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	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
2	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
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	Cytogenetic risk stratification in chronic myelomonocytic leukemia. Haematologica, 2011, 96, 375-383.	3.5	226
11	Recurrent involvement of the REL and BCL11Aloci in classical Hodgkin lymphoma. Blood, 2002, 99, 1474-1477.	1.4	224
12	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
13	Promoter hypermethylation of cancer-related genes: a strong independent prognostic factor in acute lymphoblastic leukemia. Blood, 2004, 104, 2492-2498.	1.4	204
14	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
15	Measurable Residual Disease by Next-Generation Flow Cytometry in Multiple Myeloma. Journal of Clinical Oncology, 2020, 38, 784-792.	1.6	175
16	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
17	Cytogenetic complexity in chronic lymphocytic leukemia: definitions, associations, and clinical impact. Blood, 2019, 133, 1205-1216.	1.4	164
18	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

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19	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
20	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
21	Epigenetic regulation of Wnt-signaling pathway in acute lymphoblastic leukemia. Blood, 2007, 109, 3462-3469.	1.4	153
22	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
23	Exome sequencing reveals novel and recurrent mutations with clinical impact in blastic plasmacytoid dendritic cell neoplasm. Leukemia, 2014, 28, 823-829.	7.2	148
24	Epigenetic Regulation of MicroRNAs in Acute Lymphoblastic Leukemia. Journal of Clinical Oncology, 2009, 27, 1316-1322.	1.6	131
25	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
26	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	5.5	118
27	Cancer Epigenetics and Methylation. Science, 2002, 297, 1807d-1808.	12.6	116
28	A Comprehensive Microarray-Based DNA Methylation Study of 367 Hematological Neoplasms. PLoS ONE, 2009, 4, e6986.	2.5	115
29	Impact of adjunct cytogenetic abnormalities for prognostic stratification in patients with myelodysplastic syndrome and deletion 5q. Leukemia, 2011, 25, 110-120.	7.2	113
30	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
31	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
32	MicroRNA expression profiling in Imatinib-resistant Chronic Myeloid Leukemia patients without clinically significant ABL1-mutations. Molecular Cancer, 2009, 8, 69.	19.2	101
33	Reversion of epigenetically mediated BIM silencing overcomes chemoresistance in Burkitt lymphoma. Blood, 2010, 116, 2531-2542.	1.4	96
34	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
35	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
36	Multicolor spectral karyotyping identifies new recurring breakpoints and translocations in multiple myeloma. Blood, 1998, 92, 1743-8.	1.4	85

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37	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
38	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
39	Multicolor-FICTION. American Journal of Pathology, 2002, 161, 413-420.	3.8	81
40	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
41	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
42	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
43	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
44	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
45	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
46	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
47	DNA Methylation Profiles and Their Relationship with Cytogenetic Status in Adult Acute Myeloid Leukemia. PLoS ONE, 2010, 5, e12197.	2.5	73
48	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
49	Disruption and aberrant expression of HMGA2 as a consequence of diverse chromosomal translocations in myeloid malignancies. Leukemia, 2005, 19, 245-252.	7.2	69
50	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
51	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
52	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
53	Molecular cytogenetic detection of chromosomal breakpoints in T-cell receptor gene loci. Leukemia, 2003, 17, 738-745.	7.2	66
54	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

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55	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
56	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
57	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
58	Mutation Patterns of 16 Genes in Primary and Secondary Acute Myeloid Leukemia (AML) with Normal Cytogenetics. PLoS ONE, 2012, 7, e42334.	2.5	60
59	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
60	TP53is frequently altered by methylation, mutation, and/or deletion in acute lymphoblastic leukaemia. Molecular Carcinogenesis, 2003, 38, 201-208.	2.7	58
61	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
62	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
63	Frequent and Simultaneous Epigenetic Inactivation of TP53 Pathway Genes in Acute Lymphoblastic Leukemia. PLoS ONE, 2011, 6, e17012.	2.5	52
64	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
65	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
66	Epigenetic Inactivation of the Groucho Homologue Gene TLE1 in Hematologic Malignancies. Cancer Research, 2008, 68, 4116-4122.	0.9	50
67	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
68	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
69	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
70	Identification of overexpressed genes in frequently gained/amplified chromosome regions in multiple myeloma. Haematologica, 2006, 91, 184-91.	3.5	48
71	Long-Range Epigenetic Silencing Associates with Deregulation of Ikaros Targets in Colorectal Cancer Cells. Molecular Cancer Research, 2011, 9, 1139-1151.	3.4	47
72	Molecular heterogeneity in AML/MDS patients with 3q21q26 rearrangements. Genes Chromosomes and Cancer, 2004, 40, 179-189.	2.8	46

