Jo Vandesompele

List of Publications by Year
in descending order

325 papers	61,706 citations	3933 88 h-index	932 240 g-index
376 all docs	376 docs citations	376 times ranked	84479 citing authors

#	Article	IF	Citations
1	Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. Genome Biology, 2002, 3, RESEARCH0034.	9.6	16,304
2	The MIQE Guidelines: Minimum Information for Publication of Quantitative Real-Time PCR Experiments. Clinical Chemistry, 2009, 55, 611-622.	3.2	12,487
3	qBase relative quantification framework and software for management and automated analysis of real-time quantitative PCR data. Genome Biology, 2007, 8, R19.	9.6	3,580
4	miR-9, a MYC/MYCN-activated microRNA, regulates E-cadherin and cancer metastasis. Nature Cell Biology, 2010, 12, 247-256.	10.3	1,216
5	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. Nature Genetics, 2012, 44, 1104-1110.	21.4	1,186
6	EV-TRACK: transparent reporting and centralizing knowledge in extracellular vesicle research. Nature Methods, 2017, 14, 228-232.	19.0	886
7	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	17.5	883
8	A novel and universal method for microRNA RT-qPCR data normalization. Genome Biology, 2009, 10, R64.	9.6	849
9	The impact of disparate isolation methods for extracellular vesicles on downstream RNA profiling. Journal of Extracellular Vesicles, 2014, 3, .	12.2	725
10	The Digital MIQE Guidelines: Minimum Information for Publication of Quantitative Digital PCR Experiments. Clinical Chemistry, 2013, 59, 892-902.	3.2	723
11	How to do successful gene expression analysis using real-time PCR. Methods, 2010, 50, 227-230.	3.8	582
12	Evaluation of quantitative miRNA expression platforms in the microRNA quality control (miRQC) study. Nature Methods, 2014, 11, 809-815.	19.0	564
13	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
14	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. Nucleic Acids Research, 2013, 41, D246-D251.	14.5	488
15	Melanoma addiction to the long non-coding RNA SAMMSON. Nature, 2016, 531, 518-522.	27.8	488
16	Gain of Chromosome Arm 17q and Adverse Outcome in Patients with Neuroblastoma. New England Journal of Medicine, 1999, 340, 1954-1961.	27.0	456
17	Standardization of real-time PCR gene expression data from independent biological replicates. Analytical Biochemistry, 2008, 379, 127-129.	2.4	417
18	Loss-of-function mutations in LEMD3 result in osteopoikilosis, Buschke-Ollendorff syndrome and melorheostosis. Nature Genetics, 2004, 36, 1213-1218.	21.4	410

#	Article	IF	Citations
19	LNCipedia 5: towards a reference set of human long non-coding RNAs. Nucleic Acids Research, 2019, 47, D135-D139.	14.5	403
20	Emerging patterns of cryptic chromosomal imbalance in patients with idiopathic mental retardation and multiple congenital anomalies: a new series of 140 patients and review of published reports. Journal of Medical Genetics, 2006, 43, 625-633.	3.2	342
21	LIN28B induces neuroblastoma and enhances MYCN levels via let-7 suppression. Nature Genetics, 2012, 44, 1199-1206.	21.4	336
22	Selection and validation of a set of reliable reference genes for quantitative sod gene expression analysis in C. elegans. BMC Molecular Biology, 2008, 9, 9.	3.0	327
23	Amphiregulin and Epiregulin mRNA Expression in Primary Tumors Predicts Outcome in Metastatic Colorectal Cancer Treated With Cetuximab. Journal of Clinical Oncology, 2009, 27, 5068-5074.	1.6	325
24	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. Genome Biology, 2015, 16, 133.	8.8	325
25	An update on LNCipedia: a database for annotated human lncRNA sequences. Nucleic Acids Research, 2015, 43, D174-D180.	14.5	298
26	The miR-17-92 MicroRNA Cluster Regulates Multiple Components of the TGF-β Pathway in Neuroblastoma. Molecular Cell, 2010, 40, 762-773.	9.7	279
27	Accurate and objective copy number profiling using real-time quantitative PCR. Methods, 2010, 50, 262-270.	3.8	273
