Frank Speleman

List of Publications by Year
in descending order

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437 papers	49,276 citations	4120 87 h-index	1820 210 g-index
461 all docs	461 docs citations	461 times ranked	61107 citing authors

#	Article	IF	Citations
1	Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. Genome Biology, 2002, 3, research0034.1.	13.9	16,304
2	qBase relative quantification framework and software for management and automated analysis of real-time quantitative PCR data. Genome Biology, 2007, 8, R19.	13.9	3,580
3	miR-9, a MYC/MYCN-activated microRNA, regulates E-cadherin and cancer metastasis. Nature Cell Biology, 2010, 12, 247-256.	4.6	1,216
4	Identification of ALK as a major familial neuroblastoma predisposition gene. Nature, 2008, 455, 930-935.	13.7	1,207
5	A novel and universal method for microRNA RT-qPCR data normalization. Genome Biology, 2009, 10, R64.	13.9	849
6	Loss-of-function mutations in FGFR1 cause autosomal dominant Kallmann syndrome. Nature Genetics, 2003, 33, 463-465.	9.4	764
7	Recurrent Rearrangements of Chromosome 1q21.1 and Variable Pediatric Phenotypes. New England Journal of Medicine, 2008, 359, 1685-1699.	13.9	663
8	RNA G-quadruplexes cause eIF4A-dependent oncogene translation in cancer. Nature, 2014, 513, 65-70.	13.7	506
9	EWS and ATF-1 gene fusion induced by t(12;22) translocation in malignant melanoma of soft parts. Nature Genetics, 1993, 4, 341-345.	9.4	483
10	Exhaustive mutation analysis of theNF1 gene allows identification of 95% of mutations and reveals a high frequency of unusual splicing defects. Human Mutation, 2000, 15, 541-555.	1.1	477
11	Gain of Chromosome Arm 17q and Adverse Outcome in Patients with Neuroblastoma. New England Journal of Medicine, 1999, 340, 1954-1961.	13.9	456
12	Genome dynamics of the human embryonic kidney 293 lineage in response to cell biology manipulations. Nature Communications, 2014, 5, 4767.	5.8	421
13	Loss-of-function mutations in LEMD3 result in osteopoikilosis, Buschke-Ollendorff syndrome and melorheostosis. Nature Genetics, 2004, 36, 1213-1218.	9.4	410
14	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. Journal of Medical Genetics, 2006, 43, 625-633.	1.5	342
15	LIN28B induces neuroblastoma and enhances MYCN levels via let-7 suppression. Nature Genetics, 2012, 44, 1199-1206.	9.4	336
16	International consensus for neuroblastoma molecular diagnostics: report from the International Neuroblastoma Risk Group (INRG) Biology Committee. British Journal of Cancer, 2009, 100, 1471-1482.	2.9	330
17	Overall Genomic Pattern Is a Predictor of Outcome in Neuroblastoma. Journal of Clinical Oncology, 2009, 27, 1026-1033.	0.8	288
18	PHF6 mutations in T-cell acute lymphoblastic leukemia. Nature Genetics, 2010, 42, 338-342.	9.4	282

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19	The miR-17-92 MicroRNA Cluster Regulates Multiple Components of the TGF-Î² Pathway in Neuroblastoma. Molecular Cell, 2010, 40, 762-773.	4.5	279
20	High-throughput stem-loop RT-qPCR miRNA expression profiling using minute amounts of input RNA. Nucleic Acids Research, 2008, 36, e143-e143.	6.5	261
21	Mutational dynamics between primary and relapse neuroblastomas. Nature Genetics, 2015, 47, 872-877.	9.4	253
22	Duplication of the MYB oncogene in T cell acute lymphoblastic leukemia. Nature Genetics, 2007, 39, 593-595.	9.4	252
23	Further delineation of the 15q13 microdeletion and duplication syndromes: a clinical spectrum varying from non-pathogenic to a severe outcome. Journal of Medical Genetics, 2009, 46, 511-523.	1.5	250
24	A cooperative microRNA-tumor suppressor gene network in acute T-cell lymphoblastic leukemia (T-ALL). Nature Genetics, 2011, 43, 673-678.	9.4	244
25	Meta-analysis of Neuroblastomas Reveals a Skewed ALK Mutation Spectrum in Tumors with MYCN Amplification. Clinical Cancer Research, 2010, 16, 4353-4362.	3.2	243
