

Michael M Hoffman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4558193/publications.pdf>

Version: 2024-02-01

37
papers

26,307
citations

218381

26
h-index

344852

36
g-index

58
all docs

58
docs citations

58
times ranked

47363
citing authors

#	ARTICLE	IF	CITATIONS
1	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
2	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	13.7	2,421
3	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	2.4	1,708
4	Opportunities and obstacles for deep learning in biology and medicine. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20170387.	1.5	1,282
5	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
6	Sensitive tumour detection and classification using plasma cell-free DNA methylomes. <i>Nature</i> , 2018, 563, 579-583.	13.7	624
7	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. <i>Nature Methods</i> , 2012, 9, 473-476.	9.0	562
8	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , 2013, 41, 827-841.	6.5	490
9	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014, 512, 449-452.	13.7	363
10	Machine learning for integrating data in biology and medicine: Principles, practice, and opportunities. <i>Information Fusion</i> , 2019, 50, 71-91.	11.7	340
11	Transparency and reproducibility in artificial intelligence. <i>Nature</i> , 2020, 586, E14-E16.	13.7	233
12	Classification and interaction in random forests. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1690-1692.	3.3	150
13	Extending reference assembly models. <i>Genome Biology</i> , 2015, 16, 13.	3.8	139
14	AANT: the Amino Acid-Nucleotide Interaction Database. <i>Nucleic Acids Research</i> , 2004, 32, 174D-181.	6.5	120
15	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
16	Reproducibility standards for machine learning in the life sciences. <i>Nature Methods</i> , 2021, 18, 1132-1135.	9.0	96
17	Umap and Bimap: quantifying genome and methylome mappability. <i>Nucleic Acids Research</i> , 2018, 46, e120.	6.5	94
18	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	94

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19	Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell-type-specific expression. <i>Genome Research</i> , 2015, 25, 544-557.	2.4	74
20	DNAMod: the DNA modification database. <i>Journal of Cheminformatics</i> , 2019, 11, 30.	2.8	53
21	Tumor-Naïve Multimodal Profiling of Circulating Tumor DNA in Head and Neck Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2021, 27, 4230-4244.	3.2	53
22	A dynamic Bayesian network for identifying protein-binding footprints from single molecule-based sequencing data. <i>Bioinformatics</i> , 2010, 26, i334-i342.	1.8	43
23	Statistical Inference, Learning and Models in Big Data. <i>International Statistical Review</i> , 2016, 84, 371-389.	1.1	42
24	A unified encyclopedia of human functional DNA elements through fully automated annotation of 164 human cell types. <i>Genome Biology</i> , 2019, 20, 180.	3.8	37
25	Top considerations for creating bioinformatics software documentation. <i>Briefings in Bioinformatics</i> , 2018, 19, 693-699.	3.2	33
26	ChromNet: Learning the human chromatin network from all ENCODE ChIP-seq data. <i>Genome Biology</i> , 2016, 17, 82.	3.8	31
27	Segway 2.0: Gaussian mixture models and minibatch training. <i>Bioinformatics</i> , 2018, 34, 669-671.	1.8	31
28	Estimating the Neutral Rate of Nucleotide Substitution Using Introns. <i>Molecular Biology and Evolution</i> , 2006, 24, 522-531.	3.5	29
29	Sharing biological data: why, when, and how. <i>FEBS Letters</i> , 2021, 595, 847-863.	1.3	26
30	An effective model for natural selection in promoters. <i>Genome Research</i> , 2010, 20, 685-692.	2.4	24
31	The Genomdata format for storing large-scale functional genomics data. <i>Bioinformatics</i> , 2010, 26, 1458-1459.	1.8	21
32	Segmentation and genome annotation algorithms for identifying chromatin state and other genomic patterns. <i>PLoS Computational Biology</i> , 2021, 17, e1009423.	1.5	21
33	Exploratory analysis of genomic segmentations with Segtools. <i>BMC Bioinformatics</i> , 2011, 12, 415.	1.2	20
34	Virtual ChIP-seq: predicting transcription factor binding by learning from the transcriptome. <i>Genome Biology</i> , 2022, 23, .	3.8	14
35	Assessing and assuring interoperability of a genomics file format. <i>Bioinformatics</i> , 2022, 38, 3327-3336.	1.8	3
36	Determining the epigenome using DNA alone. <i>Nature Methods</i> , 2015, 12, 191-192.	9.0	0

#	ARTICLE	IF	CITATIONS
37	Readers respond to Nature's™ Editorial on historical monuments. Nature, 0, , .	13.7	0