

John W Whitaker

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

9,833
citations

279701

23
h-index

414303

32
g-index

34
all docs

34
docs citations

34
times ranked

22101
citing authors

#	ARTICLE	IF	CITATIONS
1	Response to Marchetti et al.. Journal of Investigative Dermatology, 2022, 142, 232-234.	0.3	2
2	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
3	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
4	Identification of DNA motifs that regulate DNA methylation. Nucleic Acids Research, 2019, 47, 6753-6768.	6.5	32
5	Epigenomic analysis reveals DNA motifs regulating histone modifications in human and mouse. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3668-3677.	3.3	35
6	Comprehensive epigenetic landscape of rheumatoid arthritis fibroblast-like synoviocytes. Nature Communications, 2018, 9, 1921.	5.8	119
7	Constructing 3D interaction maps from 1D epigenomes. Nature Communications, 2016, 7, 10812.	5.8	135
8	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.	3.3	23
9	Integrative genomic deconvolution of rheumatoid arthritis GWAS loci into gene and cell type associations. Genome Biology, 2016, 17, 79.	3.8	70
10	Gene Transcription Regulation by the Interplay of an Enhancer Risk Allele and DNA Methylation in Rheumatoid Arthritis. Arthritis and Rheumatology, 2016, 68, 2637-2645.	2.9	41
11	Abnormal PTPN11 enhancer methylation promotes rheumatoid arthritis fibroblast-like synoviocyte aggressiveness and joint inflammation. JCI Insight, 2016, 1, .	2.3	34
12	The Transcriptional Response to DNA-Double-Strand Breaks in Physcomitrella patens. PLoS ONE, 2016, 11, e0161204.	1.1	29
13	DNA Methylome Signature in Synoviocytes From Patients With Early Rheumatoid Arthritis Compared to Synoviocytes From Patients With Longstanding Rheumatoid Arthritis. Arthritis and Rheumatology, 2015, 67, 1978-1980.	2.9	74
14	Integrative Omics Analysis of Rheumatoid Arthritis Identifies Non-Obvious Therapeutic Targets. PLoS ONE, 2015, 10, e0124254.	1.1	48
15	Human body epigenome maps reveal noncanonical DNA methylation variation. Nature, 2015, 523, 212-216.	13.7	605
16	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
17	The Rheumatoid Arthritis Risk Gene <i>LBH</i> Regulates Growth in Fibroblast-like Synoviocytes. Arthritis and Rheumatology, 2015, 67, 1193-1202.	2.9	56
18	Computational schemes for the prediction and annotation of enhancers from epigenomic assays. Methods, 2015, 72, 86-94.	1.9	26

#	ARTICLE	IF	CITATIONS
19	Predicting the human epigenome from DNA motifs. <i>Nature Methods</i> , 2015, 12, 265-272.	9.0	121
20	An imprinted rheumatoid arthritis methylome signature reflects pathogenic phenotype. <i>Genome Medicine</i> , 2013, 5, 40.	3.6	99
21	Predicting enhancer transcription and activity from chromatin modifications. <i>Nucleic Acids Research</i> , 2013, 41, 10032-10043.	6.5	128
22	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1134-1148.	13.5	689
23	STAR: an integrated solution to management and visualization of sequencing data. <i>Bioinformatics</i> , 2013, 29, 3204-3210.	1.8	13
24	DNA methylome signature in rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 110-117.	0.5	283
25	Global identification of transcriptional regulators of pluripotency and differentiation in embryonic stem cells. <i>Nucleic Acids Research</i> , 2012, 40, 8199-8209.	6.5	9
26	Mutagen structure and transcriptional response: Induction of distinct transcriptional profiles in <i>Salmonella</i> TA100 by the drinking water mutagen MX and its homologues. <i>Environmental and Molecular Mutagenesis</i> , 2010, 51, 69-79.	0.9	3
27	Transferomics: Seeing the Evolutionary Forest Using Phylogenetic Trees. , 2010, , 101-114.		0
28	metaTIGER: a metabolic evolution resource. <i>Nucleic Acids Research</i> , 2009, 37, D531-D538.	6.5	32
29	Alio intuitu: the automated reconstruction of the metabolic networks of parasites. <i>Trends in Parasitology</i> , 2009, 25, 396-397.	1.5	2
30	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.	13.9	56
31	Prediction of horizontal gene transfers in eukaryotes: approaches and challenges. <i>Biochemical Society Transactions</i> , 2009, 37, 792-795.	1.6	19