Maria J Calasanz

List of Publications by Year
in descending order

256	13,254	25034	26613
papers	citations	57 h-index	107 g-index

265	265	265	15342
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Chromosome banding analysis and genomic microarrays are both useful but not equivalent methods for genomic complexity risk stratification in chronic lymphocytic leukemia patients. Haematologica, 2022, 107, 593-603.	3.5	18
2	Insights into the mechanisms underlying aberrant SOX11 oncogene expression in mantle cell lymphoma. Leukemia, 2022, 36, 583-587.	7.2	5
3	Landscape and clinical significance of long noncoding <scp>RNAs</scp> involved in multiple myeloma expressed fusion transcripts. American Journal of Hematology, 2022, 97, .	4.1	1
4	Preneoplastic somatic mutations including MYD88 ^{L265P} in lymphoplasmacytic lymphoma. Science Advances, 2022, 8, eabl4644.	10.3	21
5	A Machine Learning Model Based on Tumor and Immune Biomarkers to Predict Undetectable MRD and Survival Outcomes in Multiple Myeloma. Clinical Cancer Research, 2022, 28, 2598-2609.	7.0	14
6	Characteristics and Outcomes of Adult Patients in the PETHEMA Registry with Relapsed or Refractory FLT3-ITD Mutation-Positive Acute Myeloid Leukemia. Cancers, 2022, 14, 2817.	3.7	0
7	Circulating Tumor Cells for the Staging of Patients With Newly Diagnosed Transplant-Eligible Multiple Myeloma. Journal of Clinical Oncology, 2022, 40, 3151-3161.	1.6	40
8	Deep MRD profiling defines outcome and unveils different modes of treatment resistance in standard- and high-risk myeloma. Blood, 2021, 137, 49-60.	1.4	80
9	Endogenous Retroelement Activation by Epigenetic Therapy Reverses the Warburg Effect and Elicits Mitochondrial-Mediated Cancer Cell Death. Cancer Discovery, 2021, 11, 1268-1285.	9.4	42
10	Measurable residual disease in elderly acute myeloid leukemia: results from the PETHEMA-FLUGAZA phase 3 clinical trial. Blood Advances, 2021, 5, 760-770.	5.2	18
11	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. Leukemia, 2021, 35, 1438-1450.	7.2	28
12	Lenalidomide and dexamethasone with or without clarithromycin in patients with multiple myeloma ineligible for autologous transplant: a randomized trial. Blood Cancer Journal, 2021, 11, 101.	6.2	14
13	Myelodysplastic syndromes with 20q deletion: incidence, prognostic value and impact on response to azacitidine of ASXL1 chromosomal deletion and genetic mutations. British Journal of Haematology, 2021, 194, 708-717.	2.5	7
14	Prognostic heterogeneity of adult Bâ€cell precursor acute lymphoblastic leukaemia patients with t(1;19)(q23;p13)/ TCF3â€PBX1 treated with measurable residual diseaseâ€oriented protocols. British Journal of Haematology, 2021, , .	2.5	2
15	Transcriptional profiling of circulating tumor cells in multiple myeloma: a new model to understand disease dissemination. Leukemia, 2020, 34, 589-603.	7.2	41
16	Spanish Guidelines for the use of targeted deep sequencing in myelodysplastic syndromes and chronic myelomonocytic leukaemia. British Journal of Haematology, 2020, 188, 605-622.	2.5	25
17	Measurable Residual Disease by Next-Generation Flow Cytometry in Multiple Myeloma. Journal of Clinical Oncology, 2020, 38, 784-792.	1.6	175
18	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. Genome Research, 2020, 30, 1217-1227.	5.5	35

#	Article	IF	Citations
19	Assessment of Minimal Residual Disease by Next Generation Sequencing in Peripheral Blood as a Complementary Tool for Personalized Transplant Monitoring in Myeloid Neoplasms. Journal of Clinical Medicine, 2020, 9, 3818.	2.4	9
20	Circulating tumor cells for comprehensive and multiregional non-invasive genetic characterization of multiple myeloma. Leukemia, 2020, 34, 3007-3018.	7.2	26
21	Impaired Condensin Complex and Aurora B kinase underlie mitotic and chromosomal defects in hyperdiploid B-cell ALL. Blood, 2020, 136, 313-327.	1.4	16
22	Molecular profiling of immunoglobulin heavy-chain gene rearrangements unveils new potential prognostic markers for multiple myeloma patients. Blood Cancer Journal, 2020, 10, 14.	6.2	16
23	Assessment of the clinical utility of four NGS panels in myeloid malignancies. Suggestions for NGS panel choice or design. PLoS ONE, 2020, 15, e0227986.	2.5	33
24	Strategy for identification of a potential inherited leukemia predisposition in a 299 patientâ€™s cohort with tumor-only sequencing data. Leukemia Research, 2020, 95, 106386.	0.8	3
25	Discordances between Immunofixation (IFx) and Minimal Residual Disease (MRD) Assessment with Next-Generation Flow (NGF) and Sequencing (NGS) in Patients (Pts) with Multiple Myeloma (MM): Clinical and Pathogenic Significance. Blood, 2020, 136, 5-6.	1.4	2
26	Biological and clinical significance of dysplastic hematopoiesis in patients with newly diagnosed multiple myeloma. Blood, 2020, 135, 2375-2387.	1.4	24
27	PLZF-RARÎ±, NPM1-RARÎ±, and Other Acute Promyelocytic Leukemia Variants: The PETHEMA Registry Experience and Systematic Literature Review. Cancers, 2020, 12, 1313.	3.7	20
28	Measurable Residual Disease (MRD) in Elderly Acute Myeloid Leukemia (AML): Results from the Pethema-Flugaza Phase III Clinical Trial. Blood, 2020, 136, 32-32.	1.4	0
29	Myelodysplastic Syndromes with 20q Deletion: Incidence, Prognostic Value and Impact on Response to Azacitidine of ASXL1 Chromosomal Deletion and Genetic Mutations. Blood, 2020, 136, 1-2.	1.4	0
30	Clinical Validation of a NGS Capture Panel to Identify Mutations, Copy Number Variations and Translocations in Patients with Multiple Myeloma. Blood, 2020, 136, 13-14.	1.4	1
31	WaldenstrÃ¶m's Macroglobulinemia (WM) Is Preceded By Clonal Lymphopoiesis Including MYD88 L265P in Progenitor B Cells. Blood, 2020, 136, 42-43.	1.4	1
32	Epigenomic profiling of myelofibrosis reveals widespread DNA methylation changes in enhancer elements and ZFP36L1 as a potential tumor suppressor gene that is epigenetically regulated. Haematologica, 2019, 104, 1572-1579.	3.5	16
33	Prognostic implications of MRD assessment in multiple myeloma patients: comparison of Next-Generation Sequencing and Next-Generation Flow. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e47.	0.4	2
34	Role of lncRNAs as prognostic factor and potential therapeutic target in Multiple Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e354-e355.	0.4	1
35	Circulating Tumor Cells (CTCs) for Comprehensive and Multiregional Non-Invasive Genetic Characterization of Multiple Myeloma (MM). Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e351.	0.4	0
36	Clinical significance of complex karyotype at diagnosis in pediatric and adult patients with de novo acute promyelocytic leukemia treated with ATRA and chemotherapy. Leukemia and Lymphoma, 2019, 60, 1146-1155.	1.3	12

