

Katleen De Preter

List of Publications by Year in descending order

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Version: 2024-02-01

126
papers

22,865
citations

66343

42
h-index

15732

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.	2.8	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.	8.2	5
3	Comprehensive RNA dataset of tissue and plasma from patients with esophageal cancer or precursor lesions. <i>Scientific Data</i> , 2022, 9, 86.	5.3	1
4	RRM2 enhances MYCN-driven neuroblastoma formation and acts as a synergistic target with CHK1 inhibition. <i>Science Advances</i> , 2022, 8, .	10.3	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.	2.7	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.	2.7	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.	2.8	3
8	Evaluation of a marker independent isolation method for circulating tumor cells in esophageal adenocarcinoma. <i>PLoS ONE</i> , 2021, 16, e0251052.	2.5	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.	1.6	30
10	The RNA Atlas expands the catalog of human non-coding RNAs. <i>Nature Biotechnology</i> , 2021, 39, 1453-1465.	17.5	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.	3.7	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.	2.5	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.	2.7	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.	7.1	17
15	Benchmarking of cell type deconvolution pipelines for transcriptomics data. <i>Nature Communications</i> , 2020, 11, 5650.	12.8	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.	4.5	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.	3.3	20
18	Integrative analysis identifies lincRNAs up- and downstream of neuroblastoma driver genes. <i>Scientific Reports</i> , 2019, 9, 5685.	3.3	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.	0.7	1
20	ALK positively regulates MYCN activity through repression of HBP1 expression. <i>Oncogene</i> , 2019, 38, 2690-2705.	5.9	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.	9.4	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.	6.3	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.	0.9	48
24	Computational deconvolution of transcriptomics data from mixed cell populations. <i>Bioinformatics</i> , 2018, 34, 1969-1979.	4.1	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.	2.1	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.	2.4	47
27	Biallelic and monoallelic ESR2 variants associated with 46,XY disorders of sex development. <i>Genetics in Medicine</i> , 2018, 20, 717-727.	2.4	28
28	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. <i>Nature Communications</i> , 2018, 9, 4866.	12.8	91
29	Integrated proximal proteomics reveals IRS2 as a determinant of cell survival in ALK-driven neuroblastoma. <i>Science Signaling</i> , 2018, 11, .	3.6	33
30	In silico discovery of a FOXM1 driven embryonal signaling pathway in therapy resistant neuroblastoma tumors. <i>Scientific Reports</i> , 2018, 8, 17468.	3.3	11
31	IncGraph: Incremental graphlet counting for topology optimisation. <i>PLoS ONE</i> , 2018, 13, e0195997.	2.5	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.	7.0	48
33	Meta-mining of copy number profiles of high-risk neuroblastoma tumors. <i>Scientific Data</i> , 2018, 5, 180240.	5.3	27
34	Circulating microRNA biomarkers for metastatic disease in neuroblastoma patients. <i>JCI Insight</i> , 2018, 3, .	5.0	28
35	The mutational landscape of MYCN, Lin28b and ALK F1174L driven murine neuroblastoma mimics human disease. <i>Oncotarget</i> , 2018, 9, 8334-8349.	1.8	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.	3.5	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. Expert Opinion on Drug Discovery, 2017, 12, 1-11.	5.0	28
38	Shallow Whole Genome Sequencing on Circulating Cell-Free DNA Allows Reliable Noninvasive Copy-Number Profiling in Neuroblastoma Patients. Clinical Cancer Research, 2017, 23, 6305-6314.	7.0	113
39	Zipper plot: visualizing transcriptional activity of genomic regions. BMC Bioinformatics, 2017, 18, 231.	2.6	5
40	Targeting tachykinin receptors in neuroblastoma. Oncotarget, 2017, 8, 430-443.	1.8	19
41	Early and late effects of pharmacological ALK inhibition on the neuroblastoma transcriptome. Oncotarget, 2017, 8, 106820-106832.	1.8	2
42	Glutathione biosynthesis is upregulated at the initiation of MYCN-driven neuroblastoma tumorigenesis. Molecular Oncology, 2016, 10, 866-878.	4.6	23
