

Maria J Calasanz

List of Publications by Year in descending order

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256
papers

13,254
citations

24978

57
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265
docs citations

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times ranked

15342
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. <i>Haematologica</i> , 2022, 107, 593-603.	1.7	18
2	Insights into the mechanisms underlying aberrant SOX11 oncogene expression in mantle cell lymphoma. <i>Leukemia</i> , 2022, 36, 583-587.	3.3	5
3	Landscape and clinical significance of long noncoding <i>lncRNAs</i> involved in multiple myeloma expressed fusion transcripts. <i>American Journal of Hematology</i> , 2022, 97, .	2.0	1
4	Preneoplastic somatic mutations including <i>MYD88</i> ^{L265P} in lymphoplasmacytic lymphoma. <i>Science Advances</i> , 2022, 8, eabl4644.	4.7	21
5	A Machine Learning Model Based on Tumor and Immune Biomarkers to Predict Undetectable MRD and Survival Outcomes in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2022, 28, 2598-2609.	3.2	14
6	Characteristics and Outcomes of Adult Patients in the PETHEMA Registry with Relapsed or Refractory FLT3-ITD Mutation-Positive Acute Myeloid Leukemia. <i>Cancers</i> , 2022, 14, 2817.	1.7	0
7	Circulating Tumor Cells for the Staging of Patients With Newly Diagnosed Transplant-Eligible Multiple Myeloma. <i>Journal of Clinical Oncology</i> , 2022, 40, 3151-3161.	0.8	40
8	Deep MRD profiling defines outcome and unveils different modes of treatment resistance in standard- and high-risk myeloma. <i>Blood</i> , 2021, 137, 49-60.	0.6	80
9	Endogenous Retroelement Activation by Epigenetic Therapy Reverses the Warburg Effect and Elicits Mitochondrial-Mediated Cancer Cell Death. <i>Cancer Discovery</i> , 2021, 11, 1268-1285.	7.7	42
10	Measurable residual disease in elderly acute myeloid leukemia: results from the PETHEMA-FLUGAZA phase 3 clinical trial. <i>Blood Advances</i> , 2021, 5, 760-770.	2.5	18
11	Characterization of complete <i>lncRNAs</i> transcriptome reveals the functional and clinical impact of <i>lncRNAs</i> in multiple myeloma. <i>Leukemia</i> , 2021, 35, 1438-1450.	3.3	28
12	Lenalidomide and dexamethasone with or without clarithromycin in patients with multiple myeloma ineligible for autologous transplant: a randomized trial. <i>Blood Cancer Journal</i> , 2021, 11, 101.	2.8	14
13	Myelodysplastic syndromes with 20q deletion: incidence, prognostic value and impact on response to azacitidine of <i>ASXL1</i> chromosomal deletion and genetic mutations. <i>British Journal of Haematology</i> , 2021, 194, 708-717.	1.2	7
14	Prognostic heterogeneity of adult <i>B</i> -cell precursor acute lymphoblastic leukaemia patients with t(1;19)(q23;p13)/ <i>TCF3</i> - <i>PBX1</i> treated with measurable residual disease-oriented protocols. <i>British Journal of Haematology</i> , 2021, , .	1.2	2
15	Transcriptional profiling of circulating tumor cells in multiple myeloma: a new model to understand disease dissemination. <i>Leukemia</i> , 2020, 34, 589-603.	3.3	41
16	Spanish Guidelines for the use of targeted deep sequencing in myelodysplastic syndromes and chronic myelomonocytic leukaemia. <i>British Journal of Haematology</i> , 2020, 188, 605-622.	1.2	25
17	Measurable Residual Disease by Next-Generation Flow Cytometry in Multiple Myeloma. <i>Journal of Clinical Oncology</i> , 2020, 38, 784-792.	0.8	175
18	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. <i>Genome Research</i> , 2020, 30, 1217-1227.	2.4	35

