

# Jordana T Bell

## List of Publications by Year in descending order

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Version: 2024-02-01

106  
papers

19,425  
citations

24978

57  
h-index

30010

103  
g-index

122  
all docs

122  
docs citations

122  
times ranked

29739  
citing authors

#	ARTICLE	IF	CITATIONS
1	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	13.5	2,523
2	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016, 19, 731-743.	5.1	831
3	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	1.4	786
4	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011, 12, R10.	3.8	754
5	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	13.7	743
6	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	9.4	701
7	Proton pump inhibitors alter the composition of the gut microbiota. <i>Gut</i> , 2016, 65, 749-756.	6.1	682
8	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	9.4	676
9	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
10	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
11	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015, 16, 191.	3.8	612
12	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
13	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018, 50, 790-795.	9.4	482
14	Interplay between the human gut microbiome and host metabolism. <i>Nature Communications</i> , 2019, 10, 4505.	5.8	450
15	Gut microbiota associations with common diseases and prescription medications in a population-based cohort. <i>Nature Communications</i> , 2018, 9, 2655.	5.8	411
16	Biomarkers for Type 2 Diabetes and Impaired Fasting Glucose Using a Nontargeted Metabolomics Approach. <i>Diabetes</i> , 2013, 62, 4270-4276.	0.3	356
17	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. <i>ELife</i> , 2013, 2, e01102.	2.8	355
18	A twin approach to unraveling epigenetics. <i>Trends in Genetics</i> , 2011, 27, 116-125.	2.9	350

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19	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
20	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016, 8, 8.	3.6	297
21	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
22	Metabolomic markers reveal novel pathways of ageing and early development in human populations. <i>International Journal of Epidemiology</i> , 2013, 42, 1111-1119.	0.9	241
23	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
24	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	1.4	198
25	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	3.8	183
26	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
27	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
28	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. <i>Genome Biology</i> , 2015, 16, 14.	3.8	165
29	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020, 28, 258-272.e6.	5.1	160
30	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
31	Epigenetics of discordant monozygotic twins: implications for disease. <i>Genome Medicine</i> , 2014, 6, 60.	3.6	157
32	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
33	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	5.8	151
34	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
35	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013, 34, 102-108.	1.3	135
36	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015, 10, e0134311.	1.1	134

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37	Novel genetic variants associated with lumbar disc degeneration in northern Europeans: a meta-analysis of 4600 subjects. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 1141-1148.	0.5	118
38	TwinsUK: The UK Adult Twin Registry Update. <i>Twin Research and Human Genetics</i> , 2019, 22, 523-529.	0.3	116
39	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
40	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	4.9	109
41	Glycosylation of Immunoglobulin G: Role of Genetic and Epigenetic Influences. <i>PLoS ONE</i> , 2013, 8, e82558.	1.1	105
42	coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns. <i>BMC Bioinformatics</i> , 2015, 16, 131.	1.2	104
43	Genetic impacts on DNA methylation: research findings and future perspectives. <i>Genome Biology</i> , 2021, 22, 127.	3.8	101
44	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014, 5, 5719.	5.8	100
45	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
46	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
47	The value of twins in epigenetic epidemiology. <i>International Journal of Epidemiology</i> , 2012, 41, 140-150.	0.9	88
48	Eight Common Genetic Variants Associated with Serum DHEAS Levels Suggest a Key Role in Ageing Mechanisms. <i>PLoS Genetics</i> , 2011, 7, e1002025.	1.5	87
49	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014, 15, R56.	13.9	87
50	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. <i>PLoS ONE</i> , 2013, 8, e55923.	1.1	83
51	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
52	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015, 6, 5681.	5.8	75
53	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	2.8	73
54	DNA methylation studies using twins: what are they telling us?. <i>Genome Biology</i> , 2012, 13, 172.	13.9	72