26	RTPrimerDB: the Real-Time PCR primer and probe database. Nucleic Acids Research, 2003, 31, 122-123.	6.5	240
27	A mechanistic classification of clinical phenotypes in neuroblastoma. Science, 2018, 362, 1165-1170.	6.0	213
28	Elimination of Primerâ€“Dimer Artifacts and Genomic Coamplification Using a Two-Step SYBR Green I Real-Time RT-PCR. Analytical Biochemistry, 2002, 303, 95-98.	1.1	201
29	ABT-199 mediated inhibition of BCL-2 as a novel therapeutic strategy in T-cell acute lymphoblastic leukemia. Blood, 2014, 124, 3738-3747.	0.6	198
30	Molecular pathogenesis of multiple gastrointestinal stromal tumors in NF1 patients. Human Molecular Genetics, 2006, 15, 1015-1023.	1.4	195
31	Tumor formation and inactivation of RIZ1, an Rb-binding member of a nuclear protein-methyltransferase superfamily. Genes and Development, 2001, 15, 2250-2262.	2.7	181
32	Predicting outcomes for children with neuroblastoma using a multigene-expression signature: a retrospective SIOPEN/COG/GPOH study. Lancet Oncology, The, 2009, 10, 663-671.	5.1	176
33	Emergence of New ALK Mutations at Relapse of Neuroblastoma. Journal of Clinical Oncology, 2014, 32, 2727-2734.	0.8	176
34	ALK activation by the CLTC-ALK fusion is a recurrent event in large B-cell lymphoma. Blood, 2003, 102, 2638-2641.	0.6	174
35	Lysine-specific demethylase 1 restricts hematopoietic progenitor proliferation and is essential for terminal differentiation. Leukemia, 2012, 26, 2039-2051.	3.3	171
36	The H3K27me3 demethylase UTX is a gender-specific tumor suppressor in T-cell acute lymphoblastic leukemia. Blood, 2015, 125, 13-21.	0.6	168

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37	Quantification of MYCN, DDX1, and NAG Gene Copy Number in Neuroblastoma Using a Real-Time Quantitative PCR Assay. Modern Pathology, 2002, 15, 159-166.	2.9	167
38	Unequivocal Delineation of Clinicogenetic Subgroups and Development of a New Model for Improved Outcome Prediction in Neuroblastoma. Journal of Clinical Oncology, 2005, 23, 2280-2299.	0.8	160
39	Molecular Dissection of Isolated Disease Features in Mosaic Neurofibromatosis Type 1. American Journal of Human Genetics, 2007, 81, 243-251.	2.6	157
40	Evidence for two tumour suppressor loci on chromosomal bands 1p35â€“36 involved in neuroblastoma: one probably imprinted, another associated with N-myc amplification. Human Molecular Genetics, 1995, 4, 535-539.	1.4	154
41	Expression profiling suggests underexpression of the GABAA receptor subunit Î´ in the fragile X knockout mouse model. Neurobiology of Disease, 2006, 21, 346-357.	2.1	151
42	Segmental chromosomal alterations have prognostic impact in neuroblastoma: a report from the INRG project. British Journal of Cancer, 2012, 107, 1418-1422.	2.9	151
43	Targeted Expression of Mutated ALK Induces Neuroblastoma in Transgenic Mice. Science Translational Medicine, 2012, 4, 141ra91.	5.8	147
44	Targeting MYCN-Driven Transcription By BET-Bromodomain Inhibition. Clinical Cancer Research, 2016, 22, 2470-2481.	3.2	147
45	Measurable impact of RNA quality on gene expression results from quantitative PCR. Nucleic Acids Research, 2011, 39, e63-e63.	6.5	146
46	Guidelines for molecular karyotyping in constitutional genetic diagnosis. European Journal of Human Genetics, 2007, 15, 1105-1114.	1.4	144
47	PHF6 mutations in adult acute myeloid leukemia. Leukemia, 2011, 25, 130-134.	3.3	142
48	Clinical significance of HOX11L2 expression linked to t(5;14)(q35;q32), of HOX11 expression, and of SIL-TAL fusion in childhood T-cell malignancies: results of EORTC studies 58881 and 58951. Blood, 2004, 103, 442-450.	0.6	141
49	Molecular Karyotyping: Array CGH Quality Criteria for Constitutional Genetic Diagnosis. Journal of Histochemistry and Cytochemistry, 2005, 53, 413-422.	1.3	141