28	Selection of reference genes for quantitative real-time PCR in bovine preimplantation embryos. BMC Developmental Biology, 2005, 5, 27.	2.1	269
29	High-throughput stem-loop RT-qPCR miRNA expression profiling using minute amounts of input RNA. Nucleic Acids Research, 2008, 36, e143-e143.	14.5	261
30	The need for transparency and good practices in the qPCR literature. Nature Methods, 2013, 10, 1063-1067.	19.0	251
31	The Digital MIQE Guidelines Update: Minimum Information for Publication of Quantitative Digital PCR Experiments for 2020. Clinical Chemistry, 2020, 66, 1012-1029.	3.2	247
32	Meta-analysis of Neuroblastomas Reveals a Skewed *ALK* Mutation Spectrum in Tumors with *MYCN* Amplification. Clinical Cancer Research, 2010, 16, 4353-4362.	7.0	243
33	RTPrimerDB: the Real-Time PCR primer and probe database. Nucleic Acids Research, 2003, 31, 122-123.	14.5	240
34	Distinct transcriptional MYCN/c-MYC activities are associated with spontaneous regression or malignant progression in neuroblastomas. Genome Biology, 2008, 9, R150.	9.6	215
35	A mechanistic classification of clinical phenotypes in neuroblastoma. Science, 2018, 362, 1165-1170.	12.6	213
36	MicroRNA Expression in Induced Sputum of Smokers and Patients with Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2011, 183, 898-906.	5.6	209

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37	Elimination of Primer–Dimer Artifacts and Genomic Coamplification Using a Two-Step SYBR Green I Real-Time RT-PCR. Analytical Biochemistry, 2002, 303, 95-98.	2.4	201
38	Evaluation of qPCR curve analysis methods for reliable biomarker discovery: Bias, resolution, precision, and implications. Methods, 2013, 59, 32-46.	3.8	197
39	MicroRNA expression profiling to identify and validate reference genes for relative quantification in colorectal cancer. BMC Cancer, 2010, 10, 173.	2.6	193
40	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. Nucleic Acids Research, 2010, 38, 5919-5928.	14.5	183
41	Computational deconvolution of transcriptomics data from mixed cell populations. Bioinformatics, 2018, 34, 1969-1979.	4.1	181
42	Predicting outcomes for children with neuroblastoma using a multigene-expression signature: a retrospective SIOPEN/COG/GPOH study. Lancet Oncology, The, 2009, 10, 663-671.	10.7	176
43	Lysine-specific demethylase 1 restricts hematopoietic progenitor proliferation and is essential for terminal differentiation. Leukemia, 2012, 26, 2039-2051.	7.2	171
44	Increased levels of systemic LPS-positive bacterial extracellular vesicles in patients with intestinal barrier dysfunction. Gut, 2020, 69, 191-193.	12.1	171
45	Asthma inflammatory phenotypes show differential microRNA expression in sputum. Journal of Allergy and Clinical Immunology, 2016, 137, 1433-1446.	2.9	168
46	Quantification of MYCN, DDX1, and NAG Gene Copy Number in Neuroblastoma Using a Real-Time Quantitative PCR Assay. Modern Pathology, 2002, 15, 159-166.	5.5	167
47	Unequivocal Delineation of Clinicogenetic Subgroups and Development of a New Model for Improved Outcome Prediction in Neuroblastoma. Journal of Clinical Oncology, 2005, 23, 2280-2299.	1.6	160
48	Molecular Dissection of Isolated Disease Features in Mosaic Neurofibromatosis Type 1. American Journal of Human Genetics, 2007, 81, 243-251.	6.2	157
49	Development of a new set of reference genes for normalization of real-time RT-PCR data of porcine backfat and longissimus dorsi muscle, and evaluation with PPARGC1A. BMC Biotechnology, 2006, 6, 41.	3.3	153
50	Single-Nucleotide Polymorphisms and Other Mismatches Reduce Performance of Quantitative PCR Assays. Clinical Chemistry, 2013, 59, 1470-1480.	3.2	153
51	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	14.5	153
52	Expression profiling suggests underexpression of the GABAA receptor subunit δ in the fragile X knockout mouse model. Neurobiology of Disease, 2006, 21, 346-357.	4.4	151
