

Jo Vandesompele

List of Publications by Year in Descending Order

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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.

314
papers

48,942
citations

82
h-index

220
g-index

376
ext. papers

56,511
ext. citations

8.5
avg, IF

7.26
L-index

#	Paper	IF	Citations
314	Transient nuclear lamin A/C accretion aids in recovery from vapor nanobubble-induced permeabilisation of the plasma membrane.. <i>Cellular and Molecular Life Sciences</i> , 2022 , 79, 23	10.3	2
313	RNA biomarkers from proximal liquid biopsy for diagnosis of ovarian cancer.. <i>Neoplasia</i> , 2022 , 24, 155-164	6.4	1
312	Comprehensive RNA dataset of tissue and plasma from patients with esophageal cancer or precursor lesions.. <i>Scientific Data</i> , 2022 , 9, 86	8.2	0
311	Evaluation of efficiency and sensitivity of 1D and 2D sample pooling strategies for SARS-CoV-2 RT-qPCR screening purposes.. <i>Scientific Reports</i> , 2022 , 12, 6603	4.9	0
310	The dangers of using Cq to quantify nucleic acid in biological samples; a lesson from COVID-19. <i>Clinical Chemistry</i> , 2021 ,	5.5	4
309	MISpheroid: a knowledgebase and transparency tool for minimum information in spheroid identity. <i>Nature Methods</i> , 2021 , 18, 1294-1303	21.6	4
308	Genome-wide study of the effect of blood collection tubes on the cell-free DNA methylome. <i>Epigenetics</i> , 2021 , 16, 797-807	5.7	6
307	A G316A Polymorphism in the Ornithine Decarboxylase Gene Promoter Modulates MYCN-Driven Childhood Neuroblastoma. <i>Cancers</i> , 2021 , 13,	6.6	1
306	Messenger RNA capture sequencing of extracellular RNA from human biofluids using a comprehensive set of spike-in controls. <i>STAR Protocols</i> , 2021 , 2, 100475	1.4	1
305	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021 , 39, 1453-1465	44.5	15
304	The MicroRNA Landscape of Acute Beta Cell Destruction in Type 1 Diabetic Recipients of Intraportal Islet Grafts. <i>Cells</i> , 2021 , 10,	7.9	2
303	Closing the circle: current state and perspectives of circular RNA databases. <i>Briefings in Bioinformatics</i> , 2021 , 22, 288-297	13.4	37
302	Minimally invasive classification of paediatric solid tumours using reduced representation bisulphite sequencing of cell-free DNA: a proof-of-principle study. <i>Epigenetics</i> , 2021 , 16, 196-208	5.7	7
301	Candidate RNA biomarkers in biofluids for early diagnosis of ovarian cancer: A systematic review. <i>Gynecologic Oncology</i> , 2021 , 160, 633-642	4.9	10
300	Targeted Therapy of -Rearranged Neuroblastoma with BET Bromodomain Inhibitor and Proteasome Inhibitor Combination Therapy. <i>Clinical Cancer Research</i> , 2021 , 27, 1438-1451	12.9	8
299	Recurrent chromosomal imbalances provide selective advantage to human embryonic stem cells under enhanced replicative stress conditions. <i>Genes Chromosomes and Cancer</i> , 2021 , 60, 272-281	5	0
298	Circulating RNA biomarkers in diffuse large B-cell lymphoma: a systematic review. <i>Experimental Hematology and Oncology</i> , 2021 , 10, 13	7.8	3

