

Jo Vandesompele

List of Publications by Citations

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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	Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. <i>Genome Biology</i> , 2002 , 3, RESEARCH0034	18.3	13446
313	The MIQE guidelines: minimum information for publication of quantitative real-time PCR experiments. <i>Clinical Chemistry</i> , 2009 , 55, 611-22	5.5	9710
312	qBase relative quantification framework and software for management and automated analysis of real-time quantitative PCR data. <i>Genome Biology</i> , 2007 , 8, R19	18.3	2794
311	miR-9, a MYC/MYCN-activated microRNA, regulates E-cadherin and cancer metastasis. <i>Nature Cell Biology</i> , 2010 , 12, 247-56	23.4	1102
310	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012 , 44, 1104-10	36.3	919
309	A novel and universal method for microRNA RT-qPCR data normalization. <i>Genome Biology</i> , 2009 , 10, R64	18.3	746
308	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
307	EV-TRACK: transparent reporting and centralizing knowledge in extracellular vesicle research. <i>Nature Methods</i> , 2017 , 14, 228-232	21.6	560
306	The digital MIQE guidelines: Minimum Information for Publication of Quantitative Digital PCR Experiments. <i>Clinical Chemistry</i> , 2013 , 59, 892-902	5.5	554
305	The impact of disparate isolation methods for extracellular vesicles on downstream RNA profiling. <i>Journal of Extracellular Vesicles</i> , 2014 , 3,	16.4	533
304	How to do successful gene expression analysis using real-time PCR. <i>Methods</i> , 2010 , 50, 227-30	4.6	470
303	Evaluation of quantitative miRNA expression platforms in the microRNA quality control (miRQC) study. <i>Nature Methods</i> , 2014 , 11, 809-15	21.6	463
302	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96	44.5	417
301	LNCipedia: a database for annotated human lncRNA transcript sequences and structures. <i>Nucleic Acids Research</i> , 2013 , 41, D246-51	20.1	400
300	Gain of chromosome arm 17q and adverse outcome in patients with neuroblastoma. <i>New England Journal of Medicine</i> , 1999 , 340, 1954-61	59.2	380
299	Melanoma addiction to the long non-coding RNA SAMMSON. <i>Nature</i> , 2016 , 531, 518-22	50.4	355
298	Loss-of-function mutations in LEMD3 result in osteopoikilosis, Buschke-Ollendorff syndrome and melorheostosis. <i>Nature Genetics</i> , 2004 , 36, 1213-8	36.3	344

297	Standardization of real-time PCR gene expression data from independent biological replicates. <i>Analytical Biochemistry</i> , 2008 , 379, 127-9	3.1	329
296	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, 625-33	5.8	305
295	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, 5068-74	2.2	284
294	LIN28B induces neuroblastoma and enhances MYCN levels via let-7 suppression. <i>Nature Genetics</i> , 2012 , 44, 1199-206	36.3	273
293	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	4.5	261
292	The miR-17-92 microRNA cluster regulates multiple components of the TGF- β pathway in neuroblastoma. <i>Molecular Cell</i> , 2010 , 40, 762-73	17.6	247
291	Accurate and objective copy number profiling using real-time quantitative PCR. <i>Methods</i> , 2010 , 50, 262-70	4.0	242
290	High-throughput stem-loop RT-qPCR miRNA expression profiling using minute amounts of input RNA. <i>Nucleic Acids Research</i> , 2008 , 36, e143	20.1	242
289	Selection of reference genes for quantitative real-time PCR in bovine preimplantation embryos. <i>BMC Developmental Biology</i> , 2005 , 5, 27	3.1	234
288	LNCipedia 5: towards a reference set of human long non-coding RNAs. <i>Nucleic Acids Research</i> , 2019 , 47, D135-D139	20.1	215
287	An update on LNCipedia: a database for annotated human lncRNA sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D174-80	20.1	212
286	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015 , 16, 133	18.3	212
285	Meta-analysis of neuroblastomas reveals a skewed ALK mutation spectrum in tumors with MYCN amplification. <i>Clinical Cancer Research</i> , 2010 , 16, 4353-62	12.9	208
284	The need for transparency and good practices in the qPCR literature. <i>Nature Methods</i> , 2013 , 10, 1063-7	21.6	197
283	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	10.2	187
282	RTPrimerDB: the real-time PCR primer and probe database. <i>Nucleic Acids Research</i> , 2003 , 31, 122-3	20.1	187
281	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, 95-8	3.1	186
280	MicroRNA expression profiling to identify and validate reference genes for relative quantification in colorectal cancer. <i>BMC Cancer</i> , 2010 , 10, 173	4.8	182

