

Nicolas Bertin

List of Publications by Year in descending order

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46
papers

15,978
citations

126708

33
h-index

243296

44
g-index

52
all docs

52
docs citations

52
times ranked

24560
citing authors

#	ARTICLE	IF	CITATIONS
1	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
2	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
3	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. <i>Nature</i> , 2004, 430, 88-93.	13.7	1,683
4	A Map of the Interactome Network of the Metazoan <i>C. elegans</i> . <i>Science</i> , 2004, 303, 540-543.	6.0	1,587
5	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
6	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	3.8	687
7	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 140, 744-752.	13.5	667
8	Network modeling links breast cancer susceptibility and centrosome dysfunction. <i>Nature Genetics</i> , 2007, 39, 1338-1349.	9.4	602
9	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	6.0	517
10	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. <i>Genome Research</i> , 2004, 14, 1107-1118.	2.4	516
11	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456
12	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
13	<i>C. elegans</i> ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression. <i>Nature Genetics</i> , 2003, 34, 35-41.	9.4	347
14	Effect of sampling on topology predictions of protein-protein interaction networks. <i>Nature Biotechnology</i> , 2005, 23, 839-844.	9.4	302
15	Genome-scale analysis of in vivo spatiotemporal promoter activity in <i>Caenorhabditis elegans</i> . <i>Nature Biotechnology</i> , 2007, 25, 663-668.	9.4	286
16	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566.	9.4	271
17	Functional Genomic Analysis of RNA Interference in <i>C. elegans</i> . <i>Science</i> , 2005, 308, 1164-1167.	6.0	266
18	Predictive models of molecular machines involved in <i>Caenorhabditis elegans</i> early embryogenesis. <i>Nature</i> , 2005, 436, 861-865.	13.7	260

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19	Empirically controlled mapping of the <i>Caenorhabditis elegans</i> protein-protein interactome network. <i>Nature Methods</i> , 2009, 6, 47-54.	9.0	260
20	Unexpected expression of $\hat{1}\alpha$ - and $\hat{1}\beta$ -globin in mesencephalic dopaminergic neurons and glial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15454-15459.	3.3	240
21	Human ORFeome Version 1.1: A Platform for Reverse Proteomics. <i>Genome Research</i> , 2004, 14, 2128-2135.	2.4	208
22	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011, 21, 1150-1159.	2.4	172
23	Integrating Interactome, Phenome, and Transcriptome Mapping Data for the <i>C. elegans</i> Germline. <i>Current Biology</i> , 2002, 12, 1952-1958.	1.8	170
24	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , 2014, 32, 217-219.	9.4	163
25	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	9.0	152
26	Systematic Interactome Mapping and Genetic Perturbation Analysis of a <i>C. elegans</i> TGF- $\hat{1}\beta$ Signaling Network. <i>Molecular Cell</i> , 2004, 13, 469-482.	4.5	136
27	Differential roles of epigenetic changes and <i>Foxp3</i> expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5289-5294.	3.3	111
28	Confirmation of Organized Modularity in the Yeast Interactome. <i>PLoS Biology</i> , 2007, 5, e153.	2.6	86
29	Generation of the <i>Brucella melitensis</i> ORFeome Version 1.1. <i>Genome Research</i> , 2004, 14, 2201-2206.	2.4	77
30	Super-Enhancers and Broad H3K4me3 Domains Form Complex Gene Regulatory Circuits Involving Chromatin Interactions. <i>Scientific Reports</i> , 2017, 7, 2186.	1.6	70
31	Promoter architecture of mouse olfactory receptor genes. <i>Genome Research</i> , 2012, 22, 486-497.	2.4	52
32	Digital expression profiling of the compartmentalized translome of Purkinje neurons. <i>Genome Research</i> , 2014, 24, 1396-1410.	2.4	49
33	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 73-83.	0.5	39
34	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017, 4, 170147.	2.4	29
35	A resource of ribosomal RNA-depleted RNA-Seq data from different normal adult and fetal human tissues. <i>Scientific Data</i> , 2015, 2, 150063.	2.4	24
36	Comprehensive Characterization of Transcriptional Activity during Influenza A Virus Infection Reveals Biases in Cap-Snatching of Host RNA Sequences. <i>Journal of Virology</i> , 2020, 94, .	1.5	14

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37	NanoCAGE analysis of the mouse olfactory epithelium identifies the expression of vomeronasal receptors and of proximal LINE elements. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 41.	1.8	11
38	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
39	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , 2014, 15, 1177.	1.2	10
40	Development of a high-throughput method for the systematic identification of human proteins nuclear translocation potential. <i>BMC Cell Biology</i> , 2009, 10, 69.	3.0	5
41	Lymphocyte cytosolic protein 1 (LCP1) is a novel TRAF3 dysregulation biomarker with potential prognostic value in multiple myeloma. <i>Genome Instability & Disease</i> , 2020, 1, 286-299.	0.5	5
42	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010, 141, 369.	13.5	4
43	Reply to Toward the complete interactome. <i>Nature Biotechnology</i> , 2006, 24, 615-615.	9.4	1
44	A model of the BRCA1/BRCA2 network. <i>Breast Cancer Research</i> , 2005, 7, 1.	2.2	0
45	Using CAGE Data for Quantitative Expression. , 2009, , 101-121.		0
46	Forward and Reverse Proteomics. , 2003, , 255-276.		0