50	An integrative genomics screen uncovers ncRNA T-UCR functions in neuroblastoma tumours. Oncogene, 2010, 29, 3583-3592.	2.6	141
51	The TLX1 oncogene drives aneuploidy in T cell transformation. Nature Medicine, 2010, 16, 1321-1327.	15.2	139
52	I;17 translocations and other chromosome 17 rearrangements in human primary neuroblastoma tumors and cell lines. Genes Chromosomes and Cancer, 1994, 10, 103-114.	1.5	134
53	Human fetal neuroblast and neuroblastoma transcriptome analysis confirms neuroblast origin and highlights neuroblastoma candidate genes. Genome Biology, 2006, 7, R84.	13.9	134
54	MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits proliferation and survival. Cell Death and Differentiation, 2011, 18, 974-984.	5.0	133

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55	Small-Molecule MDM2 Antagonists as a New Therapy Concept for Neuroblastoma. Cancer Research, 2006, 66, 9646-9655.	0.4	132
56	RTPrimerDB: the portal for real-time PCR primers and probes. Nucleic Acids Research, 2009, 37, D942-D945.	6.5	132
57	Prognostic Impact of Gene Expressionâ€“Based Classification for Neuroblastoma. Journal of Clinical Oncology, 2010, 28, 3506-3515.	0.8	129
58	A Novel Gene Family NBPF: Intricate Structure Generated by Gene Duplications During Primate Evolution. Molecular Biology and Evolution, 2005, 22, 2265-2274.	3.5	128
59	NOTCH1 and FBXW7 mutations have a favorable impact on early response to treatment, but not on outcome, in children with T-cell acute lymphoblastic leukemia (T-ALL) treated on EORTC trials 58881 and 58951. Leukemia, 2010, 24, 2023-2031.	3.3	125
60	Identification of a Third EXT-like Gene (EXTL3) Belonging to the EXT Gene Family. Genomics, 1998, 47, 230-237.	1.3	124
61	BET bromodomain protein inhibition is a therapeutic option for medulloblastoma. Oncotarget, 2013, 4, 2080-2095.	0.8	122
62	Genetic heterogeneity of neuroblastoma studied by comparative genomic hybridization. , 1998, 23, 141-152.		121
63	Therapeutic targeting of the MYC signal by inhibition of histone chaperone FACT in neuroblastoma. Science Translational Medicine, 2015, 7, 312ra176.	5.8	120
64	Expression analyses identify MLL as a prominent target of 11q23 amplification and support an etiologic role for MLL gain of function in myeloid malignancies. Blood, 2004, 103, 229-235.	0.6	117
65	Long noncoding RNA expression profiling in cancer: Challenges and opportunities. Genes Chromosomes and Cancer, 2019, 58, 191-199.	1.5	117
66	Quality Assessment of Genetic Markers Used for Therapy Stratification. Journal of Clinical Oncology, 2003, 21, 2077-2084.	0.8	113
67	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.	3.2	113
68	Comparative genomic hybridization (CGH) analysis of stage 4 neuroblastoma reveals high frequency of 11q deletion in tumors lackingMYCN amplification. International Journal of Cancer, 2001, 91, 680-686.	2.3	112
69	Widespread Dysregulation of MiRNAs by MYCN Amplification and Chromosomal Imbalances in Neuroblastoma: Association of miRNA Expression with Survival. PLoS ONE, 2009, 4, e7850.	1.1	112
70	MYCN/c-MYC-induced microRNAs repress coding gene networks associated with poor outcome in MYCN/c-MYC-activated tumors. Oncogene, 2010, 29, 1394-1404.	2.6	112
71	A Cre-conditional MYCN-driven neuroblastoma mouse model as an improved tool for preclinical studies. Oncogene, 2015, 34, 3357-3368.	2.6	112
72	Comprehensive Analysis of Transcriptome Variation Uncovers Known and Novel Driver Events in T-Cell Acute Lymphoblastic Leukemia. PLoS Genetics, 2013, 9, e1003997.	1.5	110

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73	The H3K27me3 demethylase UTX in normal development and disease. Epigenetics, 2014, 9, 658-668.	1.3	109
74	Delineation of two distinct 6p deletion syndromes. Human Genetics, 1999, 104, 64-72.	1.8	108
75	RTPrimerDB: the real-time PCR primer and probe database, major update 2006. Nucleic Acids Research, 2006, 34, D684-D688.	6.5	107
