

# Jordana T. Bell

## List of Publications by Year in descending order

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Version: 2024-02-01

108  
papers

18,674  
citations

31902

53  
h-index

22102

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.	5.8	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.	1.6	18
3	Adipose methylome integrative-omic analyses reveal genetic and dietary metabolic health drivers and insulin resistance classifiers. <i>Genome Medicine</i> , 2022, 14, .	3.6	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.	0.9	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.	3.8	19
6	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	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.	1.8	14
8	Novel DNA methylation signatures of tobacco smoking with trans-ethnic effects. <i>Clinical Epigenetics</i> , 2021, 13, 36.	1.8	53
9	Genetic impacts on DNA methylation: research findings and future perspectives. <i>Genome Biology</i> , 2021, 22, 127.	3.8	101
10	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	5.8	35
11	The genomic loci of specific human tRNA genes exhibit ageing-related DNA hypermethylation. <i>Nature Communications</i> , 2021, 12, 2655.	5.8	10
12	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
13	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	5.8	18
14	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. <i>European Journal of Epidemiology</i> , 2021, 36, 1143-1155.	2.5	10
15	Childhood growth and development and DNA methylation age in mid-life. <i>Clinical Epigenetics</i> , 2021, 13, 155.	1.8	5
16	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	5.8	26
17	Estrogen and COVID-19 symptoms: Associations in women from the COVID Symptom Study. <i>PLoS ONE</i> , 2021, 16, e0257051.	1.1	68
18	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	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.	1.8	7
20	DNA methylation signatures of incident coronary heart disease: findings from epigenome-wide association studies. <i>Clinical Epigenetics</i> , 2021, 13, 186.	1.8	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.	1.7	35
22	Red Wine Consumption Associated With Increased Gut Microbiota $\alpha$ -Diversity in 3 Independent Cohorts. <i>Gastroenterology</i> , 2020, 158, 270-272.e2.	0.6	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.	0.8	4
24	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	5.8	43
25	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. <i>Gut Microbes</i> , 2020, 11, 1632-1642.	4.3	65
26	Dysregulated Antibody, Natural Killer Cell and Immune Mediator Profiles in Autoimmune Thyroid Diseases. <i>Cells</i> , 2020, 9, 665.	1.8	18
27	Colonic microbiota is associated with inflammation and host epigenomic alterations in inflammatory bowel disease. <i>Nature Communications</i> , 2020, 11, 1512.	5.8	167
28	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020, 28, 258-272.e6.	5.1	160
29	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020, 12, 14092-14124.	1.4	15
30	Dissecting the role of the gut microbiota and diet on visceral fat mass accumulation. <i>Scientific Reports</i> , 2019, 9, 9758.	1.6	41
31	TwinsUK: The UK Adult Twin Registry Update. <i>Twin Research and Human Genetics</i> , 2019, 22, 523-529.	0.3	116
32	Interplay between the human gut microbiome and host metabolism. <i>Nature Communications</i> , 2019, 10, 4505.	5.8	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.	2.2	46
34	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019, 10, 2581.	5.8	62
35	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. <i>Clinical Epigenetics</i> , 2019, 11, 27.	1.8	37
36	Virome Diversity Correlates with Intestinal Microbiome Diversity in Adult Monozygotic Twins. <i>Cell Host and Microbe</i> , 2019, 25, 261-272.e5.	5.1	159

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37	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
38	Heritability of skewed X-inactivation in female twins is tissue-specific and associated with age. <i>Nature Communications</i> , 2019, 10, 5339.	5.8	47
39	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	1.4	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.	9.4	143
41	CWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	5.8	151
42	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	1.4	30
43	Meta-analysis of epigenome-wide association studies of cognitive abilities. <i>Molecular Psychiatry</i> , 2018, 23, 2133-2144.	4.1	68
44	Obligatory and facilitative allelic variation in the DNA methylome within common disease-associated loci. <i>Nature Communications</i> , 2018, 9, 8.	5.8	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.	1.4	77
46	A DNA methylation biomarker of alcohol consumption. <i>Molecular Psychiatry</i> , 2018, 23, 422-433.	4.1	280
47	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 637-648.	1.1	33
48	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Gut Microbes</i> , 2018, 9, 61-67.	4.3	41
49	090â€¦DNA 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, .	0.9	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.	2.0	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.	1.7	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.	1.6	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.	1.8	110
54	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. <i>Nature Communications</i> , 2018, 9, 3738.	5.8	24