53	DNA methylation silences miR-132 in prostate cancer. Oncogene, 2013, 32, 127-134.	5.9	151
54	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. Science Translational Medicine, 2012, 4, 141ra91.	12.4	147

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55	Measurable impact of RNA quality on gene expression results from quantitative PCR. Nucleic Acids Research, 2011, 39, e63-e63.	14.5	146
56	miRNA Expression Profiling: From Reference Genes to Global Mean Normalization. Methods in Molecular Biology, 2012, 822, 261-272.	0.9	143
57	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. Oncogene, 2010, 29, 3583-3592.	5.9	141
58	Monoallelic but not biallelic loss of Dicer1 promotes tumorigenesis in vivo. Cell Death and Differentiation, 2010, 17, 633-641.	11.2	140
59	Human fetal neuroblast and neuroblastoma transcriptome analysis confirms neuroblast origin and highlights neuroblastoma candidate genes. Genome Biology, 2006, 7, R84.	9.6	134
60	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. Cell Death and Differentiation, 2011, 18, 974-984.	11.2	133
61	Small-Molecule MDM2 Antagonists as a New Therapy Concept for Neuroblastoma. Cancer Research, 2006, 66, 9646-9655.	0.9	132
62	RTPrimerDB: the portal for real-time PCR primers and probes. Nucleic Acids Research, 2009, 37, D942-D945.	14.5	132
63	Prognostic Impact of Gene Expression–Based Classification for Neuroblastoma. Journal of Clinical Oncology, 2010, 28, 3506-3515.	1.6	129
64	RDML: structured language and reporting guidelines for real-time quantitative PCR data. Nucleic Acids Research, 2009, 37, 2065-2069.	14.5	123
65	Genetic heterogeneity of neuroblastoma studied by comparative genomic hybridization. Genes Chromosomes and Cancer, 1998, 23, 141-152.	2.8	121
66	Quantification of splice variants using real-time PCR. Nucleic Acids Research, 2001, 29, 68e-68.	14.5	119
67	Cross-Cohort Analysis Identifies a TEAD4–MYCN Positive Feedback Loop as the Core Regulatory Element of High-Risk Neuroblastoma. Cancer Discovery, 2018, 8, 582-599.	9.4	119
68	Alternative Routes to Induce Naïve Pluripotency in Human Embryonic Stem Cells. Stem Cells, 2015, 33, 2686-2698.	3.2	118
69	Expression analyses identify MLL as a prominent target of 11q23 amplification and support an etiologic role for MLL gain of function in myeloid malignancies. Blood, 2004, 103, 229-235.	1.4	117
70	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. Genes Chromosomes and Cancer, 2019, 58, 191-199.	2.8	117
71	Comparative genomic hybridization (CGH) analysis of stage 4 neuroblastoma reveals high frequency of 11q deletion in tumors lackingMYCN amplification. International Journal of Cancer, 2001, 91, 680-686.	5.1	112
72	Widespread Dysregulation of MiRNAs by MYCN Amplification and Chromosomal Imbalances in Neuroblastoma: Association of miRNA Expression with Survival. PLoS ONE, 2009, 4, e7850.	2.5	112

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73	MYCN/c-MYC-induced microRNAs repress coding gene networks associated with poor outcome in MYCN/c-MYC-activated tumors. Oncogene, 2010, 29, 1394-1404.	5.9	112
74	Selection of Reliable Reference Genes for RT-qPCR Analysis. Methods in Molecular Biology, 2014, 1160, 19-26.	0.9	112
75	The cancer-associated microprotein CASIMO1 controls cell proliferation and interacts with squalene epoxidase modulating lipid droplet formation. Oncogene, 2018, 37, 4750-4768.	5.9	111
76	MicroRNA Profiling Reveals a Role for MicroRNA-218-5p in the Pathogenesis of Chronic Obstructive Pulmonary Disease. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 43-56.	5.6	108
77	RTPrimerDB: the real-time PCR primer and probe database, major update 2006. Nucleic Acids Research, 2006, 34, D684-D688.	14.5	107
