

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	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	9.4	60
2	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
3	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
4	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
5	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
6	Twin and family epigenetic studies of type 2 diabetes. , 2021, , 105-118.		0
7	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
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 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
10	Genetic impacts on DNA methylation: research findings and future perspectives. <i>Genome Biology</i> , 2021, 22, 127.	3.8	101
11	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. <i>Nature Communications</i> , 2021, 12, 2830.	5.8	35
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	DNA methylation signatures of incident coronary heart disease: findings from epigenome-wide association studies. <i>Clinical Epigenetics</i> , 2021, 13, 186.	1.8	32
20	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
21	Red Wine Consumption Associated With Increased Gut Microbiota α -Diversity in 3 Independent Cohorts. <i>Gastroenterology</i> , 2020, 158, 270-272.e2.	0.6	58
22	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	5.8	43
23	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. <i>Gut Microbes</i> , 2020, 11, 1632-1642.	4.3	65
24	Arrhythmic Gut Microbiome Signatures Predict Risk of Type 2 Diabetes. <i>Cell Host and Microbe</i> , 2020, 28, 258-272.e6.	5.1	160
25	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
26	Dissecting the role of the gut microbiota and diet on visceral fat mass accumulation. <i>Scientific Reports</i> , 2019, 9, 9758.	1.6	41
27	TwinsUK: The UK Adult Twin Registry Update. <i>Twin Research and Human Genetics</i> , 2019, 22, 523-529.	0.3	116
28	Interplay between the human gut microbiome and host metabolism. <i>Nature Communications</i> , 2019, 10, 4505.	5.8	450
29	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. <i>Nature Communications</i> , 2019, 10, 2581.	5.8	62
30	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. <i>Clinical Epigenetics</i> , 2019, 11, 27.	1.8	37
31	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
32	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
33	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
34	DNA methylation-based estimator of telomere length. <i>Aging</i> , 2019, 11, 5895-5923.	1.4	198
35	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
36	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018, 9, 387.	5.8	151

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37	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	1.4	30
38	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
39	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 637-648.	1.1	33
40	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Gut Microbes</i> , 2018, 9, 61-67.	4.3	41
41	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
42	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
43	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
44	Increased DNA methylation variability in rheumatoid arthritis-discordant monozygotic twins. <i>Genome Medicine</i> , 2018, 10, 64.	3.6	71
45	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018, 50, 790-795.	9.4	482
46	Meta-analysis of human genome-microbiome association studies: the MiBioGen consortium initiative. <i>Microbiome</i> , 2018, 6, 101.	4.9	109
47	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
48	Gut microbiota associations with common diseases and prescription medications in a population-based cohort. <i>Nature Communications</i> , 2018, 9, 2655.	5.8	411
49	Detection of stable community structures within gut microbiota co-occurrence networks from different human populations. <i>PeerJ</i> , 2018, 6, e4303.	0.9	48
50	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
51	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
52	DNA methylation changes at infertility genes in newborn twins conceived by in vitro fertilisation. <i>Genome Medicine</i> , 2017, 9, 28.	3.6	47
53	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
54	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017, 81, 383-394.	2.8	73

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55	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	13.7	743
56	Epigenetic discrimination of identical twins from blood under the forensic scenario. <i>Forensic Science International: Genetics</i> , 2017, 31, 67-80.	1.6	35
57	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
58	Epigenetic Signatures at AQP3 and SOCS3 Engage in Low-Grade Inflammation across Different Tissues. <i>PLoS ONE</i> , 2016, 11, e0166015.	1.1	14
59	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. <i>Human Molecular Genetics</i> , 2016, 25, 4339-4349.	1.4	11
60	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
61	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
62	Genetic Determinants of the Gut Microbiome in UK Twins. <i>Cell Host and Microbe</i> , 2016, 19, 731-743.	5.1	831
63	Heritable components of the human fecal microbiome are associated with visceral fat. <i>Genome Biology</i> , 2016, 17, 189.	3.8	183
64	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
65	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
66	Integrative DNA methylome analysis of pan-cancer biomarkers in cancer discordant monozygotic twin-pairs. <i>Clinical Epigenetics</i> , 2016, 8, 7.	1.8	32
67	Signatures of early frailty in the gut microbiota. <i>Genome Medicine</i> , 2016, 8, 8.	3.6	297
68	Proton pump inhibitors alter the composition of the gut microbiota. <i>Gut</i> , 2016, 65, 749-756.	6.1	682
69	Genetic and environmental impacts on DNA methylation levels in twins. <i>Epigenomics</i> , 2016, 8, 105-117.	1.0	31
70	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. <i>PLoS ONE</i> , 2016, 11, e0153672.	1.1	69
71	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	1.4	786
72	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

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73	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
74	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
75	Gut-Microbiota-Metabolite Axis in Early Renal Function Decline. <i>PLoS ONE</i> , 2015, 10, e0134311.	1.1	134
76	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015, 6, 5681.	5.8	75
77	coMET: visualisation of regional epigenome-wide association scan results and DNA co-methylation patterns. <i>BMC Bioinformatics</i> , 2015, 16, 131.	1.2	104
78	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
79	Twin Studies and Epigenetics. , 2015, , 683-702.		3
80	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
81	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements. <i>Genome Biology</i> , 2015, 16, 14.	3.8	165
82	Host genetic variation impacts microbiome composition across human body sites. <i>Genome Biology</i> , 2015, 16, 191.	3.8	612
83	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014, 5, 5719.	5.8	100
84	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014, 15, R56.	13.9	87
85	Human Genetics Shape the Gut Microbiome. <i>Cell</i> , 2014, 159, 789-799.	13.5	2,523
86	Epigenetics of discordant monozygotic twins: implications for disease. <i>Genome Medicine</i> , 2014, 6, 60.	3.6	157
87	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
88	Epigenome-Wide DNA Methylation in Hearing Ability: New Mechanisms for an Old Problem. <i>PLoS ONE</i> , 2014, 9, e105729.	1.1	23
89	Biomarkers for Type 2 Diabetes and Impaired Fasting Glucose Using a Nontargeted Metabolomics Approach. <i>Diabetes</i> , 2013, 62, 4270-4276.	0.3	356
90	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

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91	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
92	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
93	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
94	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
95	Glycosylation of Immunoglobulin G: Role of Genetic and Epigenetic Influences. <i>PLoS ONE</i> , 2013, 8, e82558.	1.1	105
96	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
97	Analytical Considerations for Epigenome-Wide Association Scans of Complex Traits. , 2013, , 319-338.		0
98	The value of twins in epigenetic epidemiology. <i>International Journal of Epidemiology</i> , 2012, 41, 140-150.	0.9	88
99	DNA methylation studies using twins: what are they telling us?. <i>Genome Biology</i> , 2012, 13, 172.	13.9	72
100	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
101	Using epigenome-wide association scans of DNA methylation in age-related complex human traits. <i>Epigenomics</i> , 2012, 4, 511-526.	1.0	42
102	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	9.4	701
103	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011, 12, R10.	3.8	754
104	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
105	A twin approach to unraveling epigenetics. <i>Trends in Genetics</i> , 2011, 27, 116-125.	2.9	350
106	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