## Santiago Marco-Sola

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The GEM mapper: fast, accurate and versatile alignment by filtration. Nature Methods, 2012, 9, 1185-1188.	19.0	500
2	Fast gap-affine pairwise alignment using the wavefront algorithm. Bioinformatics, 2021, 37, 456-463.	4.1	75
3	From Wetâ€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
4	gemBS: high throughput processing for DNA methylation data from bisulfite sequencing. Bioinformatics, 2019, 35, 737-742.	4.1	39
5	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. BMC Genomics, 2017, 18, 7.	2.8	30
6	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
7	Thread-cooperative, bit-parallel computation of levenshtein distance on GPU. , 2014, , .		25
8	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
9	Efficient Alignment of Illumina‣ike Highâ€Throughput Sequencing Reads with the GEnomic Multiâ€ŧool (GEM) Mapper. Current Protocols in Bioinformatics, 2015, 50, 11.13.1-11.13.20.	25.8	11
10	An FPGA Accelerator of the Wavefront Algorithm for Genomics Pairwise Alignment. , 2021, , .		8
11	Accelerating Edit-Distance Sequence Alignment on GPU Using the Wavefront Algorithm. IEEE Access, 2022, 10, 63782-63796.	4.2	7
12	FPGA Acceleration of Pre-Alignment Filters for Short Read Mapping With HLS. IEEE Access, 2022, 10, 22079-22100.	4.2	5
13	OpenCL-based FPGA Accelerator for Semi-Global Approximate String Matching Using Diagonal Bit-Vectors. , 2021, , .		3