#	Article	IF	Citations
37	Cytogenetic complexity in chronic lymphocytic leukemia: definitions, associations, and clinical impact. Blood, 2019, 133, 1205-1216.	1.4	164
38	Randomized Trial of Lenalidomide and Dexamethasone Versus Clarythromycin, Lenalidomide and Dexamethasone As First Line Treatment in Patients with Multiple Myeloma Not Candidates for Autologous Stem Cell Transplantation: Results of the GEM-Claridex Clinical Trial. Blood, 2019, 134, 694-694.	1.4	4
39	Curative Strategy (GEM-CESAR) for High-Risk Smoldering Myeloma (SMM): Carfilzomib, Lenalidomide and Dexamethasone (KRd) As Induction Followed By HDT-ASCT, Consolidation with Krd and Maintenance with Rd. Blood, 2019, 134, 781-781.	1.4	38
40	WaldenstrÃ¶m's Macroglobulinemia (WM) Is Preceded By Clonal Lymphopoiesis Including MYD88 L265P in Progenitor B Cells. Blood, 2019, 134, 1527-1527.	1.4	1
41	Qip-Mass Spectrometry in High Risk Smoldering Multiple Myeloma Patients Included in the GEM-CESAR Trial: Comparison with Conventional and Minimal Residual Disease IMWG Response Assessment. Blood, 2019, 134, 581-581.	1.4	14
42	The Pathogenesis of Multiple Myeloma (MM) Is Preceded By Mutated Lymphopoiesis and B Cell Oligoclonality That Persist in Patients with Negative Minimal Residual Disease (MRD). Blood, 2019, 134, 509-509.	1.4	2
43	Circulating Tumor Cells (CTCs) for Comprehensive and Multiregional Non-Invasive Genetic Characterization of Multiple Myeloma (MM). Blood, 2019, 134, 3064-3064.	1.4	1
44	Characterization of Complete Lncrnas Transcriptome Reveals Expression of Lncrnas As a Prognostic Factor and Linc-Smilo As a Potential Therapeutic Target in Multiple Myeloma. Blood, 2019, 134, 4323-4323.	1.4	1
45	Lncrnas As New Partners of Novel Chimeric Transcripts in Multiple Myeloma. Blood, 2019, 134, 4356-4356.	1.4	0
46	Chromosome Banding Analysis Versus Genomic Microarrays: A Comparison of Methods for Genomic Complexity Risk Stratification in Chronic Lymphocytic Leukemia Patients with Complex Karyotype. Blood, 2019, 134, 4287-4287.	1.4	1
47	Strategy for Identification of an Inherited Leukemia Predisposition in a 299 Patients Cohort with Tumor-Only Sequencing Data. Blood, 2019, 134, 1415-1415.	1.4	7
48	Cdx Report Program: Heterogeneity Revealed in Current Reporting Practices for Hemato-Oncology Companion Diagnostic (CDx) Markers in Multiple Countries. Blood, 2019, 134, 5837-5837.	1.4	0
49	Heavy and Light Chain Monitoring in High Risk Smoldering Multiple Myeloma Patients Included in the GEM-CESAR Trial: Comparison with Conventional and Minimal Residual Disease IMWG Response Assessment. Blood, 2019, 134, 1852-1852.	1.4	1
50	Richter transformation driven by Epsteinâ€“Barr virus reactivation during therapyâ€related immunosuppression in chronic lymphocytic leukaemia. Journal of Pathology, 2018, 245, 61-73.	4.5	24
51	Clinical Significance and Transcriptional Profiling of Persistent Minimal Residual Disease (MRD) in Multiple Myeloma (MM) Patients with Standard-Risk (SR) and High-Risk (HR) Cytogenetics. Blood, 2018, 132, 112-112.	1.4	3
52	Transcriptomic Profiling of Circulating Tumor Cells (CTCs) in Multiple Myeloma (MM): A New Model to Understand Disease Dissemination. Blood, 2018, 132, 245-245.	1.4	5
53	Absence of Contribution to a Differential Outcome of the Stringent Complete Response IMWG Category Respect to the Conventional CR in Multiple Myeloma. a Validation Analysis Based on the Pethema/GEM2012MENOS65 Phase III Clinical Trial. Blood, 2018, 132, 1943-1943.	1.4	3
54	Immunofixation (IF) in Urine Is Really Necessary to Define Complete Remission in Multiple Myeloma (MM)? a Subanalysis from the Pethema/GEM2012MENOS65 Phase III Clinical Trial. Blood, 2018, 132, 474-474.	1.4	0

