

# Benoit Ballester

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

9,444  
citations

201575

27  
h-index

377752

34  
g-index

39  
all docs

39  
docs citations

39  
times ranked

18118  
citing authors

#	ARTICLE	IF	CITATIONS
1	JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. <i>Nucleic Acids Research</i> , 2018, 46, D260-D266.	6.5	1,232
2	JASPAR 2020: update of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2020, 48, D87-D92.	6.5	1,039
3	JASPAR 2022: the 9th release of the open-access database of transcription factor binding profiles. <i>Nucleic Acids Research</i> , 2022, 50, D165-D173.	6.5	902
4	BioMart “ biological queries made easy. <i>BMC Genomics</i> , 2009, 10, 22.	1.2	738
5	Ensembl 2009. <i>Nucleic Acids Research</i> , 2009, 37, D690-D697.	6.5	721
6	Ensembl 2007. <i>Nucleic Acids Research</i> , 2007, 35, D610-D617.	6.5	699
7	Five-Vertebrate ChIP-seq Reveals the Evolutionary Dynamics of Transcription Factor Binding. <i>Science</i> , 2010, 328, 1036-1040.	6.0	663
8	Waves of Retrotransposon Expansion Remodel Genome Organization and CTCF Binding in Multiple Mammalian Lineages. <i>Cell</i> , 2012, 148, 335-348.	13.5	528
9	Ensembl 2008. <i>Nucleic Acids Research</i> , 2007, 36, D707-D714.	6.5	440
10	BioMart Central Portal “unified access to biological data. <i>Nucleic Acids Research</i> , 2009, 37, W23-W27.	6.5	311
11	Ensembl's 10th year. <i>Nucleic Acids Research</i> , 2010, 38, D557-D562.	6.5	251
12	ReMap 2018: an updated atlas of regulatory regions from an integrative analysis of DNA-binding ChIP-seq experiments. <i>Nucleic Acids Research</i> , 2018, 46, D267-D275.	6.5	214
13	ReMap 2022: a database of Human, Mouse, Drosophila and Arabidopsis regulatory regions from an integrative analysis of DNA-binding sequencing experiments. <i>Nucleic Acids Research</i> , 2022, 50, D316-D325.	6.5	160
14	The chromatin environment shapes DNA replication origin organization and defines origin classes. <i>Genome Research</i> , 2015, 25, 1873-1885.	2.4	149
15	High-throughput and quantitative assessment of enhancer activity in mammals by CapStarr-seq. <i>Nature Communications</i> , 2015, 6, 6905.	5.8	138
16	Gene expression profiling identifies molecular subgroups among nodal peripheral T-cell lymphomas. <i>Oncogene</i> , 2006, 25, 1560-1570.	2.6	132
17	Involvement of G-quadruplex regions in mammalian replication origin activity. <i>Nature Communications</i> , 2019, 10, 3274.	5.8	120
18	Integrative analysis of public ChIP-seq experiments reveals a complex multi-cell regulatory landscape. <i>Nucleic Acids Research</i> , 2015, 43, e27-e27.	6.5	113

#	ARTICLE	IF	CITATIONS
19	ReMap 2020: a database of regulatory regions from an integrative analysis of Human and Arabidopsis DNA-binding sequencing experiments. <i>Nucleic Acids Research</i> , 2020, 48, D180-D188.	6.5	95
20	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. <i>ELife</i> , 2014, 3, e02626.	2.8	84
21	A map of direct TF-DNA interactions in the human genome. <i>Nucleic Acids Research</i> , 2019, 47, e21-e21.	6.5	72
22	A predictable conserved DNA base composition signature defines human core DNA replication origins. <i>Nature Communications</i> , 2020, 11, 4826.	5.8	41
23	Gene profiling reveals specific oncogenic mechanisms and signaling pathways in oncocytic and papillary thyroid carcinoma. <i>Oncogene</i> , 2005, 24, 4155-4161.	2.6	40
24	Strand selective generation of endo-siRNAs from the Na/phosphate transporter gene <i>Slc34a1</i> in murine tissues. <i>Nucleic Acids Research</i> , 2009, 37, 2274-2282.	6.5	39
25	Insights gained from a comprehensive all-against-all transcription factor binding motif benchmarking study. <i>Genome Biology</i> , 2020, 21, 114.	3.8	39
26	TAF4, a subunit of transcription factor II D, directs promoter occupancy of nuclear receptor HNF4A during post-natal hepatocyte differentiation. <i>ELife</i> , 2014, 3, e03613.	2.8	35
27	The <i>Sgp3</i> Locus on Mouse Chromosome 13 Regulates Nephritogenic gp70 Autoantigen Expression and Predisposes to Autoimmunity. <i>Journal of Immunology</i> , 2003, 171, 3872-3877.	0.4	29
28	Consistent annotation of gene expression arrays. <i>BMC Genomics</i> , 2010, 11, 294.	1.2	23
29	A CpG Mutational Hotspot in a ONECUT Binding Site Accounts for the Prevalent Variant of Hemophilia B Leyden. <i>American Journal of Human Genetics</i> , 2013, 92, 460-467.	2.6	23
30	Identification of proteomic signatures of mantle cell lymphoma, small lymphocytic lymphoma, and marginal zone lymphoma biopsies by surface enhanced laser desorption/ionization-time of flight mass spectrometry. <i>Leukemia and Lymphoma</i> , 2011, 52, 648-658.	0.6	8
31	Waves of Retrotransposon Expansion Remodel Genome Organization and CTCF Binding in Multiple Mammalian Lineages. <i>Cell</i> , 2012, 148, 832.	13.5	6
32	The gene regulation knowledge commons: the action area of GREEKC. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2022, 1865, 194768.	0.9	3
33	Anomaly detection in genomic catalogues using unsupervised multi-view autoencoders. <i>BMC Bioinformatics</i> , 2021, 22, 460.	1.2	0