78	A new recurrent inversion, inv(7)(p15q34), leads to transcriptional activation of HOXA10 and HOXA11 in a subset of T-cell acute lymphoblastic leukemias. Leukemia, 2005, 19, 358-366.	7.2	106
79	ComprehensiveNF1 screening on cultured Schwann cells from neurofibromas. Human Mutation, 2006, 27, 1030-1040.	2.5	105
80	Antitumor Activity of the Selective MDM2 Antagonist Nutlin-3 Against Chemoresistant Neuroblastoma With Wild-Type p53. Journal of the National Cancer Institute, 2009, 101, 1562-1574.	6.3	105
81	Cancer-Associated Adipose Tissue Promotes Breast Cancer Progression by Paracrine Oncostatin M and Jak/STAT3 Signaling. Cancer Research, 2014, 74, 6806-6819.	0.9	105
82	Rapid detection of VHL exon deletions using real-time quantitative PCR. Laboratory Investigation, 2005, 85, 24-33.	3.7	102
83	Influence of microRNAs and Long Non-Coding RNAs in Cancer Chemoresistance. Genes, 2017, 8, 95.	2.4	102
84	Identification of miR-145 as a Key Regulator of the Pigmentary Process. Journal of Investigative Dermatology, 2013, 133, 201-209.	0.7	99
85	Renal micro<scp>RNA</scp>â€•and <scp>RNA</scp>â€•profiles in progressive chronic kidney disease. European Journal of Clinical Investigation, 2016, 46, 213-226.	3.4	96
86	The generation and use of recombinant extracellular vesicles as biological reference material. Nature Communications, 2019, 10, 3288.	12.8	96
87	High <i>ALK</i> Receptor Tyrosine Kinase Expression Supersedes <i>ALK</i> Mutation as a Determining Factor of an Unfavorable Phenotype in Primary Neuroblastoma. Clinical Cancer Research, 2011, 17, 5082-5092.	7.0	95
88	Impact of RNA quality on reference gene expression stability. BioTechniques, 2005, 39, 52-56.	1.8	92
89	miRNA Expression Profiling Enables Risk Stratification in Archived and Fresh Neuroblastoma Tumor Samples. Clinical Cancer Research, 2011, 17, 7684-7692.	7.0	92
90	MiRâ€•137 functions as a tumor suppressor in neuroblastoma by downregulating KDM1A. International Journal of Cancer, 2013, 133, 1064-1073.	5.1	91

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91	MicroRNA-193b-3p acts as a tumor suppressor by targeting the MYB oncogene in T-cell acute lymphoblastic leukemia. Leukemia, 2015, 29, 798-806.	7.2	91
92	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. International Journal of Cancer, 2010, 127, 2374-2385.	5.1	88
93	Hsa-mir-145 is the top EWS-FLI1-repressed microRNA involved in a positive feedback loop in Ewing's sarcoma. Oncogene, 2011, 30, 2173-2180.	5.9	87
94	Accurate Outcome Prediction in Neuroblastoma across Independent Data Sets Using a Multigene Signature. Clinical Cancer Research, 2010, 16, 1532-1541.	7.0	86
95	MYCN and ALKF1174L are sufficient to drive neuroblastoma development from neural crest progenitor cells. Oncogene, 2013, 32, 1059-1065.	5.9	84
96	Modulation of neuroblastoma disease pathogenesis by an extensive network of epigenetically regulated microRNAs. Oncogene, 2013, 32, 2927-2936.	5.9	84
97	Multicentre analysis of patterns of DNA gains and losses in 204 neuroblastoma tumors: How many genetic subgroups are there?. Medical and Pediatric Oncology, 2001, 36, 5-10.	1.0	82
98	Revised Risk Estimation and Treatment Stratification of Low- and Intermediate-Risk Neuroblastoma Patients by Integrating Clinical and Molecular Prognostic Markers. Clinical Cancer Research, 2015, 21, 1904-1915.	7.0	80
99	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. BMC Bioinformatics, 2005, 6, 124.	2.6	79
100	Synthetic lethality between Rb, p53 and Dicer or miR-17â€"92 in retinal progenitors suppresses retinoblastoma formation. Nature Cell Biology, 2012, 14, 958-965.	10.3	79
101	miRâ€542â€3p exerts tumor suppressive functions in neuroblastoma by downregulating <scp>S</scp>urvivin. International Journal of Cancer, 2015, 136, 1308-1320.	5.1	78
102	The RNA Atlas expands the catalog of human non-coding RNAs. Nature Biotechnology, 2021, 39, 1453-1465.	17.5	75