297	Validation of Circular RNAs Using RT-qPCR After Effective Removal of Linear RNAs by Ribonuclease R. <i>Current Protocols</i> , 2021 , 1, e181		3
296	Evaluating Diagnostic Accuracy of Saliva Sampling Methods for Severe Acute Respiratory Syndrome Coronavirus 2 Reveals Differential Sensitivity and Association with Viral Load. <i>Journal of Molecular Diagnostics</i> , 2021 , 23, 1249-1258	5.1	2
295	Robust sequential biophysical fractionation of blood plasma to study variations in the biomolecular landscape of systemically circulating extracellular vesicles across clinical conditions. <i>Journal of Extracellular Vesicles</i> , 2021 , 10, e12122	16.4	3
294	The long non-coding RNA SAMMSON is essential for uveal melanoma cell survival. <i>Oncogene</i> , 2021 ,	9.2	3
293	A public-private partnership model for COVID-19 diagnostics. <i>Nature Biotechnology</i> , 2021 , 39, 1182-1184	44.5	0
292	Custom long non-coding RNA capture enhances detection sensitivity in different human sample types. <i>RNA Biology</i> , 2021 , 1-8	4.8	0
291	Selection and validation of reference genes for accurate RT-qPCR gene expression normalization in cacao beans during fermentation. <i>Tree Genetics and Genomes</i> , 2021 , 17, 1	2.1	2
290	Distinct Notch1 and BCL11B requirements mediate human γ T cell development. <i>EMBO Reports</i> , 2020 , 21, e49006	6.5	14
289	SPsimSeq: semi-parametric simulation of bulk and single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2020 , 36, 3276-3278	7.2	12
288	Charting Extracellular Transcriptomes in The Human Biofluid RNA Atlas. <i>Cell Reports</i> , 2020 , 33, 108552	10.6	19
287	Vapor nanobubble is the more reliable photothermal mechanism for inducing endosomal escape of siRNA without disturbing cell homeostasis. <i>Journal of Controlled Release</i> , 2020 , 319, 262-275	11.7	29
286	The Digital MIQE Guidelines Update: Minimum Information for Publication of Quantitative Digital PCR Experiments for 2020. <i>Clinical Chemistry</i> , 2020 , 66, 1012-1029	5.5	85
285	When DNA gets in the way: A cautionary note for DNA contamination in extracellular RNA-seq studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 18934-18936	11.5	7
284	Cautionary Note on Contamination of Reagents Used for Molecular Detection of SARS-CoV-2. <i>Clinical Chemistry</i> , 2020 , 66, 1369-1372	5.5	20
283	Increased levels of systemic LPS-positive bacterial extracellular vesicles in patients with intestinal barrier dysfunction. <i>Gut</i> , 2020 , 69, 191-193	19.2	82
282	On the utility of RNA sample pooling to optimize cost and statistical power in RNA sequencing experiments. <i>BMC Genomics</i> , 2020 , 21, 312	4.5	24
281	SMARTer single cell total RNA sequencing. <i>Nucleic Acids Research</i> , 2019 , 47, e93	20.1	21
280	Evaluating the applicability of mouse SINEs as an alternative normalization approach for RT-qPCR in brain tissue of the APP23 model for Alzheimer's disease. <i>Journal of Neuroscience Methods</i> , 2019 , 320, 128-137	3	5

279	Purification of high-quality RNA from a small number of fluorescence activated cell sorted zebrafish cells for RNA sequencing purposes. <i>BMC Genomics</i> , 2019 , 20, 228	4.5	2
278	Integrative analysis identifies lincRNAs up- and downstream of neuroblastoma driver genes. <i>Scientific Reports</i> , 2019 , 9, 5685	4.9	6
277	The generation and use of recombinant extracellular vesicles as biological reference material. <i>Nature Communications</i> , 2019 , 10, 3288	17.4	54
276	The long noncoding RNA lincNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. <i>Nature Communications</i> , 2019 , 10, 5026	17.4	40
275	Cost-effective and robust genotyping using double-mismatch allele-specific quantitative PCR. <i>Scientific Reports</i> , 2019 , 9, 2150	4.9	18
274	Performance assessment of total RNA sequencing of human biofluids and extracellular vesicles. <i>Scientific Reports</i> , 2019 , 9, 17574	4.9	29
273	Discovery and validation of a serum microRNA signature to characterize oligo- and polymetastatic prostate cancer: not ready for prime time. <i>World Journal of Urology</i> , 2019 , 37, 2557-2564	4	14
272	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019 , 47, D221-D229	10.2	90
271	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. <i>Genes Chromosomes and Cancer</i> , 2019 , 58, 191-199	5	86
270	LNCipedia 5: towards a reference set of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019 , 47, D135-D139	20.1	215
269	Cross-Cohort Analysis Identifies a TEAD4-MYCN Positive Feedback Loop as the Core Regulatory Element of High-Risk Neuroblastoma. <i>Cancer Discovery</i> , 2018 , 8, 582-599	24.4	58
268	Comparative analysis of naive, primed and ground state pluripotency in mouse embryonic stem cells originating from the same genetic background. <i>Scientific Reports</i> , 2018 , 8, 5884	4.9	35
267	Computational deconvolution of transcriptomics data from mixed cell populations. <i>Bioinformatics</i> , 2018 , 34, 1969-1979	7.2	96
266	Prognostic and Therapeutic Implications of Circulating Androgen Receptor Gene Copy Number in Prostate Cancer Patients Using Droplet Digital Polymerase Chain Reaction. <i>Clinical Genitourinary Cancer</i> , 2018 , 16, 197-205.e5	3.3	6
265	On determining the power of digital PCR experiments. <i>Analytical and Bioanalytical Chemistry</i> , 2018 , 410, 5731-5739	4.4	2
264	Localization and Expression of Nuclear Factor of Activated T-Cells 5 in Myoblasts Exposed to Pro-inflammatory Cytokines or Hyperosmolar Stress and in Biopsies from Myositis Patients. <i>Frontiers in Physiology</i> , 2018 , 9, 126	4.6	8
263	Differential gene expression analysis tools exhibit substandard performance for long non-coding RNA-sequencing data. <i>Genome Biology</i> , 2018 , 19, 96	18.3	28
262	A high-throughput 3PUTR reporter screening identifies microRNA interactomes of cancer genes. <i>PLoS ONE</i> , 2018 , 13, e0194017	3.7	12