279	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
278	Deep sequencing reveals differential expression of microRNAs in favorable versus unfavorable neuroblastoma. <i>Nucleic Acids Research</i> , 2010 , 38, 5919-28	20.1	166
277	Distinct transcriptional MYCN/c-MYC activities are associated with spontaneous regression or malignant progression in neuroblastomas. <i>Genome Biology</i> , 2008 , 9, R150	18.3	159
276	Quantification of MYCN, DDX1, and NAG gene copy number in neuroblastoma using a real-time quantitative PCR assay. <i>Modern Pathology</i> , 2002 , 15, 159-66	9.8	155
275	Predicting outcomes for children with neuroblastoma using a multigene-expression signature: a retrospective SIOPEN/COG/GPOH study. <i>Lancet Oncology, The</i> , 2009 , 10, 663-71	21.7	145
274	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, 2280-99	2.2	145
273	Lysine-specific demethylase 1 restricts hematopoietic progenitor proliferation and is essential for terminal differentiation. <i>Leukemia</i> , 2012 , 26, 2039-51	10.7	141
272	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. <i>BMC Biotechnology</i> , 2006 , 6, 41	3.5	137
271	Expression profiling suggests underexpression of the GABA(A) receptor subunit delta in the fragile X knockout mouse model. <i>Neurobiology of Disease</i> , 2006 , 21, 346-57	7.5	133
270	Molecular dissection of isolated disease features in mosaic neurofibromatosis type 1. <i>American Journal of Human Genetics</i> , 2007 , 81, 243-51	11	133
269	Monoallelic but not biallelic loss of Dicer1 promotes tumorigenesis in vivo. <i>Cell Death and Differentiation</i> , 2010 , 17, 633-41	12.7	128
268	Asthma inflammatory phenotypes show differential microRNA expression in sputum. <i>Journal of Allergy and Clinical Immunology</i> , 2016 , 137, 1433-46	11.5	127
267	DNA methylation silences miR-132 in prostate cancer. <i>Oncogene</i> , 2013 , 32, 127-34	9.2	125
266	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010 , 29, 3583-92	9.2	125
265	Measurable impact of RNA quality on gene expression results from quantitative PCR. <i>Nucleic Acids Research</i> , 2011 , 39, e63	20.1	124
264	RTPrimerDB: the portal for real-time PCR primers and probes. <i>Nucleic Acids Research</i> , 2009 , 37, D942-5	20.1	119
263	Targeted expression of mutated ALK induces neuroblastoma in transgenic mice. <i>Science Translational Medicine</i> , 2012 , 4, 141ra91	17.5	119
262	Small-molecule MDM2 antagonists as a new therapy concept for neuroblastoma. <i>Cancer Research</i> , 2006 , 66, 9646-55	10.1	119