76	A new recurrent inversion, inv(7)(p15q34), leads to transcriptional activation of HOXA10 and HOXA11 in a subset of T-cell acute lymphoblastic leukemias. Leukemia, 2005, 19, 358-366.	3.3	106
77	ComprehensiveNF1 screening on cultured Schwann cells from neurofibromas. Human Mutation, 2006, 27, 1030-1040.	1.1	105
78	Antitumor Activity of the Selective MDM2 Antagonist Nutlin-3 Against Chemoresistant Neuroblastoma With Wild-Type p53. Journal of the National Cancer Institute, 2009, 101, 1562-1574.	3.0	105
79	Molecular cytogenetic and clinical findings inETV6/ABL1-positive leukemia. Genes Chromosomes and Cancer, 2001, 30, 274-282.	1.5	103
80	Rapid detection of VHL exon deletions using real-time quantitative PCR. Laboratory Investigation, 2005, 85, 24-33.	1.7	102
81	Deletion mapping in neuroblastoma cell lines suggests two distinct tumor suppressor genes in the 1p35-36 region, only one of which is associated with N-myc amplification. Oncogene, 1995, 10, 291-7.	2.6	101
82	Constitutional translocation t(1;17)(p36;q12â€“21) in a patient with neuroblastoma. Genes Chromosomes and Cancer, 1990, 2, 252-254.	1.5	99
83	Identification of cytogenetic subclasses and recurring chromosomal aberrations in AML and MDS with complex karyotypes using m-FISH. Genes Chromosomes and Cancer, 2002, 33, 60-72.	1.5	98
84	Novel biological insights in T-cell acute lymphoblastic leukemia. Experimental Hematology, 2015, 43, 625-639.	0.2	97
85	High ALK Receptor Tyrosine Kinase Expression Supersedes ALK Mutation as a Determining Factor of an Unfavorable Phenotype in Primary Neuroblastoma. Clinical Cancer Research, 2011, 17, 5082-5092.	3.2	95
86	Mutation analysis of P73 and TP53 in Merkel cell carcinoma. British Journal of Cancer, 2000, 82, 823-826.	2.9	94
87	Impact of RNA quality on reference gene expression stability. BioTechniques, 2005, 39, 52-56.	0.8	92
88	miRNA Expression Profiling Enables Risk Stratification in Archived and Fresh Neuroblastoma Tumor Samples. Clinical Cancer Research, 2011, 17, 7684-7692.	3.2	92
89	MiRâ€137 functions as a tumor suppressor in neuroblastoma by downregulating KDM1A. International Journal of Cancer, 2013, 133, 1064-1073.	2.3	91
90	MicroRNA-193b-3p acts as a tumor suppressor by targeting the MYB oncogene in T-cell acute lymphoblastic leukemia. Leukemia, 2015, 29, 798-806.	3.3	91

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91	TBX2 is a neuroblastoma core regulatory circuitry component enhancing MYCN/FOXM1 reactivation of DREAM targets. Nature Communications, 2018, 9, 4866.	5.8	91
92	Challenges for CNV interpretation in clinical molecular karyotyping: Lessons learned from a 1001 sample experience. European Journal of Medical Genetics, 2009, 52, 398-403.	0.7	90
93	Activated Alk triggers prolonged neurogenesis and Ret upregulation providing a therapeutic target in ALK-mutated neuroblastoma. Oncotarget, 2014, 5, 2688-2702.	0.8	89
94	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. International Journal of Cancer, 2010, 127, 2374-2385.	2.3	88
95	Hsa-mir-145 is the top EWS-FLI1-repressed microRNA involved in a positive feedback loop in Ewing's sarcoma. Oncogene, 2011, 30, 2173-2180.	2.6	87
96	Accurate Outcome Prediction in Neuroblastoma across Independent Data Sets Using a Multigene Signature. Clinical Cancer Research, 2010, 16, 1532-1541.	3.2	86
97	MYCN and ALKF1174L are sufficient to drive neuroblastoma development from neural crest progenitor cells. Oncogene, 2013, 32, 1059-1065.	2.6	84
98	Modulation of neuroblastoma disease pathogenesis by an extensive network of epigenetically regulated microRNAs. Oncogene, 2013, 32, 2927-2936.	2.6	84
99	Disease-Causing 7.4 kb Cis-Regulatory Deletion Disrupting Conserved Non-Coding Sequences and Their Interaction with the FOXL2 Promotor: Implications for Mutation Screening. PLoS Genetics, 2009, 5, e1000522.	1.5	83
