

Katleen De Preter

List of Publications by Year in descending order

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Version: 2024-02-01

126
papers

22,865
citations

66234

42
h-index

15683

125
g-index

145
all docs

145
docs citations

145
times ranked

37396
citing authors

#	ARTICLE	IF	CITATIONS
1	The feasibility of using liquid biopsies as a complementary assay for copy number aberration profiling in routinely collected paediatric cancer patient samples. <i>European Journal of Cancer</i> , 2022, 160, 12-23.	1.3	16
2	miR-99b-5p, miR-380-3p, and miR-485-3p are novel chemosensitizing miRNAs in high-risk neuroblastoma. <i>Molecular Therapy</i> , 2022, 30, 1119-1134.	3.7	5
3	Comprehensive RNA dataset of tissue and plasma from patients with esophageal cancer or precursor lesions. <i>Scientific Data</i> , 2022, 9, 86.	2.4	1
4	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. <i>Science Advances</i> , 2022, 8, .	4.7	15
5	Genome-wide study of the effect of blood collection tubes on the cell-free DNA methylome. <i>Epigenetics</i> , 2021, 16, 797-807.	1.3	21
6	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.	1.3	23
7	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.	1.5	3
8	Evaluation of a marker independent isolation method for circulating tumor cells in esophageal adenocarcinoma. <i>PLoS ONE</i> , 2021, 16, e0251052.	1.1	6
9	Frequency and Prognostic Impact of <i>ALK</i> Amplifications and Mutations in the European Neuroblastoma Study Group (SIOPEN) High-Risk Neuroblastoma Trial (HR-NBL1). <i>Journal of Clinical Oncology</i> , 2021, 39, 3377-3390.	0.8	30
10	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	9.4	75
11	MEIS2 Is an Adrenergic Core Regulatory Transcription Factor Involved in Early Initiation of TH-MYCN-Driven Neuroblastoma Formation. <i>Cancers</i> , 2021, 13, 4783.	1.7	12
12	From DNA Copy Number Gains and Tumor Dependencies to Novel Therapeutic Targets for High-Risk Neuroblastoma. <i>Journal of Personalized Medicine</i> , 2021, 11, 1286.	1.1	2
13	The pitfalls and promise of liquid biopsies for diagnosing and treating solid tumors in children: a review. <i>European Journal of Pediatrics</i> , 2020, 179, 191-202.	1.3	55
14	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.	3.3	17
15	Benchmarking of cell type deconvolution pipelines for transcriptomics data. <i>Nature Communications</i> , 2020, 11, 5650.	5.8	207
16	Distinct Notch1 and <i>BCL11B</i> requirements mediate human $\hat{3}\hat{1}\hat{2}$ T cell development. <i>EMBO Reports</i> , 2020, 21, e49006.	2.0	31
17	The ETS transcription factor ETV5 is a target of activated ALK in neuroblastoma contributing to increased tumour aggressiveness. <i>Scientific Reports</i> , 2020, 10, 218.	1.6	20
18	Integrative analysis identifies lincRNAs up- and downstream of neuroblastoma driver genes. <i>Scientific Reports</i> , 2019, 9, 5685.	1.6	14