#	Article	IF	Citations
55	The Presence of MDS-like Phenotypic Abnormalities (MDS-PA) Identifies Newly Diagnosed Multiple Myeloma (MM) Patients With MDS/AML-Related Somatic Mutations And Inferior Survival. Clinical Lymphoma, Myeloma and Leukemia, 2017, 17, e11.	0.4	0
56	Monosomal karyotype in chronic lymphocytic leukemia: Association with clinical and biological features and potential prognostic significance. American Journal of Hematology, 2017, 92, E132-E135.	4.1	1
57	The molecular pathogenesis of the NUP98-HOXA9 fusion protein in acute myeloid leukemia. Leukemia, 2017, 31, 2000-2005.	7.2	28
58	Patients with chronic lymphocytic leukemia and complex karyotype show an adverse outcome even in absence of TP53/ATM FISH deletions. Oncotarget, 2017, 8, 54297-54303.	1.8	44
59	Impact of <scp>SNP</scp> array karyotyping on the diagnosis and the outcome of chronic myelomonocytic leukemia with low risk cytogenetic features or no metaphases. American Journal of Hematology, 2016, 91, 185-192.	4.1	18
60	Homeobox NKX2-3 promotes marginal-zone lymphomagenesis by activating B-cell receptor signalling and shaping lymphocyte dynamics. Nature Communications, 2016, 7, 11889.	12.8	42
61	Refining the Breakpoints of Three New Translocations Identified in Myelodysplastic Syndromes. Acta Haematologica, 2016, 135, 94-100.	1.4	2
62	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. Cancer Cell, 2016, 30, 806-821.	16.8	103
63	Prognostic impact of chromosomal translocations in myelodysplastic syndromes and chronic myelomonocytic leukemia patients. A study by the spanish group of myelodysplastic syndromes. Genes Chromosomes and Cancer, 2016, 55, 322-327.	2.8	7
64	Use of human pharyngeal and palatine tonsils as a reservoir for the analysis of Bâ€cell ontogeny in 10 paired samples. Clinical Otolaryngology, 2016, 41, 606-611.	1.2	4
65	Targeted resequencing analysis of 31 genes commonly mutated in myeloid disorders in serial samples from myelodysplastic syndrome patients showing disease progression. Leukemia, 2016, 30, 248-250.	7.2	51
66	Non-Invasive Genetic Profiling Is Highly Applicable in Multiple Myeloma (MM) through Characterization of Circulating Tumor Cells (CTCs). Blood, 2016, 128, 801-801.	1.4	2
67	Comparison of the Molecular Spectrum of Lenalidomide-Treated Myelodysplastic Syndrome with and without Del(5q). Blood, 2016, 128, 3172-3172.	1.4	0
68	HDAC Inhibitors As Novel Targeted Therapies for NUP98-HOXA9 AML Patients. Blood, 2016, 128, 2685-2685.	1.4	2
69	The Presence of MDS-like Phenotypic Abnormalities (MDS-PA) Identifies Newly Diagnosed Multiple Myeloma (MM) Patients with MDS/AML-Related Somatic Mutations and Inferior Survival. Blood, 2016, 128, 375-375.	1.4	1
70	CSNK1A1 mutations and gene expression analysis in myelodysplastic syndromes with del(5q). British Journal of Haematology, 2015, 171, 210-214.	2.5	19
71	CIP2A high expression is a poor prognostic factor in normal karyotype acute myeloid leukemia. Haematologica, 2015, 100, e183-e185.	3.5	20
72	Correlation of myelodysplastic syndromes with i(17)(q10) and <scp>TP</scp>53 and <scp>SETBP</scp>1 mutations. British Journal of Haematology, 2015, 171, 137-141.	2.5	11

#	Article	IF	Citations
73	The GATA2 transcription factor directly binds and activates MYB expression in acute myeloid leukemia. Experimental Hematology, 2015, 43, S58.	0.4	0
74	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	5.5	118
75	The relationship of TP53 R72P polymorphism to disease outcome and TP53 mutation in myelodysplastic syndromes. Blood Cancer Journal, 2015, 5, e291-e291.	6.2	15
76	Fluorescencein situhybridization analysis does not increase detection rate for trisomy 8 in chronic myelomonocytic leukemia. Leukemia and Lymphoma, 2015, 56, 242-243.	1.3	1
77	Hypermethylation of the alternative AWT1 promoter in hematological malignancies is a highly specific marker for acute myeloid leukemias despite high expression levels. Journal of Hematology and Oncology, 2014, 7, 4.	17.0	21
78	Exome sequencing reveals novel and recurrent mutations with clinical impact in blastic plasmacytoid dendritic cell neoplasm. Leukemia, 2014, 28, 823-829.	7.2	148
79	Interstitial 13q14 deletions detected in the karyotype and translocations with concomitant deletion at 13q14 in chronic lymphocytic leukemia: Different genetic mechanisms but equivalent poorer clinical outcome. Genes Chromosomes and Cancer, 2014, 53, 788-797.	2.8	15
80	Whole-exome sequencing in del(5q) myelodysplastic syndromes in transformation to acute myeloid leukemia. Leukemia, 2014, 28, 1148-1151.	7.2	17
81	Utility of SNP Arrays in Chronic Myelomonocytic Leukemia with Low Risk Cytogenetic Features or No Metaphases. Blood, 2014, 124, 4659-4659.	1.4	0
82	Risk of Central Nervous System (CNS) Involvement in Patients with Mantle Cell Lymphoma (MCL): Analysis of Clinico-Biological Factors in a Series of 283 Cases. Blood, 2014, 124, 1677-1677.	1.4	4
83	Mutations in <scp>SETBP</scp>1 are recurrent in myelodysplastic syndromes and often coexist with cytogenetic markers associated with disease progression. British Journal of Haematology, 2013, 163, 235-239.	2.5	37
84	Characterization and prognostic implication of 17 chromosome abnormalities in myelodysplastic syndrome. Leukemia Research, 2013, 37, 769-776.	0.8	11
85	Reciprocal translocations in myelodysplastic syndromes and chronic myelomonocytic leukemias: Review of 5,654 patients with an evaluable karyotype. Genes Chromosomes and Cancer, 2013, 52, 753-763.	2.8	15
86	Functional characterization of the promoter region of the human EVI1 gene in acute myeloid leukemia: RUNX1 and ELK1 directly regulate its transcription. Oncogene, 2013, 32, 2069-2078.	5.9	23
87	Downregulation of specific miRNAs in hyperdiploid multiple myeloma mimics the oncogenic effect of IgH translocations occurring in the non-hyperdiploid subtype. Leukemia, 2013, 27, 925-931.	7.2	31
88	Response to lenalidomide in myelodysplastic syndromes with del(5q): influence of cytogenetics and mutations. British Journal of Haematology, 2013, 162, 74-86.	2.5	73
89	CBL RING finger deletions are common in core-binding factor acute myeloid leukemias. Leukemia and Lymphoma, 2013, 54, 428-431.	1.3	6
90	Landscape of somatic mutations and clonal evolution in mantle cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18250-18255.	7.1	488

