

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	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	Mutational dynamics between primary and relapse neuroblastomas. <i>Nature Genetics</i> , 2015, 47, 872-877.	9.4	253
3	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
4	Benchmarking of cell type deconvolution pipelines for transcriptomics data. <i>Nature Communications</i> , 2020, 11, 5650.	5.8	207
5	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
6	Computational deconvolution of transcriptomics data from mixed cell populations. <i>Bioinformatics</i> , 2018, 34, 1969-1979.	1.8	181
7	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
8	Asthma inflammatory phenotypes show differential microRNA expression in sputum. <i>Journal of Allergy and Clinical Immunology</i> , 2016, 137, 1433-1446.	1.5	168
9	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
10	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
11	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. <i>Science Translational Medicine</i> , 2012, 4, 141ra91.	5.8	147
12	Targeting MYCN-Driven Transcription By BET-Bromodomain Inhibition. <i>Clinical Cancer Research</i> , 2016, 22, 2470-2481.	3.2	147
13	Measurable impact of RNA quality on gene expression results from quantitative PCR. <i>Nucleic Acids Research</i> , 2011, 39, e63-e63.	6.5	146
14	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010, 29, 3583-3592.	2.6	141
15	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
16	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
17	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
18	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

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19	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
20	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
21	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
22	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
23	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXO1 reactivation of DREAM targets. <i>Nature Communications</i> , 2018, 9, 4866.	5.8	91
24	Activated <i>Alk</i> triggers prolonged neurogenesis and <i>Ret</i> upregulation providing a therapeutic target in <i>ALK</i> -mutated neuroblastoma. <i>Oncotarget</i> , 2014, 5, 2688-2702.	0.8	89
25	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. <i>International Journal of Cancer</i> , 2010, 127, 2374-2385.	2.3	88
26	MYCN and HDAC2 cooperate to repress miR-183 signaling in neuroblastoma. <i>Nucleic Acids Research</i> , 2013, 41, 6018-6033.	6.5	87
27	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
28	MYCN and <i>ALKF1174L</i> are sufficient to drive neuroblastoma development from neural crest progenitor cells. <i>Oncogene</i> , 2013, 32, 1059-1065.	2.6	84
29	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. <i>BMC Bioinformatics</i> , 2005, 6, 124.	1.2	79
30	Upregulation of MAPK Negative Feedback Regulators and <i>RET</i> in Mutant <i>ALK</i> Neuroblastoma: Implications for Targeted Treatment. <i>Clinical Cancer Research</i> , 2015, 21, 3327-3339.	3.2	76
31	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	9.4	75
32	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
33	Chromosomal and MicroRNA Expression Patterns Reveal Biologically Distinct Subgroups of 11q ^â Neuroblastoma. <i>Clinical Cancer Research</i> , 2010, 16, 2971-2978.	3.2	70
34	ArrayCGH-based classification of neuroblastoma into genomic subgroups. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 1098-1108.	1.5	67
35	Genome-wide promoter methylation analysis in neuroblastoma identifies prognostic methylation biomarkers. <i>Genome Biology</i> , 2012, 13, R95.	13.9	64
36	Copy number defects of <i>G1</i> cell 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