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19	DREAM target reactivation by core transcriptional regulators supports neuroblastoma growth. <i>Molecular and Cellular Oncology</i> , 2019, 6, 1-3.	0.3	1
20	ALK positively regulates MYCN activity through repression of HBP1 expression. <i>Oncogene</i> , 2019, 38, 2690-2705.	2.6	17
21	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
22	Genomic Amplifications and Distal 6q Loss: Novel Markers for Poor Survival in High-risk Neuroblastoma Patients. <i>Journal of the National Cancer Institute</i> , 2018, 110, 1084-1093.	3.0	73
23	Network Modeling of microRNA-mRNA Interactions in Neuroblastoma Tumorigenesis Identifies miR-204 as a Direct Inhibitor of MYCN. <i>Cancer Research</i> , 2018, 78, 3122-3134.	0.4	48
24	Computational deconvolution of transcriptomics data from mixed cell populations. <i>Bioinformatics</i> , 2018, 34, 1969-1979.	1.8	181
25	Promoter-associated proteins of EPAS1 identified by enChIP-MS – A putative role of HDX as a negative regulator. <i>Biochemical and Biophysical Research Communications</i> , 2018, 499, 291-298.	1.0	10
26	Mapping the genomic landscape of inherited retinal disease genes prioritizes genes prone to coding and noncoding copy-number variations. <i>Genetics in Medicine</i> , 2018, 20, 202-213.	1.1	47
27	Biallelic and monoallelic ESR2 variants associated with 46,XY disorders of sex development. <i>Genetics in Medicine</i> , 2018, 20, 717-727.	1.1	28
28	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. <i>Nature Communications</i> , 2018, 9, 4866.	5.8	91
29	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018, 11, .	1.6	33
30	In silico discovery of a FOXM1 driven embryonal signaling pathway in therapy resistant neuroblastoma tumors. <i>Scientific Reports</i> , 2018, 8, 17468.	1.6	11
31	IncGraph: Incremental graphlet counting for topology optimisation. <i>PLoS ONE</i> , 2018, 13, e0195997.	1.1	2
32	LDHA in Neuroblastoma Is Associated with Poor Outcome and Its Depletion Decreases Neuroblastoma Growth Independent of Aerobic Glycolysis. <i>Clinical Cancer Research</i> , 2018, 24, 5772-5783.	3.2	48
33	Meta-mining of copy number profiles of high-risk neuroblastoma tumors. <i>Scientific Data</i> , 2018, 5, 180240.	2.4	27
34	Circulating microRNA biomarkers for metastatic disease in neuroblastoma patients. <i>JCI Insight</i> , 2018, 3, .	2.3	28
35	The mutational landscape of MYCN, Lin28b and ALK F1174L driven murine neuroblastoma mimics human disease. <i>Oncotarget</i> , 2018, 9, 8334-8349.	0.8	6
36	The immunophenotypic fingerprint of patients with primary antibody deficiencies is partially present in their asymptomatic first-degree relatives. <i>Haematologica</i> , 2017, 102, 192-202.	1.7	15

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37	Accelerating drug development for neuroblastoma - New Drug Development Strategy: an Innovative Therapies for Children with Cancer, European Network for Cancer Research in Children and Adolescents and International Society of Paediatric Oncology Europe Neuroblastoma project. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 1-11.	2.5	28
38	Shallow Whole Genome Sequencing on Circulating Cell-Free DNA Allows Reliable Noninvasive Copy-Number Profiling in Neuroblastoma Patients. <i>Clinical Cancer Research</i> , 2017, 23, 6305-6314.	3.2	113
39	Zipper plot: visualizing transcriptional activity of genomic regions. <i>BMC Bioinformatics</i> , 2017, 18, 231.	1.2	5
40	Targeting tachykinin receptors in neuroblastoma. <i>Oncotarget</i> , 2017, 8, 430-443.	0.8	19
41	Early and late effects of pharmacological ALK inhibition on the neuroblastoma transcriptome. <i>Oncotarget</i> , 2017, 8, 106820-106832.	0.8	2
42	Glutathione biosynthesis is upregulated at the initiation of MYCN-driven neuroblastoma tumorigenesis. <i>Molecular Oncology</i> , 2016, 10, 866-878.	2.1	23
43	Asthma inflammatory phenotypes show differential microRNA expression in sputum. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1433-1446.	1.5	168
44	Targeting MYCN-Driven Transcription By BET-Bromodomain Inhibition. <i>Clinical Cancer Research</i> , 2016, 22, 2470-2481.	3.2	147
45	MYCN and HDAC5 transcriptionally repress <i>CD9</i> to trigger invasion and metastasis in neuroblastoma. <i>Oncotarget</i> , 2016, 7, 66344-66359.	0.8	30
46	Characterization of pancreatic glucagon-producing tumors and pituitary gland tumors in transgenic mice overexpressing <i>MYCN</i> in <i>hGFAP</i> -positive cells. <i>Oncotarget</i> , 2016, 7, 74415-74426.	0.8	21
47	Methyl-CpG-binding domain sequencing reveals a prognostic methylation signature in neuroblastoma. <i>Oncotarget</i> , 2016, 7, 1960-1972.	0.8	26
48	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, 868-877.	2.3	9
49	MYCN-driven regulatory mechanisms controlling <i>LIN28B</i> in neuroblastoma. <i>Cancer Letters</i> , 2015, 366, 123-132.	3.2	51
50	Mutational dynamics between primary and relapse neuroblastomas. <i>Nature Genetics</i> , 2015, 47, 872-877.	9.4	253
51	A Cre-conditional MYCN-driven neuroblastoma mouse model as an improved tool for preclinical studies. <i>Oncogene</i> , 2015, 34, 3357-3368.	2.6	112
52	Genome wide expression profiling of p53 regulated miRNAs in neuroblastoma. <i>Scientific Reports</i> , 2015, 5, 9027.	1.6	29
53	Upregulation of MAPK Negative Feedback Regulators and RET in Mutant ALK Neuroblastoma: Implications for Targeted Treatment. <i>Clinical Cancer Research</i> , 2015, 21, 3327-3339.	3.2	76
54	Therapeutic targeting of the MYC signal by inhibition of histone chaperone FACT in neuroblastoma. <i>Science Translational Medicine</i> , 2015, 7, 312ra176.	5.8	120