43	Asthma inflammatory phenotypes show differential microRNA expression in sputum. Journal of Allergy and Clinical Immunology, 2016, 137, 1433-1446.	2.9	168
44	Targeting MYCN-Driven Transcription By BET-Bromodomain Inhibition. Clinical Cancer Research, 2016, 22, 2470-2481.	7.0	147
45	MYCN and HDAC5 transcriptionally repress <i>CD9</i> to trigger invasion and metastasis in neuroblastoma. Oncotarget, 2016, 7, 66344-66359.	1.8	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. Oncotarget, 2016, 7, 74415-74426.	1.8	21
47	Methyl-CpG-binding domain sequencing reveals a prognostic methylation signature in neuroblastoma. Oncotarget, 2016, 7, 1960-1972.	1.8	26
48	Individual patient risk stratification of high-risk neuroblastomas using a two-gene score suited for clinical use. International Journal of Cancer, 2015, 137, 868-877.	5.1	9
49	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. Cancer Letters, 2015, 366, 123-132.	7.2	51
50	Mutational dynamics between primary and relapse neuroblastomas. Nature Genetics, 2015, 47, 872-877.	21.4	253
51	A Cre-conditional MYCN-driven neuroblastoma mouse model as an improved tool for preclinical studies. Oncogene, 2015, 34, 3357-3368.	5.9	112
52	Genome wide expression profiling of p53 regulated miRNAs in neuroblastoma. Scientific Reports, 2015, 5, 9027.	3.3	29
53	Upregulation of MAPK Negative Feedback Regulators and RET in Mutant ALK Neuroblastoma: Implications for Targeted Treatment. Clinical Cancer Research, 2015, 21, 3327-3339.	7.0	76
54	Therapeutic targeting of the MYC signal by inhibition of histone chaperone FACT in neuroblastoma. Science Translational Medicine, 2015, 7, 312ra176.	12.4	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.	1.8	38
56	ViVar: A Comprehensive Platform for the Analysis and Visualization of Structural Genomic Variation. <i>PLoS ONE</i> , 2014, 9, e113800.	2.5	45
57	Histone Chaperone CHAF1A Inhibits Differentiation and Promotes Aggressive Neuroblastoma. <i>Cancer Research</i> , 2014, 74, 765-774.	0.9	47
58	Robust Selection of Cancer Survival Signatures from High-Throughput Genomic Data Using Two-Fold Subsampling. <i>PLoS ONE</i> , 2014, 9, e108818.	2.5	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.	1.8	89
60	MYCN and ALKF1174L are sufficient to drive neuroblastoma development from neural crest progenitor cells. <i>Oncogene</i> , 2013, 32, 1059-1065.	5.9	84
61	ERBB3 is a marker of a ganglioneuroblastoma/ganglioneuroma-like expression profile in neuroblastic tumours. <i>Molecular Cancer</i> , 2013, 12, 70.	19.2	14
62	Evaluation of qPCR curve analysis methods for reliable biomarker discovery: Bias, resolution, precision, and implications. <i>Methods</i> , 2013, 59, 32-46.	3.8	197
63	Different <i>Sarcocystis</i> spp. are present in bovine eosinophilic myositis. <i>Veterinary Parasitology</i> , 2013, 197, 543-548.	1.8	41
64	MYCN and HDAC2 cooperate to repress miR-183 signaling in neuroblastoma. <i>Nucleic Acids Research</i> , 2013, 41, 6018-6033.	14.5	87
65	A p53 Drug Response Signature Identifies Prognostic Genes in High-Risk Neuroblastoma. <i>PLoS ONE</i> , 2013, 8, e79843.	2.5	34
66	Focal DNA Copy Number Changes in Neuroblastoma Target MYCN Regulated Genes. <i>PLoS ONE</i> , 2013, 8, e52321.	2.5	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.	1.2	48
68	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. <i>Science Translational Medicine</i> , 2012, 4, 141ra91.	12.4	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.	6.4	24
70	Genome-wide promoter methylation analysis in neuroblastoma identifies prognostic methylation biomarkers. <i>Genome Biology</i> , 2012, 13, R95.	9.6	64
71	N-Cadherin in Neuroblastoma Disease: Expression and Clinical Significance. <i>PLoS ONE</i> , 2012, 7, e31206.	2.5	39
72	<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.	5.1	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.	5.1	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.	2.8	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.	5.1	7
76	Cancer Gene Prioritization for Targeted Resequencing Using FitSNP Scores. <i>PLoS ONE</i> , 2012, 7, e31333.	2.5	2
77	Measurable impact of RNA quality on gene expression results from quantitative PCR. <i>Nucleic Acids Research</i> , 2011, 39, e63-e63.	14.5	146
