

Maxwell W Libbrecht

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

20
papers

1,385
citations

9
h-index

37
g-index

39
ext. papers

1,886
ext. citations

13.5
avg, IF

5.22
L-index

#	Paper	IF	Citations
20	Machine learning applications in genetics and genomics. <i>Nature Reviews Genetics</i> , 2015 , 16, 321-32	30.1	845
19	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014 , 512, 449-52	50.4	265
18	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
17	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, 544-57	9.7	50
16	PREDICTD PaRallel Epigenomics Data Imputation with Cloud-based Tensor Decomposition. <i>Nature Communications</i> , 2018 , 9, 1402	17.4	37
15	Distinct epigenetic features of differentiation-regulated replication origins. <i>Epigenetics and Chromatin</i> , 2016 , 9, 18	5.8	35
14	Segway 2.0: Gaussian mixture models and minibatch training. <i>Bioinformatics</i> , 2018 , 34, 669-671	7.2	23
13	A unified encyclopedia of human functional DNA elements through fully automated annotation of 164 human cell types. <i>Genome Biology</i> , 2019 , 20, 180	18.3	18
12	Interferometric measurement of the resonant absorption and refractive index in rubidium gas. <i>American Journal of Physics</i> , 2006 , 74, 1055-1060	0.7	17
11	Choosing panels of genomics assays using submodular optimization. <i>Genome Biology</i> , 2016 , 17, 229	18.3	9
10	Choosing non-redundant representative subsets of protein sequence data sets using submodular optimization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018 , 86, 454-466	4.2	8
9	A unified encyclopedia of human functional DNA elements through fully automated annotation of 164 human cell types		5
8	Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell type-specific expression		3
7	Segmentation and genome annotation algorithms for identifying chromatin state and other genomic patterns. <i>PLoS Computational Biology</i> , 2021 , 17, e1009423	5	2
6	INGOT-DR: an interpretable classifier for predicting drug resistance in <i>M. tuberculosis</i>		2
5	Semi-supervised segmentation and genome annotation		1
4	SigTools: Exploratory Visualization For Genomic Signals. <i>Bioinformatics</i> , 2021 ,	7.2	1

3	VSS: Variance-stabilized signals for sequencing-based genomic signals	1
2	Continuous chromatin state feature annotation of the human epigenome	1
1	SplitStrains, a tool to identify and separate mixed infections from WGS data. <i>Microbial Genomics</i> , 2021 , 7,	4-4 1