261	Circulating microRNA biomarkers for metastatic disease in neuroblastoma patients. <i>JCI Insight</i> , 2018 , 3,	9.9	22
260	The mutational landscape of , and driven murine neuroblastoma mimics human disease. <i>Oncotarget</i> , 2018 , 9, 8334-8349	3.3	3
259	A mechanistic classification of clinical phenotypes in neuroblastoma. <i>Science</i> , 2018 , 362, 1165-1170	33.3	115
258	In silico discovery of a FOXM1 driven embryonal signaling pathway in therapy resistant neuroblastoma tumors. <i>Scientific Reports</i> , 2018 , 8, 17468	4.9	8
257	Targeted Genomic Screen Reveals Focal Long Non-Coding RNA Copy Number Alterations in Cancer Cell Lines. <i>Non-coding RNA</i> , 2018 , 4,	7.1	5
256	Expressed repetitive elements are broadly applicable reference targets for normalization of reverse transcription-qPCR data in mice. <i>Scientific Reports</i> , 2018 , 8, 7642	4.9	10
255	The cancer-associated microprotein CASIMO1 controls cell proliferation and interacts with squalene epoxidase modulating lipid droplet formation. <i>Oncogene</i> , 2018 , 37, 4750-4768	9.2	64
254	Detecting long non-coding RNA biomarkers in prostate cancer liquid biopsies: Hype or hope?. <i>Non-coding RNA Research</i> , 2018 , 3, 64-74	6	23
253	A comprehensive inventory of TLX1 controlled long non-coding RNAs in T-cell acute lymphoblastic leukemia through polyA+ and total RNA sequencing. <i>Haematologica</i> , 2018 , 103, e585-e589	6.6	9
252	EV-TRACK: transparent reporting and centralizing knowledge in extracellular vesicle research. <i>Nature Methods</i> , 2017 , 14, 228-232	21.6	560
251	Reply: Direct Detection of Circulating MicroRNAs Unveiled the Absence of MicroRNA-218-5p in Smoker Subjects. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017 , 196, 533	10.2	
250	Noncoding after All: Biases in Proteomics Data Do Not Explain Observed Absence of lncRNA Translation Products. <i>Journal of Proteome Research</i> , 2017 , 16, 2508-2515	5.6	22
249	MicroRNA-184 is a downstream effector of albuminuria driving renal fibrosis in rats with diabetic nephropathy. <i>Diabetologia</i> , 2017 , 60, 1114-1125	10.3	44
248	Model-Based Classification for Digital PCR: Your Umbrella for Rain. <i>Analytical Chemistry</i> , 2017 , 89, 4461-4467	4.5	23
247	Evaluation of relative quantification of alternatively spliced transcripts using droplet digital PCR. <i>Biomolecular Detection and Quantification</i> , 2017 , 13, 40-48	12	7
246	MicroRNA Expression Analysis Using Small RNA Sequencing Discovery and RT-qPCR-Based Validation. <i>Methods in Molecular Biology</i> , 2017 , 1654, 197-208	1.4	0
245	A unified censored normal regression model for qPCR differential gene expression analysis. <i>PLoS ONE</i> , 2017 , 12, e0182832	3.7	5
244	Thermodynamic framework to assess low abundance DNA mutation detection by hybridization. <i>PLoS ONE</i> , 2017 , 12, e0177384	3.7	4

