

Dina Bellizzi

List of Publications by Year in descending order

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64
papers

2,952
citations

159585

30
h-index

168389

53
g-index

66
all docs

66
docs citations

66
times ranked

4244
citing authors

#	ARTICLE	IF	CITATIONS
1	A novel VNTR enhancer within the SIRT3 gene, a human homologue of SIR2, is associated with survival at oldest ages. <i>Genomics</i> , 2005, 85, 258-263.	2.9	339
2	Variability of the SIRT3 gene, human silent information regulator Sir2 homologue, and survivorship in the elderly. <i>Experimental Gerontology</i> , 2003, 38, 1065-1070.	2.8	268
3	The Control Region of Mitochondrial DNA Shows an Unusual CpG and Non-CpG Methylation Pattern. <i>DNA Research</i> , 2013, 20, 537-547.	3.4	221
4	DNA-demethylating and anti-tumor activity of synthetic miR-29b mimics in multiple myeloma. <i>Oncotarget</i> , 2012, 3, 1246-1258.	1.8	138
5	Global DNA methylation levels are modulated by mitochondrial DNA variants. <i>Epigenomics</i> , 2012, 4, 17-27.	2.1	117
6	miR-29b induces SOCS-1 expression by promoter demethylation and negatively regulates migration of multiple myeloma and endothelial cells. <i>Cell Cycle</i> , 2013, 12, 3650-3662.	2.6	96
7	Association of the mitochondrial DNA haplogroup J with longevity is population specific. <i>European Journal of Human Genetics</i> , 2004, 12, 1080-1082.	2.8	93
8	Global DNA methylation in old subjects is correlated with frailty. <i>Age</i> , 2012, 34, 169-179.	3.0	91
9	Exploring the Role of Genetic Variability and Lifestyle in Oxidative Stress Response for Healthy Aging and Longevity. <i>International Journal of Molecular Sciences</i> , 2013, 14, 16443-16472.	4.1	86
10	Characterization of a bidirectional promoter shared between two human genes related to aging: SIRT3 and PSMD13. <i>Genomics</i> , 2007, 89, 143-150.	2.9	78
11	Epigenetics and aging. <i>Maturitas</i> , 2013, 74, 130-136.	2.4	72
12	Estradiol Increases IRS-1 Gene Expression and Insulin Signaling in Breast Cancer Cells. <i>Biochemical and Biophysical Research Communications</i> , 2001, 288, 685-689.	2.1	64
13	Mitochondrial DNA involvement in human longevity. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2006, 1757, 1388-1399.	1.0	64
14	SIRT3 protects from hypoxia and staurosporine-mediated cell death by maintaining mitochondrial membrane potential and intracellular pH. <i>Cell Death and Differentiation</i> , 2012, 19, 1815-1825.	11.2	63
15	Methylation of the ribosomal RNA gene promoter is associated with aging and age-related decline. <i>Aging Cell</i> , 2017, 16, 966-975.	6.7	63
16	Mitochondria in health, aging and diseases: the epigenetic perspective. <i>Biogerontology</i> , 2015, 16, 569-585.	3.9	57
17	Epigenetic modifications in multiple myeloma: recent advances on the role of DNA and histone methylation. <i>Expert Opinion on Therapeutic Targets</i> , 2017, 21, 91-101.	3.4	54
18	Gene expression of cytokines and cytokine receptors is modulated by the common variability of the mitochondrial DNA in cybrid cell lines. <i>Genes To Cells</i> , 2006, 11, 883-891.	1.2	47