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19	Assessment of Minimal Residual Disease by Next Generation Sequencing in Peripheral Blood as a Complementary Tool for Personalized Transplant Monitoring in Myeloid Neoplasms. <i>Journal of Clinical Medicine</i> , 2020, 9, 3818.	1.0	9
20	Circulating tumor cells for comprehensive and multiregional non-invasive genetic characterization of multiple myeloma. <i>Leukemia</i> , 2020, 34, 3007-3018.	3.3	26
21	Impaired Condensin Complex and Aurora B kinase underlie mitotic and chromosomal defects in hyperdiploid B-cell ALL. <i>Blood</i> , 2020, 136, 313-327.	0.6	16
22	Molecular profiling of immunoglobulin heavy-chain gene rearrangements unveils new potential prognostic markers for multiple myeloma patients. <i>Blood Cancer Journal</i> , 2020, 10, 14.	2.8	16
23	Assessment of the clinical utility of four NGS panels in myeloid malignancies. Suggestions for NGS panel choice or design. <i>PLoS ONE</i> , 2020, 15, e0227986.	1.1	33
24	Strategy for identification of a potential inherited leukemia predisposition in a 299 patient's cohort with tumor-only sequencing data. <i>Leukemia Research</i> , 2020, 95, 106386.	0.4	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. <i>Blood</i> , 2020, 136, 5-6.	0.6	2
26	Biological and clinical significance of dysplastic hematopoiesis in patients with newly diagnosed multiple myeloma. <i>Blood</i> , 2020, 135, 2375-2387.	0.6	24
27	PLZF-RAR \pm , NPM1-RAR \pm , and Other Acute Promyelocytic Leukemia Variants: The PETHEMA Registry Experience and Systematic Literature Review. <i>Cancers</i> , 2020, 12, 1313.	1.7	20
28	Measurable Residual Disease (MRD) in Elderly Acute Myeloid Leukemia (AML): Results from the Pethema-Flugaza Phase III Clinical Trial. <i>Blood</i> , 2020, 136, 32-32.	0.6	0
29	Myelodysplastic Syndromes with 20q Deletion: Incidence, Prognostic Value and Impact on Response to Azacitidine of <i>ASXL1</i> Chromosomal Deletion and Genetic Mutations. <i>Blood</i> , 2020, 136, 1-2.	0.6	0
30	Clinical Validation of a NGS Capture Panel to Identify Mutations, Copy Number Variations and Translocations in Patients with Multiple Myeloma. <i>Blood</i> , 2020, 136, 13-14.	0.6	1
31	Waldenström's Macroglobulinemia (WM) Is Preceded By Clonal Lymphopoiesis Including MYD88 L265P in Progenitor B Cells. <i>Blood</i> , 2020, 136, 42-43.	0.6	1
32	Epigenomic profiling of myelofibrosis reveals widespread DNA methylation changes in enhancer elements and <i>ZFP36L1</i> as a potential tumor suppressor gene that is epigenetically regulated. <i>Haematologica</i> , 2019, 104, 1572-1579.	1.7	16
33	Prognostic implications of MRD assessment in multiple myeloma patients: comparison of Next-Generation Sequencing and Next-Generation Flow. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e47.	0.2	2
34	Role of lncRNAs as prognostic factor and potential therapeutic target in Multiple Myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e354-e355.	0.2	1
35	Circulating Tumor Cells (CTCs) for Comprehensive and Multiregional Non-Invasive Genetic Characterization of Multiple Myeloma (MM). <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e351.	0.2	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. <i>Leukemia and Lymphoma</i> , 2019, 60, 1146-1155.	0.6	12