243	High-throughput PCR assay design for targeted resequencing using primerXL. <i>BMC Bioinformatics</i> , 2017 , 18, 400	3.6	10
242	Dual targeting of MDM2 and BCL2 as a therapeutic strategy in neuroblastoma. <i>Oncotarget</i> , 2017 , 8, 57047-57056	3.3	5
241	decodeRNA- predicting non-coding RNA functions using guilt-by-association. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	11
240	Quality control of digital PCR assays and platforms. <i>Analytical and Bioanalytical Chemistry</i> , 2017 , 409, 5919-5931	4.4	8
239	Zipper plot: visualizing transcriptional activity of genomic regions. <i>BMC Bioinformatics</i> , 2017 , 18, 231	3.6	5
238	The transcriptome of lung tumor-infiltrating dendritic cells reveals a tumor-supporting phenotype and a microRNA signature with negative impact on clinical outcome. <i>Oncolimmunology</i> , 2017 , 6, e1253655	7.2	40
237	MicroRNA Profiling Reveals a Role for MicroRNA-218-5p in the Pathogenesis of Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017 , 195, 43-56	10.2	90
236	Expression Profiling Identifies the Noncoding Processed Transcript of HNRNPU with Proliferative Properties in Pancreatic Ductal Adenocarcinoma. <i>Non-coding RNA</i> , 2017 , 3,	7.1	9
235	Influence of microRNAs and Long Non-Coding RNAs in Cancer Chemoresistance. <i>Genes</i> , 2017 , 8,	4.2	79
234	Abstract LB-107: EV-TRACK: transparent reporting and centralizing knowledge of extracellular vesicles to support the validation of extracellular vesicle biomarkers in cancer research 2017 ,		4
233	Long non-coding RNAs in cutaneous melanoma: clinical perspectives. <i>Oncotarget</i> , 2017 , 8, 43470-43480	3.3	29
232	Secretome analysis of breast cancer-associated adipose tissue to identify paracrine regulators of breast cancer growth. <i>Oncotarget</i> , 2017 , 8, 47239-47249	3.3	9
231	miSTAR: miRNA target prediction through modeling quantitative and qualitative miRNA binding site information in a stacked model structure. <i>Nucleic Acids Research</i> , 2017 , 45, e51	20.1	12
230	Flexible analysis of digital PCR experiments using generalized linear mixed models. <i>Biomolecular Detection and Quantification</i> , 2016 , 9, 1-13	12	9
229	Straightforward and sensitive RT-qPCR based gene expression analysis of FFPE samples. <i>Scientific Reports</i> , 2016 , 6, 21418	4.9	22
228	Differential expression of lncRNAs during the HIV replication cycle: an underestimated layer in the HIV-host interplay. <i>Scientific Reports</i> , 2016 , 6, 36111	4.9	20
227	DNA methylation profiling of primary neuroblastoma tumors using methyl-CpG-binding domain sequencing. <i>Scientific Data</i> , 2016 , 3, 160004	8.2	10
226	Targeted resequencing and variant validation using pxlence PCR assays. <i>Biomolecular Detection and Quantification</i> , 2016 , 6, 22-6	12	1

