

Jo Vandesompele

List of Publications by Year in descending order

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Version: 2024-02-01

325
papers

61,706
citations

4136

87
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. <i>Genome Biology</i> , 2002, 3, research0034.1.	13.9	16,304
2	The MIQE Guidelines: Minimum Information for Publication of Quantitative Real-Time PCR Experiments. <i>Clinical Chemistry</i> , 2009, 55, 611-622.	1.5	12,487
3	qBase relative quantification framework and software for management and automated analysis of real-time quantitative PCR data. <i>Genome Biology</i> , 2007, 8, R19.	13.9	3,580
4	miR-9, a MYC/MYCN-activated microRNA, regulates E-cadherin and cancer metastasis. <i>Nature Cell Biology</i> , 2010, 12, 247-256.	4.6	1,216
5	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012, 44, 1104-1110.	9.4	1,186
6	EV-TRACK: transparent reporting and centralizing knowledge in extracellular vesicle research. <i>Nature Methods</i> , 2017, 14, 228-232.	9.0	886
7	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. <i>Nature Biotechnology</i> , 2014, 32, 903-914.	9.4	883
8	A novel and universal method for microRNA RT-qPCR data normalization. <i>Genome Biology</i> , 2009, 10, R64.	13.9	849
9	The impact of disparate isolation methods for extracellular vesicles on downstream RNA profiling. <i>Journal of Extracellular Vesicles</i> , 2014, 3, .	5.5	725
10	The Digital MIQE Guidelines: Minimum Information for Publication of Quantitative Digital PCR Experiments. <i>Clinical Chemistry</i> , 2013, 59, 892-902.	1.5	723
11	How to do successful gene expression analysis using real-time PCR. <i>Methods</i> , 2010, 50, 227-230.	1.9	582
12	Evaluation of quantitative miRNA expression platforms in the microRNA quality control (miRQC) study. <i>Nature Methods</i> , 2014, 11, 809-815.	9.0	564
13	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	9.4	506
14	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. <i>Nucleic Acids Research</i> , 2013, 41, D246-D251.	6.5	488
15	Melanoma addiction to the long non-coding RNA SAMMSON. <i>Nature</i> , 2016, 531, 518-522.	13.7	488
16	Gain of Chromosome Arm 17q and Adverse Outcome in Patients with Neuroblastoma. <i>New England Journal of Medicine</i> , 1999, 340, 1954-1961.	13.9	456
17	Standardization of real-time PCR gene expression data from independent biological replicates. <i>Analytical Biochemistry</i> , 2008, 379, 127-129.	1.1	417
18	Loss-of-function mutations in LEMD3 result in osteopoikilosis, Buschke-Ollendorff syndrome and melorheostosis. <i>Nature Genetics</i> , 2004, 36, 1213-1218.	9.4	410