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19	Anti-tumor Activity and Epigenetic Impact of the Polyphenol Oleacein in Multiple Myeloma. <i>Cancers</i> , 2019, 11, 990.	3.7	47
20	The allele (A)(-110) in the promoter region of the HSP70-1 gene is unfavorable to longevity in women. <i>Biogerontology</i> , 2003, 4, 215-220.	3.9	46
21	The mitochondrial DNA control region shows genetically correlated levels of heteroplasmy in leukocytes of centenarians and their offspring. <i>BMC Genomics</i> , 2007, 8, 293.	2.8	44
22	Epidemiological, genetic and epigenetic aspects of the research on healthy ageing and longevity. <i>Immunity and Ageing</i> , 2012, 9, 6.	4.2	43
23	SIRT1&SIRT3 Axis Regulates Cellular Response to Oxidative Stress and Etoposide. <i>Journal of Cellular Physiology</i> , 2017, 232, 1835-1844.	4.1	39
24	Resistance of mtDNA& depleted cells to apoptosis. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2008, 73A, 528-537.	1.5	38
25	SIRT3 gene expression: A link between inherited mitochondrial DNA variants and oxidative stress. <i>Gene</i> , 2012, 497, 323-329.	2.2	38
26	Heterogeneity of primer extension products in asymmetric PCR is due both to cleavage by a structure-specific exo/endonuclease activity of DNA polymerases and to premature stops.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 2724-2728.	7.1	37
27	The methylation of nuclear and mitochondrial DNA in ageing phenotypes and longevity. <i>Mechanisms of Ageing and Development</i> , 2017, 165, 156-161.	4.6	36
28	Centenarians as extreme phenotypes: An ecological perspective to get insight into the relationship between the genetics of longevity and age-associated diseases. <i>Mechanisms of Ageing and Development</i> , 2017, 165, 195-201.	4.6	36
29	Frequency and coverage of trinucleotide repeats in eukaryotes. <i>Gene</i> , 2003, 317, 117-125.	2.2	31
30	Age-and gender-related pattern of methylation in the <i>MT-RNR1</i> gene. <i>Epigenomics</i> , 2015, 7, 707-716.	2.1	31
31	Ageing and nutrition induce tissue-specific changes on global DNA methylation status in rats. <i>Mechanisms of Ageing and Development</i> , 2018, 174, 47-54.	4.6	31
32	Heat shock response by EBV-immortalized B-lymphocytes from centenarians and control subjects: a model to study the relevance of stress response in longevity. <i>Experimental Gerontology</i> , 2004, 39, 83-90.	2.8	30
33	Gut Microbiota as Important Mediator Between Diet and DNA Methylation and Histone Modifications in the Host. <i>Nutrients</i> , 2020, 12, 597.	4.1	30
34	Two variants located in the upstream enhancer region of human UCP1 gene affect gene expression and are correlated with human longevity. <i>Experimental Gerontology</i> , 2011, 46, 897-904.	2.8	28
35	Mitochondrial DNA variability modulates mRNA and intra-mitochondrial protein levels of HSP60 and HSP75: experimental evidence from cybrid lines. <i>Cell Stress and Chaperones</i> , 2009, 14, 265-271.	2.9	27
36	Microbiome in Blood Samples From the General Population Recruited in the MARK-AGE Project: A Pilot Study. <i>Frontiers in Microbiology</i> , 2021, 12, 707515.	3.5	27