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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	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. <i>PLoS ONE</i> , 2016, 11, e0153672.	1.1	69
57	Estrogen and COVID-19 symptoms: Associations in women from the COVID Symptom Study. <i>PLoS ONE</i> , 2021, 16, e0257051.	1.1	68
58	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. <i>Gut Microbes</i> , 2020, 11, 1632-1642.	4.3	65
59	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019, 10, 2581.	5.8	62
60	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
61	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	9.4	60
62	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
63	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
64	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
65	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018, 6, e4303.	0.9	48
66	DNA methylation changes at infertility genes in newborn twins conceived by in vitro fertilisation. <i>Genome Medicine</i> , 2017, 9, 28.	3.6	47
67	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
68	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
69	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	5.8	43
70	Using epigenome-wide association scans of DNA methylation in age-related complex human traits. <i>Epigenomics</i> , 2012, 4, 511-526.	1.0	42
71	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
72	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Gut Microbes</i> , 2018, 9, 61-67.	4.3	41

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73	Dissecting the role of the gut microbiota and diet on visceral fat mass accumulation. <i>Scientific Reports</i> , 2019, 9, 9758.	1.6	41
74	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
75	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
76	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. <i>Clinical Epigenetics</i> , 2019, 11, 27.	1.8	37
77	Epigenetic discrimination of identical twins from blood under the forensic scenario. <i>Forensic Science International: Genetics</i> , 2017, 31, 67-80.	1.6	35
78	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
79	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	5.8	35
80	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 637-648.	1.1	33
81	Integrative DNA methylome analysis of pan-cancer biomarkers in cancer discordant monozygotic twin-pairs. <i>Clinical Epigenetics</i> , 2016, 8, 7.	1.8	32
82	DNA methylation signatures of incident coronary heart disease: findings from epigenome-wide association studies. <i>Clinical Epigenetics</i> , 2021, 13, 186.	1.8	32
83	Genetic and environmental impacts on DNA methylation levels in twins. <i>Epigenomics</i> , 2016, 8, 105-117.	1.0	31
84	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	1.4	30
85	Correction: DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011, 12, 405.	13.9	27
86	Genome-wide methylation analysis of a large population sample shows neurological pathways involvement in chronic widespread musculoskeletal pain. <i>Pain</i> , 2017, 158, 1053-1062.	2.0	27
87	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
88	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	5.8	26
89	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
90	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

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91	Epigenome-Wide DNA Methylation in Hearing Ability: New Mechanisms for an Old Problem. PLoS ONE, 2014, 9, e105729.	1.1	23
92	Epigenome-wide association study of diet quality in the Women's Health Initiative and TwinsUK cohort. International Journal of Epidemiology, 2021, 50, 675-684.	0.9	19
93	Equivalent DNA methylation variation between monozygotic co-twins and unrelated individuals reveals universal epigenetic inter-individual dissimilarity. Genome Biology, 2021, 22, 18.	3.8	19
94	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. Nature Communications, 2021, 12, 3987.	5.8	18
95	ACE2 expression in adipose tissue is associated with cardio-metabolic risk factors and cell type composition—implications for COVID-19. International Journal of Obesity, 2022, 46, 1478-1486.	1.6	18
96	Investigating the Epigenetic Discrimination of Identical Twins Using Buccal Swabs, Saliva, and Cigarette Butts in the Forensic Setting. Genes, 2018, 9, 252.	1.0	17
97	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. Aging, 2020, 12, 14092-14124.	1.4	15
98	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. PLoS ONE, 2016, 11, e0166015.	1.1	14
99	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of fT3 With <i>KLF9</i> and <i>DOT1L</i> . Journal of Clinical Endocrinology and Metabolism, 2021, 106, e2191-e2202.	1.8	14
100	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. Human Molecular Genetics, 2016, 25, 4339-4349.	1.4	11
101	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. European Journal of Epidemiology, 2021, 36, 1143-1155.	2.5	10
102	Adipose methylome integrative-omic analyses reveal genetic and dietary metabolic health drivers and insulin resistance classifiers. Genome Medicine, 2022, 14, .	3.6	6
103	Childhood growth and development and DNA methylation age in mid-life. Clinical Epigenetics, 2021, 13, 155.	1.8	5
104	Twin Studies and Epigenetics. , 2015, , 683-702.		3
105	Twin and family epigenetic studies of type 2 diabetes. , 2021, , 105-118.		0
106	Analytical Considerations for Epigenome-Wide Association Scans of Complex Traits. , 2013, , 319-338.		0