

# Charles E Breeze

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4930722/publications.pdf>

Version: 2024-02-01

26  
papers

2,118  
citations

471509

17  
h-index

552781

26  
g-index

37  
all docs

37  
docs citations

37  
times ranked

5208  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic aging biomarkers and occupational exposure to benzene, trichloroethylene and formaldehyde. <i>Environment International</i> , 2022, 158, 106871.	10.0	18
2	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. <i>Genome Biology</i> , 2022, 23, 13.	8.8	19
3	A mammalian methylation array for profiling methylation levels at conserved sequences. <i>Nature Communications</i> , 2022, 13, 783.	12.8	93
4	A pan-tissue DNA methylation atlas enables in silico decomposition of human tissue methylomes at cell-type resolution. <i>Nature Methods</i> , 2022, 19, 296-306.	19.0	46
5	Cell Type-Specific Signal Analysis in Epigenome-Wide Association Studies. <i>Methods in Molecular Biology</i> , 2022, 2432, 57-71.	0.9	7
6	The missing diversity in human epigenomic studies. <i>Nature Genetics</i> , 2022, 54, 737-739.	21.4	14
7	Diversity in EWAS: current state, challenges, and solutions. <i>Genome Medicine</i> , 2022, 14, .	8.2	13
8	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. <i>EBioMedicine</i> , 2021, 63, 103157.	6.1	14
9	DNA methylation predicts age and provides insight into exceptional longevity of bats. <i>Nature Communications</i> , 2021, 12, 1615.	12.8	80
10	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. <i>Genome Medicine</i> , 2021, 13, 74.	8.2	20
11	Identical twins carry a persistent epigenetic signature of early genome programming. <i>Nature Communications</i> , 2021, 12, 5618.	12.8	26
12	Epigenetic clock and methylation studies in the rhesus macaque. <i>GeroScience</i> , 2021, 43, 2441-2453.	4.6	28
13	Commute patterns, residential traffic-related air pollution, and lung cancer risk in the prospective UK Biobank cohort study. <i>Environment International</i> , 2021, 155, 106698.	10.0	12
14	Will the COVID-19 pandemic boost access to personal health care records? Smartphone data access to tackle the modern pandemic. <i>BMJ Innovations</i> , 2021, 7, 243-244.	1.7	0
15	Deciphering the genomic, epigenomic, and transcriptomic landscapes of pre-invasive lung cancer lesions. <i>Nature Medicine</i> , 2019, 25, 517-525.	30.7	178
16	Gender-neutral HPV vaccination in the UK, rising male oropharyngeal cancer rates, and lack of HPV awareness. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 131-132.	9.1	36
17	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. <i>Bioinformatics</i> , 2019, 35, 4767-4769.	4.1	84
18	Snoring and breathing pauses during sleep: interview survey of a United Kingdom population sample reveals a significant increase in the rates of sleep apnoea and obesity over the last 20 years - data from the UK sleep survey. <i>Sleep Medicine</i> , 2019, 54, 250-256.	1.6	22

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19	Genome-wide analysis of DNA methylation in buccal cells: a study of monozygotic twins and mQTLs. <i>Epigenetics and Chromatin</i> , 2018, 11, 54.	3.9	39
20	DNA methylome analysis reveals distinct epigenetic patterns of ascending aortic dissection and bicuspid aortic valve. <i>Cardiovascular Research</i> , 2017, 113, 692-704.	3.8	33
21	A comparison of reference-based algorithms for correcting cell-type heterogeneity in Epigenome-Wide Association Studies. <i>BMC Bioinformatics</i> , 2017, 18, 105.	2.6	297
22	Epigenetic reprogramming of fallopian tube fimbriae in BRCA mutation carriers defines early ovarian cancer evolution. <i>Nature Communications</i> , 2016, 7, 11620.	12.8	56
23	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	6.4	102
24	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
25	Genetic and environmental influences interact with age and sex in shaping the human methylome. <i>Nature Communications</i> , 2016, 7, 11115.	12.8	299
26	Tissue-independent and tissue-specific patterns of DNA methylation alteration in cancer. <i>Epigenetics and Chromatin</i> , 2016, 9, 10.	3.9	40