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55	MYCN-targeting miRNAs are predominantly downregulated during MYCN-driven neuroblastoma tumor formation. <i>Oncotarget</i> , 2015, 6, 5204-5216.	0.8	38
56	ViVar: A Comprehensive Platform for the Analysis and Visualization of Structural Genomic Variation. <i>PLoS ONE</i> , 2014, 9, e113800.	1.1	45
57	Histone Chaperone CHAF1A Inhibits Differentiation and Promotes Aggressive Neuroblastoma. <i>Cancer Research</i> , 2014, 74, 765-774.	0.4	47
58	Robust Selection of Cancer Survival Signatures from High-Throughput Genomic Data Using Two-Fold Subsampling. <i>PLoS ONE</i> , 2014, 9, e108818.	1.1	6
59	Activated Alk triggers prolonged neurogenesis and Ret upregulation providing a therapeutic target in ALK-mutated neuroblastoma. <i>Oncotarget</i> , 2014, 5, 2688-2702.	0.8	89
60	MYCN and ALKF1174L are sufficient to drive neuroblastoma development from neural crest progenitor cells. <i>Oncogene</i> , 2013, 32, 1059-1065.	2.6	84
61	ERBB3 is a marker of a ganglioneuroblastoma/ganglioneuroma-like expression profile in neuroblastic tumours. <i>Molecular Cancer</i> , 2013, 12, 70.	7.9	14
62	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
63	Different <i>Sarcocystis</i> spp. are present in bovine eosinophilic myositis. <i>Veterinary Parasitology</i> , 2013, 197, 543-548.	0.7	41
64	MYCN and HDAC2 cooperate to repress miR-183 signaling in neuroblastoma. <i>Nucleic Acids Research</i> , 2013, 41, 6018-6033.	6.5	87
65	A p53 Drug Response Signature Identifies Prognostic Genes in High-Risk Neuroblastoma. <i>PLoS ONE</i> , 2013, 8, e79843.	1.1	34
66	Focal DNA Copy Number Changes in Neuroblastoma Target MYCN Regulated Genes. <i>PLoS ONE</i> , 2013, 8, e52321.	1.1	37
67	Pharmacological activation of the p53 pathway by nutlin-3 exerts anti-tumoral effects in medulloblastomas. <i>Neuro-Oncology</i> , 2012, 14, 859-869.	0.6	48
68	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. <i>Science Translational Medicine</i> , 2012, 4, 141ra91.	5.8	147
69	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, 1409-1417.	2.9	24
70	Genome-wide promoter methylation analysis in neuroblastoma identifies prognostic methylation biomarkers. <i>Genome Biology</i> , 2012, 13, R95.	13.9	64
71	N-Cadherin in Neuroblastoma Disease: Expression and Clinical Significance. <i>PLoS ONE</i> , 2012, 7, e31206.	1.1	39
72	miR-17-92 cluster 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

