# Santiago Marco-Sola

List of Publications by Year
in descending order

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|---|---|---|---|
| 13<br>papers | 817<br>citations | 1163117<br>8<br>h-index | 1372567<br>10<br>g-index |
| 18<br>all docs | 18<br>docs citations | 18<br>times ranked | 2394<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | FPGA Acceleration of Pre-Alignment Filters for Short Read Mapping With HLS. IEEE Access, 2022, 10, 22079-22100. | 4.2 | 5 |
| 2 | AnchorWave: Sensitive alignment of genomes with high sequence diversity, extensive structural polymorphism, and whole-genome duplication. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 29 |
| 3 | Accelerating Edit-Distance Sequence Alignment on GPU Using the Wavefront Algorithm. IEEE Access, 2022, 10, 63782-63796. | 4.2 | 7 |
| 4 | Fast gap-affine pairwise alignment using the wavefront algorithm. Bioinformatics, 2021, 37, 456-463. | 4.1 | 75 |
| 5 | OpenCL-based FPGA Accelerator for Semi-Global Approximate String Matching Using Diagonal Bit-Vectors. , 2021, , . | | 3 |
| 6 | An FPGA Accelerator of the Wavefront Algorithm for Genomics Pairwise Alignment. , 2021, , . | | 8 |
| 7 | gemBS: high throughput processing for DNA methylation data from bisulfite sequencing. Bioinformatics, 2019, 35, 737-742. | 4.1 | 39 |
| 8 | ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. BMC Genomics, 2017, 18, 7. | 2.8 | 30 |
| 9 | From Wet‐Lab to Variations: Concordance and Speed of Bioinformatics Pipelines for Whole Genome and Whole Exome Sequencing. Human Mutation, 2016, 37, 1263-1271. | 2.5 | 47 |
| 10 | Efficient Alignment of Illumina‐Like High‐Throughput Sequencing Reads with the GEnomic Multi‐tool (GEM) Mapper. Current Protocols in Bioinformatics, 2015, 50, 11.13.1-11.13.20. | 25.8 | 11 |
| 11 | Boosting the FM-Index on the GPU: Effective Techniques to Mitigate Random Memory Access. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1048-1059. | 3.0 | 21 |
| 12 | Thread-cooperative, bit-parallel computation of levenshtein distance on GPU. , 2014, , . | | 25 |
| 13 | The GEM mapper: fast, accurate and versatile alignment by filtration. Nature Methods, 2012, 9, 1185-1188. | 19.0 | 500 |