Giovanni Fiorito

List of Publications by Year
in descending order

65 papers	4,064 citations	168829 31 h-index	156644 58 g-index
76 all docs	76 docs citations	76 times ranked	8346 citing authors

#	Article	IF	Citations
1	Machine learning in clinical and epidemiological research: isn't it time for biostatisticians to work on it?. , 2022, 16, .		8
2	Early life adversity and age acceleration at mid-life and older ages indexed using the next-generation GrimAge and Pace of Aging epigenetic clocks. Psychoneuroendocrinology, 2022, 137, 105643.	1.3	24
3	Work-related stress and well-being in association with epigenetic age acceleration: A Northern Finland Birth Cohort 1966 Study. Aging, 2022, 14, 1128-1156.	1.4	11
4	The Role of Epigenetic Clocks in Explaining Educational Inequalities in Mortality: A Multicohort Study and Meta-analysis. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 1750-1759.	1.7	9
5	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	5.8	26
6	GrimAge Outperforms Other Epigenetic Clocks in the Prediction of Age-Related Clinical Phenotypes and All-Cause Mortality. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 741-749.	1.7	200
7	Comparative Evaluation of MaxQuant and Proteome Discoverer MS1-Based Protein Quantification Tools. Journal of Proteome Research, 2021, 20, 3497-3507.	1.8	27
8	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	5.8	35
9	Pre-diagnostic DNA methylation patterns differ according to mammographic breast density amongst women who subsequently develop breast cancer: a case-only study in the EPIC-Florence cohort. Breast Cancer Research and Treatment, 2021, 189, 435-444.	1.1	1
10	On the Stability of Feature Selection in Multiomics Data. , 2021, , .		1
11	Sex-Biased Expression of Pharmacogenes across Human Tissues. Biomolecules, 2021, 11, 1206.	1.8	5
12	DNA methylation‒based biomarkers of aging were slowed down in a two‒year diet and physical activity intervention trial: the DAMA study. Aging Cell, 2021, 20, e13439.	3.0	64
13	Epigenetic Clocks and Allostatic Load Reveal Potential Sex-Specific Drivers of Biological Aging. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 495-503.	1.7	26
14	Agnostic Cys34‒albumin adductomics and DNA methylation: Implication of N‒acetylcysteine in lung carcinogenesis years before diagnosis. International Journal of Cancer, 2020, 146, 3294-3303.	2.3	12
15	Health inequalities: Embodied evidence across biological layers. Social Science and Medicine, 2020, 246, 112781.	1.8	34
16	The Inhibitory Role of miR-486-5p on CSC Phenotype Has Diagnostic and Prognostic Potential in Colorectal Cancer. Cancers, 2020, 12, 3432.	1.7	14
17	Stochastic Epigenetic Mutations Are Associated with Risk of Breast Cancer, Lung Cancer, and Mature B-cell Neoplasms. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2026-2037.	1.1	18
18	Determinants of accelerated metabolomic and epigenetic aging in a UK cohort. Aging Cell, 2020, 19, e13149.	3.0	95

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19	Age-related DNA methylation changes are sex-specific: a comprehensive assessment. Aging, 2020, 12, 24057-24080.	1.4	55
20	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
21	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	0.7	22
22	DNA methylation, colon cancer and Mediterranean diet: results from the EPIC-Italy cohort. Epigenetics, 2019, 14, 977-988.	1.3	19
23	Maternal educational inequalities in measured body mass index trajectories in three European countries. Paediatric and Perinatal Epidemiology, 2019, 33, 226-237.	0.8	17
24	How does socio-economic position (SEP) get biologically embedded? A comparison of allostatic load and the epigenetic clock(s). Psychoneuroendocrinology, 2019, 104, 64-73.	1.3	65
25	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. Aging, 2019, 11, 2045-2070.	1.4	137
26	Lessons from Knowledge on theÂCorrelates of theÂAge of Onset of Physical Illness. , 2019, , 15-28.		0
27	Micronucleus Assay for Assessing Chromosomal Damage in Medical Workers Exposed to Anaesthetic Gases. Issues in Toxicology, 2019, , 618-635.	0.2	0
28	Allostatic load and subsequent all-cause mortality: which biological markers drive the relationship? Findings from a UK birth cohort. European Journal of Epidemiology, 2018, 33, 441-458.	2.5	95
29	Epigenome-wide association study of adiposity and future risk of obesity-related diseases. International Journal of Obesity, 2018, 42, 2022-2035.	1.6	43
30	FOXP3 , ICOS and ICOSL gene polymorphisms in systemic sclerosis: FOXP3 rs2294020 is associated with disease progression in a female Italian population. Immunobiology, 2018, 223, 112-117.	0.8	8
31	Association of DNA Methylation-Based Biological Age With Health Risk Factors and Overall and Cause-Specific Mortality. American Journal of Epidemiology, 2018, 187, 529-538.	1.6	106
32	Oxidative stress and inflammation mediate the effect of air pollution on cardio€•and cerebrovascular disease: A prospective study in nonsmokers. Environmental and Molecular Mutagenesis, 2018, 59, 234-246.	0.9	88
33	Perturbation of metabolic pathways mediates the association of air pollutants with asthma and cardiovascular diseases. Environment International, 2018, 119, 334-345.	4.8	73
34	Epigenetic supersimilarity of monozygotic twin pairs. Genome Biology, 2018, 19, 2.	3.8	89
35	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	5.5	298
36	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743

