

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
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52
all docs

52
docs citations

52
times ranked

24560
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
2	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
3	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
4	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
5	Super-Enhancers and Broad H3K4me3 Domains Form Complex Gene Regulatory Circuits Involving Chromatin Interactions. <i>Scientific Reports</i> , 2017, 7, 2186.	1.6	70
6	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017, 4, 170147.	2.4	29
7	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456
8	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
9	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	6.0	517
10	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	3.8	687
11	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
12	Differential roles of epigenetic changes and Foxp3 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
13	Digital expression profiling of the compartmentalized translome of Purkinje neurons. <i>Genome Research</i> , 2014, 24, 1396-1410.	2.4	49
14	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. <i>Nature Biotechnology</i> , 2014, 32, 217-219.	9.4	163
15	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
16	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	13.7	2,269
17	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
18	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

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19	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. BMC Genomics, 2014, 15, 1177.	1.2	10
20	Promoter architecture of mouse olfactory receptor genes. Genome Research, 2012, 22, 486-497.	2.4	52
21	Unamplified cap analysis of gene expression on a single-molecule sequencer. Genome Research, 2011, 21, 1150-1159.	2.4	172
22	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. Nature Methods, 2010, 7, 528-534.	9.0	152
23	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 140, 744-752.	13.5	667
24	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. Cell, 2010, 141, 369.	13.5	4
25	Development of a high-throughput method for the systematic identification of human proteins nuclear translocation potential. BMC Cell Biology, 2009, 10, 69.	3.0	5
26	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	9.4	408
27	Empirically controlled mapping of the Caenorhabditis elegans protein-protein interactome network. Nature Methods, 2009, 6, 47-54.	9.0	260
28	Unexpected expression of $\hat{1}\pm$ - and $\hat{1}^2$ -globin in mesencephalic dopaminergic neurons and glial cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15454-15459.	3.3	240
29	Using CAGE Data for Quantitative Expression. , 2009, , 101-121.		0
30	Confirmation of Organized Modularity in the Yeast Interactome. PLoS Biology, 2007, 5, e153.	2.6	86
31	Genome-scale analysis of in vivo spatiotemporal promoter activity in Caenorhabditis elegans. Nature Biotechnology, 2007, 25, 663-668.	9.4	286
32	Network modeling links breast cancer susceptibility and centrosome dysfunction. Nature Genetics, 2007, 39, 1338-1349.	9.4	602
33	Reply to Toward the complete interactome. Nature Biotechnology, 2006, 24, 615-615.	9.4	1
34	Effect of sampling on topology predictions of protein-protein interaction networks. Nature Biotechnology, 2005, 23, 839-844.	9.4	302
35	Predictive models of molecular machines involved in Caenorhabditis elegans early embryogenesis. Nature, 2005, 436, 861-865.	13.7	260
36	Functional Genomic Analysis of RNA Interference in C. elegans. Science, 2005, 308, 1164-1167.	6.0	266

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37	A model of the BRCA1/BRCA2 network. Breast Cancer Research, 2005, 7, 1.	2.2	0
38	Annotation Transfer Between Genomes: Protein-Protein Interologs and Protein-DNA Regulogs. Genome Research, 2004, 14, 1107-1118.	2.4	516
39	Generation of the Brucella melitensis ORFeome Version 1.1. Genome Research, 2004, 14, 2201-2206.	2.4	77
40	Human ORFeome Version 1.1: A Platform for Reverse Proteomics. Genome Research, 2004, 14, 2128-2135.	2.4	208
41	Evidence for dynamically organized modularity in the yeast protein-protein interaction network. Nature, 2004, 430, 88-93.	13.7	1,683
42	A Map of the Interactome Network of the Metazoan C. elegans. Science, 2004, 303, 540-543.	6.0	1,587
43	Systematic Interactome Mapping and Genetic Perturbation Analysis of a C. elegans TGF- β Signaling Network. Molecular Cell, 2004, 13, 469-482.	4.5	136
44	C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression. Nature Genetics, 2003, 34, 35-41.	9.4	347
45	Forward and Reverse Proteomics. , 2003, , 255-276.		0
46	Integrating Interactome, Phenome, and Transcriptome Mapping Data for the C. elegans Germline. Current Biology, 2002, 12, 1952-1958.	1.8	170