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19	LNCipedia 5: towards a reference set of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019, 47, D135-D139.	6.5	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. <i>Journal of Medical Genetics</i> , 2006, 43, 625-633.	1.5	342
21	LIN28B induces neuroblastoma and enhances MYCN levels via let-7 suppression. <i>Nature Genetics</i> , 2012, 44, 1199-1206.	9.4	336
22	Selection and validation of a set of reliable reference genes for quantitative sod gene expression analysis in <i>C. elegans</i> . <i>BMC Molecular Biology</i> , 2008, 9, 9.	3.0	327
23	Amphiregulin and Epiregulin mRNA Expression in Primary Tumors Predicts Outcome in Metastatic Colorectal Cancer Treated With Cetuximab. <i>Journal of Clinical Oncology</i> , 2009, 27, 5068-5074.	0.8	325
24	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015, 16, 133.	3.8	325
25	An update on LNCipedia: a database for annotated human lncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D174-D180.	6.5	298
26	The miR-17-92 MicroRNA Cluster Regulates Multiple Components of the TGF- β Pathway in Neuroblastoma. <i>Molecular Cell</i> , 2010, 40, 762-773.	4.5	279
27	Accurate and objective copy number profiling using real-time quantitative PCR. <i>Methods</i> , 2010, 50, 262-270.	1.9	273
28	Selection of reference genes for quantitative real-time PCR in bovine preimplantation embryos. <i>BMC Developmental Biology</i> , 2005, 5, 27.	2.1	269
29	High-throughput stem-loop RT-qPCR miRNA expression profiling using minute amounts of input RNA. <i>Nucleic Acids Research</i> , 2008, 36, e143-e143.	6.5	261
30	The need for transparency and good practices in the qPCR literature. <i>Nature Methods</i> , 2013, 10, 1063-1067.	9.0	251
31	The Digital MIQE Guidelines Update: Minimum Information for Publication of Quantitative Digital PCR Experiments for 2020. <i>Clinical Chemistry</i> , 2020, 66, 1012-1029.	1.5	247
32	Meta-analysis of Neuroblastomas Reveals a Skewed <i>ALK</i> Mutation Spectrum in Tumors with <i>MYCN</i> Amplification. <i>Clinical Cancer Research</i> , 2010, 16, 4353-4362.	3.2	243
33	RTPrimerDB: the Real-Time PCR primer and probe database. <i>Nucleic Acids Research</i> , 2003, 31, 122-123.	6.5	240
34	Distinct transcriptional MYCN/c-MYC activities are associated with spontaneous regression or malignant progression in neuroblastomas. <i>Genome Biology</i> , 2008, 9, R150.	13.9	215
35	A mechanistic classification of clinical phenotypes in neuroblastoma. <i>Science</i> , 2018, 362, 1165-1170.	6.0	213
36	MicroRNA Expression in Induced Sputum of Smokers and Patients with Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 183, 898-906.	2.5	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. <i>Analytical Biochemistry</i> , 2002, 303, 95-98.	1.1	201
38	Evaluation of qPCR curve analysis methods for reliable biomarker discovery: Bias, resolution, precision, and implications. <i>Methods</i> , 2013, 59, 32-46.	1.9	197
39	MicroRNA expression profiling to identify and validate reference genes for relative quantification in colorectal cancer. <i>BMC Cancer</i> , 2010, 10, 173.	1.1	193
40	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. <i>Nucleic Acids Research</i> , 2010, 38, 5919-5928.	6.5	183
41	Computational deconvolution of transcriptomics data from mixed cell populations. <i>Bioinformatics</i> , 2018, 34, 1969-1979.	1.8	181
42	Predicting outcomes for children with neuroblastoma using a multigene-expression signature: a retrospective SIOPEX/COG/GPOH study. <i>Lancet Oncology</i> , 2009, 10, 663-671.	5.1	176
43	Lysine-specific demethylase 1 restricts hematopoietic progenitor proliferation and is essential for terminal differentiation. <i>Leukemia</i> , 2012, 26, 2039-2051.	3.3	171
44	Increased levels of systemic LPS-positive bacterial extracellular vesicles in patients with intestinal barrier dysfunction. <i>Gut</i> , 2020, 69, 191-193.	6.1	171
45	Asthma inflammatory phenotypes show differential microRNA expression in sputum. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1433-1446.	1.5	168
46	Quantification of MYCN, DDX1, and NAG Gene Copy Number in Neuroblastoma Using a Real-Time Quantitative PCR Assay. <i>Modern Pathology</i> , 2002, 15, 159-166.	2.9	167
47	Unequivocal Delineation of Clinicogenetic Subgroups and Development of a New Model for Improved Outcome Prediction in Neuroblastoma. <i>Journal of Clinical Oncology</i> , 2005, 23, 2280-2299.	0.8	160
48	Molecular Dissection of Isolated Disease Features in Mosaic Neurofibromatosis Type 1. <i>American Journal of Human Genetics</i> , 2007, 81, 243-251.	2.6	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 PPAR γ 1A. <i>BMC Biotechnology</i> , 2006, 6, 41.	1.7	153
50	Single-Nucleotide Polymorphisms and Other Mismatches Reduce Performance of Quantitative PCR Assays. <i>Clinical Chemistry</i> , 2013, 59, 1470-1480.	1.5	153
51	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153
52	Expression profiling suggests underexpression of the GABA A receptor subunit δ in the fragile X knockout mouse model. <i>Neurobiology of Disease</i> , 2006, 21, 346-357.	2.1	151
53	DNA methylation silences miR-132 in prostate cancer. <i>Oncogene</i> , 2013, 32, 127-134.	2.6	151
54	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. <i>Science Translational Medicine</i> , 2012, 4, 141ra91.	5.8	147

