinical Epigenetics</i> , 2021, 13, 114.	1.8	11
13	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.	3.0	12
14	No association between frailty index and epigenetic clocks in Italian semi-supercentenarians. <i>Mechanisms of Ageing and Development</i> , 2021, 197, 111514.	2.2	8
15	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. <i>Npj Parkinson's Disease</i> , 2021, 7, 78.	2.5	2
16	Multimodal evaluation of the melanopsin retinal ganglion cells system in relation to circadian rhythms in Alzheimer's disease and aging. <i>Journal of the Neurological Sciences</i> , 2021, 429, 118980.	0.3	0
17	Ribosomal DNA instability: An evolutionary conserved fuel for inflammaging. <i>Ageing Research Reviews</i> , 2020, 58, 101018.	5.0	18
18	Gene duplication, rather than epigenetic changes, drives FGF4 overexpression in KIT/PDGFR α /SDH/RAS-P WT GIST. <i>Scientific Reports</i> , 2020, 10, 19829.	1.6	10

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19	Down syndrome, accelerated aging and immunosenescence. <i>Seminars in Immunopathology</i> , 2020, 42, 635-645.	2.8	35
20	The Human Body as a Super Network: Digital Methods to Analyze the Propagation of Aging. <i>Frontiers in Aging Neuroscience</i> , 2020, 12, 136.	1.7	24
21	Analysis of Epigenetic Age Predictors in Pain-Related Conditions. <i>Frontiers in Public Health</i> , 2020, 8, 172.	1.3	8
22	Small extracellular vesicles deliver miRâ€21 and miRâ€17 as proâ€senescence effectors to endothelial cells. <i>Journal of Extracellular Vesicles</i> , 2020, 9, 1725285.	5.5	104
23	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.	1.7	12
24	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.	2.1	76
25	Lamin A involvement in ageing processes. <i>Ageing Research Reviews</i> , 2020, 62, 101073.	5.0	41
26	Age-related DNA methylation changes are sex-specific: a comprehensive assessment. <i>Aging</i> , 2020, 12, 24057-24080.	1.4	55
27	Network markers of DNA methylation in neurodegenerative diseases. , 2020, , .		1
28	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.	1.7	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. <i>Journal of Translational Medicine</i> , 2019, 17, 250.	1.8	4
30	Age-Related DNA Methylation Changes: Potential Impact on Skeletal Muscle Aging in Humans. <i>Frontiers in Physiology</i> , 2019, 10, 996.	1.3	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. <i>Epigenomics</i> , 2019, 11, 587-604.	1.0	29
32	The Impact of Caloric Restriction on the Epigenetic Signatures of Aging. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2022.	1.8	71
33	Down Syndrome, Ageing and Epigenetics. <i>Sub-Cellular Biochemistry</i> , 2019, 91, 161-193.	1.0	10
34	Accelerated bioâ€cognitive aging in Down syndrome: State of the art and possible deceleration strategies. <i>Aging Cell</i> , 2019, 18, e12903.	3.0	47
35	The peculiar aging of human liver: A geroscience perspective within transplant context. <i>Ageing Research Reviews</i> , 2019, 51, 24-34.	5.0	35
36	Genomic stability, anti-inflammatory phenotype, and up-regulation of the RNaseH2 in cells from centenarians. <i>Cell Death and Differentiation</i> , 2019, 26, 1845-1858.	5.0	37