#	Article	IF	Citations
91	Single nucleotide polymorphism array karyotyping: A diagnostic and prognostic tool in myelodysplastic syndromes with unsuccessful conventional cytogenetic testing. Genes Chromosomes and Cancer, 2013, 52, 1167-1177.	2.8	44
92	Biallelic losses of 13q do not confer a poorer outcome in chronic lymphocytic leukaemia: analysis of 627 patients with isolated 13q deletion. British Journal of Haematology, 2013, 163, 47-54.	2.5	13
93	Aberrant DNA methylation profile of chronic and transformed classic Philadelphia-negative myeloproliferative neoplasms. Haematologica, 2013, 98, 1414-1420.	3.5	46
94	Downregulation of PPP2R5E is a common event in acute myeloid leukemia that affects the oncogenic potential of leukemic cells. Haematologica, 2013, 98, e103-e104.	3.5	25
95	Molecular Subsets of Mantle Cell Lymphoma Defined by the IGHV Mutational Status and SOX11 Expression Have Distinct Biologic and Clinical Features. Cancer Research, 2012, 72, 5307-5316.	0.9	231
96	Preclinical activity of LBH589 alone or in combination with chemotherapy in a xenogeneic mouse model of human acute lymphoblastic leukemia. Leukemia, 2012, 26, 1517-1526.	7.2	41
97	Overexpression of GATA2 predicts an adverse prognosis for patients with acute myeloid leukemia and it is associated with distinct molecular abnormalities. Leukemia, 2012, 26, 550-554.	7.2	64
98	Mutation Patterns of 16 Genes in Primary and Secondary Acute Myeloid Leukemia (AML) with Normal Cytogenetics. PLoS ONE, 2012, 7, e42334.	2.5	60
99	Overexpression of SET is a recurrent event associated with poor outcome and contributes to protein phosphatase 2A inhibition in acute myeloid leukemia. Haematologica, 2012, 97, 543-550.	3.5	105
100	RomÃ¡n-GÃ³mez J, Cordeu L, Agirre X, JimÃ©nez-Velasco A, San JosÃ©-Eneriz E, Garate L, Calasanz MJ, Heiniger A, Torres A, Prosper F. Epigenetic regulation of Wnt-signaling pathway in acute lymphoblastic leukemia. Blood. 2007;109(8):3462â€“3469.. Blood, 2012, 120, 3625-3625.	1.4	4
101	Highâ€throughput sequencing analysis of the chromosome 7q32 deletion reveals <scp>IRF</scp>5 as a potential tumour suppressor in splenic marginalâ€zone lymphoma. British Journal of Haematology, 2012, 158, 712-726.	2.5	45
102	Chromatin modifications induced by the AML1-ETO fusion protein reversibly silence its genomic targets through AML1 and Sp1 binding motifs. Leukemia, 2012, 26, 1329-1337.	7.2	30
103	TET2 Mutations Are Associated with Specific 5-Methylcytosine and 5-Hydroxymethylcytosine Profiles in Patients with Chronic Myelomonocytic Leukemia. PLoS ONE, 2012, 7, e31605.	2.5	70
104	Integration of SNP and mRNA Arrays with MicroRNA Profiling Reveals That MiR-370 Is Upregulated and Targets NF1 in Acute Myeloid Leukemia. PLoS ONE, 2012, 7, e47717.	2.5	36
105	Abstract 2205: The EVI1 human protein regulates its own transcription. Role of the different isoforms. , 2012, , .		0
106	Abstract 85: RUNX1 and ELK1 directly regulate the transcription of EVI1 during megakaryocytic differentiation. , 2012, , .		0
107	Association of MDM2 Gene Polymorphisms SNP285 and 309 with Myelodysplastic Syndromes (MDS) Susceptibility and Outcome.. Blood, 2012, 120, 2823-2823.	1.4	0
108	Cytogenetic risk stratification in chronic myelomonocytic leukemia. Haematologica, 2011, 96, 375-383.	3.5	226

#	Article	IF	Citations
109	Epigenetic Activation of SOX11 in Lymphoid Neoplasms by Histone Modifications. PLoS ONE, 2011, 6, e21382.	2.5	38
110	NPM1 gene deletions in myelodysplastic syndromes with 5q- and complex karyotype. Haematologica, 2011, 96, 784-785.	3.5	8
111	Prognostic value of FLT3 mutations in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and anthracycline monochemotherapy. Haematologica, 2011, 96, 1470-1477.	3.5	59
112	LMO2 expression reflects the different stages of blast maturation and genetic features in B-cell acute lymphoblastic leukemia and predicts clinical outcome. Haematologica, 2011, 96, 980-986.	3.5	26
113	Down-regulation of EVI1 is associated with epigenetic alterations and good prognosis in patients with acute myeloid leukemia. Haematologica, 2011, 96, 1448-1456.	3.5	45
114	Deregulation of FGFR1 and CDK6 oncogenic pathways in acute lymphoblastic leukaemia harbouring epigenetic modifications of the MIR9 family. British Journal of Haematology, 2011, 155, 73-83.	2.5	53
115	Impact of adjunct cytogenetic abnormalities for prognostic stratification in patients with myelodysplastic syndrome and deletion 5q. Leukemia, 2011, 25, 110-120.	7.2	113
116	PP2A impaired activity is a common event in acute myeloid leukemia and its activation by forskolin has a potent anti-leukemic effect. Leukemia, 2011, 25, 606-614.	7.2	124
117	Long-Range Epigenetic Silencing Associates with Deregulation of Ikaros Targets in Colorectal Cancer Cells. Molecular Cancer Research, 2011, 9, 1139-1151.	3.4	47
118	A cyclin-D1 interaction with BAX underlies its oncogenic role and potential as a therapeutic target in mantle cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12461-12466.	7.1	50
119	Frequent and Simultaneous Epigenetic Inactivation of TP53 Pathway Genes in Acute Lymphoblastic Leukemia. PLoS ONE, 2011, 6, e17012.	2.5	52
120	Homeobox NKX2-3 Is Over-Expressed in Human B-Cell Lymphomas and Drives Marginal Zone B-Cell Lymphomagenesis in Mice. Blood, 2011, 118, 260-260.	1.4	0
121	SETBP1 overexpression is a novel leukemogenic mechanism that predicts adverse outcome in elderly patients with acute myeloid leukemia. Blood, 2010, 115, 615-625.	1.4	154
122	Cytogenetic aberrations and their prognostic value in a series of 330 splenic marginal zone B-cell lymphomas: a multicenter study of the Splenic B-Cell Lymphoma Group. Blood, 2010, 116, 1479-1488.	1.4	174
123	Reversion of epigenetically mediated BIM silencing overcomes chemoresistance in Burkitt lymphoma. Blood, 2010, 116, 2531-2542.	1.4	96
124	Additional chromosome abnormalities in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and chemotherapy. Haematologica, 2010, 95, 424-431.	3.5	84
125	A new potential oncogenic mutation in the FERM domain of JAK2 in BCR/ABL1-negative and V617F-negative chronic myeloproliferative neoplasms revealed by a comprehensive screening of 17 tyrosine kinase coding genes. Cancer Genetics and Cytogenetics, 2010, 199, 1-8.	1.0	10
126	Incidence and prognostic impact of secondary cytogenetic aberrations in a series of 145 patients with mantle cell lymphoma. Genes Chromosomes and Cancer, 2010, 49, 439-451.	2.8	68