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55	Measurable impact of RNA quality on gene expression results from quantitative PCR. <i>Nucleic Acids Research</i> , 2011, 39, e63-e63.	6.5	146
56	miRNA Expression Profiling: From Reference Genes to Global Mean Normalization. <i>Methods in Molecular Biology</i> , 2012, 822, 261-272.	0.4	143
57	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010, 29, 3583-3592.	2.6	141
58	Monoallelic but not biallelic loss of Dicer1 promotes tumorigenesis in vivo. <i>Cell Death and Differentiation</i> , 2010, 17, 633-641.	5.0	140
59	Human fetal neuroblast and neuroblastoma transcriptome analysis confirms neuroblast origin and highlights neuroblastoma candidate genes. <i>Genome Biology</i> , 2006, 7, R84.	13.9	134
60	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. <i>Cell Death and Differentiation</i> , 2011, 18, 974-984.	5.0	133
61	Small-Molecule MDM2 Antagonists as a New Therapy Concept for Neuroblastoma. <i>Cancer Research</i> , 2006, 66, 9646-9655.	0.4	132
62	RTPrimerDB: the portal for real-time PCR primers and probes. <i>Nucleic Acids Research</i> , 2009, 37, D942-D945.	6.5	132
63	Prognostic Impact of Gene Expression-Based Classification for Neuroblastoma. <i>Journal of Clinical Oncology</i> , 2010, 28, 3506-3515.	0.8	129
64	RDML: structured language and reporting guidelines for real-time quantitative PCR data. <i>Nucleic Acids Research</i> , 2009, 37, 2065-2069.	6.5	123
65	Genetic heterogeneity of neuroblastoma studied by comparative genomic hybridization. , 1998, 23, 141-152.		121
66	Quantification of splice variants using real-time PCR. <i>Nucleic Acids Research</i> , 2001, 29, 68e-68.	6.5	119
67	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.	7.7	119
68	Alternative Routes to Induce Naïve Pluripotency in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2015, 33, 2686-2698.	1.4	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. <i>Blood</i> , 2004, 103, 229-235.	0.6	117
70	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. <i>Genes Chromosomes and Cancer</i> , 2019, 58, 191-199.	1.5	117
71	Comparative genomic hybridization (CGH) analysis of stage 4 neuroblastoma reveals high frequency of 11q deletion in tumors lacking MYCN amplification. <i>International Journal of Cancer</i> , 2001, 91, 680-686.	2.3	112
72	Widespread Dysregulation of MiRNAs by MYCN Amplification and Chromosomal Imbalances in Neuroblastoma: Association of miRNA Expression with Survival. <i>PLoS ONE</i> , 2009, 4, e7850.	1.1	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. <i>Oncogene</i> , 2010, 29, 1394-1404.	2.6	112
74	Selection of Reliable Reference Genes for RT-qPCR Analysis. <i>Methods in Molecular Biology</i> , 2014, 1160, 19-26.	0.4	112
75	The cancer-associated microprotein CASIMO1 controls cell proliferation and interacts with squalene epoxidase modulating lipid droplet formation. <i>Oncogene</i> , 2018, 37, 4750-4768.	2.6	111
76	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.	2.5	108
77	RTPrimerDB: the real-time PCR primer and probe database, major update 2006. <i>Nucleic Acids Research</i> , 2006, 34, D684-D688.	6.5	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. <i>Leukemia</i> , 2005, 19, 358-366.	3.3	106
79	ComprehensiveNF1 screening on cultured Schwann cells from neurofibromas. <i>Human Mutation</i> , 2006, 27, 1030-1040.	1.1	105
80	Antitumor Activity of the Selective MDM2 Antagonist Nutlin-3 Against Chemoresistant Neuroblastoma With Wild-Type p53. <i>Journal of the National Cancer Institute</i> , 2009, 101, 1562-1574.	3.0	105
81	Cancer-Associated Adipose Tissue Promotes Breast Cancer Progression by Paracrine Oncostatin M and Jak/STAT3 Signaling. <i>Cancer Research</i> , 2014, 74, 6806-6819.	0.4	105
82	Rapid detection of VHL exon deletions using real-time quantitative PCR. <i>Laboratory Investigation</i> , 2005, 85, 24-33.	1.7	102
83	Influence of microRNAs and Long Non-Coding RNAs in Cancer Chemoresistance. <i>Genes</i> , 2017, 8, 95.	1.0	102
84	Identification of miR-145 as a Key Regulator of the Pigmentary Process. <i>Journal of Investigative Dermatology</i> , 2013, 133, 201-209.	0.3	99
85	Renal microRNA and lncRNA profiles in progressive chronic kidney disease. <i>European Journal of Clinical Investigation</i> , 2016, 46, 213-226.	1.7	96
86	The generation and use of recombinant extracellular vesicles as biological reference material. <i>Nature Communications</i> , 2019, 10, 3288.	5.8	96
87	High ALK Receptor Tyrosine Kinase Expression Supersedes ALK Mutation as a Determining Factor of an Unfavorable Phenotype in Primary Neuroblastoma. <i>Clinical Cancer Research</i> , 2011, 17, 5082-5092.	3.2	95
88	Impact of RNA quality on reference gene expression stability. <i>BioTechniques</i> , 2005, 39, 52-56.	0.8	92
89	miRNA Expression Profiling Enables Risk Stratification in Archived and Fresh Neuroblastoma Tumor Samples. <i>Clinical Cancer Research</i> , 2011, 17, 7684-7692.	3.2	92
90	MIR137 functions as a tumor suppressor in neuroblastoma by downregulating KDM1A. <i>International Journal of Cancer</i> , 2013, 133, 1064-1073.	2.3	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. <i>Leukemia</i> , 2015, 29, 798-806.	3.3	91
92	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. <i>International Journal of Cancer</i> , 2010, 127, 2374-2385.	2.3	88
93	Hsa-mir-145 is the top EWS-FLI1-repressed microRNA involved in a positive feedback loop in Ewing's sarcoma. <i>Oncogene</i> , 2011, 30, 2173-2180.	2.6	87
94	Accurate Outcome Prediction in Neuroblastoma across Independent Data Sets Using a Multigene Signature. <i>Clinical Cancer Research</i> , 2010, 16, 1532-1541.	3.2	86
95	MYCN and ALK1174L are sufficient to drive neuroblastoma development from neural crest progenitor cells. <i>Oncogene</i> , 2013, 32, 1059-1065.	2.6	84
96	Modulation of neuroblastoma disease pathogenesis by an extensive network of epigenetically regulated microRNAs. <i>Oncogene</i> , 2013, 32, 2927-2936.	2.6	84
97	Multicentre analysis of patterns of DNA gains and losses in 204 neuroblastoma tumors: How many genetic subgroups are there?. <i>Medical and Pediatric Oncology</i> , 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. <i>Clinical Cancer Research</i> , 2015, 21, 1904-1915.	3.2	80
99	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. <i>BMC Bioinformatics</i> , 2005, 6, 124.	1.2	79
100	Synthetic lethality between Rb, p53 and Dicer or miR-17-92 in retinal progenitors suppresses retinoblastoma formation. <i>Nature Cell Biology</i> , 2012, 14, 958-965.	4.6	79
101	miR-542-3p exerts tumor suppressive functions in neuroblastoma by downregulating <i>urvivin</i> . <i>International Journal of Cancer</i> , 2015, 136, 1308-1320.	2.3	78
102	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	9.4	75
103	Closing the circle: current state and perspectives of circular RNA databases. <i>Briefings in Bioinformatics</i> , 2021, 22, 288-297.	3.2	74
104	miRBase Tracker: keeping track of microRNA annotation changes. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	1.4	73
105	The microRNA body map: dissecting microRNA function through integrative genomics. <i>Nucleic Acids Research</i> , 2011, 39, e136-e136.	6.5	72
106	Non-coding RNAs in the pathogenesis of COPD. <i>Thorax</i> , 2015, 70, 782-791.	2.7	71
107	Chromosomal and MicroRNA Expression Patterns Reveal Biologically Distinct Subgroups of 11q ⁺ Neuroblastoma. <i>Clinical Cancer Research</i> , 2010, 16, 2971-2978.	3.2	70
108	ArrayCGH-based classification of neuroblastoma into genomic subgroups. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 1098-1108.	1.5	67