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37	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
38	Comparison of miRNA profiles of microdissected Hodgkin/Reedâ€Sternberg cells and Hodgkin cell lines <i>versus</i> CD77⁺ Bâ€cells reveals a distinct subset of differentially expressed miRNAs. <i>British Journal of Haematology</i> , 2009, 147, 686-690.	1.2	55
39	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
40	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. <i>Cancer Letters</i> , 2015, 366, 123-132.	3.2	51
41	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
42	Network Modeling of microRNAâ€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
43	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
44	Histone Chaperone CHAF1A Inhibits Differentiation and Promotes Aggressive Neuroblastoma. <i>Cancer Research</i> , 2014, 74, 765-774.	0.4	47
45	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
46	ViVar: A Comprehensive Platform for the Analysis and Visualization of Structural Genomic Variation. <i>PLoS ONE</i> , 2014, 9, e113800.	1.1	45
47	<i>Dickkopfâ€3</i> is regulated by the MYCNâ€induced miRâ€17â€92 cluster in neuroblastoma. <i>International Journal of Cancer</i> , 2012, 130, 2591-2598.	2.3	43
48	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
49	Different Sarcocystis spp. are present in bovine eosinophilic myositis. <i>Veterinary Parasitology</i> , 2013, 197, 543-548.	0.7	41
50	N-Cadherin in Neuroblastoma Disease: Expression and Clinical Significance. <i>PLoS ONE</i> , 2012, 7, e31206.	1.1	39
51	ID2 expression in neuroblastoma does not correlate to MYCN levels and lacks prognostic value. <i>Oncogene</i> , 2003, 22, 456-460.	2.6	38
52	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
53	MYCN-targeting miRNAs are predominantly downregulated during MYCN-driven neuroblastoma tumor formation. <i>Oncotarget</i> , 2015, 6, 5204-5216.	0.8	38
54	Identification of a novel recurrent 1q42.2â€qter 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

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55	Focal DNA Copy Number Changes in Neuroblastoma Target MYCN Regulated Genes. PLoS ONE, 2013, 8, e52321.	1.1	37
56	Detection of DNA copy number alterations in cancer by array comparative genomic hybridization. Genetics in Medicine, 2007, 9, 574-584.	1.1	36
57	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.	1.1	34
58	Copy number alterations and copy number variation in cancer: close encounters of the bad kind. Cytogenetic and Genome Research, 2008, 123, 176-182.	0.6	34
59	The emerging molecular pathogenesis of neuroblastoma: implications for improved risk assessment and targeted therapy. Genome Medicine, 2009, 1, 74.	3.6	34
60	A p53 Drug Response Signature Identifies Prognostic Genes in High-Risk Neuroblastoma. PLoS ONE, 2013, 8, e79843.	1.1	34
61	A detailed inventory of DNA copy number alterations in four commonly used Hodgkin's lymphoma cell lines. Haematologica, 2007, 92, 913-920.	1.7	33
62	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. Science Signaling, 2018, 11, .	1.6	33
63	Distinct Notch1 and <i>BCL11B</i> requirements mediate human $\hat{3}^{\hat{1}}/\hat{1}\pm\hat{1}^2$ T cell development. EMBO Reports, 2020, 21, e49006.	2.0	31
64	Frequency and Prognostic Impact of <i>ALK</i> Amplifications and Mutations in the European Neuroblastoma Study Group (SIOPEN) High-Risk Neuroblastoma Trial (HR-NBL1). Journal of Clinical Oncology, 2021, 39, 3377-3390.	0.8	30
65	MYCN and HDAC5 transcriptionally repress <i>CD9</i> to trigger invasion and metastasis in neuroblastoma. Oncotarget, 2016, 7, 66344-66359.	0.8	30
66	Multiplex Amplicon Quantification (MAQ), a fast and efficient method for the simultaneous detection of copy number alterations in neuroblastoma. BMC Genomics, 2010, 11, 298.	1.2	29
67	Genome wide expression profiling of p53 regulated miRNAs in neuroblastoma. Scientific Reports, 2015, 5, 9027.	1.6	29
68	Application of laser capture microdissection in genetic analysis of neuroblastoma and neuroblastoma precursor cells. Cancer Letters, 2003, 197, 53-61.	3.2	28
69	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. Expert Opinion on Drug Discovery, 2017, 12, 1-11.	2.5	28
70	Biallelic and monoallelic ESR2 variants associated with 46,XY disorders of sex development. Genetics in Medicine, 2018, 20, 717-727.	1.1	28
71	Circulating microRNA biomarkers for metastatic disease in neuroblastoma patients. JCI Insight, 2018, 3, .	2.3	28
72	A 6-gene signature identifies four molecular subgroups of neuroblastoma. Cancer Cell International, 2011, 11, 9.	1.8	27