103	Closing the circle: current state and perspectives of circular RNA databases. Briefings in Bioinformatics, 2021, 22, 288-297.	6.5	74
104	miRBase Tracker: keeping track of microRNA annotation changes. Database: the Journal of Biological Databases and Curation, 2014, 2014, .	3.0	73
105	The microRNA body map: dissecting microRNA function through integrative genomics. Nucleic Acids Research, 2011, 39, e136-e136.	14.5	72
106	Non-coding RNAs in the pathogenesis of COPD. Thorax, 2015, 70, 782-791.	5.6	71
107	Chromosomal and MicroRNA Expression Patterns Reveal Biologically Distinct Subgroups of 11qâˆ' Neuroblastoma. Clinical Cancer Research, 2010, 16, 2971-2978.	7.0	70
108	ArrayCGHâ€based classification of neuroblastoma into genomic subgroups. Genes Chromosomes and Cancer, 2007, 46, 1098-1108.	2.8	67

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109	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. Nature Communications, 2019, 10, 5026.	12.8	67
110	Real-Time Quantitative PCR as an Alternative to Southern Blot or Fluorescence *In Situ* Hybridization for Detection of Gene Copy Number Changes. , 2007, 353, 205-226.		64
111	Genome-wide promoter methylation analysis in neuroblastoma identifies prognostic methylation biomarkers. Genome Biology, 2012, 13, R95.	9.6	64
112	Gene-expression profiling reveals distinct expression patterns for Classic versus Variant Merkel cell phenotypes and new classifier genes to distinguish Merkel cell from small-cell lung carcinoma. Oncogene, 2004, 23, 2732-2742.	5.9	63
113	Primer Sequence Disclosure: A Clarification of the MIQE Guidelines. Clinical Chemistry, 2011, 57, 919-921.	3.2	63
114	Functional Analysis of the p53 Pathway in Neuroblastoma Cells Using the Small-Molecule MDM2 Antagonist Nutlin-3. Molecular Cancer Therapeutics, 2011, 10, 983-993.	4.1	61
115	Positional gene enrichment analysis of gene sets for high-resolution identification of overrepresented chromosomal regions. Nucleic Acids Research, 2008, 36, e43-e43.	14.5	56
116	On the utility of RNA sample pooling to optimize cost and statistical power in RNA sequencing experiments. BMC Genomics, 2020, 21, 312.	2.8	56
117	The humanFOXL2 mutation database. Human Mutation, 2004, 24, 189-193.	2.5	55
118	Comparison of miRNA profiles of microdissected Hodgkin/Reed–Sternberg cells and Hodgkin cell lines *versus* CD77⁺ B cells reveals a distinct subset of differentially expressed miRNAs. British Journal of Haematology, 2009, 147, 686-690.	2.5	55
119	Oncogenic activation of FOXR1 by 11q23 intrachromosomal deletion-fusions in neuroblastoma. Oncogene, 2012, 31, 1571-1581.	5.9	55
120	MicroRNA-128-3p is a novel oncomiR targeting PHF6 in T-cell acute lymphoblastic leukemia. Haematologica, 2014, 99, 1326-1333.	3.5	55
121	Escape from p53-mediated tumor surveillance in neuroblastoma: switching off the p14ARF-MDM2-p53 axis. Cell Death and Differentiation, 2009, 16, 1563-1572.	11.2	54
122	Aberrant methylation of candidate tumor suppressor genes in neuroblastoma. Cancer Letters, 2009, 273, 336-346.	7.2	54
123	MicroRNA-184 is a downstream effector of albuminuria driving renal fibrosis in rats with diabetic nephropathy. Diabetologia, 2017, 60, 1114-1125.	6.3	54
124	Comparative analysis of naive, primed and ground state pluripotency in mouse embryonic stem cells originating from the same genetic background. Scientific Reports, 2018, 8, 5884.	3.3	54
125	Differential mucosal expression of Th17-related genes between the inflamed colon and ileum of patients with inflammatory bowel disease. BMC Immunology, 2010, 11, 61.	2.2	53
126	Accurate RT-qPCR gene expression analysis on cell culture lysates. Scientific Reports, 2012, 2, 222.	3.3	52

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127	Murine M cells express annexin V specifically. Journal of Pathology, 2006, 209, 240-249.	4.5	51
