

# John R Edwards

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2150626/publications.pdf>

Version: 2024-02-01

20  
papers

1,825  
citations

623734

14  
h-index

794594

19  
g-index

20  
all docs

20  
docs citations

20  
times ranked

3767  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation and DNA methyltransferases. <i>Epigenetics and Chromatin</i> , 2017, 10, 23.	3.9	360
2	Stromal senescence establishes an immunosuppressive microenvironment that drives tumorigenesis. <i>Nature Communications</i> , 2016, 7, 11762.	12.8	290
3	Reprogrammable CRISPR/Cas9-based system for inducing site-specific DNA methylation. <i>Biology Open</i> , 2016, 5, 866-874.	1.2	228
4	Notes on the role of dynamic DNA methylation in mammalian development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6796-6799.	7.1	200
5	Chromatin and sequence features that define the fine and gross structure of genomic methylation patterns. <i>Genome Research</i> , 2010, 20, 972-980.	5.5	160
6	FBXL10 protects Polycomb-bound genes from hypermethylation. <i>Nature Genetics</i> , 2015, 47, 479-485.	21.4	136
7	Epigenetic coordination of embryonic heart transcription by dynamically regulated long noncoding RNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12264-12269.	7.1	128
8	Discovering high-resolution patterns of differential DNA methylation that correlate with gene expression changes. <i>Nucleic Acids Research</i> , 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. <i>Epigenetics</i> , 2013, 8, 431-444.	2.7	50
10	Modeling complex patterns of differential DNA methylation that associate with gene expression changes. <i>Nucleic Acids Research</i> , 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. <i>Breast Cancer Research</i> , 2016, 18, 13.	5.0	41
12	Methylation-directed glycosylation of chromatin factors represses retrotransposon promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 14292-14298.	7.1	28
13	Abnormal X chromosome inactivation and sex-specific gene dysregulation after ablation of FBXL10. <i>Epigenetics and Chromatin</i> , 2016, 9, 22.	3.9	19
14	DNA Methylation and Regulatory Elements during Chicken Germline Stem Cell Differentiation. <i>Stem Cell Reports</i> , 2018, 10, 1793-1806.	4.8	19
15	Epigenomic regulation of human T-cell leukemia virus by chromatin-insulator CTCF. <i>PLoS Pathogens</i> , 2021, 17, e1009577.	4.7	12
16	Determining subpopulation methylation profiles from bisulfite sequencing data of heterogeneous samples using DXM. <i>Nucleic Acids Research</i> , 2021, 49, e93-e93.	14.5	7
17	Methylation Abnormalities in Mammary Carcinoma: The Methylation Suicide Hypothesis. <i>Journal of Cancer Therapy</i> , 2014, 05, 1311-1324.	0.4	5
18	Reply to Wilkinson: Minor role of programmed methylation and demethylation in mammalian development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2117-E2117.	7.1	1

#	ARTICLE	IF	CITATIONS
19	Integrated Analysis of DNA Methylation, Hydroxymethylation, and Gene Expression Data Using ME-Class2. <i>Methods in Molecular Biology</i> , 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. <i>Blood</i> , 2018, 132, 2604-2604.	1.4	0