#	Article	IF	Citations
127	EVI1 controls proliferation in acute myeloid leukaemia through modulation of miR-1-2. British Journal of Cancer, 2010, 103, 1292-1296.	6.4	33
128	Analysis of genomic breakpoints in p190 and p210 BCRâ€“ABL indicate distinct mechanisms of formation. Leukemia, 2010, 24, 1742-1750.	7.2	43
129	Frequent mutation of the polycomb-associated gene ASXL1 in the myelodysplastic syndromes and in acute myeloid leukemia. Leukemia, 2010, 24, 1062-1065.	7.2	231
130	Bcr/Abl Interferes with the Fanconi Anemia/BRCA Pathway: Implications in the Chromosomal Instability of Chronic Myeloid Leukemia Cells. PLoS ONE, 2010, 5, e15525.	2.5	20
131	Silencing of hsa-miR-124 by EVI1 in cell lines and patients with acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, E167-8; author reply E169-70.	7.1	30
132	Response to lenalidomide in a patient with myelodysplastic syndrome with isolated del(5q) and JAK2 V617F mutation. Leukemia and Lymphoma, 2010, 51, 1941-1943.	1.3	7
133	Quantification ofPDGFRAalternative transcripts improves the screening forXâ€“PDGFRAfusions by reverse transcriptase-polymerase chain reaction. Leukemia and Lymphoma, 2010, 51, 1720-1726.	1.3	0
134	Frequent Mutation of the Polycomb-Associated Gene ASXL1 In Acute Myeloid Leukemia Secondary to Myelodysplastic Syndrome or Chronic Myelomonocytic Leukemia. Blood, 2010, 116, 2940-2940.	1.4	1
135	DNA Methylation Profiles and Their Relationship with Cytogenetic Status in Adult Acute Myeloid Leukemia. PLoS ONE, 2010, 5, e12197.	2.5	73
136	A Novel Pro-Survival Function of Cyclin-D1 Underlies Its Oncogenic Role and Potential as a Therapeutic Target In Mantle Cell Lymphoma. Blood, 2010, 116, 769-769.	1.4	0
137	A Comprehensive Microarray-Based DNA Methylation Study of 367 Hematological Neoplasms. PLoS ONE, 2009, 4, e6986.	2.5	115
138	Epigenetic Regulation of MicroRNAs in Acute Lymphoblastic Leukemia. Journal of Clinical Oncology, 2009, 27, 1316-1322.	1.6	131
139	A novel t(7;13)(p12;q33âˆ¼q34) in AML-M2. Cancer Genetics and Cytogenetics, 2009, 195, 198-200.	1.0	1
140	Guidelines for HER2 testing in breast cancer: a national consensus of the Spanish Society of Pathology (SEAP) and the Spanish Society of Medical Oncology (SEOM). Clinical and Translational Oncology, 2009, 11, 363-375.	2.4	15
141	C005 Prognostic impact of the proportion of aberrant metaphases in patients with a primary myelodysplastic syndrome. Leukemia Research, 2009, 33, S33-S34.	0.8	0
142	P029 Prognostic relevance of specific chromosomal abnormalities in chronic myelomonocytic leukemia. Leukemia Research, 2009, 33, S74-S75.	0.8	0
143	P030 Prognostic impact on survival of an unsuccessful conventional cytogenetic study in patients with myelodysplastic syndromes (MDS). Leukemia Research, 2009, 33, S75-S76.	0.8	5
144	Biallelic inactivation of TRAF3 in a subset of B-cell lymphomas with interstitial del(14)(q24.1q32.33). Leukemia, 2009, 23, 2153-2155.	7.2	50

#	Article	IF	Citations
145	MicroRNA expression profiling in Imatinib-resistant Chronic Myeloid Leukemia patients without clinically significant ABL1-mutations. Molecular Cancer, 2009, 8, 69.	19.2	101
146	Epigenetic Silencing of the Tumor Suppressor MicroRNAHsa-miR-124aRegulates CDK6 Expression and Confers a Poor Prognosis in Acute Lymphoblastic Leukemia. Cancer Research, 2009, 69, 4443-4453.	0.9	299
147	Deregulated expression of cytokine receptor gene, CRLF2, is involved in lymphoid transformation in B-cell precursor acute lymphoblastic leukemia. Blood, 2009, 114, 2688-2698.	1.4	445
148	Molecular cytogenetics in translational oncology: when chromosomes meet genomics. Clinical and Translational Oncology, 2008, 10, 20-29.	2.4	7
149	Resistance to Imatinib Mesylate-induced apoptosis in acute lymphoblastic leukemia is associated with PTEN down-regulation due to promoter hypermethylation. Leukemia Research, 2008, 32, 709-716.	0.8	39
150	Low frequency of JAK2 exon 12 mutations in classic and atypical CMPDs. Leukemia Research, 2008, 32, 1485-1487.	0.8	3
151	Methylation status of SOCS1 and SOCS3 in BCR-ABL negative and JAK2V617F negative chronic myeloproliferative neoplasms. Leukemia Research, 2008, 32, 1638-1640.	0.8	16
152	BCRâ€ABL1â€induced expression of HSPA8 promotes cell survival in chronic myeloid leukaemia. British Journal of Haematology, 2008, 142, 571-582.	2.5	33
153	A new dic(7;12)(p12.21;p12.2) chromosome aberration in a case of acute myeloid leukemia. Cancer Genetics and Cytogenetics, 2008, 185, 102-105.	1.0	2
154	Down-Regulation of hsa-miR-10a in Chronic Myeloid Leukemia CD34+ Cells Increases USF2-Mediated Cell Growth. Molecular Cancer Research, 2008, 6, 1830-1840.	3.4	208
155	Epigenetic Inactivation of the Groucho Homologue Gene TLE1 in Hematologic Malignancies. Cancer Research, 2008, 68, 4116-4122.	0.9	50
156	Fluorescence in situ hybridization improves the detection of 5q31 deletion in myelodysplastic syndromes without cytogenetic evidence of 5q-. Haematologica, 2008, 93, 1001-1008.	3.5	36
157	Risk-adapted treatment of acute promyelocytic leukemia with all-trans retinoic acid and anthracycline monochemotherapy: long-term outcome of the LPA 99 multicenter study by the PETHEMA Group. Blood, 2008, 112, 3130-3134.	1.4	154
158	Epigenetic regulation of Wnt-signaling pathway in acute lymphoblastic leukemia. Blood, 2007, 109, 3462-3469.	1.4	153
159	Neurofibromatosis 1, and Not TP53, Seems to Be the Main Target of Chromosome 17 Deletions in De Novo Acute Myeloid Leukemia. Journal of Clinical Oncology, 2007, 25, 1151-1152.	1.6	8
160	The potential effect of gender in combination with common genetic polymorphisms of drug-metabolizing enzymes on the risk of developing acute leukemia. Haematologica, 2007, 92, 308-314.	3.5	76
161	Five members of the CEBP transcription factor family are targeted by recurrent IGH translocations in B-cell precursor acute lymphoblastic leukemia (BCP-ALL). Blood, 2007, 109, 3451-3461.	1.4	188
162	DNA profiling analysis of 100 consecutive de novo acute myeloid leukemia cases reveals patterns of genomic instability that affect all cytogenetic risk groups. Leukemia, 2007, 21, 1224-1231.	7.2	50

