Maxwell W Libbrecht

List of Publications by Year in Descending Order

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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.

| 2O | 1,385 | 9 | 37 |
|-------------|----------------------|---------|---------|
| papers | citations | h-index | g-index |
| 39 | 1,886 ext. citations | 13.5 | 5.22 |
| ext. papers | | avg, IF | L-index |

| # | Paper | IF | Citations |
|----|---|----------------|-----------|
| 20 | SigTools: Exploratory Visualization For Genomic Signals. <i>Bioinformatics</i> , 2021 , | 7.2 | 1 |
| 19 | Segmentation and genome annotation algorithms for identifying chromatin state and other genomic patterns. <i>PLoS Computational Biology</i> , 2021 , 17, e1009423 | 5 | 2 |
| 18 | SplitStrains, a tool to identify and separate mixed infections from WGS data. <i>Microbial Genomics</i> , 2021 , 7, | 4.4 | 1 |
| 17 | Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698 | 50.4 | 61 |
| 16 | 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 |
| 15 | PREDICTD PaRallel Epigenomics Data Imputation with Cloud-based Tensor Decomposition. <i>Nature Communications</i> , 2018 , 9, 1402 | 17.4 | 37 |
| 14 | 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 |
| 13 | Segway 2.0: Gaussian mixture models and minibatch training. <i>Bioinformatics</i> , 2018 , 34, 669-671 | 7.2 | 23 |
| 12 | Choosing panels of genomics assays using submodular optimization. <i>Genome Biology</i> , 2016 , 17, 229 | 18.3 | 9 |
| 11 | Distinct epigenetic features of differentiation-regulated replication origins. <i>Epigenetics and Chromatin</i> , 2016 , 9, 18 | 5.8 | 35 |
| 10 | 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, 544-5 | 5 7 9.7 | 50 |
| 9 | Machine learning applications in genetics and genomics. <i>Nature Reviews Genetics</i> , 2015 , 16, 321-32 | 30.1 | 845 |
| 8 | Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014 , 512, 449-52 | 50.4 | 265 |
| 7 | 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 |
| 6 | Semi-supervised segmentation and genome annotation | | 1 |
| 5 | Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell type-specific expression | | 3 |
| 4 | A unified encyclopedia of human functional DNA elements through fully automated annotation of 164 human cell types | | 5 |

LIST OF PUBLICATIONS

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| 2 | INGOT-DR: an interpretable classifier for predicting drug resistance in M. tuberculosis | 2 |
|---|---|---|
| 1 | Continuous chromatin state feature annotation of the human epigenome | 1 |

VSS: Variance-stabilized signals for sequencing-based genomic signals

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