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73	Identification of a novel recurrent 1q42.2â€¹qter deletion in high risk <i>MYCN</i> single copy 11q deleted neuroblastomas. <i>International Journal of Cancer</i> , 2012, 130, 2599-2606.	2.3	37
74	Copy number defects of G1â€¹Cell cycle genes in neuroblastoma are frequent and correlate with high expression of <i>E2F</i> target genes and a poor prognosis. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 10-19.	1.5	57
75	Isolation of disseminated neuroblastoma cells from bone marrow aspirates for pretreatment risk assessment by array comparative genomic hybridization. <i>International Journal of Cancer</i> , 2012, 130, 1098-1108.	2.3	7
76	Cancer Gene Prioritization for Targeted Resequencing Using FitSNP Scores. <i>PLoS ONE</i> , 2012, 7, e31333.	1.1	2
77	Measurable impact of RNA quality on gene expression results from quantitative PCR. <i>Nucleic Acids Research</i> , 2011, 39, e63-e63.	6.5	146
78	Identification of tumoral glial precursor cells in neuroblastoma. <i>Cancer Letters</i> , 2011, 312, 73-81.	3.2	9
79	EV1<i>â€¹</i>mediated down regulation of <i>MIR449A</i> is essential for the survival of EV1 positive leukaemic cells. <i>British Journal of Haematology</i> , 2011, 154, 337-348.	1.2	20
80	Neuroblastoma genetics and phenotype: A tale of heterogeneity. <i>Seminars in Cancer Biology</i> , 2011, 21, 238-244.	4.3	25
81	A 6-gene signature identifies four molecular subgroups of neuroblastoma. <i>Cancer Cell International</i> , 2011, 11, 9.	1.8	27
82	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
83	High <i>ALK</i> Receptor Tyrosine Kinase Expression Supersedes <i>ALK</i> Mutation as a Determining Factor of an Unfavorable Phenotype in Primary Neuroblastoma. <i>Clinical Cancer Research</i> , 2011, 17, 5082-5092.	3.2	95
84	Multiplex Amplicon Quantification (MAQ), a fast and efficient method for the simultaneous detection of copy number alterations in neuroblastoma. <i>BMC Genomics</i> , 2010, 11, 298.	1.2	29
85	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. <i>International Journal of Cancer</i> , 2010, 127, 2374-2385.	2.3	88
86	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
87	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010, 29, 3583-3592.	2.6	141
88	Chromosomal and MicroRNA Expression Patterns Reveal Biologically Distinct Subgroups of 11qâ€¹ Neuroblastoma. <i>Clinical Cancer Research</i> , 2010, 16, 2971-2978.	3.2	70
89	The Quassinoid Derivative NBT-272 Targets Both the AKT and ERK Signaling Pathways in Embryonal Tumors. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 3145-3157.	1.9	14
90	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

