JosÃ© I MartÃ-n-Subero

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1825314/publications.pdf

Version: 2024-02-01

164	14,095	20759	22764
papers	citations	60 h-index	112 g-index

172	172	172	19161
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Insights into the mechanisms underlying aberrant SOX11 oncogene expression in mantle cell lymphoma. Leukemia, 2022, 36, 583-587.	3.3	5
2	Landscape and clinical significance of long noncoding <scp>RNAs</scp> involved in multiple myeloma expressed fusion transcripts. American Journal of Hematology, 2022, 97, .	2.0	1
3	Towards precision medicine in lymphoid malignancies. Journal of Internal Medicine, 2022, 292, 221-242.	2.7	9
4	Comprehensive characterization of the epigenetic landscape in Multiple Myeloma. Theranostics, 2022, 12, 1715-1729.	4.6	10
5	PanCancer analysis of somatic mutations in repetitive regions reveals recurrent mutations in snRNA U2. Npj Genomic Medicine, 2022, 7, 19.	1.7	2
6	IGLV3-21R110 identifies an aggressive biological subtype of chronic lymphocytic leukemia with intermediate epigenetics. Blood, 2021, 137, 2935-2946.	0.6	49
7	Genomic and transcriptomic correlates of Richter transformation in chronic lymphocytic leukemia. Blood, 2021, 137, 2800-2816.	0.6	51
8	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. Nature Communications, 2021, 12, 651.	5.8	67
9	Characterization of complete lncRNAs transcriptome reveals the functional and clinical impact of lncRNAs in multiple myeloma. Leukemia, 2021, 35, 1438-1450.	3.3	28
10	EOMES is essential for antitumor activity of CD8+ T cells in chronic lymphocytic leukemia. Leukemia, 2021, 35, 3152-3162.	3.3	26
11	Extramedullary multiple myeloma patient derived orthotopic xenograft with high disturbed genome: combined exhaustive molecular and therapeutic studies. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	5
12	Gene expression derived from alternative promoters improves prognostic stratification in multiple myeloma. Leukemia, 2021, 35, 3012-3016.	3.3	11
13	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	3.3	34
14	Cereblon enhancer methylation and IMiD resistance in multiple myeloma. Blood, 2021, 138, 1721-1726.	0.6	25
15	The hydroxymethylome of multiple myeloma identifies FAM72D as a 1q21 marker linked to proliferation. Haematologica, 2020, 105, 774-783.	1.7	23
16	The proliferative history shapes the DNA methylome of B-cell tumors and predicts clinical outcome. Nature Cancer, 2020, 1, 1066-1081.	5.7	51
17	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. Genome Research, 2020, 30, 1217-1227.	2.4	35
18	Chronic lymphocytic leukemias with trisomy 12 show a distinct DNA methylation profile linked to altered chromatin activation. Haematologica, 2020, 105, 2864-2867.	1.7	11