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37	The impact of nutrients on the aging rate: A complex interaction of demographic, environmental and genetic factors. <i>Mechanisms of Ageing and Development</i> , 2016, 154, 49-61.	4.6	26
38	Evidence that the mouse insulin receptor substrate-1 belongs to the gene family on which the promoter is activated by estrogen receptor I \pm through its interaction with Sp1. <i>Journal of Molecular Endocrinology</i> , 2006, 36, 91-105.	2.5	25
39	A New Robust Epigenetic Model for Forensic Age Prediction. <i>Journal of Forensic Sciences</i> , 2020, 65, 1424-1431.	1.6	24
40	Identification of GATA2 and AP-1 Activator Elements within the Enhancer VNTR Occurring in Intron 5 of the Human SIRT3 Gene. <i>Molecules and Cells</i> , 2009, 28, 87-92.	2.6	22
41	Mitochondrial function, mitochondrial DNA and ageing: a reappraisal. <i>Biogerontology</i> , 2010, 11, 575-588.	3.9	21
42	Estradiol via estrogen receptor beta influences ROS levels through the transcriptional regulation of SIRT3 in human seminoma TCam-2 cells. <i>Tumor Biology</i> , 2017, 39, 101042831770164.	1.8	19
43	The influences on human longevity by HUMTHO1.STR polymorphism (Tyrosine Hydroxylase gene). <i>Mechanisms of Ageing and Development</i> , 2002, 123, 1403-1410.	4.6	18
44	A novel sampling design to explore gene-longevity associations: the ECHA study. <i>European Journal of Human Genetics</i> , 2008, 16, 236-242.	2.8	18
45	Mitochondrial genome and epigenome two sides of the same coin. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 888-908.	3.0	16
46	Epigenetic signature: implications for mitochondrial quality control in human aging. <i>Aging</i> , 2019, 11, 1240-1251.	3.1	16
47	Experimental testing of a mathematical model relevant to the extrinsic pathway of apoptosis. <i>Cell Stress and Chaperones</i> , 2010, 15, 13-23.	2.9	13
48	Directed Organization of DNA Filaments in a Soft Matter Template. <i>Langmuir</i> , 2013, 29, 3398-3403.	3.5	12
49	Antibacterial Activity and Epigenetic Remodeling of Essential Oils from Calabrian Aromatic Plants. <i>Nutrients</i> , 2022, 14, 391.	4.1	11
50	Individual DNA Methylation Profile is Correlated with Age and can be Targeted to Modulate Healthy Aging and Longevity. <i>Current Pharmaceutical Design</i> , 2019, 25, 4139-4149.	1.9	8
51	rRNA-gene methylation and biological aging. <i>Aging</i> , 2018, 10, 7-8.	3.1	7
52	Triplet repeats, over-expanded in neuromuscular diseases, are under-represented in mammalian DNA: a survey of models. <i>Brain Research Bulletin</i> , 2001, 56, 265-271.	3.0	6
53	Multi-Tissue DNA Methylation Remodeling at Mitochondrial Quality Control Genes According to Diet in Rat Aging Models. <i>Nutrients</i> , 2020, 12, 460.	4.1	6
54	EQUILIBRIUM, STABILITY AND DYNAMICAL RESPONSE IN A MODEL OF THE EXTRINSIC APOPTOSIS PATHWAY. <i>Journal of Biological Systems</i> , 2007, 15, 261-285.	1.4	5

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55	A Genetic Variant of ASCT2 Hampers In Vitro RNA Splicing and Correlates with Human Longevity. <i>Rejuvenation Research</i> , 2018, 21, 193-199.	1.8	5
56	Epigenetic Regulation of Mitochondrial Quality Control Genes in Multiple Myeloma: A Sequenom MassARRAY Pilot Investigation on HMCLs. <i>Journal of Clinical Medicine</i> , 2021, 10, 1295.	2.4	5
57	Impact of Nutrition on Age-Related Epigenetic RNA Modifications in Rats. <i>Nutrients</i> , 2022, 14, 1232.	4.1	5
58	Epigenetics and Ageing. , 2019, , 99-133.		3
59	A model for the involvement of Okazaki fragments maturation in the expansion of short tandem repeats. <i>Gene</i> , 2001, 276, 153-159.	2.2	2
60	Aging and Longevity between Genetic Background and Lifestyle Intervention. <i>BioMed Research International</i> , 2014, 2014, 1-2.	1.9	2
61	Mini Nutritional Assessment Scores Indicate Higher Risk for Prospective Mortality and Contrasting Correlation With Age-Related Epigenetic Biomarkers. <i>Frontiers in Endocrinology</i> , 2019, 10, 672.	3.5	1
62	Dynamical analysis of the programmed cell death pathway. , 2007, , .		1
63	MiR-29b Exerts Anti-Multiple Myeloma Activity by Targeting Key Oncogenic Pathways and Modulating DNA Methylation Profile.. <i>Blood</i> , 2012, 120, 2941-2941.	1.4	1
64	A procedure for cloning genomic DNA fragments with increasing thermoresistance. <i>Gene</i> , 1998, 219, 63-71.	2.2	0