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109	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. <i>Nature Communications</i> , 2019, 10, 5026.	5.8	67
110	Real-Time Quantitative PCR as an Alternative to Southern Blot or Fluorescence <i>In Situ</i> 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. <i>Genome Biology</i> , 2012, 13, R95.	13.9	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. <i>Oncogene</i> , 2004, 23, 2732-2742.	2.6	63
113	Primer Sequence Disclosure: A Clarification of the MIQE Guidelines. <i>Clinical Chemistry</i> , 2011, 57, 919-921.	1.5	63
114	Functional Analysis of the p53 Pathway in Neuroblastoma Cells Using the Small-Molecule MDM2 Antagonist Nutlin-3. <i>Molecular Cancer Therapeutics</i> , 2011, 10, 983-993.	1.9	61
115	Positional gene enrichment analysis of gene sets for high-resolution identification of overrepresented chromosomal regions. <i>Nucleic Acids Research</i> , 2008, 36, e43-e43.	6.5	56
116	On the utility of RNA sample pooling to optimize cost and statistical power in RNA sequencing experiments. <i>BMC Genomics</i> , 2020, 21, 312.	1.2	56
117	The humanFOXL2 mutation database. <i>Human Mutation</i> , 2004, 24, 189-193.	1.1	55
118	Comparison of miRNA profiles of microdissected Hodgkin/Reed-Sternberg cells and Hodgkin cell lines <i>versus</i> CD77 ⁺ B-cells reveals a distinct subset of differentially expressed miRNAs. <i>British Journal of Haematology</i> , 2009, 147, 686-690.	1.2	55
119	Oncogenic activation of FOXR1 by 11q23 intrachromosomal deletion-fusions in neuroblastoma. <i>Oncogene</i> , 2012, 31, 1571-1581.	2.6	55
120	MicroRNA-128-3p is a novel oncomiR targeting PHF6 in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2014, 99, 1326-1333.	1.7	55
121	Escape from p53-mediated tumor surveillance in neuroblastoma: switching off the p14ARF-MDM2-p53 axis. <i>Cell Death and Differentiation</i> , 2009, 16, 1563-1572.	5.0	54
122	Aberrant methylation of candidate tumor suppressor genes in neuroblastoma. <i>Cancer Letters</i> , 2009, 273, 336-346.	3.2	54
123	MicroRNA-184 is a downstream effector of albuminuria driving renal fibrosis in rats with diabetic nephropathy. <i>Diabetologia</i> , 2017, 60, 1114-1125.	2.9	54
124	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.	1.6	54
125	Differential mucosal expression of Th17-related genes between the inflamed colon and ileum of patients with inflammatory bowel disease. <i>BMC Immunology</i> , 2010, 11, 61.	0.9	53
126	Accurate RT-qPCR gene expression analysis on cell culture lysates. <i>Scientific Reports</i> , 2012, 2, 222.	1.6	52