261	miRNA expression profiling: from reference genes to global mean normalization. <i>Methods in Molecular Biology</i> , 2012 , 822, 261-72	1.4	118
260	A mechanistic classification of clinical phenotypes in neuroblastoma. <i>Science</i> , 2018 , 362, 1165-1170	33.3	115
259	Single-nucleotide polymorphisms and other mismatches reduce performance of quantitative PCR assays. <i>Clinical Chemistry</i> , 2013 , 59, 1470-80	5.5	114
258	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. <i>Cell Death and Differentiation</i> , 2011 , 18, 974-84	12.7	113
257	Human fetal neuroblast and neuroblastoma transcriptome analysis confirms neuroblast origin and highlights neuroblastoma candidate genes. <i>Genome Biology</i> , 2006 , 7, R84	18.3	111
256	RDML: structured language and reporting guidelines for real-time quantitative PCR data. <i>Nucleic Acids Research</i> , 2009 , 37, 2065-9	20.1	107
255	Prognostic impact of gene expression-based classification for neuroblastoma. <i>Journal of Clinical Oncology</i> , 2010 , 28, 3506-15	2.2	106
254	Genetic heterogeneity of neuroblastoma studied by comparative genomic hybridization. <i>Genes Chromosomes and Cancer</i> , 1998 , 23, 141-52	5	106
253	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, 229-35	2.2	105
252	MYCN/c-MYC-induced microRNAs repress coding gene networks associated with poor outcome in MYCN/c-MYC-activated tumors. <i>Oncogene</i> , 2010 , 29, 1394-404	9.2	104
251	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	3.7	104
250	Quantification of splice variants using real-time PCR. <i>Nucleic Acids Research</i> , 2001 , 29, E68-8	20.1	104
249	RTPrimerDB: the real-time PCR primer and probe database, major update 2006. <i>Nucleic Acids Research</i> , 2006 , 34, D684-8	20.1	98
248	Computational deconvolution of transcriptomics data from mixed cell populations. <i>Bioinformatics</i> , 2018 , 34, 1969-1979	7.2	96
247	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, 358-66	10.7	95
246	Rapid detection of VHL exon deletions using real-time quantitative PCR. <i>Laboratory Investigation</i> , 2005 , 85, 24-33	5.9	95
245	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, 680-6	7.5	95
244	Alternative Routes to Induce Naïve Pluripotency in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2015 , 33, 2686-98	5.8	91

243	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
242	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, 1562-74	9.7	90
241	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019 , 47, D221-D229	10.29	90
240	Comprehensive NF1 screening on cultured Schwann cells from neurofibromas. <i>Human Mutation</i> , 2006 , 27, 1030-40	4.7	87
239	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. <i>Genes Chromosomes and Cancer</i> , 2019 , 58, 191-199	5	86
238	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
237	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
236	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
235	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, 5082-92	12.9	83
234	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
233	Selection of reliable reference genes for RT-qPCR analysis. <i>Methods in Molecular Biology</i> , 2014 , 1160, 19-26	1.4	81
232	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
231	Impact of RNA quality on reference gene expression stability. <i>BioTechniques</i> , 2005 , 39, 52, 54, 56	2.5	80
230	Influence of microRNAs and Long Non-Coding RNAs in Cancer Chemoresistance. <i>Genes</i> , 2017 , 8,	4.2	79
229	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. <i>International Journal of Cancer</i> , 2010 , 127, 2374-85	7.5	79
228	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
227	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. <i>BMC Bioinformatics</i> , 2005 , 6, 124	3.6	74
226	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, 2173-80	9.2	73

225	Modulation of neuroblastoma disease pathogenesis by an extensive network of epigenetically regulated microRNAs. <i>Oncogene</i> , 2013 , 32, 2927-36	9.2	72
224	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		72
223	MYCN and ALKF1174L are sufficient to drive neuroblastoma development from neural crest progenitor cells. <i>Oncogene</i> , 2013 , 32, 1059-65	9.2	71
222	miRBase Tracker: keeping track of microRNA annotation changes. <i>Database: the Journal of Biological Databases and Curation</i> , 2014 , 2014,	5	71
221	Renal microRNA- and RNA-profiles in progressive chronic kidney disease. <i>European Journal of Clinical Investigation</i> , 2016 , 46, 213-26	4.6	71
220	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
219	Accurate outcome prediction in neuroblastoma across independent data sets using a multigene signature. <i>Clinical Cancer Research</i> , 2010 , 16, 1532-41	12.9	69
218	miRNA expression profiling enables risk stratification in archived and fresh neuroblastoma tumor samples. <i>Clinical Cancer Research</i> , 2011 , 17, 7684-92	12.9	69
217	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
216	Chromosomal and microRNA expression patterns reveal biologically distinct subgroups of 11q-neuroblastoma. <i>Clinical Cancer Research</i> , 2010 , 16, 2971-8	12.9	65
215	The microRNA body map: dissecting microRNA function through integrative genomics. <i>Nucleic Acids Research</i> , 2011 , 39, e136	20.1	64
214	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
213	ArrayCGH-based classification of neuroblastoma into genomic subgroups. <i>Genes Chromosomes and Cancer</i> , 2007 , 46, 1098-108	5	62
212	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
211	Functional analysis of the p53 pathway in neuroblastoma cells using the small-molecule MDM2 antagonist nutlin-3. <i>Molecular Cancer Therapeutics</i> , 2011 , 10, 983-93	6.1	57
210	Real-time quantitative PCR as an alternative to Southern blot or fluorescence in situ hybridization for detection of gene copy number changes. <i>Methods in Molecular Biology</i> , 2007 , 353, 205-26	1.4	56
209	The generation and use of recombinant extracellular vesicles as biological reference material. <i>Nature Communications</i> , 2019 , 10, 3288	17.4	54
208	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