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55	Increased DNA methylation variability in rheumatoid arthritis-discordant monozygotic twins. <i>Genome Medicine</i> , 2018, 10, 64.	3.6	71
56	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018, 50, 790-795.	9.4	482
57	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	4.9	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.	1.0	17
59	Gut microbiota associations with common diseases and prescription medications in a population-based cohort. <i>Nature Communications</i> , 2018, 9, 2655.	5.8	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.	1.1	11
61	GWAS 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.	7.1	436
62	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018, 6, e4303.	0.9	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.	3.1	49
64	DNA methylation changes at infertility genes in newborn twins conceived by in vitro fertilisation. <i>Genome Medicine</i> , 2017, 9, 28.	3.6	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.	0.3	26
66	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	2.8	73
67	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	13.7	743
68	Epigenetic discrimination of identical twins from blood under the forensic scenario. <i>Forensic Science International: Genetics</i> , 2017, 31, 67-80.	1.6	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.	1.1	32
70	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
71	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , 2016, 11, e0166015.	1.1	14
72	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016, 25, 4339-4349.	1.4	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.	2.9	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.	1.8	42
75	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016, 19, 731-743.	5.1	831
76	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	3.8	183
77	Novel regional age-associated DNA methylation changes within human common disease-associated loci. <i>Genome Biology</i> , 2016, 17, 193.	3.8	29
78	Exploring the molecular basis of age-related disease comorbidities using a multi-omics graphical model. <i>Scientific Reports</i> , 2016, 6, 37646.	1.6	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.	1.2	61
80	Integrative DNA methylome analysis of pan-cancer biomarkers in cancer discordant monozygotic twin-pairs. <i>Clinical Epigenetics</i> , 2016, 8, 7.	1.8	32
81	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016, 8, 8.	3.6	297
82	Epigenetic associations of type 2 diabetes and BMI in an Arab population. <i>Clinical Epigenetics</i> , 2016, 8, 13.	1.8	110
83	Proton pump inhibitors alter the composition of the gut microbiota. <i>Gut</i> , 2016, 65, 749-756.	6.1	682
84	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. <i>PLoS ONE</i> , 2016, 11, e0153672.	1.1	69
85	Metabolomics profiling reveals novel markers for leukocyte telomere length. <i>Aging</i> , 2016, 8, 77-86.	1.4	33
86	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	1.4	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.	0.9	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.	0.3	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.	3.8	90
90	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015, 10, e0134311.	1.1	134

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91	coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns. <i>BMC Bioinformatics</i> , 2015, 16, 131.	1.2	104
92	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015, 6, 7208.	5.8	178
93	Power and sample size estimation for epigenome-wide association scans to detect differential DNA methylation. <i>International Journal of Epidemiology</i> , 2015, 44, 1429-1441.	0.9	178
94	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. <i>Genome Biology</i> , 2015, 16, 14.	3.8	165
95	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015, 16, 191.	3.8	612
96	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. <i>Epigenetics</i> , 2014, 9, 1382-1396.	1.3	285
97	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014, 5, 5719.	5.8	100
98	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	1.5	80
99	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	13.5	2,523
100	Epigenetics of discordant monozygotic twins: implications for disease. <i>Genome Medicine</i> , 2014, 6, 60.	3.6	157
101	Obesity accelerates epigenetic aging of human liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15538-15543.	3.3	620
102	Epigenome-Wide DNA Methylation in Hearing Ability: New Mechanisms for an Old Problem. <i>PLoS ONE</i> , 2014, 9, e105729.	1.1	23
103	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. <i>American Journal of Human Genetics</i> , 2013, 93, 876-890.	2.6	330
104	The value of twins in epigenetic epidemiology. <i>International Journal of Epidemiology</i> , 2012, 41, 140-150.	0.9	88
105	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. <i>PLoS Genetics</i> , 2012, 8, e1002629.	1.5	620
106	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	9.4	701
107	Genome-Wide Association Scan Allowing for Epistasis in Type 2 Diabetes. <i>Annals of Human Genetics</i> , 2011, 75, 10-19.	0.3	34
108	A twin approach to unraveling epigenetics. <i>Trends in Genetics</i> , 2011, 27, 116-125.	2.9	350