#	Article	IF	Citations
19	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. Blood, 2020, 136, 1419-1432.	0.6	131
20	A lncRNA-SWI/SNF complex crosstalk controls transcriptional activation at specific promoter regions. Nature Communications, 2020, 11, 936.	5.8	69
21	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. Nature Communications, 2019, 10, 3615.	5.8	32
22	Expression of <scp>ELF</scp>1, a lymphoid <scp>ETS</scp> domainâ€containing transcription factor, is recurrently lost in classical Hodgkin lymphoma. British Journal of Haematology, 2019, 185, 79-88.	1.2	9
23	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.	1.7	16
24	Impaired CpG Demethylation in Common Variable Immunodeficiency Associates With B Cell Phenotype and Proliferation Rate. Frontiers in Immunology, 2019, 10, 878.	2.2	19
25	Long non-coding RNAs discriminate the stages and gene regulatory states of human humoral immune response. Nature Communications, 2019, 10, 821.	5.8	73
26	DNA methylation profiles in chronic lymphocytic leukemia patients treated with chemoimmunotherapy. Clinical Epigenetics, 2019, 11, 177.	1.8	15
27	Integrated epigenomic and transcriptomic analysis reveals TP63 as a novel player in clinically aggressive chronic lymphocytic leukemia. International Journal of Cancer, 2019, 144, 2695-2706.	2.3	24
28	DNA methylation profiling of hepatosplenic T-cell lymphoma. Haematologica, 2019, 104, e104-e107.	1.7	11
29	Expression of the transcribed ultraconserved region 70 and the related long nonâ€coding <scp>RNA AC</scp>092652.2â€202 has prognostic value in Chronic Lymphocytic Leukaemia. British Journal of Haematology, 2019, 184, 1045-1050.	1.2	10
30	Whole-genome sequencing of chronic lymphocytic leukaemia reveals distinct differences in the mutational landscape between IgHVmut and IgHVunmut subgroups. Leukemia, 2018, 32, 332-342.	3.3	49
31	Charting the dynamic epigenome during B-cell development. Seminars in Cancer Biology, 2018, 51, 139-148.	4.3	22
32	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157
33	Insight into origins, mechanisms, and utility of DNA methylation in B-cell malignancies. Blood, 2018, 132, 999-1006.	0.6	24
34	Cyclin D1 overexpression induces global transcriptional downregulation in lymphoid neoplasms. Journal of Clinical Investigation, 2018, 128, 4132-4147.	3.9	31
35	Discovery of first-in-class reversible dual small molecule inhibitors against G9a and DNMTs in hematological malignancies. Nature Communications, 2017, 8, 15424.	5.8	109
36	LMO2-negative Expression Predicts the Presence of MYC Translocations in Aggressive B-Cell Lymphomas. American Journal of Surgical Pathology, 2017, 41, 877-886.	2.1	19

#	Article	IF	Citations
37	DNA methylation profiling of pediatric Bâ€cell lymphoblastic leukemia with KMT2A rearrangement identifies hypomethylation at enhancer sites. Pediatric Blood and Cancer, 2017, 64, e26251.	0.8	20
38	Differentiation stage of myeloma plasma cells: biological and clinical significance. Leukemia, 2017, 31, 382-392.	3.3	83
39	In silico deconvolution and purification of cancer epigenomes. Oncoscience, 2017, 4, 25-26.	0.9	6
40	Genetic Predisposition to Chronic Lymphocytic Leukemia Is Mediated by a BMF Super-Enhancer Polymorphism. Cell Reports, 2016, 16, 2061-2067.	2.9	58
41	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. Cancer Cell, 2016, 30, 806-821.	7.7	103
42	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
43	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. Cell Reports, 2016, 17, 2101-2111.	2.9	54
44	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	9.4	270
45	The DNA Methylomes of Cancer. , 2016, , 183-207.		1
46	Mutations in CHD2 cause defective association with active chromatin in chronic lymphocytic leukemia. Blood, 2015, 126, 195-202.	0.6	50
47	Aberrant epigenome in <scp>iPSC</scp> â€derived dopaminergic neurons from Parkinson's disease patients. EMBO Molecular Medicine, 2015, 7, 1529-1546.	3.3	117
48	Cell-Cycle-Dependent Reconfiguration of the DNA Methylome during Terminal Differentiation of Human B Cells into Plasma Cells. Cell Reports, 2015, 13, 1059-1071.	2.9	65
49	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. Nature Genetics, 2015, 47, 746-756.	9.4	278
50	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. Genome Research, 2015, 25, 478-487.	2.4	118
51	Epigenetic remodeling in B-cell acute lymphoblastic leukemia occurs in two tracks and employs embryonic stem cell-like signatures. Nucleic Acids Research, 2015, 43, 2590-2602.	6.5	42
52	DNA methylation fingerprint of neuroblastoma reveals new biological and clinical insights. Genomics Data, 2015, 5, 360-363.	1.3	8
53	NF-Î²B activation impairs somatic cell reprogramming in ageing. Nature Cell Biology, 2015, 17, 1004-1013.	4.6	91
54	DNA methylation fingerprint of neuroblastoma reveals new biological and clinical insights. Epigenomics, 2015, 7, 1137-1153.	1.0	40

