

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

136740
32
h-index

168136
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. <i>Nucleic Acids Research</i> , 2021, 49, D892-D898.	6.5	57
2	LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. <i>Nature Communications</i> , 2021, 12, 925.	5.8	18
3	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.	5.7	11
4	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	5.8	11
5	The choice of negative control antisense oligonucleotides dramatically impacts downstream analysis depending on the cellular background. <i>BMC Genomic Data</i> , 2021, 22, 33.	0.7	0
6	A field guide to cultivating computational biology. <i>PLoS Biology</i> , 2021, 19, e3001419.	2.6	6
7	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020, 30, 1060-1072.	2.4	109
8	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020, 30, 951-961.	2.4	29
9	Recounting the FANTOM CAGE-Associated Transcriptome. <i>Genome Research</i> , 2020, 30, 1073-1081.	2.4	35
10	Recent advances in functional genome analysis. <i>F1000Research</i> , 2018, 7, 1968.	0.8	16
11	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
12	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	9.4	456
13	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015, 347, 1010-1014.	6.0	517
14	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015, 16, 22.	3.8	687
15	Transcriptome analysis of controlled and therapy-resistant childhood asthma reveals distinct gene expression profiles. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 136, 638-648.	1.5	59
16	Batf2/Irf1 Induces Inflammatory Responses in Classically Activated Macrophages, Lipopolysaccharides, and Mycobacterial Infection. <i>Journal of Immunology</i> , 2015, 194, 6035-6044.	0.4	83
17	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015, 43, 6969-6982.	6.5	54
18	Paradigm shifts in genomics through the FANTOM projects. <i>Mammalian Genome</i> , 2015, 26, 391-402.	1.0	96

#	ARTICLE	IF	CITATIONS
19	PAPD5-mediated 3' adenylation 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, 11467-11472.	3.3	130
20	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
21	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, 531-536.	1.0	14
22	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014, 123, e79-e89.	0.6	72
23	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
24	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
25	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014, 123, e58-e67.	0.6	175
26	Multiplicity of 5' Cap Structures Present on Short RNAs. <i>PLoS ONE</i> , 2014, 9, e102895.	1.1	29
27	Identification of ZNF395 as a novel modulator of adipogenesis. <i>Experimental Cell Research</i> , 2013, 319, 68-76.	1.2	32
28	Comparison of RNA- or LNA-hybrid oligonucleotides in template-switching reactions for high-speed sequencing library preparation. <i>BMC Genomics</i> , 2013, 14, 665.	1.2	23
29	Temporal dynamics and transcriptional control using single-cell gene expression analysis. <i>Genome Biology</i> , 2013, 14, R118.	13.9	43
30	Effect of Thiazole Orange Doubly Labeled Thymidine on DNA Duplex Formation. <i>Biochemistry</i> , 2012, 51, 6056-6067.	1.2	13
31	Reconstruction of Monocyte Transcriptional Regulatory Network Accompanies Monocytic Functions in Human Fibroblasts. <i>PLoS ONE</i> , 2012, 7, e33474.	1.1	36
32	Site-specific DICER and DROSHA RNA products control the DNA-damage response. <i>Nature</i> , 2012, 488, 231-235.	13.7	460
33	Optimization of turn-back primers in isothermal amplification. <i>Nucleic Acids Research</i> , 2011, 39, e59-e59.	6.5	66
34	Hierarchical Evolution of the Bacterial Sporulation Network. <i>Current Biology</i> , 2010, 20, R735-R745.	1.8	183
35	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010, 20, 257-264.	2.4	126
36	A comprehensive survey of 3' animal miRNA modification events and a possible role for 3' adenylation in modulating miRNA targeting effectiveness. <i>Genome Research</i> , 2010, 20, 1398-1410.	2.4	309

#	ARTICLE	IF	CITATIONS
37	Probabilistic resolution of multi-mapping reads in massively parallel sequencing data using MuMRescueLite. <i>Bioinformatics</i> , 2009, 25, 2613-2614.	1.8	41
38	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
39	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009, 25, 1422-1423.	1.8	4,097
40	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009, 10, R39.	13.9	67
41	DBTBS: a database of transcriptional regulation in <i>Bacillus subtilis</i> containing upstream intergenic conservation information. <i>Nucleic Acids Research</i> , 2008, 36, D93-D96.	6.5	339
42	Deep cap analysis gene expression (CAGE): genome-wide identification of promoters, quantification of their expression, and network inference. <i>BioTechniques</i> , 2008, 44, 627-632.	0.8	87
43	Hon-yaku: a biology-driven Bayesian methodology for identifying translation initiation sites in prokaryotes. <i>BMC Bioinformatics</i> , 2007, 8, 47.	1.2	23
44	Prediction of Transcriptional Terminators in <i>Bacillus subtilis</i> and Related Species. <i>PLoS Computational Biology</i> , 2005, 1, e25.	1.5	158
45	Predicting gene regulation by sigma factors in <i>Bacillus subtilis</i> from genome-wide data. <i>Bioinformatics</i> , 2004, 20, i101-i108.	1.8	25
46	Open source clustering software. <i>Bioinformatics</i> , 2004, 20, 1453-1454.	1.8	2,768
47	Cold phase fluid model of the longitudinal dynamics of space-charge-dominated beams. <i>Physics of Plasmas</i> , 2003, 10, 855-861.	0.7	15
48	Statistical analysis of a small set of time-ordered gene expression data using linear splines. <i>Bioinformatics</i> , 2002, 18, 1477-1485.	1.8	54
49	Overview of theory and modeling in the heavy ion fusion virtual national laboratory. <i>Laser and Particle Beams</i> , 2002, 20, 377-384.	0.4	14
50	Inferring Gene Regulatory Networks from Time-Ordered Gene Expression Data Using Differential Equations. <i>Lecture Notes in Computer Science</i> , 2002, , 267-274.	1.0	32
51	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.	0.7	8
52	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.	0.7	6
53	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.	0.7	11
54	A Model for Pulsed Activation Accounting for Circulation, Extraction, and Makeup. <i>Fusion Science and Technology</i> , 1998, 34, 974-979.	0.6	3