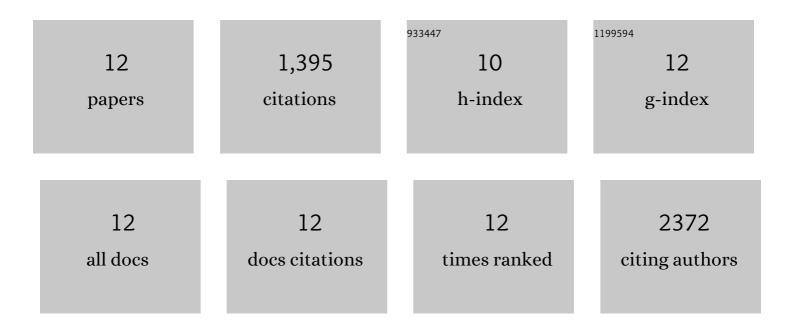
Stéphane Robin

List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Integrative epigenomic mapping defines four main chromatin states in Arabidopsis. EMBO Journal, 2011, 30, 1928-1938. | 7.8 | 600 |
| 2 | A statistical approach for array CGH data analysis. BMC Bioinformatics, 2005, 6, 27. | 2.6 | 256 |
| 3 | The MatP/matS Site-Specific System Organizes the Terminus Region of the E. coli Chromosome into a Macrodomain. Cell, 2008, 135, 475-485. | 28.9 | 252 |
| 4 | Joint segmentation, calling, and normalization of multiple CGH profiles. Biostatistics, 2011, 12, 413-428. | 1.5 | 88 |
| 5 | Identification of DNA Motifs Implicated in Maintenance of Bacterial Core Genomes by Predictive Modeling. PLoS Genetics, 2007, 3, e153. | 3.5 | 63 |
| 6 | Hidden Markov Models with mixtures as emission distributions. Statistics and Computing, 2014, 24, 493-504. | 1.5 | 42 |
| 7 | Statistical tests to compare motif count exceptionalities. BMC Bioinformatics, 2007, 8, 84. | 2.6 | 28 |
| 8 | ChIPmix: mixture model of regressions for two-color ChIP–chip analysis. Bioinformatics, 2008, 24, i181-i186. | 4.1 | 22 |
| 9 | Segmentor3IsBack: an R package for the fast and exact segmentation of Seq-data. Algorithms for Molecular Biology, 2014, 9, 6. | 1.2 | 21 |
| 10 | Genomic Instability: A Stronger Prognostic Marker Than Proliferation for Early Stage Luminal Breast Carcinomas. PLoS ONE, 2013, 8, e76496. | 2.5 | 16 |
| 11 | SegCorr a statistical procedure for the detection of genomic regions of correlated expression. BMC Bioinformatics, 2017, 18, 333. | 2.6 | 5 |
| 12 | A factor model approach for the joint segmentation with betweenâ€series correlation. Scandinavian Journal of Statistics, 2019, 46, 686-705. | 1.4 | 2 |