#	Article	IF	Citations
55	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2015, 526, 519-524.	13.7	749
56	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. Nature Genetics, 2015, 47, 1316-1325.	9.4	119
57	A B-cell epigenetic signature defines three biologic subgroups of chronic lymphocytic leukemia with clinical impact. Leukemia, 2015, 29, 598-605.	3.3	129
58	The chromatin remodeller CHD8 is required for E2F-dependent transcription activation of S-phase genes. Nucleic Acids Research, 2014, 42, 2185-2196.	6.5	72
59	Assessment of SOX11 Expression in Routine Lymphoma Tissue Sections. American Journal of Surgical Pathology, 2014, 38, 86-93.	2.1	58
60	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	2.4	175
61	A familial disorder of altered DNA-methylation. Journal of Medical Genetics, 2014, 51, 407-412.	1.5	24
62	Breakpoint characterization of the der(19)t(11;19)(q13;p13) in the ovarian cancer cell line SKOVâ€3. Genes Chromosomes and Cancer, 2013, 52, 512-522.	1.5	6
63	Intragenic DNA methylation in transcriptional regulation, normal differentiation and cancer. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 1161-1174.	0.9	188
64	microRNA Expression Profiles Identify Subtypes of Mantle Cell Lymphoma with Different Clinicobiological Characteristics. Clinical Cancer Research, 2013, 19, 3121-3129.	3.2	35
65	Genomeâ€wide methylation analyses identify a subset of mantle cell lymphoma with a high number of methylated CpGs and aggressive clinicopathological features. International Journal of Cancer, 2013, 133, 2852-2863.	2.3	15
66	Lowâ€grade and highâ€grade mammary carcinomas in WAPâ€T transgenic mice are independent entities distinguished by Met expression. International Journal of Cancer, 2013, 132, 1300-1310.	2.3	15
67	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.	3.3	488
68	Genetic and epigenetic basis of chronic lymphocytic leukemia. Current Opinion in Hematology, 2013, 20, 362-368.	1.2	34
69	DNA methylation map of mouse and human brain identifies target genes in Alzheimerâ€™s disease. Brain, 2013, 136, 3018-3027.	3.7	129
70	SOX11 regulates PAX5 expression and blocks terminal B-cell differentiation in aggressive mantle cell lymphoma. Blood, 2013, 121, 2175-2185.	0.6	129
71	Aberrant DNA methylation profile of chronic and transformed classic Philadelphia-negative myeloproliferative neoplasms. Haematologica, 2013, 98, 1414-1420.	1.7	46
72	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.	3.3	41