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127	Murine M cells express annexin V specifically. <i>Journal of Pathology</i> , 2006, 209, 240-249.	2.1	51
128	EV11s consistently expressed as principal transcript in common and rare recurrent 3q26 rearrangements. <i>Genes Chromosomes and Cancer</i> , 2006, 45, 349-356.	1.5	51
129	Identification and expression analysis of genes associated with bovine blastocyst formation. <i>BMC Developmental Biology</i> , 2007, 7, 64.	2.1	51
130	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. <i>Cancer Letters</i> , 2015, 366, 123-132.	3.2	51
131	Neuroblastoma epigenetics: From candidate gene approaches to genome-wide screenings. <i>Epigenetics</i> , 2011, 6, 962-970.	1.3	50
132	The Notch driven long non-coding RNA repertoire in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2014, 99, 1808-1816.	1.7	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. <i>Oncolmmunology</i> , 2017, 6, e1253655.	2.1	50
134	Charting Extracellular Transcriptomes in The Human Biofluid RNA Atlas. <i>Cell Reports</i> , 2020, 33, 108552.	2.9	50
135	Neuroblastoma cells with overexpressed MYCN retain their capacity to undergo neuronal differentiation. <i>Laboratory Investigation</i> , 2004, 84, 406-417.	1.7	49
136	Molecular diagnostics for congenital hearing loss including 15 deafness genes using a next generation sequencing platform. <i>BMC Medical Genomics</i> , 2012, 5, 17.	0.7	49
137	A Constitutional Translocation t(1;17)(p36.2;q11.2) in a Neuroblastoma Patient Disrupts the Human NBPF1 and ACCN1 Genes. <i>PLoS ONE</i> , 2008, 3, e2207.	1.1	49
138	Translocation-excision-deletion-amplification mechanism leading to nonsyntenic coamplification of MYC and ATBF1. <i>Genes Chromosomes and Cancer</i> , 2006, 45, 107-117.	1.5	47
139	Combined M-FISH and CGH analysis allows comprehensive description of genetic alterations in neuroblastoma cell lines. <i>Genes Chromosomes and Cancer</i> , 2001, 32, 126-135.	1.5	46
140	Performance assessment of total RNA sequencing of human biofluids and extracellular vesicles. <i>Scientific Reports</i> , 2019, 9, 17574.	1.6	46
141	Cautionary Note on Contamination of Reagents Used for Molecular Detection of SARS-CoV-2. <i>Clinical Chemistry</i> , 2020, 66, 1369-1372.	1.5	46
142	Regulatory microRNA Network Identification in Bovine Blastocyst Development. <i>Stem Cells and Development</i> , 2013, 22, 1907-1920.	1.1	45
143	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.	4.8	45
144	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.	1.8	44