100	Multicentre analysis of patterns of DNA gains and losses in 204 neuroblastoma tumors: How many genetic subgroups are there?. Medical and Pediatric Oncology, 2001, 36, 5-10.	1.0	82
101	Combined karyotyping, CGH and M-FISH analysis allows detailed characterization of unidentified chromosomal rearrangements in Merkel cell carcinoma. International Journal of Cancer, 2002, 101, 137-145.	2.3	80
102	Revised Risk Estimation and Treatment Stratification of Low- and Intermediate-Risk Neuroblastoma Patients by Integrating Clinical and Molecular Prognostic Markers. Clinical Cancer Research, 2015, 21, 1904-1915.	3.2	80
103	t(5;14)/HOX11L2-positive T-cell acute lymphoblastic leukemia. A collaborative study of the Groupe FranÃ§ais de CytogÃ©nÃ©tique HÃ©matologique (GFCH). Leukemia, 2003, 17, 1851-1857.	3.3	79
104	arrayCGHbase: an analysis platform for comparative genomic hybridization microarrays. BMC Bioinformatics, 2005, 6, 124.	1.2	79
105	Synthetic lethality between Rb, p53 and Dicer or miR-17â€“92 in retinal progenitors suppresses retinoblastoma formation. Nature Cell Biology, 2012, 14, 958-965.	4.6	79
106	miRâ€542â€3p exerts tumor suppressive functions in neuroblastoma by downregulating <scp>S</scp>urvivin. International Journal of Cancer, 2015, 136, 1308-1320.	2.3	78
107	Identification and Characterization of a Novel Member of the EXT Gene Family, EXTL2. European Journal of Human Genetics, 1997, 5, 382-389.	1.4	77
108	Smoothing waves in array CGH tumor profiles. Bioinformatics, 2009, 25, 1099-1104.	1.8	76

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109	Upregulation of MAPK Negative Feedback Regulators and RET in Mutant ALK Neuroblastoma: Implications for Targeted Treatment. Clinical Cancer Research, 2015, 21, 3327-3339.	3.2	76
110	ZEB2 drives immature T-cell lymphoblastic leukaemia development via enhanced tumour-initiating potential and IL-7 receptor signalling. Nature Communications, 2015, 6, 5794.	5.8	75
111	The Î±E-catenin gene (CTNNA1) acts as an invasion-suppressor gene in human colon cancer cells. Oncogene, 1999, 18, 905-915.	2.6	73
112	Genomic Amplifications and Distal 6q Loss: Novel Markers for Poor Survival in High-risk Neuroblastoma Patients. Journal of the National Cancer Institute, 2018, 110, 1084-1093.	3.0	73
113	PAX5/IGH rearrangement is a recurrent finding in a subset of aggressive B-NHL with complex chromosomal rearrangements. Genes Chromosomes and Cancer, 2005, 44, 218-223.	1.5	72
114	Molecular cytogenetic study of 126 unselected T-ALL cases reveals high incidence of TCRÎ² locus rearrangements and putative new T-cell oncogenes. Leukemia, 2006, 20, 1238-1244.	3.3	72
115	Subtelomeric imbalances in phenotypically normal individuals. Human Mutation, 2007, 28, 958-967.	1.1	72
116	The microRNA body map: dissecting microRNA function through integrative genomics. Nucleic Acids Research, 2011, 39, e136-e136.	6.5	72
117	Chromosomal and MicroRNA Expression Patterns Reveal Biologically Distinct Subgroups of 11qâ^' Neuroblastoma. Clinical Cancer Research, 2010, 16, 2971-2978.	3.2	70
118	Detailed characterization of 12 supernumerary ring chromosomes using microâ€FISH and search for uniparental disomy. American Journal of Medical Genetics Part A, 2001, 99, 223-233.	2.4	68
119	Proneural and proneuroendocrine transcription factor expression in cutaneous mechanoreceptor (Merkel) cells and Merkel cell carcinoma. International Journal of Cancer, 2002, 101, 103-110.	2.3	68
120	ArrayCGHâ€based classification of neuroblastoma into genomic subgroups. Genes Chromosomes and Cancer, 2007, 46, 1098-1108.	1.5	67
121	i(12p) in a malignant ovarian tumor. Cancer Genetics and Cytogenetics, 1990, 45, 49-53.	1.0	65
