

# Guillermo Barturen

## List of Publications by Year in descending order

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Version: 2024-02-01

22  
papers

1,036  
citations

567281

15  
h-index

642732

23  
g-index

26  
all docs

26  
docs citations

26  
times ranked

1951  
citing authors

#	ARTICLE	IF	CITATIONS
1	geno5mC: A Database to Explore the Association between Genetic Variation (SNPs) and CpG Methylation in the Human Genome. <i>Journal of Molecular Biology</i> , 2021, 433, 166709.	4.2	1
2	Integrative Analysis Reveals a Molecular Stratification of Systemic Autoimmune Diseases. <i>Arthritis and Rheumatology</i> , 2021, 73, 1073-1085.	5.6	81
3	Expression Quantitative Trait Locus Analysis in Systemic Sclerosis Identifies New Candidate Genes Associated With Multiple Aspects of Disease Pathology. <i>Arthritis and Rheumatology</i> , 2021, 73, 1288-1300.	5.6	9
4	A comprehensive database for integrated analysis of omics data in autoimmune diseases. <i>BMC Bioinformatics</i> , 2021, 22, 343.	2.6	12
5	A new molecular classification to drive precision treatment strategies in primary Sjögren's syndrome. <i>Nature Communications</i> , 2021, 12, 3523.	12.8	67
6	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. <i>Nature Communications</i> , 2021, 12, 4854.	12.8	42
7	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
8	Integrative epigenomics in Sjögren's syndrome reveals novel pathways and a strong interaction between the HLA, autoantibodies and the interferon signature. <i>Scientific Reports</i> , 2021, 11, 23292.	3.3	16
9	Genome-wide whole blood transcriptome profiling in a large European cohort of systemic sclerosis patients. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 1218-1226.	0.9	26
10	Moving towards a molecular taxonomy of autoimmune rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2018, 14, 75-93.	8.0	80
11	Gene expression profiling comes closer to the clinic. <i>Nature Reviews Rheumatology</i> , 2017, 13, 69-70.	8.0	2
12	SLE redefined on the basis of molecular pathways. <i>Best Practice and Research in Clinical Rheumatology</i> , 2017, 31, 291-305.	3.3	10
13	NGSmethDB 2017: enhanced methylomes and differential methylation. <i>Nucleic Acids Research</i> , 2017, 45, D97-D103.	14.5	16
14	sRNAtoolbox: an integrated collection of small RNA research tools. <i>Nucleic Acids Research</i> , 2015, 43, W467-W473.	14.5	238
15	NGSmethDB: an updated genome resource for high quality, single-cytosine resolution methylomes. <i>Nucleic Acids Research</i> , 2014, 42, D53-D59.	14.5	22
16	DNA clustering and genome complexity. <i>Computational Biology and Chemistry</i> , 2014, 53, 71-78.	2.3	12
17	CpGislandEVO: A Database and Genome Browser for Comparative Evolutionary Genomics of CpG Islands. <i>BioMed Research International</i> , 2013, 2013, 1-6.	1.9	4
18	MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. <i>F1000Research</i> , 2013, 2, 217.	1.6	42

#	ARTICLE	IF	CITATIONS
19	MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. F1000Research, 2013, 2, 217.	1.6	30
20	Clustering of DNA words and biological function: A proof of principle. Journal of Theoretical Biology, 2012, 297, 127-136.	1.7	22
21	WordCluster: detecting clusters of DNA words and genomic elements. Algorithms for Molecular Biology, 2011, 6, 2.	1.2	21
22	Prediction of CpG-island function: CpG clustering vs. sliding-window methods. BMC Genomics, 2010, 11, 327.	2.8	40