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73	Aberrant DNA methylation profile of chronic and transformed classic Philadelphia-negative myeloproliferative neoplasms. Haematologica, 2013, 98, 1414-1420.	3.5	46
74	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
75	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
76	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
77	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
78	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
79	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
80	Analysis of genomic breakpoints in p190 and p210 BCRâ€“ABL indicate distinct mechanisms of formation. Leukemia, 2010, 24, 1742-1750.	7.2	43
81	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
82	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
83	JAK2 V617F mutation in classic chronic myeloproliferative diseases: a report on a series of 349 patients. Leukemia, 2006, 20, 534-535.	7.2	41
84	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
85	Transcriptional profiling of circulating tumor cells in multiple myeloma: a new model to understand disease dissemination. Leukemia, 2020, 34, 589-603.	7.2	41
86	Genomic imbalances detected by comparative genomic hybridization are prognostic markers in invasive ductal breast carcinomas. Histopathology, 2002, 40, 547-555.	2.9	40
87	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
88	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
89	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
90	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

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91	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
92	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
93	Epigenetic Activation of SOX11 in Lymphoid Neoplasms by Histone Modifications. PLoS ONE, 2011, 6, e21382.	2.5	38
94	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
95	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
96	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
97	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
98	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
99	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. Genome Research, 2020, 30, 1217-1227.	5.5	35
100	BCRâ€ABL1â€induced expression of HSPA8 promotes cell survival in chronic myeloid leukaemia. British Journal of Haematology, 2008, 142, 571-582.	2.5	33
101	EVI1 controls proliferation in acute myeloid leukaemia through modulation of miR-1-2. British Journal of Cancer, 2010, 103, 1292-1296.	6.4	33
102	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
103	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
104	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
105	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
106	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
107	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
108	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

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109	Frequent gain of chromosome 19 in megakaryoblastic leukemias detected by comparative genomic hybridization. Genes Chromosomes and Cancer, 2001, 32, 285-293.	2.8	29
110	JAK2-V617F activating mutation in acute myeloid leukemia: prognostic impact and association with other molecular markers. Leukemia, 2007, 21, 2386-2390.	7.2	29
111	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
112	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
113	The molecular pathogenesis of the NUP98-HOXA9 fusion protein in acute myeloid leukemia. Leukemia, 2017, 31, 2000-2005.	7.2	28
114	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. Leukemia, 2021, 35, 1438-1450.	7.2	28
115	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
116	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
117	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
118	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
119	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
120	Circulating tumor cells for comprehensive and multiregional non-invasive genetic characterization of multiple myeloma. Leukemia, 2020, 34, 3007-3018.	7.2	26
121	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
122	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
123	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
124	Cytogenetic profile of myelodysplastic syndromes with complex karyotypes: an analysis using spectral karyotyping. Cancer Genetics and Cytogenetics, 2004, 153, 39-47.	1.0	24
125	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
126	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

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127	Biological and clinical significance of dysplastic hematopoiesis in patients with newly diagnosed multiple myeloma. Blood, 2020, 135, 2375-2387.	1.4	24
128	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
129	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
130	Preneoplastic somatic mutations including MYD88 ^{L265P} in lymphoplasmacytic lymphoma. Science Advances, 2022, 8, eabl4644.	10.3	21
131	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
132	CIP2A high expression is a poor prognostic factor in normal karyotype acute myeloid leukemia. Haematologica, 2015, 100, e183-e185.	3.5	20
133	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
134	Emergence of secondary acute leukemia in a patient treated for osteosarcoma: implications of germline TP53 mutations. , 1998, 30, 165-169.		19
135	CSNK1A1 mutations and gene expression analysis in myelodysplastic syndromes with del(5q). British Journal of Haematology, 2015, 171, 210-214.	2.5	19
136	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
137	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
138	Secondary myelodysplastic syndrome after treatment for promyelocytic leukemia. Cancer Genetics and Cytogenetics, 2003, 143, 178-181.	1.0	18
139	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
140	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
141	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
142	Cytogenetic data in 41 patients with multiple myeloma. Cancer Genetics and Cytogenetics, 1994, 78, 210-213.	1.0	17
143	Geographic differences in the incidence of cytogenetic abnormalities of acute myelogenous leukemia (AML) in Spain. Leukemia Research, 2006, 30, 943-948.	0.8	17
144	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

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145	Whole-exome sequencing in del(5q) myelodysplastic syndromes in transformation to acute myeloid leukemia. Leukemia, 2014, 28, 1148-1151.	7.2	17
146	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
147	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
148	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
149	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
150	Heterogeneity of structural abnormalities in the 7q31.3â¯¼q34 region in myeloid malignancies. Cancer Genetics and Cytogenetics, 2004, 150, 136-143.	1.0	15
151	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
152	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
153	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
154	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
155	Chromosomal abnormalities clustering in multiple myeloma reveals cytogenetic subgroups with nonrandom acquisition of chromosomal changes. Leukemia, 2004, 18, 654-657.	7.2	14
156	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
157	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
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