78	Identification of tumoral glial precursor cells in neuroblastoma. <i>Cancer Letters</i> , 2011, 312, 73-81.	7.2	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.	2.5	20
80	Neuroblastoma genetics and phenotype: A tale of heterogeneity. <i>Seminars in Cancer Biology</i> , 2011, 21, 238-244.	9.6	25
81	A 6-gene signature identifies four molecular subgroups of neuroblastoma. <i>Cancer Cell International</i> , 2011, 11, 9.	4.1	27
82	miRNA Expression Profiling Enables Risk Stratification in Archived and Fresh Neuroblastoma Tumor Samples. <i>Clinical Cancer Research</i> , 2011, 17, 7684-7692.	7.0	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.	7.0	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.	2.8	29
85	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. <i>International Journal of Cancer</i> , 2010, 127, 2374-2385.	5.1	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.	5.9	112
87	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. <i>Oncogene</i> , 2010, 29, 3583-3592.	5.9	141
88	Chromosomal and MicroRNA Expression Patterns Reveal Biologically Distinct Subgroups of 11qâ€¹ Neuroblastoma. <i>Clinical Cancer Research</i> , 2010, 16, 2971-2978.	7.0	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.	4.1	14
90	Accurate Outcome Prediction in Neuroblastoma across Independent Data Sets Using a Multigene Signature. <i>Clinical Cancer Research</i> , 2010, 16, 1532-1541.	7.0	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.	7.0	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.	7.0	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.	14.5	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.	1.4	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.	2.5	55
97	The emerging molecular pathogenesis of neuroblastoma: implications for improved risk assessment and targeted therapy. <i>Genome Medicine</i> , 2009, 1, 74.	8.2	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.	10.7	176
99	59-gene prognostic signature sub-stratifies high-risk neuroblastoma patients. <i>Lancet Oncology</i> , The, 2009, 10, 1030.	10.7	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.	1.4	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.	5.1	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.	2.8	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.	2.6	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.	1.1	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.	7.2	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.	14.5	56
107	MicroRNA Profiling of EVI1 Deregulated Myeloid Leukemia. <i>Blood</i> , 2008, 112, 5322-5322.	1.4	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.	1.4	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.	2.4	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.	3.5	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.	5.1	20
112	ArrayCGH-based classification of neuroblastoma into genomic subgroups. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 1098-1108.	2.8	67
113	Human fetal neuroblast and neuroblastoma transcriptome analysis confirms neuroblast origin and highlights neuroblastoma candidate genes. <i>Genome Biology</i> , 2006, 7, R84.	9.6	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.	5.1	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.	1.1	16
116	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. <i>BMC Bioinformatics</i> , 2005, 6, 124.	2.6	79
117	Positional and functional mapping of a neuroblastoma differentiation gene on chromosome 11. <i>BMC Genomics</i> , 2005, 6, 97.	2.8	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.	1.6	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.	1.6	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.	2.8	22
121	No evidence for involvement of SDHD in neuroblastoma pathogenesis. <i>BMC Cancer</i> , 2004, 4, 55.	2.6	17
122	ID2 expression in neuroblastoma does not correlate to MYCN levels and lacks prognostic value. <i>Oncogene</i> , 2003, 22, 456-460.	5.9	38
123	Application of laser capture microdissection in genetic analysis of neuroblastoma and neuroblastoma precursor cells. <i>Cancer Letters</i> , 2003, 197, 53-61.	7.2	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.	9.6	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.	5.5	167
126	DNA Copy Number Changes and Beyond. <i>Pediatric and Adolescent Medicine</i> , 0, , 10-22.	0.4	0