207	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, 2732-42	9.2	53
206	Non-coding RNAs in the pathogenesis of COPD. <i>Thorax</i> , 2015 , 70, 782-91	7.3	52
205	Primer sequence disclosure: a clarification of the MIQE guidelines. <i>Clinical Chemistry</i> , 2011 , 57, 919-21	5.5	52
204	Genome-wide promoter methylation analysis in neuroblastoma identifies prognostic methylation biomarkers. <i>Genome Biology</i> , 2012 , 13, R95	18.3	51
203	The human FOXL2 mutation database. <i>Human Mutation</i> , 2004 , 24, 189-93	4.7	50
202	Aberrant methylation of candidate tumor suppressor genes in neuroblastoma. <i>Cancer Letters</i> , 2009 , 273, 336-46	9.9	49
201	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
200	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
199	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	3.7	46
198	Positional gene enrichment analysis of gene sets for high-resolution identification of overrepresented chromosomal regions. <i>Nucleic Acids Research</i> , 2008 , 36, e43	20.1	46
197	Identification and expression analysis of genes associated with bovine blastocyst formation. <i>BMC Developmental Biology</i> , 2007 , 7, 64	3.1	46
196	Murine M cells express annexin V specifically. <i>Journal of Pathology</i> , 2006 , 209, 240-9	9.4	46
195	EVI1 is consistently expressed as principal transcript in common and rare recurrent 3q26 rearrangements. <i>Genes Chromosomes and Cancer</i> , 2006 , 45, 349-56	5	45
194	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
193	Oncogenic activation of FOXR1 by 11q23 intrachromosomal deletion-fusions in neuroblastoma. <i>Oncogene</i> , 2012 , 31, 1571-81	9.2	44
192	Escape from p53-mediated tumor surveillance in neuroblastoma: switching off the p14(ARF)-MDM2-p53 axis. <i>Cell Death and Differentiation</i> , 2009 , 16, 1563-72	12.7	43
191	Combined M-FISH and CGH analysis allows comprehensive description of genetic alterations in neuroblastoma cell lines. <i>Genes Chromosomes and Cancer</i> , 2001 , 32, 126-35	5	43
190	The long noncoding RNA lncNB1 promotes tumorigenesis by interacting with ribosomal protein RPL35. <i>Nature Communications</i> , 2019 , 10, 5026	17.4	40

