

# Michiel J L De Hoon

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7414898/publications.pdf>

Version: 2024-02-01

54  
papers

15,173  
citations

136950

32  
h-index

168389

53  
g-index

59  
all docs

59  
docs citations

59  
times ranked

29854  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. Nature Communications, 2021, 12, 925.	12.8	18
3	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
4	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
5	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
6	A field guide to cultivating computational biology. PLoS Biology, 2021, 19, e3001419.	5.6	6
7	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
8	Comparative transcriptomics of primary cells in vertebrates. Genome Research, 2020, 30, 951-961.	5.5	29
9	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	5.5	35
10	Recent advances in functional genome analysis. F1000Research, 2018, 7, 1968.	1.6	16
11	An atlas of human long non-coding RNAs with accurate 5' ends. Nature, 2017, 543, 199-204.	27.8	898
12	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	17.5	456
13	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. Science, 2015, 347, 1010-1014.	12.6	517
14	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
15	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
16	Batf2/Irf1 Induces Inflammatory Responses in Classically Activated Macrophages, Lipopolysaccharides, and Mycobacterial Infection. Journal of Immunology, 2015, 194, 6035-6044.	0.8	83
17	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. Nucleic Acids Research, 2015, 43, 6969-6982.	14.5	54
18	Paradigm shifts in genomics through the FANTOM projects. Mammalian Genome, 2015, 26, 391-402.	2.2	96

#	ARTICLE	IF	CITATIONS
19	PAPD5-mediated 3' 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
20	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
21	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
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	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
24	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
25	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. Blood, 2014, 123, e58-e67.	1.4	175
26	Multiplicity of 5' Cap Structures Present on Short RNAs. PLoS ONE, 2014, 9, e102895.	2.5	29
27	Identification of ZNF395 as a novel modulator of adipogenesis. Experimental Cell Research, 2013, 319, 68-76.	2.6	32
28	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
29	Temporal dynamics and transcriptional control using single-cell gene expression analysis. Genome Biology, 2013, 14, R118.	9.6	43
30	Effect of Thiazole Orange Doubly Labeled Thymidine on DNA Duplex Formation. Biochemistry, 2012, 51, 6056-6067.	2.5	13
31	Reconstruction of Monocyte Transcriptional Regulatory Network Accompanies Monocytic Functions in Human Fibroblasts. PLoS ONE, 2012, 7, e33474.	2.5	36
32	Site-specific DICER and DROSHA RNA products control the DNA-damage response. Nature, 2012, 488, 231-235.	27.8	460
33	Optimization of turn-back primers in isothermal amplification. Nucleic Acids Research, 2011, 39, e59-e59.	14.5	66
34	Hierarchical Evolution of the Bacterial Sporulation Network. Current Biology, 2010, 20, R735-R745.	3.9	183
35	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
36	A comprehensive survey of 3' animal miRNA modification events and a possible role for 3' adenylation in modulating miRNA targeting effectiveness. Genome Research, 2010, 20, 1398-1410.	5.5	309

#	ARTICLE	IF	CITATIONS
37	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRescueLite. Bioinformatics, 2009, 25, 2613-2614.	4.1	41
38	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
39	Biopython: freely available Python tools for computational molecular biology and bioinformatics. Bioinformatics, 2009, 25, 1422-1423.	4.1	4,097
40	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. Genome Biology, 2009, 10, R39.	9.6	67
41	DBTBS: a database of transcriptional regulation in Bacillus subtilis containing upstream intergenic conservation information. Nucleic Acids Research, 2008, 36, D93-D96.	14.5	339
42	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
43	Hon-yaku: a biology-driven Bayesian methodology for identifying translation initiation sites in prokaryotes. BMC Bioinformatics, 2007, 8, 47.	2.6	23
44	Prediction of Transcriptional Terminators in Bacillus subtilis and Related Species. PLoS Computational Biology, 2005, 1, e25.	3.2	158
45	Predicting gene regulation by sigma factors in Bacillus subtilis from genome-wide data. Bioinformatics, 2004, 20, i101-i108.	4.1	25
46	Open source clustering software. Bioinformatics, 2004, 20, 1453-1454.	4.1	2,768
47	Cold phase fluid model of the longitudinal dynamics of space-charge-dominated beams. Physics of Plasmas, 2003, 10, 855-861.	1.9	15
48	Statistical analysis of a small set of time-ordered gene expression data using linear splines. Bioinformatics, 2002, 18, 1477-1485.	4.1	54
49	Overview of theory and modeling in the heavy ion fusion virtual national laboratory. Laser and Particle Beams, 2002, 20, 377-384.	1.0	14
50	Inferring Gene Regulatory Networks from Time-Ordered Gene Expression Data Using Differential Equations. Lecture Notes in Computer Science, 2002, , 267-274.	1.3	32
51	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
52	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
53	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
54	A Model for Pulsed Activation Accounting for Circulation, Extraction, and Makeup. Fusion Science and Technology, 1998, 34, 974-979.	0.6	3