Michiel J L De Hoon

List of Publications by Year
in descending order

54	15,173	136950	168389
papers	citations	32	53
		h-index	g-index

59	59	59	29854
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Biopython: freely available Python tools for computational molecular biology and bioinformatics. Bioinformatics, 2009, 25, 1422-1423.	4.1	4,097
2	Open source clustering software. Bioinformatics, 2004, 20, 1453-1454.	4.1	2,768
3	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
4	An atlas of human long non-coding RNAs with accurate 5â€² ends. Nature, 2017, 543, 199-204.	27.8	898
5	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
6	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
7	Site-specific DICER and DROSHA RNA products control the DNA-damage response. Nature, 2012, 488, 231-235.	27.8	460
8	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456
9	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	21.4	408
10	DBTBS: a database of transcriptional regulation in Bacillus subtilis containing upstream intergenic conservation information. Nucleic Acids Research, 2008, 36, D93-D96.	14.5	339
11	A comprehensive survey of 3â€² animal miRNA modification events and a possible role for 3â€² adenylation in modulating miRNA targeting effectiveness. Genome Research, 2010, 20, 1398-1410.	5.5	309
12	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. Nature Genetics, 2014, 46, 558-566.	21.4	271
13	Hierarchical Evolution of the Bacterial Sporulation Network. Current Biology, 2010, 20, R735-R745.	3.9	183
14	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. Blood, 2014, 123, e58-e67.	1.4	175
15	Prediction of Transcriptional Terminators in Bacillus subtilis and Related Species. PLoS Computational Biology, 2005, 1, e25.	3.2	158
16	PAPD5-mediated 3â€² adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11467-11472.	7.1	130
17	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. Genome Research, 2010, 20, 257-264.	5.5	126
18	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109

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19	Paradigm shifts in genomics through the FANTOM projects. Mammalian Genome, 2015, 26, 391-402.	2.2	96
20	Deep cap analysis gene expression (CAGE): genome-wide identification of promoters, quantification of their expression, and network inference. BioTechniques, 2008, 44, 627-632.	1.8	87
21	Batf2/Irf1 Induces Inflammatory Responses in Classically Activated Macrophages, Lipopolysaccharides, and Mycobacterial Infection. Journal of Immunology, 2015, 194, 6035-6044.	0.8	83
22	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. Blood, 2014, 123, e79-e89.	1.4	72
23	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. Genome Biology, 2009, 10, R39.	9.6	67
24	Optimization of turn-back primers in isothermal amplification. Nucleic Acids Research, 2011, 39, e59-e59.	14.5	66
25	Transcriptome analysis of controlled and therapy-resistant childhood asthma reveals distinct gene expression profiles. Journal of Allergy and Clinical Immunology, 2015, 136, 638-648.	2.9	59
26	FANTOM enters 20th year: expansion of transcriptomic atlases and functional annotation of non-coding RNAs. Nucleic Acids Research, 2021, 49, D892-D898.	14.5	57
27	Statistical analysis of a small set of time-ordered gene expression data using linear splines. Bioinformatics, 2002, 18, 1477-1485.	4.1	54
28	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. Nucleic Acids Research, 2015, 43, 6969-6982.	14.5	54
29	Temporal dynamics and transcriptional control using single-cell gene expression analysis. Genome Biology, 2013, 14, R118.	9.6	43
30	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRescueLite. Bioinformatics, 2009, 25, 2613-2614.	4.1	41
31	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. Molecular Genetics and Metabolism, 2014, 112, 73-83.	1.1	39
32	Reconstruction of Monocyte Transcriptional Regulatory Network Accompanies Monocytic Functions in Human Fibroblasts. PLoS ONE, 2012, 7, e33474.	2.5	36
33	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	5.5	35
34	Identification of ZNF395 as a novel modulator of adipogenesis. Experimental Cell Research, 2013, 319, 68-76.	2.6	32
35	Inferring Gene Regulatory Networks from Time-Ordered Gene Expression Data Using Differential Equations. Lecture Notes in Computer Science, 2002, , 267-274.	1.3	32
36	Comparative transcriptomics of primary cells in vertebrates. Genome Research, 2020, 30, 951-961.	5.5	29

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37	Multiplicity of 5′ Cap Structures Present on Short RNAs. PLoS ONE, 2014, 9, e102895.	2.5	29
38	Predicting gene regulation by sigma factors in Bacillus subtilis from genome-wide data. Bioinformatics, 2004, 20, i101-i108.	4.1	25
39	Hon-yaku: a biology-driven Bayesian methodology for identifying translation initiation sites in prokaryotes. BMC Bioinformatics, 2007, 8, 47.	2.6	23
40	Comparison of RNA- or LNA-hybrid oligonucleotides in template-switching reactions for high-speed sequencing library preparation. BMC Genomics, 2013, 14, 665.	2.8	23
41	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. Nature Communications, 2021, 12, 925.	12.8	18
42	Recent advances in functional genome analysis. F1000Research, 2018, 7, 1968.	1.6	16
43	Cold phase fluid model of the longitudinal dynamics of space-charge-dominated beams. Physics of Plasmas, 2003, 10, 855-861.	1.9	15
44	Overview of theory and modeling in the heavy ion fusion virtual national laboratory. Laser and Particle Beams, 2002, 20, 377-384.	1.0	14
45	Systemic identification of estrogen-regulated genes in breast cancer cells through cap analysis of gene expression mapping. Biochemical and Biophysical Research Communications, 2014, 447, 531-536.	2.1	14
46	Effect of Thiazole Orange Doubly Labeled Thymidine on DNA Duplex Formation. Biochemistry, 2012, 51, 6056-6067.	2.5	13
47	Planning for an integrated research experiment. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2001, 464, 621-628.	1.6	11
48	Combined inhibition of XIAP and BCL2 drives maximal therapeutic efficacy in genetically diverse aggressive acute myeloid leukemia. Nature Cancer, 2021, 2, 340-356.	13.2	11
49	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
50	Results from the scaled final focus experiment. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2001, 464, 126-133.	1.6	8
51	Simulation of the LBNL scaled final focus experiment. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2001, 464, 278-283.	1.6	6
52	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	5.6	6
53	A Model for Pulsed Activation Accounting for Circulation, Extraction, and Makeup. Fusion Science and Technology, 1998, 34, 974-979.	0.6	3
54	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. BMC Genomic Data, 2021, 22, 33.	1.7	0