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37	Cytogenetic complexity in chronic lymphocytic leukemia: definitions, associations, and clinical impact. <i>Blood</i> , 2019, 133, 1205-1216.	0.6	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. <i>Blood</i> , 2019, 134, 694-694.	0.6	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. <i>Blood</i> , 2019, 134, 781-781.	0.6	38
40	Waldenström's Macroglobulinemia (WM) Is Preceded By Clonal Lymphopoiesis Including MYD88 L265P in Progenitor B Cells. <i>Blood</i> , 2019, 134, 1527-1527.	0.6	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. <i>Blood</i> , 2019, 134, 581-581.	0.6	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). <i>Blood</i> , 2019, 134, 509-509.	0.6	2
43	Circulating Tumor Cells (CTCs) for Comprehensive and Multiregional Non-Invasive Genetic Characterization of Multiple Myeloma (MM). <i>Blood</i> , 2019, 134, 3064-3064.	0.6	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. <i>Blood</i> , 2019, 134, 4323-4323.	0.6	1
45	Lncrnas As New Partners of Novel Chimeric Transcripts in Multiple Myeloma. <i>Blood</i> , 2019, 134, 4356-4356.	0.6	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. <i>Blood</i> , 2019, 134, 4287-4287.	0.6	1
47	Strategy for Identification of an Inherited Leukemia Predisposition in a 299 Patients Cohort with Tumor-Only Sequencing Data. <i>Blood</i> , 2019, 134, 1415-1415.	0.6	7
48	Cdx Report Program: Heterogeneity Revealed in Current Reporting Practices for Hemato-Oncology Companion Diagnostic (CDx) Markers in Multiple Countries. <i>Blood</i> , 2019, 134, 5837-5837.	0.6	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. <i>Blood</i> , 2019, 134, 1852-1852.	0.6	1
50	Richter transformation driven by Epstein-Barr virus reactivation during therapy-related immunosuppression in chronic lymphocytic leukaemia. <i>Journal of Pathology</i> , 2018, 245, 61-73.	2.1	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. <i>Blood</i> , 2018, 132, 112-112.	0.6	3
52	Transcriptomic Profiling of Circulating Tumor Cells (CTCs) in Multiple Myeloma (MM): A New Model to Understand Disease Dissemination. <i>Blood</i> , 2018, 132, 245-245.	0.6	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. <i>Blood</i> , 2018, 132, 1943-1943.	0.6	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. <i>Blood</i> , 2018, 132, 474-474.	0.6	0

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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. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2017, 17, e11.	0.2	0
56	Monosomal karyotype in chronic lymphocytic leukemia: Association with clinical and biological features and potential prognostic significance. <i>American Journal of Hematology</i> , 2017, 92, E132-E135.	2.0	1
57	The molecular pathogenesis of the NUP98-HOXA9 fusion protein in acute myeloid leukemia. <i>Leukemia</i> , 2017, 31, 2000-2005.	3.3	28
58	Patients with chronic lymphocytic leukemia and complex karyotype show an adverse outcome even in absence of <i>TP53/ATM FISH</i> deletions. <i>Oncotarget</i> , 2017, 8, 54297-54303.	0.8	44
59	Impact of <i>SNP</i> array karyotyping on the diagnosis and the outcome of chronic myelomonocytic leukemia with low risk cytogenetic features or no metaphases. <i>American Journal of Hematology</i> , 2016, 91, 185-192.	2.0	18
60	Homeobox NKX2-3 promotes marginal-zone lymphomagenesis by activating B-cell receptor signalling and shaping lymphocyte dynamics. <i>Nature Communications</i> , 2016, 7, 11889.	5.8	42
61	Refining the Breakpoints of Three New Translocations Identified in Myelodysplastic Syndromes. <i>Acta Haematologica</i> , 2016, 135, 94-100.	0.7	2
62	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. <i>Cancer Cell</i> , 2016, 30, 806-821.	7.7	103
63	Prognostic impact of chromosomal translocations in myelodysplastic syndromes and chronic myelomonocytic leukemia patients. A study by the spanish group of myelodysplastic syndromes. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 322-327.	1.5	7
64	Use of human pharyngeal and palatine tonsils as a reservoir for the analysis of B cell ontogeny in 10 paired samples. <i>Clinical Otolaryngology</i> , 2016, 41, 606-611.	0.6	4
65	Targeted resequencing analysis of 31 genes commonly mutated in myeloid disorders in serial samples from myelodysplastic syndrome patients showing disease progression. <i>Leukemia</i> , 2016, 30, 248-250.	3.3	51
66	Non-Invasive Genetic Profiling Is Highly Applicable in Multiple Myeloma (MM) through Characterization of Circulating Tumor Cells (CTCs). <i>Blood</i> , 2016, 128, 801-801.	0.6	2
67	Comparison of the Molecular Spectrum of Lenalidomide-Treated Myelodysplastic Syndrome with and without Del(5q). <i>Blood</i> , 2016, 128, 3172-3172.	0.6	0
68	HDAC Inhibitors As Novel Targeted Therapies for NUP98-HOXA9 AML Patients. <i>Blood</i> , 2016, 128, 2685-2685.	0.6	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. <i>Blood</i> , 2016, 128, 375-375.	0.6	1
70	<i>CSNK1A1</i> mutations and gene expression analysis in myelodysplastic syndromes with del(5q). <i>British Journal of Haematology</i> , 2015, 171, 210-214.	1.2	19
71	CIP2A high expression is a poor prognostic factor in normal karyotype acute myeloid leukemia. <i>Haematologica</i> , 2015, 100, e183-e185.	1.7	20
72	Correlation of myelodysplastic syndromes with i(17)(q10) and <i>TP53</i> and <i>SETBP1</i> mutations. <i>British Journal of Haematology</i> , 2015, 171, 137-141.	1.2	11