122	Pallister-killian syndrome: Characterization of the isochromosome 12p by fluorescentIn Situ hybridization. American Journal of Medical Genetics Part A, 1991, 41, 381-387.	2.4	65
123	High-Resolution Fluorescence Mapping of 46 DNA Markers to the Short Arm of Human Chromosome 1. Genomics, 1993, 18, 71-78.	1.3	64
124	Real-Time Quantitative PCR as an Alternative to Southern Blot or Fluorescence In Situ Hybridization for Detection of Gene Copy Number Changes. , 2007, 353, 205-226.		64
125	Acute myeloid leukaemia with 8p11 (MYST3) rearrangement: an integrated cytologic, cytogenetic and molecular study by the groupe francophone de cytogÃ©nÃ©tique hÃ©matologique. Leukemia, 2008, 22, 1567-1575.	3.3	64
126	Array comparative genomic hybridization and flow cytometry analysis of spontaneous abortions and mors in utero samples. BMC Medical Genetics, 2009, 10, 89.	2.1	64

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127	Genome-wide promoter methylation analysis in neuroblastoma identifies prognostic methylation biomarkers. Genome Biology, 2012, 13, R95.	13.9	64
128	Cytogenetic analysis of a mesenchymal hamartoma of the liver. Cancer Genetics and Cytogenetics, 1989, 40, 29-32.	1.0	63
129	Frequent allelic loss at 10q23 but low incidence ofPTEN mutations in merkel cell carcinoma. International Journal of Cancer, 2001, 92, 409-413.	2.3	63
130	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. Oncogene, 2004, 23, 2732-2742.	2.6	63
131	Functional Analysis of the p53 Pathway in Neuroblastoma Cells Using the Small-Molecule MDM2 Antagonist Nutlin-3. Molecular Cancer Therapeutics, 2011, 10, 983-993.	1.9	61
132	Hyperdiploidy with 58-66 chromosomes in childhood B-acute lymphoblastic leukemia is highly curable: 58951 CLG-EORTC results. Blood, 2013, 121, 2415-2423.	0.6	61
133	Epigenetics in Tâ€cell acute lymphoblastic leukemia. Immunological Reviews, 2015, 263, 50-67.	2.8	61
134	1p36: Every subband a suppressor?. European Journal of Cancer, 1995, 31, 538-541.	1.3	60
135	Osteopoikilosis, short stature and mental retardation as key features of a new microdeletion syndrome on 12q14. Journal of Medical Genetics, 2007, 44, 264-268.	1.5	58
136	Recurrent 1;17 translocations in human neuroblastoma reveal nonhomologous mitotic recombination during the S/G2 phase as a novel mechanism for loss of heterozygosity. American Journal of Human Genetics, 1994, 55, 341-7.	2.6	58
137	Characteristic pattern of chromosomal gains and losses in Merkel cell carcinoma detected by comparative genomic hybridization. Cancer Research, 1998, 58, 1503-8.	0.4	58
138	Six cases of 7p deletion: Clinical, cytogenetic, and molecular studies. American Journal of Medical Genetics Part A, 1994, 51, 270-276.	2.4	57
139	Interstitial telomeric sequences at the junction site of a jumping translocation. Human Genetics, 1997, 99, 735-737.	1.8	57
140	Copy number defects of G1â€cell cycle genes in neuroblastoma are frequent and correlate with high expression of E2F target genes and a poor prognosis. Genes Chromosomes and Cancer, 2012, 51, 10-19.	1.5	57
141	GATA3 induces human T-cell commitment by restraining Notch activity and repressing NK-cell fate. Nature Communications, 2016, 7, 11171.	5.8	57
142	Chromosomal aberrations in Bloom syndrome patients with myeloid malignancies. Cancer Genetics and Cytogenetics, 2001, 128, 39-42.	1.0	56
143	Somatic loss of wild typeNF1 allele in neurofibromas: Comparison ofNF1 microdeletion and non-microdeletion patients. Genes Chromosomes and Cancer, 2006, 45, 893-904.	1.5	56
144	Positional gene enrichment analysis of gene sets for high-resolution identification of overrepresented chromosomal regions. Nucleic Acids Research, 2008, 36, e43-e43.	6.5	56

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145	Comparison of miRNA profiles of microdissected Hodgkin/Reedâ€Sternberg cells and Hodgkin cell lines versus CD77⁺ Bâ€cells reveals a distinct subset of differentially expressed miRNAs. British Journal of Haematology, 2009, 147, 686-690.	1.2	55