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145	<i>Dickkopf3</i> is regulated by the MYCN-induced miR-17-92 cluster in neuroblastoma. <i>International Journal of Cancer</i> , 2012, 130, 2591-2598.	2.3	43
146	Flexible, Scalable, and Efficient Targeted Resequencing on a Benchtop Sequencer for Variant Detection in Clinical Practice. <i>Human Mutation</i> , 2015, 36, 379-387.	1.1	43
147	Differential gene expression analysis tools exhibit substandard performance for long non-coding RNA-sequencing data. <i>Genome Biology</i> , 2018, 19, 96.	3.8	43
148	Quantification of NF1 transcripts reveals novel highly expressed splice variants. <i>FEBS Letters</i> , 2002, 522, 71-76.	1.3	41
149	Meta-mining of Neuroblastoma and Neuroblast Gene Expression Profiles Reveals Candidate Therapeutic Compounds. <i>Clinical Cancer Research</i> , 2009, 15, 3690-3696.	3.2	41
150	The Dangers of Using Cq to Quantify Nucleic Acid in Biological Samples: A Lesson From COVID-19. <i>Clinical Chemistry</i> , 2021, 68, 153-162.	1.5	41
151	<i>M</i> <i>R</i> 34a deficiency accelerates medulloblastoma formation <i>in vivo</i> . <i>International Journal of Cancer</i> , 2015, 136, 2293-2303.	2.3	40
152	Practical Tools to Implement Massive Parallel Pyrosequencing of PCR Products in Next Generation Molecular Diagnostics. <i>PLoS ONE</i> , 2011, 6, e25531.	1.1	40
153	Massively parallel sequencing for early molecular diagnosis in Leber congenital amaurosis. <i>Genetics in Medicine</i> , 2012, 14, 576-585.	1.1	39
154	N-Cadherin in Neuroblastoma Disease: Expression and Clinical Significance. <i>PLoS ONE</i> , 2012, 7, e31206.	1.1	39
155	Pharmacologic activation of wild-type p53 by nutlin therapy in childhood cancer. <i>Cancer Letters</i> , 2014, 344, 157-165.	3.2	39
156	ID2 expression in neuroblastoma does not correlate to MYCN levels and lacks prognostic value. <i>Oncogene</i> , 2003, 22, 456-460.	2.6	38
157	RNA pre-amplification enables large-scale RT-qPCR gene-expression studies on limiting sample amounts. <i>BMC Research Notes</i> , 2009, 2, 235.	0.6	38
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