Michael M Hoffman

List of Publications by Year in Descending Order

48 papers	19,140 citations	23 h-index	58 g-index
58 ext. papers	23,740 ext. citations	17.7 avg, IF	8.25 L-index

#	Paper	IF	Citations
48	Virtual ChIP-seq: predicting transcription factor binding by learning from the transcriptome. *Genome Biology*, **2022**, 23,	18.3	1
47	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
46	Segmentation and genome annotation algorithms for identifying chromatin state and other genomic patterns. *PLoS Computational Biology*, **2021**, 17, e1009423	5	2
45	Tumor-Naïve Multimodal Profiling of Circulating Tumor DNA in Head and Neck Squamous Cell Carcinoma. *Clinical Cancer Research*, **2021**, 27, 4230-4244	12.9	9
44	Reproducibility standards for machine learning in the life sciences. *Nature Methods*, **2021**, 18, 1132-1135	21.6	14
43	Transparency and reproducibility in artificial intelligence. *Nature*, **2020**, 586, E14-E16	50.4	85
42	Functional annotation of human long noncoding RNAs via molecular phenotyping. *Genome Research*, **2020**, 30, 1060-1072	9.7	41
41	A unified encyclopedia of human functional DNA elements through fully automated annotation of 164 human cell types. *Genome Biology*, **2019**, 20, 180	18.3	18
40	DNAmod: the DNA modification database. *Journal of Cheminformatics*, **2019**, 11, 30	8.6	29
39	Machine Learning for Integrating Data in Biology and Medicine: Principles, Practice, and Opportunities. *Information Fusion*, **2019**, 50, 71-91	16.7	170
38	Opportunities and obstacles for deep learning in biology and medicine. *Journal of the Royal Society Interface*, **2018**, 15,	4.1	780
37	Classification and interaction in random forests. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 1690-1692	11.5	69
36	Segway 2.0: Gaussian mixture models and minibatch training. *Bioinformatics*, **2018**, 34, 669-671	7.2	23
35	Top considerations for creating bioinformatics software documentation. *Briefings in Bioinformatics*, **2018**, 19, 693-699	13.4	15
34	Sensitive tumour detection and classification using plasma cell-free DNA methylomes. *Nature*, **2018** , 563, 579-583	50.4	344
33	Umap and Bismap: quantifying genome and methylome mappability. *Nucleic Acids Research*, **2018**, 46, e120	20.1	57
32	ChromNet: Learning the human chromatin network from all ENCODE ChIP-seq data. *Genome Biology*, **2016**, 17, 82	18.3	26

31	Statistical Inference, Learning and Models in Big Data. *International Statistical Review*, **2016**, 84, 371-389	1.4	28
30	Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell-type-specific expression. *Genome Research*, **2015**, 25, 544-57	9.7	50
29	Determining the epigenome using DNA alone. *Nature Methods*, **2015**, 12, 191-2	21.6	
28	Extending reference assembly models. *Genome Biology*, **2015**, 16, 13	18.3	107
27	Comparative analysis of metazoan chromatin organization. *Nature*, **2014**, 512, 449-52	50.4	265
26	Integrative annotation of chromatin elements from ENCODE data. *Nucleic Acids Research*, **2013**, 41, 827-41	10.1	383
25	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
24	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. *Genome Research*, **2012**, 22, 1813-31	9.7	1211
23	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. *Nature Methods*, **2012**, 9, 473-6	21.6	419
22	A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biology*, **2011**, 9, e1001046	9.7	1060
21	Exploratory analysis of genomic segmentations with Segtools. *BMC Bioinformatics*, **2011**, 12, 415	3.6	14
20	The Genomedata format for storing large-scale functional genomics data. *Bioinformatics*, **2010**, 26, 1458-9	7.2	15
19	A dynamic Bayesian network for identifying protein-binding footprints from single molecule-based sequencing data. *Bioinformatics*, **2010**, 26, i334-42	7.2	37
18	An effective model for natural selection in promoters. *Genome Research*, **2010**, 20, 685-92	9.7	22
17	Estimating the neutral rate of nucleotide substitution using introns. *Molecular Biology and Evolution*, **2007**, 24, 522-31	8.3	25
16	AANT: the Amino Acid-Nucleotide Interaction Database. *Nucleic Acids Research*, **2004**, 32, D174-81	20.1	104
15	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature*, **2004**, 432, 695-716	50.4	2143
14	Semi-supervised segmentation and genome annotation		1

13	Modeling methyl-sensitive transcription factor motifs with an expanded epigenetic alphabet	9
12	DNAmod: the DNA modification database	6
11	A unified encyclopedia of human functional DNA elements through fully automated annotation of 164 human cell types	5
10	Umap and Bismap: quantifying genome and methylome mappability	4
9	Opportunities and obstacles for deep learning in biology and medicine	45
8	Virtual ChIP-seq: predicting transcription factor binding by learning from the transcriptome	12
7	BEHST: genomic set enrichment analysis enhanced through integration of chromatin long-range interactions	4
6	Viral integration transforms chromatin to drive oncogenesis	2
5	Unsupervised analysis of multi-experiment transcriptomic patterns with SegRNA identifies unannotated transcripts	2
4	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping	6
3	Semi-automated genome annotation using epigenomic data and Segway	1
2	Functional annotation of human long noncoding RNAs using chromatin conformation data	1
1	Sensitive and reproducible cell-free methylome quantification with synthetic spike-in controls	1