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73	The GATA2 transcription factor directly binds and activates MYB expression in acute myeloid leukemia. <i>Experimental Hematology</i> , 2015, 43, S58.	0.2	0
74	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	2.4	118
75	The relationship of TP53 R72P polymorphism to disease outcome and TP53 mutation in myelodysplastic syndromes. <i>Blood Cancer Journal</i> , 2015, 5, e291-e291.	2.8	15
76	Fluorescence in situ hybridization analysis does not increase detection rate for trisomy 8 in chronic myelomonocytic leukemia. <i>Leukemia and Lymphoma</i> , 2015, 56, 242-243.	0.6	1
77	Hypermethylation of the alternative AWT1 promoter in hematological malignancies is a highly specific marker for acute myeloid leukemias despite high expression levels. <i>Journal of Hematology and Oncology</i> , 2014, 7, 4.	6.9	21
78	Exome sequencing reveals novel and recurrent mutations with clinical impact in blastic plasmacytoid dendritic cell neoplasm. <i>Leukemia</i> , 2014, 28, 823-829.	3.3	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. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 788-797.	1.5	15
80	Whole-exome sequencing in del(5q) myelodysplastic syndromes in transformation to acute myeloid leukemia. <i>Leukemia</i> , 2014, 28, 1148-1151.	3.3	17
81	Utility of SNP Arrays in Chronic Myelomonocytic Leukemia with Low Risk Cytogenetic Features or No Metaphases. <i>Blood</i> , 2014, 124, 4659-4659.	0.6	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. <i>Blood</i> , 2014, 124, 1677-1677.	0.6	4
83	Mutations in <i>SETBP1</i> are recurrent in myelodysplastic syndromes and often coexist with cytogenetic markers associated with disease progression. <i>British Journal of Haematology</i> , 2013, 163, 235-239.	1.2	37
84	Characterization and prognostic implication of 17 chromosome abnormalities in myelodysplastic syndrome. <i>Leukemia Research</i> , 2013, 37, 769-776.	0.4	11
85	Reciprocal translocations in myelodysplastic syndromes and chronic myelomonocytic leukemias: Review of 5,654 patients with an evaluable karyotype. <i>Genes Chromosomes and Cancer</i> , 2013, 52, 753-763.	1.5	15
86	Functional characterization of the promoter region of the human EVI1 gene in acute myeloid leukemia: RUNX1 and ELK1 directly regulate its transcription. <i>Oncogene</i> , 2013, 32, 2069-2078.	2.6	23
87	Downregulation of specific miRNAs in hyperdiploid multiple myeloma mimics the oncogenic effect of IgH translocations occurring in the non-hyperdiploid subtype. <i>Leukemia</i> , 2013, 27, 925-931.	3.3	31
88	Response to lenalidomide in myelodysplastic syndromes with del(5q): influence of cytogenetics and mutations. <i>British Journal of Haematology</i> , 2013, 162, 74-86.	1.2	73
89	CBL RING finger deletions are common in core-binding factor acute myeloid leukemias. <i>Leukemia and Lymphoma</i> , 2013, 54, 428-431.	0.6	6
90	Landscape of somatic mutations and clonal evolution in mantle cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18250-18255.	3.3	488