225	Melanoma addiction to the long non-coding RNA SAMMSON. <i>Nature</i> , 2016 , 531, 518-22	50.4	355
224	Methyl-CpG-binding domain sequencing reveals a prognostic methylation signature in neuroblastoma. <i>Oncotarget</i> , 2016 , 7, 1960-72	3.3	16
223	Long non-coding RNA expression profiling in the NCI60 cancer cell line panel using high-throughput RT-qPCR. <i>Scientific Data</i> , 2016 , 3, 160052	8.2	4
222	Depletion of tRNA-halves enables effective small RNA sequencing of low-input murine serum samples. <i>Scientific Reports</i> , 2016 , 6, 37876	4.9	8
221	Long noncoding RNA signatures define oncogenic subtypes in T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2016 , 30, 1927-30	10.7	26
220	Asthma inflammatory phenotypes show differential microRNA expression in sputum. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 137, 1433-46	11.5	127
219	Stage 4S neuroblastoma tumors show a characteristic DNA methylation portrait. <i>Epigenetics</i> , 2016 , 11, 761-771	5.7	15
218	RT-qPCR gene expression analysis in zebrafish: Preanalytical precautions and use of expressed repetitive elements for normalization. <i>Methods in Cell Biology</i> , 2016 , 135, 329-42	1.8	6
217	Renal microRNA- and RNA-profiles in progressive chronic kidney disease. <i>European Journal of Clinical Investigation</i> , 2016 , 46, 213-26	4.6	71
216	Individual patient risk stratification of high-risk neuroblastomas using a two-gene score suited for clinical use. <i>International Journal of Cancer</i> , 2015 , 137, 868-77	7.5	8
215	An update on LNCipedia: a database for annotated human lncRNA sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D174-80	20.1	212
214	RNA expression signatures and posttranscriptional regulation in diabetic nephropathy. <i>Nephrology Dialysis Transplantation</i> , 2015 , 30 Suppl 4, iv35-42	4.3	25
213	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. <i>Cancer Letters</i> , 2015 , 366, 123-32	9.9	31
212	Identification of miRNAs contributing to neuroblastoma chemoresistance. <i>Computational and Structural Biotechnology Journal</i> , 2015 , 13, 307-19	6.8	17
211	Genome wide expression profiling of p53 regulated miRNAs in neuroblastoma. <i>Scientific Reports</i> , 2015 , 5, 9027	4.9	26
210	RDML-Ninja and RDMLdb for standardized exchange of qPCR data. <i>BMC Bioinformatics</i> , 2015 , 16, 197	3.6	9
209	Non-coding RNAs and respiratory disease. <i>Thorax</i> , 2015 , 70, 388-90	7.3	13
208	miR-542-3p exerts tumor suppressive functions in neuroblastoma by downregulating Survivin. <i>International Journal of Cancer</i> , 2015 , 136, 1308-20	7.5	65

207	Revised risk estimation and treatment stratification of low- and intermediate-risk neuroblastoma patients by integrating clinical and molecular prognostic markers. <i>Clinical Cancer Research</i> , 2015 , 21, 1904-15	12.9	53
206	MicroRNA-193b-3p acts as a tumor suppressor by targeting the MYB oncogene in T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2015 , 29, 798-806	10.7	80
205	Inhibition of CDK4/6 as a novel therapeutic option for neuroblastoma. <i>Cancer Cell International</i> , 2015 , 15, 76	6.4	26
204	MiR-34a deficiency accelerates medulloblastoma formation in vivo. <i>International Journal of Cancer</i> , 2015 , 136, 2293-303	7.5	32
203	Alternative Routes to Induce Naïve Pluripotency in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2015 , 33, 2686-98	5.8	91
202	Flexible, scalable, and efficient targeted resequencing on a benchtop sequencer for variant detection in clinical practice. <i>Human Mutation</i> , 2015 , 36, 379-87	4.7	34
201	Non-coding RNAs in the pathogenesis of COPD. <i>Thorax</i> , 2015 , 70, 782-91	7.3	52
200	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015 , 16, 133	18.3	212
199	MYCN-targeting miRNAs are predominantly downregulated during MYCN-driven neuroblastoma tumor formation. <i>Oncotarget</i> , 2015 , 6, 5204-16	3.3	32
198	RT-qPCR-based quantification of small non-coding RNAs. <i>Methods in Molecular Biology</i> , 2015 , 1296, 85-102	10.4	12
197	Lung tumours reprogram pulmonary dendritic cell immunogenicity at the microRNA level. <i>International Journal of Cancer</i> , 2014 , 135, 2868-77	7.5	22
196	Cancer-associated adipose tissue promotes breast cancer progression by paracrine oncostatin M and Jak/STAT3 signaling. <i>Cancer Research</i> , 2014 , 74, 6806-19	10.1	83
195	The Notch driven long non-coding RNA repertoire in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2014 , 99, 1808-16	6.6	36
194	Early targets of miR-34a in neuroblastoma. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2114-31	7.6	22
193	Target enrichment using parallel nanoliter quantitative PCR amplification. <i>BMC Genomics</i> , 2014 , 15, 184	4.5	16
192	Illumina sequencing of 15 deafness genes using fragmented amplicons. <i>BMC Research Notes</i> , 2014 , 7, 509	2.3	
191	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , 2014 , 32, 903-14	44.5	618
190	Evaluation of quantitative miRNA expression platforms in the microRNA quality control (miRQC) study. <i>Nature Methods</i> , 2014 , 11, 809-15	21.6	463