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91	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
92	Predicting outcomes for children with neuroblastoma. <i>Discovery Medicine</i> , 2010, 10, 29-36.	0.5	15
93	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
94	External oligonucleotide standards enable cross laboratory comparison and exchange of real-time quantitative PCR data. <i>Nucleic Acids Research</i> , 2009, 37, e138-e138.	6.5	25
95	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
96	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, 686-690.	1.2	55
97	The emerging molecular pathogenesis of neuroblastoma: implications for improved risk assessment and targeted therapy. <i>Genome Medicine</i> , 2009, 1, 74.	3.6	34
98	Predicting outcomes for children with neuroblastoma using a multigene-expression signature: a retrospective SIOPEN/COG/GPOH study. <i>Lancet Oncology</i> , The, 2009, 10, 663-671.	5.1	176
99	59-gene prognostic signature sub-stratifies high-risk neuroblastoma patients. <i>Lancet Oncology</i> , The, 2009, 10, 1030.	5.1	11
100	Downregulation of MiR-449a Is Essential for the Survival of EVI1 Positive Leukemic Cells through Modulation of NOTCH1 and BCL2. <i>Blood</i> , 2009, 114, 361-361.	0.6	0
101	Identification of 2 putative critical segments of 17q gain in neuroblastoma through integrative genomics. <i>International Journal of Cancer</i> , 2008, 122, 1177-1182.	2.3	22
102	Aberrant splicing of the <i>PTPRD</i> gene mimics microdeletions identified at this locus in neuroblastomas. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 197-202.	1.5	22
103	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.	1.1	34
104	Copy number alterations and copy number variation in cancer: close encounters of the bad kind. <i>Cytogenetic and Genome Research</i> , 2008, 123, 176-182.	0.6	34
105	Low-cost dedicated mini-arrays for high-throughput analysis of DNA copy-number alterations in neuroblastoma. <i>Cancer Letters</i> , 2008, 269, 111-116.	3.2	2
106	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
107	MicroRNA Profiling of EVI1 Deregulated Myeloid Leukemia. <i>Blood</i> , 2008, 112, 5322-5322.	0.6	0
108	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>Blood</i> , 2008, 112, 4488-4488.	0.6	0

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109	Detection of DNA copy number alterations in cancer by array comparative genomic hybridization. <i>Genetics in Medicine</i> , 2007, 9, 574-584.	1.1	36
110	A detailed inventory of DNA copy number alterations in four commonly used Hodgkin's lymphoma cell lines. <i>Haematologica</i> , 2007, 92, 913-920.	1.7	33
111	High resolution tiling-path BAC array deletion mapping suggests commonly involved 3p21-p22 tumor suppressor genes in neuroblastoma and more frequent tumors. <i>International Journal of Cancer</i> , 2007, 120, 533-538.	2.3	20
112	ArrayCGH-based classification of neuroblastoma into genomic subgroups. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 1098-1108.	1.5	67
113	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
114	The von Hippel-Lindau tumor suppressor gene expression level has prognostic value in neuroblastoma. <i>International Journal of Cancer</i> , 2006, 119, 624-629.	2.3	14
115	Genome wide measurement of DNA copy number changes in neuroblastoma: dissecting amplicons and mapping losses, gains and breakpoints. <i>Cytogenetic and Genome Research</i> , 2006, 115, 273-282.	0.6	16
116	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. <i>BMC Bioinformatics</i> , 2005, 6, 124.	1.2	79
117	Positional and functional mapping of a neuroblastoma differentiation gene on chromosome 11. <i>BMC Genomics</i> , 2005, 6, 97.	1.2	19
118	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
119	No Evidence for Correlation of DDX1 Gene Amplification With Improved Survival Probability in Patients With MYCN-Amplified Neuroblastomas. <i>Journal of Clinical Oncology</i> , 2005, 23, 3167-3168.	0.8	24
120	Combined subtractive cDNA cloning and array CGH: an efficient approach for identification of overexpressed genes in DNA amplicons. <i>BMC Genomics</i> , 2004, 5, 11.	1.2	22
121	No evidence for involvement of SDHD in neuroblastoma pathogenesis. <i>BMC Cancer</i> , 2004, 4, 55.	1.1	17
122	ID2 expression in neuroblastoma does not correlate to MYCN levels and lacks prognostic value. <i>Oncogene</i> , 2003, 22, 456-460.	2.6	38
123	Application of laser capture microdissection in genetic analysis of neuroblastoma and neuroblastoma precursor cells. <i>Cancer Letters</i> , 2003, 197, 53-61.	3.2	28
124	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
125	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
126	DNA Copy Number Changes and Beyond. <i>Pediatric and Adolescent Medicine</i> , 0, , 10-22.	0.4	0