Guillermo Barturen

List of Publications by Year
in descending order

22 papers	1,036 citations	566801 15 h-index	642321 23 g-index
26 all docs	26 docs citations	26 times ranked	1951 citing authors

#	Article	IF	Citations
1	sRNAtoolbox: an integrated collection of small RNA research tools. Nucleic Acids Research, 2015, 43, W467-W473.	6.5	238
2	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
3	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. Arthritis and Rheumatology, 2021, 73, 1073-1085.	2.9	81
4	Moving towards a molecular taxonomy of autoimmune rheumatic diseases. Nature Reviews Rheumatology, 2018, 14, 75-93.	3.5	80
5	A new molecular classification to drive precision treatment strategies in primary SjÃ¶grenâ€™s syndrome. Nature Communications, 2021, 12, 3523.	5.8	67
6	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature Communications, 2021, 12, 4854.	5.8	42
7	MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. F1000Research, 2013, 2, 217.	0.8	42
8	Prediction of CpG-island function: CpG clustering vs. sliding-window methods. BMC Genomics, 2010, 11, 327.	1.2	40
9	MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. F1000Research, 2013, 2, 217.	0.8	30
10	Genome-wide whole blood transcriptome profiling in a large European cohort of systemic sclerosis patients. Annals of the Rheumatic Diseases, 2020, 79, 1218-1226.	0.5	26
11	Clustering of DNA words and biological function: A proof of principle. Journal of Theoretical Biology, 2012, 297, 127-136.	0.8	22
12	NGSmethDB: an updated genome resource for high quality, single-cytosine resolution methylomes. Nucleic Acids Research, 2014, 42, D53-D59.	6.5	22
13	WordCluster: detecting clusters of DNA words and genomic elements. Algorithms for Molecular Biology, 2011, 6, 2.	0.3	21
14	NGSmethDB 2017: enhanced methylomes and differential methylation. Nucleic Acids Research, 2017, 45, D97-D103.	6.5	16
15	Integrative epigenomics in SjÃ¶grenÂ´s syndrome reveals novel pathways and a strong interaction between the HLA, autoantibodies and the interferon signature. Scientific Reports, 2021, 11, 23292.	1.6	16
16	DNA clustering and genome complexity. Computational Biology and Chemistry, 2014, 53, 71-78.	1.1	12
17	A comprehensive database for integrated analysis of omics data in autoimmune diseases. BMC Bioinformatics, 2021, 22, 343.	1.2	12
18	SLE redefined on the basis of molecular pathways. Best Practice and Research in Clinical Rheumatology, 2017, 31, 291-305.	1.4	10

#	Article	IF	Citations
19	Expression Quantitative Trait Locus Analysis in Systemic Sclerosis Identifies New Candidate Genes Associated With Multiple Aspects of Disease Pathology. Arthritis and Rheumatology, 2021, 73, 1288-1300.	2.9	9
20	<i>CpGislandEVO</i>: A Database and Genome Browser for Comparative Evolutionary Genomics of CpG Islands. BioMed Research International, 2013, 2013, 1-6.	0.9	4
21	Gene expression profiling comes closer to the clinic. Nature Reviews Rheumatology, 2017, 13, 69-70.	3.5	2
22	geno5mC: A Database to Explore the Association between Genetic Variation (SNPs) and CpG Methylation in the Human Genome. Journal of Molecular Biology, 2021, 433, 166709.	2.0	1