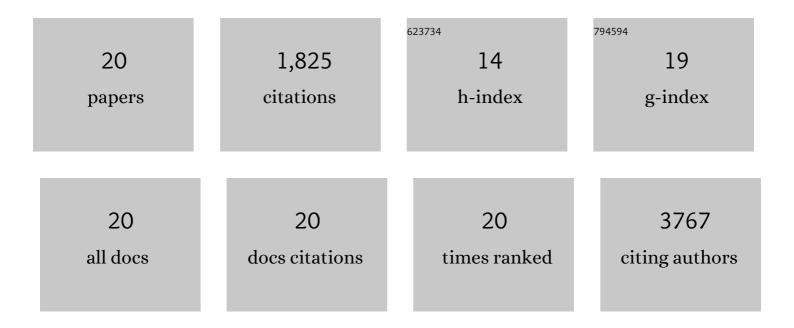
John R Edwards

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	DNA methylation and DNA methyltransferases. Epigenetics and Chromatin, 2017, 10, 23.	3.9	360
2	Stromal senescence establishes an immunosuppressive microenvironment that drives tumorigenesis. Nature Communications, 2016, 7, 11762.	12.8	290
3	Reprogrammable CRISPR/Cas9-based system for inducing site-specific DNA methylation. Biology Open, 2016, 5, 866-874.	1.2	228
4	Notes on the role of dynamic DNA methylation in mammalian development. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6796-6799.	7.1	200
5	Chromatin and sequence features that define the fine and gross structure of genomic methylation patterns. Genome Research, 2010, 20, 972-980.	5.5	160
6	FBXL10 protects Polycomb-bound genes from hypermethylation. Nature Genetics, 2015, 47, 479-485.	21.4	136
7	Epigenetic coordination of embryonic heart transcription by dynamically regulated long noncoding RNAs. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12264-12269.	7.1	128
8	Discovering high-resolution patterns of differential DNA methylation that correlate with gene expression changes. Nucleic Acids Research, 2013, 41, 6816-6827.	14.5	94
9	DNMT gene expression and methylome in Marek's disease resistant and susceptible chickens prior to and following infection by MDV. Epigenetics, 2013, 8, 431-444.	2.7	50
10	Modeling complex patterns of differential DNA methylation that associate with gene expression changes. Nucleic Acids Research, 2017, 45, 5100-5111.	14.5	46
11	p53 deficiency linked to B cell translocation gene 2 (BTG2) loss enhances metastatic potential by promoting tumor growth in primary and metastatic sites in patient-derived xenograft (PDX) models of triple-negative breast cancer. Breast Cancer Research, 2016, 18, 13.	5.0	41
12	Methylation-directed glycosylation of chromatin factors represses retrotransposon promoters. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 14292-14298.	7.1	28
13	Abnormal X chromosome inactivation and sex-specific gene dysregulation after ablation of FBXL10. Epigenetics and Chromatin, 2016, 9, 22.	3.9	19
14	DNA Methylation and Regulatory Elements during Chicken Germline Stem Cell Differentiation. Stem Cell Reports, 2018, 10, 1793-1806.	4.8	19
15	Epigenomic regulation of human T-cell leukemia virus by chromatin-insulator CTCF. PLoS Pathogens, 2021, 17, e1009577.	4.7	12
16	Determining subpopulation methylation profiles from bisulfite sequencing data of heterogeneous samples using DXM. Nucleic Acids Research, 2021, 49, e93-e93.	14.5	7
17	Methylation Abnormalities in Mammary Carcinoma: The Methylation Suicide Hypothesis. Journal of Cancer Therapy, 2014, 05, 1311-1324.	0.4	5
18	Reply to Wilkinson: Minor role of programmed methylation and demethylation in mammalian development. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2117-E2117.	7.1	1

#	Article	IF	CITATIONS
19	Integrated Analysis of DNA Methylation, Hydroxymethylation, and Gene Expression Data Using ME-Class2. Methods in Molecular Biology, 2021, 2198, 467-489.	0.9	1
20	A Novel Method to Identify Epigenetic Subclones with Increased Fitness from Genomic DNA Methylation Data of Lymphoma and Leukemia Patients. Blood, 2018, 132, 2604-2604.	1.4	0