

Jordana T Bell

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

114
papers

12,335
citations

50
h-index

111
g-index

122
ext. papers

16,420
ext. citations

12.2
avg, IF

6.1
L-index

#	Paper	IF	Citations
114	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function.. <i>Nature Genetics</i> , 2022 ,	36.3	6
113	The Utility of Twins for Epigenetic Analysis 2022 , 213-233		0
112	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.. <i>Nature Communications</i> , 2022 , 13, 2408	17.4	1
111	DNA methylation signatures of incident coronary heart disease: findings from epigenome-wide association studies. <i>Clinical Epigenetics</i> , 2021 , 13, 186	7.7	2
110	Genetic impacts on DNA methylation: research findings and future perspectives. <i>Genome Biology</i> , 2021 , 22, 127	18.3	16
109	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021 , 12, 2830	17.4	9
108	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021 , 22, 194	18.3	14
107	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021 , 12, 3987	17.4	3
106	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. <i>European Journal of Epidemiology</i> , 2021 , 36, 1143-1155	12.1	4
105	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	7.8	8
104	Twin and family epigenetic studies of type 2 diabetes 2021 , 105-118		
103	Equivalent DNA methylation variation between monozygotic co-twins and unrelated individuals reveals universal epigenetic inter-individual dissimilarity. <i>Genome Biology</i> , 2021 , 22, 18	18.3	5
102	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
101	Epigenome-Wide Association Study of Thyroid Function Traits Identifies Novel Associations of FT3 With KLF9 and DOT1L. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, e2191-e2202	5.6	2
100	Childhood growth and development and DNA methylation age in mid-life. <i>Clinical Epigenetics</i> , 2021 , 13, 155	7.7	1
99	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021 , 12, 5618	17.4	6
98	Estrogen and COVID-19 symptoms: Associations in women from the COVID Symptom Study. <i>PLoS ONE</i> , 2021 , 16, e0257051	3.7	14

97	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
96	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020 , 11, 2865	17.4	18
95	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. <i>Gut Microbes</i> , 2020 , 11, 1632-1642	8.8	22
94	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020 , 28, 258-272.e6	23.4	68
93	DNA Methylation Age and Physical and Cognitive Aging. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020 , 75, 504-511	6.4	8
92	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. <i>Aging</i> , 2020 , 12, 14092-14124	5.6	6
91	ACE2 expression in adipose tissue is associated with COVID-19 cardio-metabolic risk factors and cell type composition 2020 ,		4
90	Red Wine Consumption Associated With Increased Gut Microbiota Diversity in 3 Independent Cohorts. <i>Gastroenterology</i> , 2020 , 158, 270-272.e2	13.3	31
89	Interplay between the human gut microbiome and host metabolism. <i>Nature Communications</i> , 2019 , 10, 4505	17.4	197
88	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019 , 10, 2581	17.4	31
87	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. <i>Clinical Epigenetics</i> , 2019 , 11, 27	7.7	17
86	Dissecting the role of the gut microbiota and diet on visceral fat mass accumulation. <i>Scientific Reports</i> , 2019 , 9, 9758	4.9	22
85	TwinsUK: The UK Adult Twin Registry Update. <i>Twin Research and Human Genetics</i> , 2019 , 22, 523-529	2.2	51
84	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019 , 11, 5895-5923	5.6	69
83	Virome Diversity Correlates with Intestinal Microbiome Diversity in Adult Monozygotic Twins. <i>Cell Host and Microbe</i> , 2019 , 25, 261-272.e5	23.4	89
82	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019 , 20, 249	18.3	248
81	Heritability of skewed X-inactivation in female twins is tissue-specific and associated with age. <i>Nature Communications</i> , 2019 , 10, 5339	17.4	19
80	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	36.3	82

79	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018 , 9, 387	17.4	106
78	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018 , 27, 1106-1121	5.6	21
77	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	5.6	43
76	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018 , 1862, 637-648	4	25
75	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018 , 6, 101	16.6	53
74	Investigating the Epigenetic Discrimination of Identical Twins Using Buccal Swabs, Saliva, and Cigarette Butts in the Forensic Setting. <i>Genes</i> , 2018 , 9,	4.2	11
73	Gut microbiota associations with common diseases and prescription medications in a population-based cohort. <i>Nature Communications</i> , 2018 , 9, 2655	17.4	225
72	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018 , 6, e4303	3.1	28
71	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Gut Microbes</i> , 2018 , 9, 61-67	8.8	27
70	Multi-OMICS analyses of frailty and chronic widespread musculoskeletal pain suggest involvement of shared neurological pathways. <i>Pain</i> , 2018 , 159, 2565-2572	8	24
69	An Investigation Into Physical Frailty as a Link Between the Gut Microbiome and Cognitive Health. <i>Frontiers in Aging Neuroscience</i> , 2018 , 10, 398	5.3	27
68	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. <i>Clinical Epigenetics</i> , 2018 , 10, 126	7.7	56
67	Increased DNA methylation variability in rheumatoid arthritis-discordant monozygotic twins. <i>Genome Medicine</i> , 2018 , 10, 64	14.4	48
66	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018 , 50, 790-795	6.3	262
65	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	6.3	33
64	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	8	21
63	DNA methylation changes at infertility genes in newborn twins conceived by in vitro fertilisation. <i>Genome Medicine</i> , 2017 , 9, 28	14.4	28
62	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	4.3	16

