

Michiel J L De Hoon

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56
papers

10,660
citations

30
h-index

59
g-index

59
ext. papers

13,600
ext. citations

12.2
avg, IF

5.51
L-index

#	Paper	IF	Citations
56	Open source clustering software. <i>Bioinformatics</i> , 2004 , 20, 1453-4	7.2	2321
55	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009 , 25, 1422-3	7.2	2308
54	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
53	An atlas of human long non-coding RNAs with accurate 5Xends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
52	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015 , 16, 22	18.3	443
51	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015 , 347, 1010-4	33.3	384
50	Site-specific DICER and DROSHA RNA products control the DNA-damage response. <i>Nature</i> , 2012 , 488, 231-5	50.4	380
49	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
48	DBTBS: a database of transcriptional regulation in <i>Bacillus subtilis</i> containing upstream intergenic conservation information. <i>Nucleic Acids Research</i> , 2008 , 36, D93-6	20.1	290
47	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017 , 35, 872-878	44.5	282
46	A comprehensive survey of 3Xanimal miRNA modification events and a possible role for 3Xadenylation in modulating miRNA targeting effectiveness. <i>Genome Research</i> , 2010 , 20, 1398-410	9.7	269
45	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014 , 46, 558-66	36.3	203
44	Hierarchical evolution of the bacterial sporulation network. <i>Current Biology</i> , 2010 , 20, R735-45	6.3	145
43	Prediction of transcriptional terminators in <i>Bacillus subtilis</i> and related species. <i>PLoS Computational Biology</i> , 2005 , 1, e25	5	140
42	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014 , 123, e58-67	2.2	126
41	PAPD5-mediated 3Xadenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11467-72	11.5	106
40	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010 , 20, 257-64	9.7	105

39	Deep cap analysis gene expression (CAGE): genome-wide identification of promoters, quantification of their expression, and network inference. <i>BioTechniques</i> , 2008 , 44, 627-8, 630, 632	2.5	74
38	Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , 2015 , 26, 391-402	3.2	73
37	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014 , 123, e79-89	2.2	59
36	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009 , 10, R39	18.3	56
35	Optimization of turn-back primers in isothermal amplification. <i>Nucleic Acids Research</i> , 2011 , 39, e59	20.1	54
34	Batf2/Irf1 induces inflammatory responses in classically activated macrophages, lipopolysaccharides, and mycobacterial infection. <i>Journal of Immunology</i> , 2015 , 194, 6035-44	5.3	49
33	Statistical analysis of a small set of time-ordered gene expression data using linear splines. <i>Bioinformatics</i> , 2002 , 18, 1477-85	7.2	48
32	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072	9.7	41
31	Transcriptome analysis of controlled and therapy-resistant childhood asthma reveals distinct gene expression profiles. <i>Journal of Allergy and Clinical Immunology</i> , 2015 , 136, 638-48	11.5	40
30	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015 , 43, 6969-82	20.1	38
29	Temporal dynamics and transcriptional control using single-cell gene expression analysis. <i>Genome Biology</i> , 2013 , 14, R118	18.3	34
28	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRescueLite. <i>Bioinformatics</i> , 2009 , 25, 2613-4	7.2	32
27	Reconstruction of monocyte transcriptional regulatory network accompanies monocytic functions in human fibroblasts. <i>PLoS ONE</i> , 2012 , 7, e33474	3.7	31
26	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	3.7	25
25	Identification of ZNF395 as a novel modulator of adipogenesis. <i>Experimental Cell Research</i> , 2013 , 319, 68-76	4.2	25
24	Multiplicity of 5Xcap structures present on short RNAs. <i>PLoS ONE</i> , 2014 , 9, e102895	3.7	22
23	Inferring Gene Regulatory Networks from Time-Ordered Gene Expression Data Using Differential Equations. <i>Lecture Notes in Computer Science</i> , 2002 , 267-274	0.9	22
22	Predicting gene regulation by sigma factors in <i>Bacillus subtilis</i> from genome-wide data. <i>Bioinformatics</i> , 2004 , 20 Suppl 1, i101-8	7.2	21

21	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. <i>Nucleic Acids Research</i> , 2021 , 49, D892-D898	20.1	19
20	Hon-yaku: a biology-driven Bayesian methodology for identifying translation initiation sites in prokaryotes. <i>BMC Bioinformatics</i> , 2007 , 8, 47	3.6	18
19	Comparison of RNA- or LNA-hybrid oligonucleotides in template-switching reactions for high-speed sequencing library preparation. <i>BMC Genomics</i> , 2013 , 14, 665	4.5	17
18	Cold phase fluid model of the longitudinal dynamics of space-charge-dominated beams. <i>Physics of Plasmas</i> , 2003 , 10, 855-861	2.1	15
17	Overview of theory and modeling in the heavy ion fusion virtual national laboratory. <i>Laser and Particle Beams</i> , 2002 , 20, 377-384	0.9	14
16	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020 , 30, 1073-1081	9.7	13
15	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020 , 30, 951-961	9.7	12
14	Effect of thiazole orange doubly labeled thymidine on DNA duplex formation. <i>Biochemistry</i> , 2012 , 51, 6056-67	3.2	11
13	Systemic identification of estrogen-regulated genes in breast cancer cells through cap analysis of gene expression mapping. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 447, 531-6	3.4	10
12	Recent advances in functional genome analysis. <i>F1000Research</i> , 2018 , 7,	3.6	10
11	Planning for an integrated research experiment. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2001 , 464, 621-628 ^{1,2}		9
10	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6
9	Results from the scaled final focus experiment. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2001 , 464, 126-133 ^{1,2}		5
8	Simulation of the LBNL scaled final focus experiment. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2001 , 464, 278-283 ^{1,2}		4
7	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. <i>Nature Communications</i> , 2021 , 12, 925	17.4	4
6	A Model for Pulsed Activation Accounting for Circulation, Extraction, and Makeup. <i>Fusion Science and Technology</i> , 1998 , 34, 974-979		3
5	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021 , 12, 3297	17.4	3
4	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021 , 19, e3001419	9.7	2

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| 3 | Functional annotation of human long noncoding RNAs using chromatin conformation data | 1 |
| 2 | Combined inhibition of XIAP and BCL2 drives maximal therapeutic efficacy in genetically diverse aggressive acute myeloid leukemia.. <i>Nature Cancer</i> , 2021 , 2, 340-356 | 15.4 ○ |
| 1 | The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. <i>BMC Genomic Data</i> , 2021 , 22, 33 | ○ |