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37	Responders and non-responders to influenza vaccination: A DNA methylation approach on blood cells. <i>Experimental Gerontology</i> , 2018, 105, 94-100.	1.2	39
38	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.	1.7	16
39	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.	2.7	29
40	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.	1.4	11
41	Age-Related Epigenetic Derangement upon Reprogramming and Differentiation of Cells from the Elderly. <i>Genes</i> , 2018, 9, 39.	1.0	11
42	Epigenetic DNA methylation changes in episodic and chronic migraine. <i>Neurological Sciences</i> , 2018, 39, 67-68.	0.9	24
43	Impact of demography and population dynamics on the genetic architecture of human longevity. <i>Aging</i> , 2018, 10, 1947-1963.	1.4	16
44	The methylation of nuclear and mitochondrial DNA in ageing phenotypes and longevity. <i>Mechanisms of Ageing and Development</i> , 2017, 165, 156-161.	2.2	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. <i>Radiation and Environmental Biophysics</i> , 2017, 56, 193-200.	0.6	16
46	The epigenetic landscape of age-related diseases: the geroscience perspective. <i>Biogerontology</i> , 2017, 18, 549-559.	2.0	62
47	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.	1.7	66
48	Genome-wide DNA methylation analysis in blood cells from patients with Werner syndrome. <i>Clinical Epigenetics</i> , 2017, 9, 92.	1.8	33
49	Aberrant methylation patterns in colorectal cancer: a meta-analysis. <i>Oncotarget</i> , 2017, 8, 12820-12830.	0.8	15
50	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.	0.8	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. <i>Oncotarget</i> , 2017, 8, 37091-37103.	0.8	19
52	Epigenome-wide association study in hepatocellular carcinoma: Identification of stochastic epigenetic mutations through an innovative statistical approach. <i>Oncotarget</i> , 2017, 8, 41890-41902.	0.8	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. <i>Genome Biology and Evolution</i> , 2016, 8, 2760-2773.	1.1	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. <i>Aging Cell</i> , 2016, 15, 755-765.	3.0	60
56	Inferring chronological age from DNA methylation patterns of human teeth. <i>American Journal of Physical Anthropology</i> , 2016, 159, 585-595.	2.1	60
57	Systems medicine of inflammaging. <i>Briefings in Bioinformatics</i> , 2016, 17, 527-540.	3.2	35
58	Analysis of the machinery and intermediates of the 5hmC-mediated DNA demethylation pathway in aging on samples from the MARK-AGE Study. <i>Aging</i> , 2016, 8, 1896-1922.	1.4	36
59	Accelerated epigenetic aging in Down syndrome. <i>Aging Cell</i> , 2015, 14, 491-495.	3.0	446
60	Genomics and epigenomics. <i>Journal of Headache and Pain</i> , 2015, 16, A7.	2.5	2
61	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.	1.1	81
62	Statistical strategies and stochastic predictive models for the MARK-AGE data. <i>Mechanisms of Ageing and Development</i> , 2015, 151, 45-53.	2.2	3
63	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.	1.1	71
64	The epigenetic side of human adaptation: hypotheses, evidences and theories. <i>Annals of Human Biology</i> , 2015, 42, 1-9.	0.4	31
65	A meta-analysis on age-associated changes in blood DNA methylation: results from an original analysis pipeline for Infinium 450k data. <i>Aging</i> , 2015, 7, 97-109.	1.4	46
66	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.	1.4	68
67	Decreased epigenetic age of PBMCs from Italian semi-supercentenarians and their offspring. <i>Aging</i> , 2015, 7, 1159-1170.	1.4	276
68	From lifetime to evolution: timescales of human gut microbiota adaptation. <i>Frontiers in Microbiology</i> , 2014, 5, 587.	1.5	91
69	Identification of a DNA methylation signature in blood cells from persons with Down Syndrome. <i>Aging</i> , 2014, 7, 82-96.	1.4	92
70	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.	0.9	25
71	Present and future of anti-ageing epigenetic diets. <i>Mechanisms of Ageing and Development</i> , 2014, 136-137, 101-115.	2.2	76
72	The nucleolar size is associated to the methylation status of ribosomal DNA in breast carcinomas. <i>BMC Cancer</i> , 2014, 14, 361.	1.1	22

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73	TET2 gene expression and 5-hydroxymethylcytosine level in multiple sclerosis peripheral blood cells. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2014, 1842, 1130-1136.	1.8	55
74	Poly(ADP-ribosyl)ation is involved in the epigenetic control of TET1 gene transcription. <i>Oncotarget</i> , 2014, 5, 10356-10367.	0.8	36
75	ADP-ribose polymer depletion leads to nuclear Ctfc re-localization and chromatin rearrangement. <i>Biochemical Journal</i> , 2013, 449, 623-630.	1.7	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. <i>Aging</i> , 2013, 5, 373-385.	1.4	57
77	Immune System, Cell Senescence, Aging and Longevity - Inflamm-Aging Reappraised. <i>Current Pharmaceutical Design</i> , 2013, 19, 1675-1679.	0.9	101
78	Genes of Human Longevity: An Endless Quest?. <i>Current Vascular Pharmacology</i> , 2013, 12, 707-717.	0.8	22
79	Immune system, cell senescence, aging and longevity--inflamm-aging reappraised. <i>Current Pharmaceutical Design</i> , 2013, 19, 1675-9.	0.9	144
80	ADP-ribose polymers localized on Ctfc-Parp1-Dnmt1 complex prevent methylation of Ctfc target sites. <i>Biochemical Journal</i> , 2012, 441, 645-652.	1.7	110
81	Methylation of <i>ELOVL2</i> gene as a new epigenetic marker of age. <i>Aging Cell</i> , 2012, 11, 1132-1134.	3.0	362
82	Poly(ADP-ribosyl)ation Acts in the DNA Demethylation of Mouse Primordial Germ Cells Also with DNA Damage-Independent Roles. <i>PLoS ONE</i> , 2012, 7, e46927.	1.1	60
83	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.	0.2	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. <i>Aging</i> , 2012, 4, 509-520.	1.4	33
85	Poly(ADP-ribosyl)ation affects stabilization of Che-1 protein in response to DNA damage. <i>DNA Repair</i> , 2011, 10, 380-389.	1.3	18
86	Validation of suitable internal control genes for expression studies in aging. <i>Mechanisms of Ageing and Development</i> , 2010, 131, 89-95.	2.2	60
87	Parp1 Localizes within the Dnmt1 Promoter and Protects Its Unmethylated State by Its Enzymatic Activity. <i>PLoS ONE</i> , 2009, 4, e4717.	1.1	97
88	Origin and evolution of the c.844_845ins68/c.833T>C mutations within the cystathionine Î²-synthase gene in great apes. <i>FEBS Letters</i> , 2008, 582, 423-426.	1.3	5