61	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017 , 81, 383-394	4	51
60	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017 , 541, 81-86	50.4	511
59	Epigenetic discrimination of identical twins from blood under the forensic scenario. <i>Forensic Science International: Genetics</i> , 2017 , 31, 67-80	4.3	21
58	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83
57	Exploring the molecular basis of age-related disease comorbidities using a multi-omics graphical model. <i>Scientific Reports</i> , 2016 , 6, 37646	4.9	33
56	ABO antigen and secretor statuses are not associated with gut microbiota composition in 1,500 twins. <i>BMC Genomics</i> , 2016 , 17, 941	4.5	49
55	Integrative DNA methylome analysis of pan-cancer biomarkers in cancer discordant monozygotic twin-pairs. <i>Clinical Epigenetics</i> , 2016 , 8, 7	7.7	21
54	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016 , 8, 8	14.4	200
53	Proton pump inhibitors alter the composition of the gut microbiota. <i>Gut</i> , 2016 , 65, 749-56	19.2	454
52	Genetic and environmental impacts on DNA methylation levels in twins. <i>Epigenomics</i> , 2016 , 8, 105-17	4.4	17
51	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. <i>PLoS ONE</i> , 2016 , 11, e0153672	3.7	48
50	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Ageing</i> , 2016 , 8, 1844-1865	5.6	531
49	A heritability-based comparison of methods used to cluster 16S rRNA gene sequences into operational taxonomic units. <i>PeerJ</i> , 2016 , 4, e2341	3.1	23
48	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , 2016 , 11, e0166015	3.7	10
47	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016 , 25, 4339-4349	5.6	7
46	Shotgun Metagenomics of 250 Adult Twins Reveals Genetic and Environmental Impacts on the Gut Microbiome. <i>Cell Systems</i> , 2016 , 3, 572-584.e3	10.6	172
45	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, 2450-9	5.6	31
44	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016 , 19, 731-43	23.4	547

43	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016 , 17, 189	18.3	124
42	Twin Studies and Epigenetics 2015 , 683-702		1
41	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	7.8	121
40	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. <i>Genome Biology</i> , 2015 , 16, 14	18.3	108
39	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015 , 16, 191	18.3	428
38	DNA Methylation Changes in the IGF1R Gene in Birth Weight Discordant Adult Monozygotic Twins. <i>Twin Research and Human Genetics</i> , 2015 , 18, 635-46	2.2	20
37	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	18.3	70
36	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015 , 10, e0134311	3.7	85
35	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015 , 6, 5681	17.4	56
34	coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns. <i>BMC Bioinformatics</i> , 2015 , 16, 131	3.6	79
33	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015 , 6, 7208	17.4	126
32	Human genetics shape the gut microbiome. <i>Cell</i> , 2014 , 159, 789-99	56.2	1750
31	Epigenetics of discordant monozygotic twins: implications for disease. <i>Genome Medicine</i> , 2014 , 6, 60	14.4	116
30	Obesity accelerates epigenetic aging of human liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15538-43	11.5	456
29	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014 , 5, 5719	17.4	85
28	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014 , 15, R56	18.3	73
27	Epigenome-wide DNA methylation in hearing ability: new mechanisms for an old problem. <i>PLoS ONE</i> , 2014 , 9, e105729	3.7	15
26	Biomarkers for type 2 diabetes and impaired fasting glucose using a nontargeted metabolomics approach. <i>Diabetes</i> , 2013 , 62, 4270-6	0.9	268

25	Metabolomic markers reveal novel pathways of ageing and early development in human populations. <i>International Journal of Epidemiology</i> , 2013 , 42, 1111-9	7.8	166
24	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, 876-90	11	269
23	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	3.7	71
22	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013 , 34, 102-8	4.6	117
21	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, 1141-8	2.4	84
20	Glycosylation of immunoglobulin g: role of genetic and epigenetic influences. <i>PLoS ONE</i> , 2013 , 8, e82558	3.7	70
19	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. <i>ELife</i> , 2013 , 2, e01102	8.9	247
18	Analytical Considerations for Epigenome-Wide Association Scans of Complex Traits 2013 , 319-338		
17	The value of twins in epigenetic epidemiology. <i>International Journal of Epidemiology</i> , 2012 , 41, 140-50	7.8	73
16	DNA methylation studies using twins: what are they telling us?. <i>Genome Biology</i> , 2012 , 13, 172	18.3	56
15	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	6	501
14	Using epigenome-wide association scans of DNA methylation in age-related complex human traits. <i>Epigenomics</i> , 2012 , 4, 511-26	4.4	39
13	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012 , 44, 1084-93	16.3	572
12	Correction: DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines 2011 , 12, 405		22
11	A twin approach to unraveling epigenetics. <i>Trends in Genetics</i> , 2011 , 27, 116-25	8.5	268
10	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011 , 12, R10	18.3	651
9	Eight common genetic variants associated with serum DHEAS levels suggest a key role in ageing mechanisms. <i>PLoS Genetics</i> , 2011 , 7, e1002025	6	69
8	Arrhythmic gut microbiome signatures for risk profiling of Type-2 Diabetes		1

7	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort	4
6	Large-scale association analyses identify host factors influencing human gut microbiome composition	9
5	Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing	8
4	Genomic and phenomic insights from an atlas of genetic effects on DNA methylation	7
3	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health	2
2	Interplay between the human gut microbiome and host metabolism	3
1	GWAS of epigenetic ageing rates in blood reveals a critical role for TERT	1