189	Pharmacologic activation of wild-type p53 by nutlin therapy in childhood cancer. <i>Cancer Letters</i> , 2014 , 344, 157-65	9.9	33
188	The impact of disparate isolation methods for extracellular vesicles on downstream RNA profiling. <i>Journal of Extracellular Vesicles</i> , 2014 , 3,	16.4	533
187	Expressed repeat elements improve RT-qPCR normalization across a wide range of zebrafish gene expression studies. <i>PLoS ONE</i> , 2014 , 9, e109091	3.7	27
186	CASP8 SNP D302H (rs1045485) is associated with worse survival in MYCN-amplified neuroblastoma patients. <i>PLoS ONE</i> , 2014 , 9, e114696	3.7	14
185	miRBase Tracker: keeping track of microRNA annotation changes. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014,	5	71
184	MicroRNA-128-3p is a novel oncomiR targeting PHF6 in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2014 , 99, 1326-33	6.6	47
183	Lack of association between MDM2 promoter SNP309 and clinical outcome in patients with neuroblastoma. <i>Pediatric Blood and Cancer</i> , 2014 , 61, 1867-70	3	4
182	Ectopic microRNA-150-5p transcription sensitizes glucocorticoid therapy response in MM1S multiple myeloma cells but fails to overcome hormone therapy resistance in MM1R cells. <i>PLoS ONE</i> , 2014 , 9, e113842	3.7	31
181	Selection of reliable reference genes for RT-qPCR analysis. <i>Methods in Molecular Biology</i> , 2014 , 1160, 19-26	1.4	81
180	The NOTCH1 Driven Long Non-Coding RNA Repertoire in T-Cell Acute Lymphoblastic Leukemia. <i>Blood</i> , 2014 , 124, 900-900	2.2	
179	MYCN and ALKF1174L are sufficient to drive neuroblastoma development from neural crest progenitor cells. <i>Oncogene</i> , 2013 , 32, 1059-65	9.2	71
178	Modulation of neuroblastoma disease pathogenesis by an extensive network of epigenetically regulated microRNAs. <i>Oncogene</i> , 2013 , 32, 2927-36	9.2	72
177	The need for transparency and good practices in the qPCR literature. <i>Nature Methods</i> , 2013 , 10, 1063-7	21.6	197
176	Of flies, mice and men: a systematic approach to understanding the early life origins of chronic lung disease. <i>Thorax</i> , 2013 , 68, 380-4	7.3	33
175	Reference loci for RT-qPCR analysis of differentiating human embryonic stem cells. <i>BMC Molecular Biology</i> , 2013 , 14, 21	4.5	27
174	Evaluation of qPCR curve analysis methods for reliable biomarker discovery: bias, resolution, precision, and implications. <i>Methods</i> , 2013 , 59, 32-46	4.6	168
173	MiR-137 functions as a tumor suppressor in neuroblastoma by downregulating KDM1A. <i>International Journal of Cancer</i> , 2013 , 133, 1064-73	7.5	84
172	Regulatory microRNA network identification in bovine blastocyst development. <i>Stem Cells and Development</i> , 2013 , 22, 1907-20	4.4	32