#	Article	IF	Citations
163	A comprehensive genetic and histopathologic analysis identifies two subgroups of B-cell malignancies carrying a t(14;19)(q32;q13) or variant BCL3-translocation. Leukemia, 2007, 21, 1532-1544.	7.2	85
164	Role of MTHFR (677, 1298) haplotype in the risk of developing secondary leukemia after treatment of breast cancer and hematological malignancies. Leukemia, 2007, 21, 1413-1422.	7.2	45
165	JAK2-V617F activating mutation in acute myeloid leukemia: prognostic impact and association with other molecular markers. Leukemia, 2007, 21, 2386-2390.	7.2	29
166	Profile of polymorphisms of drug-metabolising enzymes and the risk of therapy-related leukaemia. British Journal of Haematology, 2007, 136, 590-596.	2.5	75
167	Simultaneous translocations of FGFR3/MMSET and CCND1 into two different IGH alleles in multiple myeloma: lack of concurrent activation of both proto-oncogenes. Cancer Genetics and Cytogenetics, 2007, 175, 65.e1-65.e5.	1.0	3
168	Multiple myeloma primary cells show a highly rearranged unbalanced genome with amplifications and homozygous deletions irrespective of the presence of immunoglobulin-related chromosome translocations. Haematologica, 2007, 92, 795-802.	3.5	28
169	Multicolor interphase cytogenetics for the study of plasma cell dyscrasias. Oncology Reports, 2007, 18, 1099-106.	2.6	6
170	Downregulation of DBC1 expression in acute lymphoblastic leukaemia is mediated by aberrant methylation of its promoter. British Journal of Haematology, 2006, 134, 137-144.	2.5	30
171	JAK2 V617F mutation in classic chronic myeloproliferative diseases: a report on a series of 349 patients. Leukemia, 2006, 20, 534-535.	7.2	41
172	ASPP1, a common activator of TP53, is inactivated by aberrant methylation of its promoter in acute lymphoblastic leukemia. Oncogene, 2006, 25, 1862-1870.	5.9	63
173	Geographic differences in the incidence of cytogenetic abnormalities of acute myelogenous leukemia (AML) in Spain. Leukemia Research, 2006, 30, 943-948.	0.8	17
174	Interphase FISH for the detection of breakpoints in IG loci and chromosomal changes with adverse prognostic impact in multiple myeloma with normal karyotypes. Cancer Genetics and Cytogenetics, 2006, 167, 183-185.	1.0	2
175	Identification of recurrent chromosomal breakpoints in multiple myeloma with complex karyotypes by combined G-banding, spectral karyotyping, and fluorescence in situ hybridization analyses. Cancer Genetics and Cytogenetics, 2006, 169, 143-149.	1.0	17
176	Abnormal methylation of the commonPARK2andPACRGpromoter is associated with downregulation of gene expression in acute lymphoblastic leukemia and chronic myeloid leukemia. International Journal of Cancer, 2006, 118, 1945-1953.	5.1	77
177	CpG Island Methylator Phenotype Redefines the Prognostic Effect of t(12;21) in Childhood Acute Lymphoblastic Leukemia. Clinical Cancer Research, 2006, 12, 4845-4850.	7.0	62
178	Identification of overexpressed genes in frequently gained/amplified chromosome regions in multiple myeloma. Haematologica, 2006, 91, 184-91.	3.5	48
179	Lack of association of CYP3A4-V polymorphism with the risk of treatment-related leukemia. Leukemia Research, 2005, 29, 595-597.	0.8	10
180	p53 Aberrations do not predict individual response to fludarabine in patients with B-cell chronic lymphocytic leukaemia in advanced stages Rai III/IV. British Journal of Haematology, 2005, 129, 53-59.	2.5	31

#	Article	IF	Citations
181	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. Nature Genetics, 2005, 37, 391-400.	21.4	1,710
182	Disruption and aberrant expression of HMGA2 as a consequence of diverse chromosomal translocations in myeloid malignancies. Leukemia, 2005, 19, 245-252.	7.2	69
183	NUP98 is fused to HOXA9 in a variant complex t(7;11;13;17) in a patient with AML-M2. Cancer Genetics and Cytogenetics, 2005, 157, 151-156.	1.0	7
184	Coexistence of different clonal populations harboring the b3a2 (p210) and e1a2 (p190) BCR-ABL1 fusion transcripts in chronic myelogenous leukemia resistant to imatinib. Cancer Genetics and Cytogenetics, 2005, 160, 22-26.	1.0	11
185	Analysis of myelodysplastic syndromes with complex karyotypes by highâ€resolution comparative genomic hybridization and subtelomeric CGH array. Genes Chromosomes and Cancer, 2005, 42, 287-298.	2.8	40
186	Amplification ofIGH/MYC fusion in clinically aggressiveIGH/BCL2-positive germinal center B-cell lymphomas. Genes Chromosomes and Cancer, 2005, 43, 414-423.	2.8	37
187	FISH analysis of hematological neoplasias with 1p36 rearrangements allows the definition of a cluster of 2.5ï¿½Mb included in the minimal region deleted in 1p36 deletion syndrome. Human Genetics, 2005, 116, 476-485.	3.8	7
188	Pediatric Meningosarcoma: Clinical Evolution and Genetic Instability. Pediatric Neurology, 2005, 32, 352-354.	2.1	2
189	GATA2 Is Overexpressed in 46% of Patients with AML and Normal Karyotype. The Mutational Pattern FLT3-ITD/GATA2/WT1 Could Define a Group of Patients with Normal Karyotype and AML-M1 Subtype.. Blood, 2005, 106, 2378-2378.	1.4	1
190	GATA2 May Contribute with EVI1 to the Leukemogenic Mechanism in Patients with 3q21q26 Rearrangements.. Blood, 2005, 106, 2852-2852.	1.4	0
191	Genetic Aberrations and Response to Fludarabine as First Line Treatment in a Serie of B-CLL Patients.. Blood, 2005, 106, 2131-2131.	1.4	0
192	A Gain of Function Mutation in JAK2 Is Frequently Found in Patients with AML-M2 and Normal Karyotype.. Blood, 2005, 106, 2366-2366.	1.4	40
193	Identification of novel cytogenetic markers with prognostic significance in a series of 968 patients with primary myelodysplastic syndromes. Haematologica, 2005, 90, 1168-78.	3.5	163
194	NIN, a Gene Encoding a CEP110-Like Centrosomal Protein, Is Fused to PDGFRB in a Patient with a t(5;14)(q33;q24) and an Imatinib-Responsive Myeloproliferative Disorder 1. Cancer Research, 2004, 64, 2673-2676.	0.9	67
195	Î±CP-4, Encoded by a Putative Tumor Suppressor Gene at 3p21, But Not Its Alternative Splice Variant Î±CP-4a, Is Underexpressed in Lung Cancer. Cancer Research, 2004, 64, 4171-4179.	0.9	27
196	Chromosomal abnormalities clustering in multiple myeloma reveals cytogenetic subgroups with nonrandom acquisition of chromosomal changes. Leukemia, 2004, 18, 654-657.	7.2	14
197	Cryptic ins(2;11) with clonal evolution showing amplification of 11q23â€“q25 either on hsr(11) or on dmin, in a patient with AML-M2. Leukemia, 2004, 18, 2041-2044.	7.2	6
198	Molecular characterization of a t(1;3)(p36;q21) in a patient with MDS. MEL1 is widely expressed in normal tissues, including bone marrow, and it is not overexpressed in the t(1;3) cells. Oncogene, 2004, 23, 311-316.	5.9	30