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91	Single nucleotide polymorphism array karyotyping: A diagnostic and prognostic tool in myelodysplastic syndromes with unsuccessful conventional cytogenetic testing. <i>Genes Chromosomes and Cancer</i> , 2013, 52, 1167-1177.	1.5	44
92	Biallelic losses of 13q do not confer a poorer outcome in chronic lymphocytic leukaemia: analysis of 627 patients with isolated 13q deletion. <i>British Journal of Haematology</i> , 2013, 163, 47-54.	1.2	13
93	Aberrant DNA methylation profile of chronic and transformed classic Philadelphia-negative myeloproliferative neoplasms. <i>Haematologica</i> , 2013, 98, 1414-1420.	1.7	46
94	Downregulation of PPP2R5E is a common event in acute myeloid leukemia that affects the oncogenic potential of leukemic cells. <i>Haematologica</i> , 2013, 98, e103-e104.	1.7	25
95	Molecular Subsets of Mantle Cell Lymphoma Defined by the <i>IGHV</i> Mutational Status and SOX11 Expression Have Distinct Biologic and Clinical Features. <i>Cancer Research</i> , 2012, 72, 5307-5316.	0.4	231
96	Preclinical activity of LBH589 alone or in combination with chemotherapy in a xenogeneic mouse model of human acute lymphoblastic leukemia. <i>Leukemia</i> , 2012, 26, 1517-1526.	3.3	41
97	Overexpression of GATA2 predicts an adverse prognosis for patients with acute myeloid leukemia and it is associated with distinct molecular abnormalities. <i>Leukemia</i> , 2012, 26, 550-554.	3.3	64
98	Mutation Patterns of 16 Genes in Primary and Secondary Acute Myeloid Leukemia (AML) with Normal Cytogenetics. <i>PLoS ONE</i> , 2012, 7, e42334.	1.1	60
99	Overexpression of SET is a recurrent event associated with poor outcome and contributes to protein phosphatase 2A inhibition in acute myeloid leukemia. <i>Haematologica</i> , 2012, 97, 543-550.	1.7	105
100	Román-Gómez J, Cordeu L, Agirre X, Jimenez-Velasco A, San José-Eneriz E, Garate L, Calasanz MJ, Heiniger A, Torres A, Prosper F. Epigenetic regulation of Wnt-signaling pathway in acute lymphoblastic leukemia. <i>Blood</i> . 2007;109(8):3462-3469. <i>Blood</i> , 2012, 120, 3625-3625.	0.6	4
101	High-throughput sequencing analysis of the chromosome 7q32 deletion reveals <i>IRF5</i> as a potential tumour suppressor in splenic marginal zone lymphoma. <i>British Journal of Haematology</i> , 2012, 158, 712-726.	1.2	45
102	Chromatin modifications induced by the AML1-ETO fusion protein reversibly silence its genomic targets through AML1 and Sp1 binding motifs. <i>Leukemia</i> , 2012, 26, 1329-1337.	3.3	30
103	TET2 Mutations Are Associated with Specific 5-Methylcytosine and 5-Hydroxymethylcytosine Profiles in Patients with Chronic Myelomonocytic Leukemia. <i>PLoS ONE</i> , 2012, 7, e31605.	1.1	70
104	Integration of SNP and mRNA Arrays with MicroRNA Profiling Reveals That MiR-370 Is Upregulated and Targets NF1 in Acute Myeloid Leukemia. <i>PLoS ONE</i> , 2012, 7, e47717.	1.1	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. <i>Blood</i> , 2012, 120, 2823-2823.	0.6	0
108	Cytogenetic risk stratification in chronic myelomonocytic leukemia. <i>Haematologica</i> , 2011, 96, 375-383.	1.7	226