171	Identification of miR-145 as a key regulator of the pigmentary process. <i>Journal of Investigative Dermatology</i> , 2013 , 133, 201-9	4.3	74
170	The digital MIQE guidelines: Minimum Information for Publication of Quantitative Digital PCR Experiments. <i>Clinical Chemistry</i> , 2013 , 59, 892-902	5.5	554
169	Single-nucleotide polymorphisms and other mismatches reduce performance of quantitative PCR assays. <i>Clinical Chemistry</i> , 2013 , 59, 1470-80	5.5	114
168	DNA methylation silences miR-132 in prostate cancer. <i>Oncogene</i> , 2013 , 32, 127-34	9.2	125
167	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. <i>Nucleic Acids Research</i> , 2013 , 41, D246-51	20.1	400
166	Effective Alu repeat based RT-Qpcr normalization in cancer cell perturbation experiments. <i>PLoS ONE</i> , 2013 , 8, e71776	3.7	9
165	Focal DNA copy number changes in neuroblastoma target MYCN regulated genes. <i>PLoS ONE</i> , 2013 , 8, e52321	3.7	31
164	CLL cells respond to B-Cell receptor stimulation with a microRNA/mRNA signature associated with MYC activation and cell cycle progression. <i>PLoS ONE</i> , 2013 , 8, e60275	3.7	27
163	Expanding The TLX1-Regulome In T Cell Acute Lymphoblastic Leukemia Towards Long Non-Coding RNAs. <i>Blood</i> , 2013 , 122, 813-813	2.2	
162	Lysine-specific demethylase 1 restricts hematopoietic progenitor proliferation and is essential for terminal differentiation. <i>Leukemia</i> , 2012 , 26, 2039-51	10.7	141
161	microRNAs in colon cancer: a roadmap for discovery. <i>FEBS Letters</i> , 2012 , 586, 3000-7	3.8	29
160	Genome-wide promoter methylation analysis in neuroblastoma identifies prognostic methylation biomarkers. <i>Genome Biology</i> , 2012 , 13, R95	18.3	51
159	Synthetic lethality between Rb, p53 and Dicer or miR-17-92 in retinal progenitors suppresses retinoblastoma formation. <i>Nature Cell Biology</i> , 2012 , 14, 958-65	23.4	69
158	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012 , 44, 1104-10	36.3	919
157	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. <i>BMC Medical Genomics</i> , 2012 , 5, 17	3.7	46
156	LIN28B induces neuroblastoma and enhances MYCN levels via let-7 suppression. <i>Nature Genetics</i> , 2012 , 44, 1199-206	36.3	273
155	N-cadherin in neuroblastoma disease: expression and clinical significance. <i>PLoS ONE</i> , 2012 , 7, e31206	3.7	27
154	miRNA expression profiling: from reference genes to global mean normalization. <i>Methods in Molecular Biology</i> , 2012 , 822, 261-72	1.4	118

153	Whole-genome RT-qPCR microRNA expression profiling. <i>Methods in Molecular Biology</i> , 2012 , 815, 121-30	4	3
152	Dickkopf-3 is regulated by the MYCN-induced miR-17-92 cluster in neuroblastoma. <i>International Journal of Cancer</i> , 2012 , 130, 2591-8	7.5	36
151	Identification of a novel recurrent 1q42.2-1qter deletion in high risk MYCN single copy 11q deleted neuroblastomas. <i>International Journal of Cancer</i> , 2012 , 130, 2599-606	7.5	31
150	Accurate RT-qPCR gene expression analysis on cell culture lysates. <i>Scientific Reports</i> , 2012 , 2, 222	4.9	38
149	Targeted expression of mutated ALK induces neuroblastoma in transgenic mice. <i>Science Translational Medicine</i> , 2012 , 4, 141ra91	17.5	119
148	Oncogenic activation of FOXR1 by 11q23 intrachromosomal deletion-fusions in neuroblastoma. <i>Oncogene</i> , 2012 , 31, 1571-81	9.2	44
147	Massively parallel sequencing for early molecular diagnosis in Leber congenital amaurosis. <i>Genetics in Medicine</i> , 2012 , 14, 576-85	8.1	37
146	Exon-level expression analyses identify MYCN and NTRK1 as major determinants of alternative exon usage and robustly predict primary neuroblastoma outcome. <i>British Journal of Cancer</i> , 2012 , 107, 1409-17	8.7	19
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2	The RNA Atlas, a single nucleotide resolution map of the human transcriptome		4
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