#	Article	IF	Citations
199	Cytogenetic Patterns in 384 Northern-Spanish Patients with Haematological Disorders. Hereditas, 2004, 118, 79-85.	1.4	1
200	Heterogeneity of structural abnormalities in the 7q31.3âˆ¼q34 region in myeloid malignancies. Cancer Genetics and Cytogenetics, 2004, 150, 136-143.	1.0	15
201	Remission of acute monocytic leukemia, secondary to treatment with epipodophyllotoxins, in a patient with t(8;16)(p11;p13) and MYST3â€“CREBBP fusion. Cancer Genetics and Cytogenetics, 2004, 152, 177-178.	1.0	1
202	Cytogenetic profile of myelodysplastic syndromes with complex karyotypes: an analysis using spectral karyotyping. Cancer Genetics and Cytogenetics, 2004, 153, 39-47.	1.0	24
203	Molecular heterogeneity in AML/MDS patients with 3q21q26 rearrangements. Genes Chromosomes and Cancer, 2004, 40, 179-189.	2.8	46
204	Promoter hypermethylation of cancer-related genes: a strong independent prognostic factor in acute lymphoblastic leukemia. Blood, 2004, 104, 2492-2498.	1.4	204
205	NALP1 is a transcriptional target for cAMP-response-element-binding protein (CREB) in myeloid leukaemia cells. Biochemical Journal, 2004, 384, 281-286.	3.7	24
206	Clinical variability of patients with the t(6;8)(q27;p12) and FGFR1OP-FGFR1 fusion: two further cases. The Hematology Journal, 2004, 5, 534-537.	1.4	49
207	Molecular cytogenetic characterization of breakpoints in 19 patients with hematologic malignancies and 12p unbalanced translocations. Cancer Genetics and Cytogenetics, 2003, 142, 115-119.	1.0	6
208	Secondary myelodysplastic syndrome after treatment for promyelocytic leukemia. Cancer Genetics and Cytogenetics, 2003, 143, 178-181.	1.0	18
209	Array comparative genomic hybridization analysis of myelodysplastic syndromes with complex karyotypes. A technical evaluation. Cancer Genetics and Cytogenetics, 2003, 144, 87-89.	1.0	6
210	t(10;16)(q22;p13) and MORFâ€“CREBBP fusion is a recurrent event in acute myeloid leukemia. Genes Chromosomes and Cancer, 2003, 36, 402-405.	2.8	28
211	De novo erythroleukemia chromosome features include multiple rearrangements, with special involvement of chromosomes 11 and 19. Genes Chromosomes and Cancer, 2003, 36, 406-412.	2.8	27
212	Identification of candidate tumor-suppressor genes in 6q27 by combined deletion mapping and electronic expression profiling in lymphoid neoplasms. Genes Chromosomes and Cancer, 2003, 37, 421-426.	2.8	39
213	TP53is frequently altered by methylation, mutation, and/or deletion in acute lymphoblastic leukaemia. Molecular Carcinogenesis, 2003, 38, 201-208.	2.7	58
214	Novel translocations that disrupt the plateletâ€derived growth factor receptor Î² (PDGFRB) gene in BCRâ€“ABLâ€negative chronic myeloproliferative disorders. British Journal of Haematology, 2003, 120, 251-256.	2.5	87
215	Molecular cytogenetic detection of chromosomal breakpoints in T-cell receptor gene loci. Leukemia, 2003, 17, 738-745.	7.2	66
216	Abnormalities on 1q and 7q are associated with poor outcome in sporadic Burkitt's lymphoma. A cytogenetic and comparative genomic hybridization study. Leukemia, 2003, 17, 2016-2024.	7.2	76