128	EVI1is consistently expressed as principal transcript in common and rare recurrent 3q26 rearrangements. Genes Chromosomes and Cancer, 2006, 45, 349-356.	2.8	51
129	Identification and expression analysis of genes associated with bovine blastocyst formation. BMC Developmental Biology, 2007, 7, 64.	2.1	51
130	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. Cancer Letters, 2015, 366, 123-132.	7.2	51
131	Neuroblastoma epigenetics: From candidate gene approaches to genome-wide screenings. Epigenetics, 2011, 6, 962-970.	2.7	50
132	The Notch driven long non-coding RNA repertoire in T-cell acute lymphoblastic leukemia. Haematologica, 2014, 99, 1808-1816.	3.5	50
133	The transcriptome of lung tumor-infiltrating dendritic cells reveals a tumor-supporting phenotype and a microRNA signature with negative impact on clinical outcome. OncoImmunology, 2017, 6, e1253655.	4.6	50
134	Charting Extracellular Transcriptomes in The Human Biofluid RNA Atlas. Cell Reports, 2020, 33, 108552.	6.4	50
135	Neuroblastoma cells with overexpressed MYCN retain their capacity to undergo neuronal differentiation. Laboratory Investigation, 2004, 84, 406-417.	3.7	49
136	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. BMC Medical Genomics, 2012, 5, 17.	1.5	49
137	A Constitutional Translocation t(1;17)(p36.2;q11.2) in a Neuroblastoma Patient Disrupts the Human NBPF1 and ACCN1 Genes. PLoS ONE, 2008, 3, e2207.	2.5	49
138	Translocationâ€"excisionâ€"deletionâ€"amplification mechanism leading to nonsyntenic coamplification of <i>MYC</i> and <i>ATBF1</i>. Genes Chromosomes and Cancer, 2006, 45, 107-117.	2.8	47
139	Combined M-FISH and CGH analysis allows comprehensive description of genetic alterations in neuroblastoma cell lines. Genes Chromosomes and Cancer, 2001, 32, 126-135.	2.8	46
140	Performance assessment of total RNA sequencing of human biofluids and extracellular vesicles. Scientific Reports, 2019, 9, 17574.	3.3	46
141	Cautionary Note on Contamination of Reagents Used for Molecular Detection of SARS-CoV-2. Clinical Chemistry, 2020, 66, 1369-1372.	3.2	46
142	Regulatory microRNA Network Identification in Bovine Blastocyst Development. Stem Cells and Development, 2013, 22, 1907-1920.	2.1	45
143	Vapor nanobubble is the more reliable photothermal mechanism for inducing endosomal escape of siRNA without disturbing cell homeostasis. Journal of Controlled Release, 2020, 319, 262-275.	9.9	45
144	Noncoding after All: Biases in Proteomics Data Do Not Explain Observed Absence of lncRNA Translation Products. Journal of Proteome Research, 2017, 16, 2508-2515.	3.7	44

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145	*Dickkopf-3* is regulated by the MYCN-induced miR-17-92 cluster in neuroblastoma. International Journal of Cancer, 2012, 130, 2591-2598.	5.1	43
146	Flexible, Scalable, and Efficient Targeted Resequencing on a Benchtop Sequencer for Variant Detection in Clinical Practice. Human Mutation, 2015, 36, 379-387.	2.5	43
147	Differential gene expression analysis tools exhibit substandard performance for long non-coding RNA-sequencing data. Genome Biology, 2018, 19, 96.	8.8	43
148	Quantification of NF1 transcripts reveals novel highly expressed splice variants. FEBS Letters, 2002, 522, 71-76.	2.8	41
149	Meta-mining of Neuroblastoma and Neuroblast Gene Expression Profiles Reveals Candidate Therapeutic Compounds. Clinical Cancer Research, 2009, 15, 3690-3696.	7.0	41
150	The Dangers of Using Cq to Quantify Nucleic Acid in Biological Samples: A Lesson From COVID-19. Clinical Chemistry, 2021, 68, 153-162.	3.2	41
151	MiR-34a deficiency accelerates medulloblastoma formation *in vivo*. International Journal of Cancer, 2015, 136, 2293-2303.	5.1	40
152	Practical Tools to Implement Massive Parallel Pyrosequencing of PCR Products in Next Generation Molecular Diagnostics. PLoS ONE, 2011, 6, e25531.	2.5	40