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109	Epigenetic Activation of SOX11 in Lymphoid Neoplasms by Histone Modifications. PLoS ONE, 2011, 6, e21382.	1.1	38
110	NPM1 gene deletions in myelodysplastic syndromes with 5q- and complex karyotype. Haematologica, 2011, 96, 784-785.	1.7	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.	1.7	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.	1.7	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.	1.7	45
114	Deregulation of <i>FGFR1</i> and <i>CDK6</i> oncogenic pathways in acute lymphoblastic leukaemia harbouring epigenetic modifications of the <i>MIR9</i> family. British Journal of Haematology, 2011, 155, 73-83.	1.2	53
115	Impact of adjunct cytogenetic abnormalities for prognostic stratification in patients with myelodysplastic syndrome and deletion 5q. Leukemia, 2011, 25, 110-120.	3.3	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.	3.3	124
117	Long-Range Epigenetic Silencing Associates with Deregulation of Ikaros Targets in Colorectal Cancer Cells. Molecular Cancer Research, 2011, 9, 1139-1151.	1.5	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.	3.3	50
119	Frequent and Simultaneous Epigenetic Inactivation of TP53 Pathway Genes in Acute Lymphoblastic Leukemia. PLoS ONE, 2011, 6, e17012.	1.1	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.	0.6	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.	0.6	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.	0.6	174
123	Reversion of epigenetically mediated BIM silencing overcomes chemoresistance in Burkitt lymphoma. Blood, 2010, 116, 2531-2542.	0.6	96
124	Additional chromosome abnormalities in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and chemotherapy. Haematologica, 2010, 95, 424-431.	1.7	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.	1.5	68

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127	EV11 controls proliferation in acute myeloid leukaemia through modulation of miR-1-2. <i>British Journal of Cancer</i> , 2010, 103, 1292-1296.	2.9	33
128	Analysis of genomic breakpoints in p190 and p210 BCR-ABL indicate distinct mechanisms of formation. <i>Leukemia</i> , 2010, 24, 1742-1750.	3.3	43
129	Frequent mutation of the polycomb-associated gene ASXL1 in the myelodysplastic syndromes and in acute myeloid leukemia. <i>Leukemia</i> , 2010, 24, 1062-1065.	3.3	231
130	Bcr/Abl Interferes with the Fanconi Anemia/BRCA Pathway: Implications in the Chromosomal Instability of Chronic Myeloid Leukemia Cells. <i>PLoS ONE</i> , 2010, 5, e15525.	1.1	20
131	Silencing of hsa-miR-124 by EV11 in cell lines and patients with acute myeloid leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, E167-8; author reply E169-70.	3.3	30
132	Response to lenalidomide in a patient with myelodysplastic syndrome with isolated del(5q) and JAK2 V617F mutation. <i>Leukemia and Lymphoma</i> , 2010, 51, 1941-1943.	0.6	7
133	Quantification of PDGFRA alternative transcripts improves the screening for PDGFRA fusions by reverse transcriptase-polymerase chain reaction. <i>Leukemia and Lymphoma</i> , 2010, 51, 1720-1726.	0.6	0
134	Frequent Mutation of the Polycomb-Associated Gene ASXL1 In Acute Myeloid Leukemia Secondary to Myelodysplastic Syndrome or Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2010, 116, 2940-2940.	0.6	1
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