#	Article	IF	Citations
217	Methylation of CpG dinucleotides and/or CCWGG motifs at the promoter of TP53 correlates with decreased gene expression in a subset of acute lymphoblastic leukemia patients. Oncogene, 2003, 22, 1070-1072.	5.9	73
218	Risk-adapted treatment of acute promyelocytic leukemia with all-trans-retinoic acid and anthracycline monochemotherapy: a multicenter study by the PETHEMA group. Blood, 2003, 103, 1237-1243.	1.4	395
219	Lack of Bcr-Abl point mutations in chronic myeloid leukemia patients in chronic phase before imatinib treatment is not predictive of response. Haematologica, 2003, 88, 1425-6.	3.5	3
220	Cancer Epigenetics and Methylation. Science, 2002, 297, 1807d-1808.	12.6	116
221	Recurrent involvement of the REL and BCL11Aloci in classical Hodgkin lymphoma. Blood, 2002, 99, 1474-1477.	1.4	224
222	Multicolor-FICTION. American Journal of Pathology, 2002, 161, 413-420.	3.8	81
223	Exon Concatenation to Increase the Efficiency of Mutation Screening by DGGE. BioTechniques, 2002, 32, 1064-1070.	1.8	5
224	Novel dic(16;18)(q11;p11) in two cases of Philadelphia chromosome positive acute B-cell lymphoblastic leukemia. Cancer Genetics and Cytogenetics, 2002, 139, 63-66.	1.0	1
225	Interphase FISH assays for the detection of translocations with breakpoints in immunoglobulin light chain loci. International Journal of Cancer, 2002, 98, 470-474.	5.1	84
226	A novel gene,MDS2,is fused toETV6/TELin a t(1;12)(p36.1;p13) in a patient with myelodysplastic syndrome. Genes Chromosomes and Cancer, 2002, 35, 11-19.	2.8	28
227	Genomic imbalances detected by comparative genomic hybridization are prognostic markers in invasive ductal breast carcinomas. Histopathology, 2002, 40, 547-555.	2.9	40
228	The Minnesota Health Partnership and Coordinated Health Care and Disability Prevention: the implementation of an integrated benefits and medical care model. Journal of Occupational Rehabilitation, 2002, 12, 43-54.	2.2	8
229	Relationship of Disability Prevention to Patient Health Status and Satisfaction With Primary Care Provider. Journal of Occupational and Environmental Medicine, 2001, 43, 706-712.	1.7	7
230	Pretreatment characteristics and clinical outcome of acute promyelocytic leukaemia patients according to the PMLâ€RARÎ± isoforms: a study of the PETHEMA group. British Journal of Haematology, 2001, 114, 99-103.	2.5	52
231	Identification of new translocations involving ETV6 in hematologic malignancies by fluorescence in situ hybridization and spectral karyotyping. Genes Chromosomes and Cancer, 2001, 31, 134-142.	2.8	64
232	Frequent gain of chromosome 19 in megakaryoblastic leukemias detected by comparative genomic hybridization. Genes Chromosomes and Cancer, 2001, 32, 285-293.	2.8	29
233	Cytogenetic and molecular characterization of a patient with simultaneous B-cell chronic lymphocytic leukemia and peripheral T-cell lymphoma. American Journal of Hematology, 2001, 68, 276-279.	4.1	13
234	Further characterization of complex chromosomal rearrangements in myeloid malignancies: spectral karyotyping adds precision in defining abnormalities associated with poor prognosis. Leukemia, 2001, 15, 1133-1136.	7.2	25

#	Article	IF	Citations
235	Insertion (22;9)(q11;q34q21) in a patient with chronic myeloid leukemia characterized by fluorescence in situ hybridization. Cancer Genetics and Cytogenetics, 2001, 125, 167-170.	1.0	3
236	Amplification of ERBB2, RARA, and TOP2A genes in a myelodysplastic syndrome transforming to acute myeloid leukemia. Cancer Genetics and Cytogenetics, 2001, 127, 174-176.	1.0	11
237	Comparative genomic hybridization and amplotyping by arbitrarily primed PCR in stage A B-CLL. Cancer Genetics and Cytogenetics, 2001, 130, 8-13.	1.0	18
238	Identification of new translocations involving ETV6 in hematologic malignancies by fluorescence in situ hybridization and spectral karyotyping. Genes Chromosomes and Cancer, 2001, 31, 134-142.	2.8	2
239	Additional cytogenetic changes do not influence the outcome of patients with newly diagnosed acute promyelocytic leukemia treated with an ATRA plus anthracyclin based protocol. A report of the Spanish group PETHEMA. Haematologica, 2001, 86, 807-13.	3.5	46
240	Multiplex-polymerase chain reaction assay for the detection of prognostically significant translocations in acute lymphoblastic leukemia. Haematologica, 2001, 86, 1254-60.	3.5	6
241	A 3-cM commonly deleted region in 6q21 in leukemias and lymphomas delineated by fluorescence in situ hybridization. Genes Chromosomes and Cancer, 2000, 27, 52-58.	2.8	67
242	Incidence, characterization and prognostic significance of chromosomal abnormalities in 640 patients with primary myelodysplastic syndromes. British Journal of Haematology, 2000, 108, 346-356.	2.5	230
243	Nonclonal Chromosomal Aberrations Induced by Anti-Tumoral Regimens in Childhood Cancer. Cancer Genetics and Cytogenetics, 2000, 121, 78-85.	1.0	12
244	Identification of novel chromosomal rearrangements in acute myelogenous leukemia involving loci on chromosome 2p23, 15q22 and 17q21. Leukemia, 1999, 13, 1534-1538.	7.2	18
245	A modified AIDA protocol with anthracycline-based consolidation results in high antileukemic efficacy and reduced toxicity in newly diagnosed PML/RARalpha-positive acute promyelocytic leukemia. PETHEMA group. Blood, 1999, 94, 3015-21.	1.4	293
246	Emergence of secondary acute leukemia in a patient treated for osteosarcoma: implications of germline TP53 mutations. , 1998, 30, 165-169.		19
247	Multicolor spectral karyotyping identifies new recurring breakpoints and translocations in multiple myeloma. Blood, 1998, 92, 1743-8.	1.4	85
248	Hypodiploidy and 22q11 rearrangements at diagnosis are associated with poor prognosis in patients with multiple myeloma. British Journal of Haematology, 1997, 98, 418-425.	2.5	39
249	Cytogenetic analysis of 280 patients with multiple myeloma and related disorders: Primary breakpoints and clinical correlations. Genes Chromosomes and Cancer, 1997, 18, 84-93.	2.8	150
250	Cytogenetic analysis of 280 patients with multiple myeloma and related disorders: primary breakpoints and clinical correlations. Genes Chromosomes and Cancer, 1997, 18, 84-93.	2.8	28
251	A variant t(14;17) in acute promyelocytic leukemia Positive response to retinoic acid treatment. Cancer Genetics and Cytogenetics, 1995, 80, 160-161.	1.0	9
252	Cytogenetic data in 41 patients with multiple myeloma. Cancer Genetics and Cytogenetics, 1994, 78, 210-213.	1.0	17

#	Article	IF	Citations
253	Complex karyotype including 14q+ marker in a case of WaldenstrÃ¶m's macroglobulinemia. Cancer Genetics and Cytogenetics, 1994, 73, 169-170.	1.0	6
254	Complex karyotype including trisomy 8 in a case of B-chronic lymphocytic leukemia. Cancer Genetics and Cytogenetics, 1992, 62, 108-109.	1.0	1
255	A new case of acute lymphoblastic leukemia B-cell type with chromosomal rearrangements involving the T-cell receptor breakpoint at band 14q11. American Journal of Hematology, 1992, 41, 137-139.	4.1	6
256	Double minute chromosomes and monosomy 7 in a lymphatic blast crisis of chronic myeloid leukemia. Cancer Genetics and Cytogenetics, 1990, 48, 133-134.	1.0	3