153	Massively parallel sequencing for early molecular diagnosis in Leber congenital amaurosis. Genetics in Medicine, 2012, 14, 576-585.	2.4	39
154	N-Cadherin in Neuroblastoma Disease: Expression and Clinical Significance. PLoS ONE, 2012, 7, e31206.	2.5	39
155	Pharmacologic activation of wild-type p53 by nutlin therapy in childhood cancer. Cancer Letters, 2014, 344, 157-165.	7.2	39
156	ID2 expression in neuroblastoma does not correlate to MYCN levels and lacks prognostic value. Oncogene, 2003, 22, 456-460.	5.9	38
157	RNA pre-amplification enables large-scale RT-qPCR gene-expression studies on limiting sample amounts. BMC Research Notes, 2009, 2, 235.	1.4	38
158	Expressed Repeat Elements Improve RT-qPCR Normalization across a Wide Range of Zebrafish Gene Expression Studies. PLoS ONE, 2014, 9, e109091.	2.5	38
159	Inhibition of CDK4/6 as a novel therapeutic option for neuroblastoma. Cancer Cell International, 2015, 15, 76.	4.1	38
160	SMARTer single cell total RNA sequencing. Nucleic Acids Research, 2019, 47, e93-e93.	14.5	38
161	Ectopic MicroRNA-150-5p Transcription Sensitizes Glucocorticoid Therapy Response in MM1S Multiple Myeloma Cells but Fails to Overcome Hormone Therapy Resistance in MM1R Cells. PLoS ONE, 2014, 9, e113842.	2.5	38
162	MYCN-targeting miRNAs are predominantly downregulated during MYCN-driven neuroblastoma tumor formation. Oncotarget, 2015, 6, 5204-5216.	1.8	38

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163	MISpheroID: a knowledgebase and transparency tool for minimum information in spheroid identity. Nature Methods, 2021, 18, 1294-1303.	19.0	38
164	Identification of a novel recurrent 1q42.2â€‘qter deletion in high risk <i>MYCN</i> single copy 11q deleted neuroblastomas. International Journal of Cancer, 2012, 130, 2599-2606.	5.1	37
165	Robust sequential biophysical fractionation of blood plasma to study variations in the biomolecular landscape of systemically circulating extracellular vesicles across clinical conditions. Journal of Extracellular Vesicles, 2021, 10, e12122.	12.2	37
166	Focal DNA Copy Number Changes in Neuroblastoma Target MYCN Regulated Genes. PLoS ONE, 2013, 8, e52321.	2.5	37
167	Modulation of the peroxisomal gene expression pattern by dehydroepiandrosterone and vitamin D: therapeutic implications. Journal of Endocrinology, 2002, 175, 779-792.	2.6	35
168	Pathological splice mutations outside the invariant AG/GT splice sites of BRCA1 exon 5 increase alternative transcript levels in the 5â€² end of the BRCA1 gene. Oncogene, 2002, 21, 4171-4175.	5.9	35
169	methBLAST and methPrimerDB: web-tools for PCR based methylation analysis. BMC Bioinformatics, 2006, 7, 496.	2.6	35
170	Selection of reference genes for quantitative real-time PCR in equine in vivo and fresh and frozen-thawed in vitro blastocysts. BMC Research Notes, 2009, 2, 246.	1.4	35
171	Model-Based Classification for Digital PCR: Your Umbrella for Rain. Analytical Chemistry, 2017, 89, 4461-4467.	6.5	35
172	Long non-coding RNAs in cutaneous melanoma: clinical perspectives. Oncotarget, 2017, 8, 43470-43480.	1.8	35
173	CADM1 is a strong neuroblastoma candidate gene that maps within a 3.72 Mb critical region of loss on 11q23. BMC Cancer, 2008, 8, 173.	2.6	34
174	The emerging molecular pathogenesis of neuroblastoma: implications for improved risk assessment and targeted therapy. Genome Medicine, 2009, 1, 74.	8.2	34
175	Of flies, mice and men: a systematic approach to understanding the early life origins of chronic lung disease. Thorax, 2013, 68, 380-384.	5.6	34
176	RNA expression signatures and posttranscriptional regulation in diabetic nephropathy. Nephrology Dialysis Transplantation, 2015, 30, iv35-iv42.	0.7	32
177	Long noncoding RNA signatures define oncogenic subtypes in T-cell acute lymphoblastic leukemia. Leukemia, 2016, 30, 1927-1930.	7.2	32
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