

John W Whitaker

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

9,833
citations

279798

23
h-index

414414

32
g-index

34
all docs

34
docs citations

34
times ranked

22101
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
2	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
3	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	28.9	689
4	Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , 2015, 523, 212-216.	27.8	605
5	DNA methylome signature in rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 110-117.	0.9	283
6	Constructing 3D interaction maps from 1D epigenomes. <i>Nature Communications</i> , 2016, 7, 10812.	12.8	135
7	Predicting enhancer transcription and activity from chromatin modifications. <i>Nucleic Acids Research</i> , 2013, 41, 10032-10043.	14.5	128
8	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	27.8	123
9	Predicting the human epigenome from DNA motifs. <i>Nature Methods</i> , 2015, 12, 265-272.	19.0	121
10	Comprehensive epigenetic landscape of rheumatoid arthritis fibroblast-like synoviocytes. <i>Nature Communications</i> , 2018, 9, 1921.	12.8	119
11	An imprinted rheumatoid arthritis methylome signature reflects pathogenic phenotype. <i>Genome Medicine</i> , 2013, 5, 40.	8.2	99
12	DNA Methylome Signature in Synoviocytes From Patients With Early Rheumatoid Arthritis Compared to Synoviocytes From Patients With Longstanding Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2015, 67, 1978-1980.	5.6	74
13	Integrative genomic deconvolution of rheumatoid arthritis GWAS loci into gene and cell type associations. <i>Genome Biology</i> , 2016, 17, 79.	8.8	70
14	The transferome of metabolic genes explored: analysis of the horizontal transfer of enzyme encoding genes in unicellular eukaryotes. <i>Genome Biology</i> , 2009, 10, R36.	9.6	56
15	The Rheumatoid Arthritis Risk Gene <i>IL1B</i> Regulates Growth in Fibroblast-like Synoviocytes. <i>Arthritis and Rheumatology</i> , 2015, 67, 1193-1202.	5.6	56
16	Integrative Omics Analysis of Rheumatoid Arthritis Identifies Non-Obvious Therapeutic Targets. <i>PLoS ONE</i> , 2015, 10, e0124254.	2.5	48
17	<i>IL1B</i> Gene Transcription Regulation by the Interplay of an Enhancer Risk Allele and DNA Methylation in Rheumatoid Arthritis. <i>Arthritis and Rheumatology</i> , 2016, 68, 2637-2645.	5.6	41
18	Epigenomic analysis reveals DNA motifs regulating histone modifications in human and mouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3668-3677.	7.1	35

#	ARTICLE	IF	CITATIONS
19	Abnormal PTPN11 enhancer methylation promotes rheumatoid arthritis fibroblast-like synoviocyte aggressiveness and joint inflammation. JCI Insight, 2016, 1, .	5.0	34
20	metaTIGER: a metabolic evolution resource. Nucleic Acids Research, 2009, 37, D531-D538.	14.5	32
21	Identification of DNA motifs that regulate DNA methylation. Nucleic Acids Research, 2019, 47, 6753-6768.	14.5	32
22	The Transcriptional Response to DNA-Double-Strand Breaks in Physcomitrella patens. PLoS ONE, 2016, 11, e0161204.	2.5	29
23	Computational schemes for the prediction and annotation of enhancers from epigenomic assays. Methods, 2015, 72, 86-94.	3.8	26
24	Epipolymorphisms associated with the clinical outcome of autoimmune arthritis affect CD4 ⁺ T cell activation pathways. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13845-13850.	7.1	23
25	Prediction of horizontal gene transfers in eukaryotes: approaches and challenges. Biochemical Society Transactions, 2009, 37, 792-795.	3.4	19
26	STAR: an integrated solution to management and visualization of sequencing data. Bioinformatics, 2013, 29, 3204-3210.	4.1	13
27	Global identification of transcriptional regulators of pluripotency and differentiation in embryonic stem cells. Nucleic Acids Research, 2012, 40, 8199-8209.	14.5	9
28	Mutagen structure and transcriptional response: Induction of distinct transcriptional profiles in <i>Salmonella</i> TA100 by the drinking water mutagen MX and its homologues. Environmental and Molecular Mutagenesis, 2010, 51, 69-79.	2.2	3
29	Alio intuitu: the automated reconstruction of the metabolic networks of parasites. Trends in Parasitology, 2009, 25, 396-397.	3.3	2
30	Response to Marchetti et al.. Journal of Investigative Dermatology, 2022, 142, 232-234.	0.7	2
31	Transferomics: Seeing the Evolutionary Forest Using Phylogenetic Trees. , 2010, , 101-114.		0