

Jordana T. Bell

List of Publications by Year in descending order

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Version: 2024-02-01

108
papers

18,674
citations

31976

53
h-index

22166

113
g-index

124
all docs

124
docs citations

124
times ranked

28392
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. <i>Nature Communications</i> , 2022, 13, 2408.	12.8	26
2	ACE2 expression in adipose tissue is associated with cardio-metabolic risk factors and cell type composition—implications for COVID-19. <i>International Journal of Obesity</i> , 2022, 46, 1478-1486.	3.4	18
3	Adipose methylome integrative-omic analyses reveal genetic and dietary metabolic health drivers and insulin resistance classifiers. <i>Genome Medicine</i> , 2022, 14, .	8.2	6
4	Epigenome-wide association study of diet quality in the Women’s Health Initiative and TwinsUK cohort. <i>International Journal of Epidemiology</i> , 2021, 50, 675-684.	1.9	19
5	Equivalent DNA methylation variation between monozygotic co-twins and unrelated individuals reveals universal epigenetic inter-individual dissimilarity. <i>Genome Biology</i> , 2021, 22, 18.	8.8	19
6	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
7	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of fT3 With <i>KLF9</i> and <i>DOT1L</i> . <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, e2191-e2202.	3.6	14
8	Novel DNA methylation signatures of tobacco smoking with trans-ethnic effects. <i>Clinical Epigenetics</i> , 2021, 13, 36.	4.1	53
9	Genetic impacts on DNA methylation: research findings and future perspectives. <i>Genome Biology</i> , 2021, 22, 127.	8.8	101
10	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	12.8	35
11	The genomic loci of specific human tRNA genes exhibit ageing-related DNA hypermethylation. <i>Nature Communications</i> , 2021, 12, 2655.	12.8	10
12	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	8.8	90
13	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	12.8	18
14	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. <i>European Journal of Epidemiology</i> , 2021, 36, 1143-1155.	5.7	10
15	Childhood growth and development and DNA methylation age in mid-life. <i>Clinical Epigenetics</i> , 2021, 13, 155.	4.1	5
16	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	12.8	26
17	Estrogen and COVID-19 symptoms: Associations in women from the COVID Symptom Study. <i>PLoS ONE</i> , 2021, 16, e0257051.	2.5	68
18	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218

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19	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. <i>Clinical Epigenetics</i> , 2021, 13, 198.	4.1	7
20	DNA methylation signatures of incident coronary heart disease: findings from epigenome-wide association studies. <i>Clinical Epigenetics</i> , 2021, 13, 186.	4.1	32
21	DNA methylation age and physical and cognitive ageing. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020, 75, 504-511.	3.6	35
22	Red Wine Consumption Associated With Increased Gut Microbiota α -Diversity in 3 Independent Cohorts. <i>Gastroenterology</i> , 2020, 158, 270-272.e2.	1.3	58
23	Faecal microbiota transplant to ERadicate gastrointestinal carriage of Antibiotic Resistant Organisms (FERARO): a prospective, randomised placebo-controlled feasibility trial. <i>BMJ Open</i> , 2020, 10, e038847.	1.9	4
24	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	12.8	43
25	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. <i>Gut Microbes</i> , 2020, 11, 1632-1642.	9.8	65
26	Dysregulated Antibody, Natural Killer Cell and Immune Mediator Profiles in Autoimmune Thyroid Diseases. <i>Cells</i> , 2020, 9, 665.	4.1	18
27	Colonic microbiota is associated with inflammation and host epigenomic alterations in inflammatory bowel disease. <i>Nature Communications</i> , 2020, 11, 1512.	12.8	167
28	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020, 28, 258-272.e6.	11.0	160
29	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	3.1	15
30	Dissecting the role of the gut microbiota and diet on visceral fat mass accumulation. <i>Scientific Reports</i> , 2019, 9, 9758.	3.3	41
31	TwinsUK: The UK Adult Twin Registry Update. <i>Twin Research and Human Genetics</i> , 2019, 22, 523-529.	0.6	116
32	Interplay between the human gut microbiome and host metabolism. <i>Nature Communications</i> , 2019, 10, 4505.	12.8	450
33	Association of dietary folate and vitamin B-12 intake with genome-wide DNA methylation in blood: a large-scale epigenome-wide association analysis in 5841 individuals. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 437-450.	4.7	46
34	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019, 10, 2581.	12.8	62
35	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. <i>Clinical Epigenetics</i> , 2019, 11, 27.	4.1	37
36	Virome Diversity Correlates with Intestinal Microbiome Diversity in Adult Monozygotic Twins. <i>Cell Host and Microbe</i> , 2019, 25, 261-272.e5.	11.0	159