146	MicroRNA-128-3p is a novel oncomiR targeting PHF6 in T-cell acute lymphoblastic leukemia. Haematologica, 2014, 99, 1326-1333.	1.7	55
147	The pitfalls and promise of liquid biopsies for diagnosing and treating solid tumors in children: a review. European Journal of Pediatrics, 2020, 179, 191-202.	1.3	55
148	Improved detection of chromosomal abnormalities in chronic lymphocytic leukemia by conventional cytogenetics using CpG oligonucleotide and interleukinâ€2 stimulation: A Belgian multicentric study. Genes Chromosomes and Cancer, 2009, 48, 843-853.	1.5	54
149	Escape from p53-mediated tumor surveillance in neuroblastoma: switching off the p14ARF-MDM2-p53 axis. Cell Death and Differentiation, 2009, 16, 1563-1572.	5.0	54
150	Aberrant methylation of candidate tumor suppressor genes in neuroblastoma. Cancer Letters, 2009, 273, 336-346.	3.2	54
151	EVI1is consistently expressed as principal transcript in common and rare recurrent 3q26 rearrangements. Genes Chromosomes and Cancer, 2006, 45, 349-356.	1.5	51
152	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. Cancer Letters, 2015, 366, 123-132.	3.2	51
153	Mapping of novel regions of DNA gain and loss by comparative genomic hybridization in esophageal carcinoma in the Black and Colored populations of South Africa. Cancer Research, 1999, 59, 1877-83.	0.4	51
154	Molecular cytogenetic analysis of 10;11 rearrangements in acute myeloid leukemia. Leukemia, 2002, 16, 344-351.	3.3	50
155	GAB2 is a novel target of 11q amplification in AML/MDS. Genes Chromosomes and Cancer, 2006, 45, 798-807.	1.5	50
156	Neuroblastoma epigenetics: From candidate gene approaches to genome-wide screenings. Epigenetics, 2011, 6, 962-970.	1.3	50
157	The Notch driven long non-coding RNA repertoire in T-cell acute lymphoblastic leukemia. Haematologica, 2014, 99, 1808-1816.	1.7	50
158	Neuroblastoma cells with overexpressed MYCN retain their capacity to undergo neuronal differentiation. Laboratory Investigation, 2004, 84, 406-417.	1.7	49
159	Genome profiling of acute myelomonocytic leukemia: alteration of the MYB locus in MYST3-linked cases. Leukemia, 2009, 23, 85-94.	3.3	49
160	Comprehensive miRNA expression profiling in human T-cell acute lymphoblastic leukemia by small RNA-sequencing. Scientific Reports, 2017, 7, 7901.	1.6	49
161	A Constitutional Translocation t(1;17)(p36.2;q11.2) in a Neuroblastoma Patient Disrupts the Human NBPF1 and ACCN1 Genes. PLoS ONE, 2008, 3, e2207.	1.1	49
162	Pharmacological activation of the p53 pathway by nutlin-3 exerts anti-tumoral effects in medulloblastomas. Neuro-Oncology, 2012, 14, 859-869.	0.6	48

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163	PRDM16 (1p36) translocations define a distinct entity of myeloid malignancies with poor prognosis but may also occur in lymphoid malignancies. British Journal of Haematology, 2012, 156, 76-88.	1.2	48
164	LIN28B overexpression defines a novel fetal-like subgroup of juvenile myelomonocytic leukemia. Blood, 2016, 127, 1163-1172.	0.6	48
165	Network Modeling of microRNAâ€“mRNA Interactions in Neuroblastoma Tumorigenesis Identifies miR-204 as a Direct Inhibitor of MYCN. Cancer Research, 2018, 78, 3122-3134.	0.4	48
166	LDHA in Neuroblastoma Is Associated with Poor Outcome and Its Depletion Decreases Neuroblastoma Growth Independent of Aerobic Glycolysis. Clinical Cancer Research, 2018, 24, 5772-5783.	3.2	48
167	Translocation-excision-deletion-amplification mechanism leading to nonsyntenic coamplification ofMYC andATBF1. Genes Chromosomes and Cancer, 2006, 45, 107-117.	1.5	47
168	Histone Chaperone CHAF1A Inhibits Differentiation and Promotes Aggressive Neuroblastoma. Cancer Research, 2014, 74, 765-774.	0.4	47
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