189	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	7.2	40
188	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. <i>British Journal of Haematology</i> , 2009 , 147, 686-90	4.5	40
187	Neuroblastoma epigenetics: from candidate gene approaches to genome-wide screenings. <i>Epigenetics</i> , 2011 , 6, 962-70	5.7	40
186	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	3.7	39
185	Accurate RT-qPCR gene expression analysis on cell culture lysates. <i>Scientific Reports</i> , 2012 , 2, 222	4.9	38
184	Neuroblastoma cells with overexpressed MYCN retain their capacity to undergo neuronal differentiation. <i>Laboratory Investigation</i> , 2004 , 84, 406-17	5.9	38
183	Meta-mining of neuroblastoma and neuroblast gene expression profiles reveals candidate therapeutic compounds. <i>Clinical Cancer Research</i> , 2009 , 15, 3690-6	12.9	37
182	Massively parallel sequencing for early molecular diagnosis in Leber congenital amaurosis. <i>Genetics in Medicine</i> , 2012 , 14, 576-85	8.1	37
181	Closing the circle: current state and perspectives of circular RNA databases. <i>Briefings in Bioinformatics</i> , 2021 , 22, 288-297	13.4	37
180	The Notch driven long non-coding RNA repertoire in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2014 , 99, 1808-16	6.6	36
179	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
178	RNA pre-amplification enables large-scale RT-qPCR gene-expression studies on limiting sample amounts. <i>BMC Research Notes</i> , 2009 , 2, 235	2.3	36
177	ID2 expression in neuroblastoma does not correlate to MYCN levels and lacks prognostic value. <i>Oncogene</i> , 2003 , 22, 456-60	9.2	36
176	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
175	Practical tools to implement massive parallel pyrosequencing of PCR products in next generation molecular diagnostics. <i>PLoS ONE</i> , 2011 , 6, e25531	3.7	35
174	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
173	Pathological splice mutations outside the invariant AG/GT splice sites of BRCA1 exon 5 increase alternative transcript levels in the 5P end of the BRCA1 gene. <i>Oncogene</i> , 2002 , 21, 4171-5	9.2	34
172	Pharmacologic activation of wild-type p53 by nutlin therapy in childhood cancer. <i>Cancer Letters</i> , 2014 , 344, 157-65	9.9	33

171	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
170	Quantification of NF1 transcripts reveals novel highly expressed splice variants. <i>FEBS Letters</i> , 2002 , 522, 71-6	3.8	33
169	Regulatory microRNA network identification in bovine blastocyst development. <i>Stem Cells and Development</i> , 2013 , 22, 1907-20	4.4	32
168	MiR-34a deficiency accelerates medulloblastoma formation in vivo. <i>International Journal of Cancer</i> , 2015 , 136, 2293-303	7.5	32
167	Selection of reference genes for quantitative real-time PCR in equine in vivo and fresh and frozen-thawed in vitro blastocysts. <i>BMC Research Notes</i> , 2009 , 2, 246	2.3	32
166	MYCN-targeting miRNAs are predominantly downregulated during MYCN-driven neuroblastoma tumor formation. <i>Oncotarget</i> , 2015 , 6, 5204-16	3.3	32
165	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. <i>Cancer Letters</i> , 2015 , 366, 123-32	9.9	31
164	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
163	methBLAST and methPrimerDB: web-tools for PCR based methylation analysis. <i>BMC Bioinformatics</i> , 2006 , 7, 496	3.6	31
162	Translocation-excision-deletion-amplification mechanism leading to nonsyntenic coamplification of MYC and ATBF1. <i>Genes Chromosomes and Cancer</i> , 2006 , 45, 107-17	5	31
161	Modulation of the peroxisomal gene expression pattern by dehydroepiandrosterone and vitamin D: therapeutic implications. <i>Journal of Endocrinology</i> , 2002 , 175, 779-92	4.7	31
160	Focal DNA copy number changes in neuroblastoma target MYCN regulated genes. <i>PLoS ONE</i> , 2013 , 8, e52321	3.7	31
159	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
158	microRNAs in colon cancer: a roadmap for discovery. <i>FEBS Letters</i> , 2012 , 586, 3000-7	3.8	29
157	Unreliable real-time PCR analysis of human endogenous retrovirus-W (HERV-W) RNA expression and DNA copy number in multiple sclerosis. <i>AIDS Research and Human Retroviruses</i> , 2009 , 25, 377-8; author reply 379-81	1.6	29
156	CADM1 is a strong neuroblastoma candidate gene that maps within a 3.72 Mb critical region of loss on 11q23. <i>BMC Cancer</i> , 2008 , 8, 173	4.8	29
155	Long non-coding RNAs in cutaneous melanoma: clinical perspectives. <i>Oncotarget</i> , 2017 , 8, 43470-43480	3.3	29
154	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

153	Performance assessment of total RNA sequencing of human biofluids and extracellular vesicles. <i>Scientific Reports</i> , 2019 , 9, 17574	4.9	29
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