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37	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	8.8	552
38	Heritability of skewed X-inactivation in female twins is tissue-specific and associated with age. <i>Nature Communications</i> , 2019, 10, 5339.	12.8	47
39	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	3.1	198
40	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018, 50, 572-580.	21.4	143
41	CWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	12.8	151
42	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	2.9	30
43	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	7.9	68
44	Obligatory and facilitative allelic variation in the DNA methylome within common disease-associated loci. <i>Nature Communications</i> , 2018, 9, 8.	12.8	107
45	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort. <i>Human Molecular Genetics</i> , 2018, 27, 732-741.	2.9	77
46	A DNA methylation biomarker of alcohol consumption. <i>Molecular Psychiatry</i> , 2018, 23, 422-433.	7.9	280
47	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 637-648.	2.4	33
48	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Gut Microbes</i> , 2018, 9, 61-67.	9.8	41
49	090â€fDNA methylation and its relationship with musculoskeletal health in older adults from the Hertfordshire Cohort Study: findings from an epigenome-wide association study. <i>Rheumatology</i> , 2018, 57, .	1.9	1
50	Multi-OMICS analyses of frailty and chronic widespread musculoskeletal pain suggest involvement of shared neurological pathways. <i>Pain</i> , 2018, 159, 2565-2572.	4.2	38
51	An Investigation Into Physical Frailty as a Link Between the Gut Microbiome and Cognitive Health. <i>Frontiers in Aging Neuroscience</i> , 2018, 10, 398.	3.4	51
52	Genome-wide methylation analysis identifies ELOVL5 as an epigenetic biomarker for the risk of type 2 diabetes mellitus. <i>Scientific Reports</i> , 2018, 8, 14862.	3.3	22
53	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. <i>Clinical Epigenetics</i> , 2018, 10, 126.	4.1	110
54	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018, 9, 3738.	12.8	24

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55	Increased DNA methylation variability in rheumatoid arthritis-discordant monozygotic twins. <i>Genome Medicine</i> , 2018, 10, 64.	8.2	71
56	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018, 50, 790-795.	21.4	482
57	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	11.1	109
58	Investigating the Epigenetic Discrimination of Identical Twins Using Buccal Swabs, Saliva, and Cigarette Butts in the Forensic Setting. <i>Genes</i> , 2018, 9, 252.	2.4	17
59	Gut microbiota associations with common diseases and prescription medications in a population-based cohort. <i>Nature Communications</i> , 2018, 9, 2655.	12.8	411
60	Associations between body size, nutrition and socioeconomic position in early life and the epigenome: A systematic review. <i>PLoS ONE</i> , 2018, 13, e0201672.	2.5	11
61	CWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal effect of schizophrenia liability. <i>Nature Neuroscience</i> , 2018, 21, 1161-1170.	14.8	436
62	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018, 6, e4303.	2.0	48
63	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. <i>Journal of Bone and Mineral Research</i> , 2017, 32, 1644-1650.	2.8	49
64	DNA methylation changes at infertility genes in newborn twins conceived by in vitro fertilisation. <i>Genome Medicine</i> , 2017, 9, 28.	8.2	47
65	Higher Nevus Count Exhibits a Distinct DNA Methylation Signature in Healthy Human Skin: Implications for Melanoma. <i>Journal of Investigative Dermatology</i> , 2017, 137, 910-920.	0.7	26
66	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	5.3	73
67	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	27.8	743
68	Epigenetic discrimination of identical twins from blood under the forensic scenario. <i>Forensic Science International: Genetics</i> , 2017, 31, 67-80.	3.1	35
69	2SNP heritability and effects of genetic variants for neutrophil-to-lymphocyte and platelet-to-lymphocyte ratio. <i>Journal of Human Genetics</i> , 2017, 62, 979-988.	2.3	32
70	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	6.2	154
71	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , 2016, 11, e0166015.	2.5	14
72	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016, 25, 4339-4349.	2.9	11

