

Stijn Van Dongen

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.

29
papers

12,010
citations

21
h-index

31
g-index

31
ext. papers

13,472
ext. citations

13.6
avg, IF

6.16
L-index

#	Paper	IF	Citations
29	miRBase: microRNA sequences, targets and gene nomenclature. <i>Nucleic Acids Research</i> , 2006 , 34, D140-40.1	40.1	3494
28	miRBase: tools for microRNA genomics. <i>Nucleic Acids Research</i> , 2008 , 36, D154-8	20.1	3326
27	Requirement of bic/microRNA-155 for normal immune function. <i>Science</i> , 2007 , 316, 608-11	33.3	1584
26	Zebrafish MiR-430 promotes deadenylation and clearance of maternal mRNAs. <i>Science</i> , 2006 , 312, 75-9	33.3	1222
25	Graph Clustering Via a Discrete Uncoupling Process. <i>SIAM Journal on Matrix Analysis and Applications</i> , 2008 , 30, 121-141	1.5	290
24	RNA editing of human microRNAs. <i>Genome Biology</i> , 2006 , 7, R27	18.3	270
23	An ENU-induced mutation of miR-96 associated with progressive hearing loss in mice. <i>Nature Genetics</i> , 2009 , 41, 614-8	36.3	249
22	Kraken: a set of tools for quality control and analysis of high-throughput sequence data. <i>Methods</i> , 2013 , 63, 41-9	4.6	242
21	Using MCL to extract clusters from networks. <i>Methods in Molecular Biology</i> , 2012 , 804, 281-95	1.4	221
20	Detecting microRNA binding and siRNA off-target effects from expression data. <i>Nature Methods</i> , 2008 , 5, 1023-5	21.6	220
19	Malignant germ cell tumors display common microRNA profiles resulting in global changes in expression of messenger RNA targets. <i>Cancer Research</i> , 2010 , 70, 2911-23	10.1	201
18	Construction, visualisation, and clustering of transcription networks from microarray expression data. <i>PLoS Computational Biology</i> , 2007 , 3, 2032-42	5	190
17	Targeted deletion of microRNA-22 promotes stress-induced cardiac dilation and contractile dysfunction. <i>Circulation</i> , 2012 , 125, 2751-61	16.7	134
16	LIN28 Expression in malignant germ cell tumors downregulates let-7 and increases oncogene levels. <i>Cancer Research</i> , 2013 , 73, 4872-84	10.1	50
15	The two most common histological subtypes of malignant germ cell tumour are distinguished by global microRNA profiles, associated with differential transcription factor expression. <i>Molecular Cancer</i> , 2010 , 9, 290	42.1	48
14	Extent, causes, and consequences of small RNA expression variation in human adipose tissue. <i>PLoS Genetics</i> , 2012 , 8, e1002704	6	43
13	Mirnova: genome-free prediction of microRNAs from small RNA sequencing data and single-cells using decision forests. <i>Nucleic Acids Research</i> , 2017 , 45, e177	20.1	35

12	Many si/shRNAs can kill cancer cells by targeting multiple survival genes through an off-target mechanism. <i>ELife</i> , 2017 , 6,	8.9	35
11	Large-scale analysis of microRNA expression, epi-transcriptomic features and biogenesis. <i>Nucleic Acids Research</i> , 2017 , 45, 1079-1090	20.1	33
10	Depletion of HPV16 early genes induces autophagy and senescence in a cervical carcinogenesis model, regardless of viral physical state. <i>Journal of Pathology</i> , 2013 , 231, 354-66	9.4	28
9	Transposon-driven transcription is a conserved feature of vertebrate spermatogenesis and transcript evolution. <i>EMBO Reports</i> , 2017 , 18, 1231-1247	6.5	26
8	MiR-277/4989 regulate transcriptional landscape during juvenile to adult transition in the parasitic helminth <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005559	4.8	21
7	Messenger RNA and microRNA profiling during early mouse EB formation. <i>Gene Expression Patterns</i> , 2011 , 11, 334-44	1.5	16
6	Exploring regulatory networks of miR-96 in the developing inner ear. <i>Scientific Reports</i> , 2016 , 6, 23363	4.9	11
5	GeneMCL in microarray analysis. <i>Computational Biology and Chemistry</i> , 2005 , 29, 354-9	3.6	10
4	Large-scale identification of microRNA targets in murine Dgcr8-deficient embryonic stem cell lines. <i>PLoS ONE</i> , 2012 , 7, e41762	3.7	8
3	Single-cell Atlas of common variable immunodeficiency shows germinal center-associated epigenetic dysregulation in B-cell responses.. <i>Nature Communications</i> , 2022 , 13, 1779	17.4	2
2	Visualization and analysis of RNA-Seq assembly graphs. <i>Nucleic Acids Research</i> , 2019 , 47, 7262-7275	20.1	1
1	Detecting MicroRNA Signatures Using Gene Expression Analysis 2014 , 129-150		