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37	Telomerase activity, telomere length and *hTERT* DNA methylation in peripheral blood mononuclear cells from monozygotic twins with discordant smoking habits. Environmental and Molecular Mutagenesis, 2017, 58, 551-559.	0.9	8
38	Social adversity and epigenetic aging: a multi-cohort study on socioeconomic differences in peripheral blood DNA methylation. Scientific Reports, 2017, 7, 16266.	1.6	181
39	An epigenome-wide association study meta-analysis of educational attainment. Molecular Psychiatry, 2017, 22, 1680-1690.	4.1	70
40	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. PLoS ONE, 2016, 11, e0166015.	1.1	14
41	Association between Beta$_1$-Adrenergic Receptor Polymorphism and Risk of ICD Shock in Heart Failure Patients. PACE - Pacing and Clinical Electrophysiology, 2016, 39, 557-564.	0.5	2
42	H2AX phosphorylation level in peripheral blood mononuclear cells as an event–free survival predictor for bladder cancer. Molecular Carcinogenesis, 2016, 55, 1833-1842.	1.3	15
43	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	3.8	251
44	DNA and chromosomal damage in medical workers exposed to anaesthetic gases assessed by the lymphocyte cytokinesis-block micronucleus (CBMN) assay. A critical review. Mutation Research - Reviews in Mutation Research, 2016, 770, 26-34.	2.4	15
45	Complex interplay between neutral and adaptive evolution shaped differential genomic background and disease susceptibility along the Italian peninsula. Scientific Reports, 2016, 6, 32513.	1.6	41
46	The Italian genome reflects the history of Europe and the Mediterranean basin. European Journal of Human Genetics, 2016, 24, 1056-1062.	1.4	40
47	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
48	Abstract 778: DNA repair capacity, chromosomal damage, methylation and gene expression levels in bladder cancer: An integrated analysis. , 2016, , .		1
49	Gene-specific DNA methylation profiles and LINE-1 hypomethylation are associated with myocardial infarction risk. Clinical Epigenetics, 2015, 7, 133.	1.8	61
50	Epigenetic signatures of internal migration in Italy. International Journal of Epidemiology, 2015, 44, 1442-1449.	0.9	17
51	Gene–asbestos interaction in malignant pleural mesothelioma susceptibility. Carcinogenesis, 2015, 36, 1129-1135.	1.3	34
52	Differentially methylated microRNAs in prediagnostic samples of subjects who developed breast cancer in the European Prospective Investigation into Nutrition and Cancer (EPIC-Italy) cohort. Carcinogenesis, 2015, 36, 1144-1153.	1.3	36
53	Early diagnosis of bladder cancer through the detection of urinary tyrosine-phosphorylated proteins. British Journal of Cancer, 2015, 113, 469-475.	2.9	12
54	Characterization of whole-genome autosomal differences of DNA methylation between men and women. Epigenetics and Chromatin, 2015, 8, 43.	1.8	176

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55	Abstract 4615: H2AX phosphorylation assays, gene expression and epigenomic profiles as markers in bladder cancer: an integrated approach. , 2015, , .		1
56	Novel Epigenetic Changes Unveiled by Monozygotic Twins Discordant for Smoking Habits. PLoS ONE, 2015, 10, e0128265.	1.1	49
57	Abstract LB-188: Epigenome-wide study in prediagnostic samples from the European Prospective Investigation into Nutrition and Cancer (EPIC-Italy) cohort: Differentially methylated microRNAs in subjects who developed breast cancer. , 2015, , .		0
58	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
59	Shorter Leukocyte Telomere Length Is Independently Associated with Poor Survival in Patients with Bladder Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2439-2446.	1.1	29
60	B-vitamins intake, DNA-methylation of One Carbon Metabolism and homocysteine pathway genes and myocardial infarction risk: The EPICOR study. Nutrition, Metabolism and Cardiovascular Diseases, 2014, 24, 483-488.	1.1	50
61	Sardinians Genetic Background Explained by Runs of Homozygosity and Genomic Regions under Positive Selection. PLoS ONE, 2014, 9, e91237.	1.1	37
62	Abstract 5367: DNA repair capacity, gene expression and epigenomic profiles in bladder cancer. , 2014, , .		0
63	A genome-wide association study for malignant mesothelioma risk. Lung Cancer, 2013, 82, 1-8.	0.9	45
64	Genetic Variants Associated with Increased Risk of Malignant Pleural Mesothelioma: A Genome-Wide Association Study. PLoS ONE, 2013, 8, e61253.	1.1	71
65	An Overview of the Genetic Structure within the Italian Population from Genome-Wide Data. PLoS ONE, 2012, 7, e43759.	1.1	49