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73	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016, 3, 572-584.e3.	6.2	261
74	Contribution of Heritability and Epigenetic Factors to Skeletal Muscle Mass Variation in United Kingdom Twins. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 2450-2459.	3.6	42
75	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016, 19, 731-743.	11.0	831
76	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	8.8	183
77	Novel regional age-associated DNA methylation changes within human common disease-associated loci. <i>Genome Biology</i> , 2016, 17, 193.	8.8	29
78	Exploring the molecular basis of age-related disease comorbidities using a multi-omics graphical model. <i>Scientific Reports</i> , 2016, 6, 37646.	3.3	45
79	ABO antigen and secretor statuses are not associated with gut microbiota composition in 1,500 twins. <i>BMC Genomics</i> , 2016, 17, 941.	2.8	61
80	Integrative DNA methylome analysis of pan-cancer biomarkers in cancer discordant monozygotic twin-pairs. <i>Clinical Epigenetics</i> , 2016, 8, 7.	4.1	32
81	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016, 8, 8.	8.2	297
82	Epigenetic associations of type 2 diabetes and BMI in an Arab population. <i>Clinical Epigenetics</i> , 2016, 8, 13.	4.1	110
83	Proton pump inhibitors alter the composition of the gut microbiota. <i>Gut</i> , 2016, 65, 749-756.	12.1	682
84	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. <i>PLoS ONE</i> , 2016, 11, e0153672.	2.5	69
85	Metabolomics profiling reveals novel markers for leukocyte telomere length. <i>Aging</i> , 2016, 8, 77-86.	3.1	33
86	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	3.1	786
87	A heritability-based comparison of methods used to cluster 16S rRNA gene sequences into operational taxonomic units. <i>PeerJ</i> , 2016, 4, e2341.	2.0	41
88	DNA Methylation Changes in the <i>IGF1R</i> Gene in Birth Weight Discordant Adult Monozygotic Twins. <i>Twin Research and Human Genetics</i> , 2015, 18, 635-646.	0.6	23
89	Population whole-genome bisulfite sequencing across two tissues highlights the environment as the principal source of human methylome variation. <i>Genome Biology</i> , 2015, 16, 290.	8.8	90
90	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015, 10, e0134311.	2.5	134

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91	coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns. BMC Bioinformatics, 2015, 16, 131.	2.6	104
92	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
93	Power and sample size estimation for epigenome-wide association scans to detect differential DNA methylation. International Journal of Epidemiology, 2015, 44, 1429-1441.	1.9	178
94	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. Genome Biology, 2015, 16, 14.	8.8	165
95	Host genetic variation impacts microbiome composition across human body sites. Genome Biology, 2015, 16, 191.	8.8	612
96	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. Epigenetics, 2014, 9, 1382-1396.	2.7	285
97	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. Nature Communications, 2014, 5, 5719.	12.8	100
98	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
99	Human Genetics Shape the Gut Microbiome. Cell, 2014, 159, 789-799.	28.9	2,523
100	Epigenetics of discordant monozygotic twins: implications for disease. Genome Medicine, 2014, 6, 60.	8.2	157
101	Obesity accelerates epigenetic aging of human liver. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15538-15543.	7.1	620
102	Epigenome-Wide DNA Methylation in Hearing Ability: New Mechanisms for an Old Problem. PLoS ONE, 2014, 9, e105729.	2.5	23
103	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. American Journal of Human Genetics, 2013, 93, 876-890.	6.2	330
104	The value of twins in epigenetic epidemiology. International Journal of Epidemiology, 2012, 41, 140-150.	1.9	88
105	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. PLoS Genetics, 2012, 8, e1002629.	3.5	620
106	Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature Genetics, 2012, 44, 1084-1089.	21.4	701
107	Genome-Wide Association Scan Allowing for Epistasis in Type 2 Diabetes. Annals of Human Genetics, 2011, 75, 10-19.	0.8	34
108	A twin approach to unraveling epigenetics. Trends in Genetics, 2011, 27, 116-125.	6.7	350