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73	Meta-mining of copy number profiles of high-risk neuroblastoma tumors. <i>Scientific Data</i> , 2018, 5, 180240.	2.4	27
74	Methyl-CpG-binding domain sequencing reveals a prognostic methylation signature in neuroblastoma. <i>Oncotarget</i> , 2016, 7, 1960-1972.	0.8	26
75	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
76	Neuroblastoma genetics and phenotype: A tale of heterogeneity. <i>Seminars in Cancer Biology</i> , 2011, 21, 238-244.	4.3	25
77	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
78	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
79	Glutathione biosynthesis is upregulated at the initiation of MYCN-driven neuroblastoma tumorigenesis. <i>Molecular Oncology</i> , 2016, 10, 866-878.	2.1	23
80	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
81	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
82	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
83	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
84	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
85	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
86	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
87	EV11-mediated down regulation of <i>MIR449A</i> is essential for the survival of EV11 positive leukaemic cells. <i>British Journal of Haematology</i> , 2011, 154, 337-348.	1.2	20
88	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
89	Positional and functional mapping of a neuroblastoma differentiation gene on chromosome 11. <i>BMC Genomics</i> , 2005, 6, 97.	1.2	19
90	Targeting tachykinin receptors in neuroblastoma. <i>Oncotarget</i> , 2017, 8, 430-443.	0.8	19

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91	No evidence for involvement of SDHD in neuroblastoma pathogenesis. <i>BMC Cancer</i> , 2004, 4, 55.	1.1	17
92	ALK positively regulates MYCN activity through repression of HBP1 expression. <i>Oncogene</i> , 2019, 38, 2690-2705.	2.6	17
93	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
94	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
95	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
96	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
97	Predicting outcomes for children with neuroblastoma. <i>Discovery Medicine</i> , 2010, 10, 29-36.	0.5	15
98	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. <i>Science Advances</i> , 2022, 8, .	4.7	15
99	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
100	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
101	ERBB3 is a marker of a ganglioneuroblastoma/ganglioneuroma-like expression profile in neuroblastic tumours. <i>Molecular Cancer</i> , 2013, 12, 70.	7.9	14
102	Integrative analysis identifies lincRNAs up- and downstream of neuroblastoma driver genes. <i>Scientific Reports</i> , 2019, 9, 5685.	1.6	14
103	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
104	59-gene prognostic signature sub-stratifies high-risk neuroblastoma patients. <i>Lancet Oncology</i> , The, 2009, 10, 1030.	5.1	11
105	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
106	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
107	Identification of tumoral glial precursor cells in neuroblastoma. <i>Cancer Letters</i> , 2011, 312, 73-81.	3.2	9
108	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

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109	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
110	Evaluation of a marker independent isolation method for circulating tumor cells in esophageal adenocarcinoma. <i>PLoS ONE</i> , 2021, 16, e0251052.	1.1	6
111	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
112	The mutational landscape of <i>MYCN</i> , <i>Lin28b</i> and <i>ALK</i> driven murine neuroblastoma mimics human disease. <i>Oncotarget</i> , 2018, 9, 8334-8349.	0.8	6
113	Zipper plot: visualizing transcriptional activity of genomic regions. <i>BMC Bioinformatics</i> , 2017, 18, 231.	1.2	5
114	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
115	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
116	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
117	IncGraph: Incremental graphlet counting for topology optimisation. <i>PLoS ONE</i> , 2018, 13, e0195997.	1.1	2
118	Cancer Gene Prioritization for Targeted Resequencing Using FitSNP Scores. <i>PLoS ONE</i> , 2012, 7, e31333.	1.1	2
119	Early and late effects of pharmacological ALK inhibition on the neuroblastoma transcriptome. <i>Oncotarget</i> , 2017, 8, 106820-106832.	0.8	2
120	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
121	DREAM target reactivation by core transcriptional regulators supports neuroblastoma growth. <i>Molecular and Cellular Oncology</i> , 2019, 6, 1-3.	0.3	1
122	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
123	DNA Copy Number Changes and Beyond. <i>Pediatric and Adolescent Medicine</i> , 0, , 10-22.	0.4	0
124	MicroRNA Profiling of EVI1 Deregulated Myeloid Leukemia. <i>Blood</i> , 2008, 112, 5322-5322.	0.6	0
125	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
126	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