#	Article	IF	Citations
73	A DNA methylation fingerprint of 1628 human samples. Genome Research, 2012, 22, 407-419.	2.4	341
74	ETS1 encoding a transcription factor involved in B-cell differentiation is recurrently deleted and down-regulated in classical Hodgkin's lymphoma. Haematologica, 2012, 97, 1612-1614.	1.7	17
75	Array-based DNA methylation analysis in classical Hodgkin lymphoma reveals new insights into the mechanisms underlying silencing of B cell-specific genes. Leukemia, 2012, 26, 185-188.	3.3	43
76	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	9.4	525
77	TET2 Mutations Are Associated with Specific 5-Methylcytosine and 5-Hydroxymethylcytosine Profiles in Patients with Chronic Myelomonocytic Leukemia. PLoS ONE, 2012, 7, e31605.	1.1	70
78	DNA Hypomethylation Affects Cancer-Related Biological Functions and Genes Relevant in Neuroblastoma Pathogenesis. PLoS ONE, 2012, 7, e48401.	1.1	31
79	Profiling Epigenetic Alterations in Disease. Advances in Experimental Medicine and Biology, 2011, 711, 162-177.	0.8	49
80	Epigenetic Activation of SOX11 in Lymphoid Neoplasms by Histone Modifications. PLoS ONE, 2011, 6, e21382.	1.1	38
81	Epigenomic profiling in polycythaemia vera and essential thrombocythaemia shows low levels of aberrant DNA methylation. Journal of Clinical Pathology, 2011, 64, 1010-1013.	1.0	20
82	Androgen Receptor Mutations Are Associated with Altered Epigenomic Programming as Evidenced by <i>HOXA5</i> Methylation. Sexual Development, 2011, 5, 70-76.	1.1	10
83	Frequent and Simultaneous Epigenetic Inactivation of TP53 Pathway Genes in Acute Lymphoblastic Leukemia. PLoS ONE, 2011, 6, e17012.	1.1	52
84	How epigenomics brings phenotype into being. Pediatric Endocrinology Reviews, 2011, 9 Suppl 1, 506-10.	1.2	9
85	Deregulation of the telomerase reverse transcriptase (TERT) gene by chromosomal translocations in B-cell malignancies. Blood, 2010, 116, 1317-1320.	0.6	44
86	Rare occurrence of biallelic CYLD gene mutations in classical Hodgkin lymphoma. Genes Chromosomes and Cancer, 2010, 49, 803-809.	1.5	37
87	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. Genome Research, 2010, 20, 170-179.	2.4	569
88	Four patients with speech delay, seizures and variable corpus callosum thickness sharing a 0.440ÂMb deletion in region 1q44 containing the HNRPU gene. European Journal of Medical Genetics, 2010, 53, 179-185.	0.7	72
89	DNA Methylation Profiles and Their Relationship with Cytogenetic Status in Adult Acute Myeloid Leukemia. PLoS ONE, 2010, 5, e12197.	1.1	73
90	A Comprehensive Microarray-Based DNA Methylation Study of 367 Hematological Neoplasms. PLoS ONE, 2009, 4, e6986.	1.1	115

#	Article	IF	Citations
91	A microarray-based DNA methylation study of glioblastoma multiforme. Epigenetics, 2009, 4, 255-264.	1.3	155
92	TNFAIP3 (A20) is a tumor suppressor gene in Hodgkin lymphoma and primary mediastinal B cell lymphoma. Journal of Experimental Medicine, 2009, 206, 981-989.	4.2	448
93	Array-based DNA methylation profiling of primary lymphomas of the central nervous system. BMC Cancer, 2009, 9, 455.	1.1	30
94	Recurrent loss, but lack of mutations, of the SMARCB1 tumor suppressor gene in T-cell prolymphocytic leukemia with TCL1Aâ€“TCRAD juxtaposition. Cancer Genetics and Cytogenetics, 2009, 192, 44-47.	1.0	21
95	GeneChip analyses point to novel pathogenetic mechanisms in mantle cell lymphoma. British Journal of Haematology, 2009, 144, 317-331.	1.2	28
96	Biallelic inactivation of TRAF3 in a subset of B-cell lymphomas with interstitial del(14)(q24.1q32.33). Leukemia, 2009, 23, 2153-2155.	3.3	50
97	Hunting for the 5th base: Techniques for analyzing DNA methylation. Biochimica Et Biophysica Acta - General Subjects, 2009, 1790, 847-862.	1.1	62
98	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.	0.4	299
99	New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. Blood, 2009, 113, 2488-2497.	0.6	133
100	TNFAIP3(A20) is a tumor suppressor gene in Hodgkin lymphoma and primary mediastinal B cell lymphoma. Journal of Cell Biology, 2009, 185, i4-i4.	2.3	1
101	Epigenetic Signatures Associated with Different Levels of Differentiation Potential in Human Stem Cells. PLoS ONE, 2009, 4, e7809.	1.1	96
102	Clinical features of maternal uniparental disomy 14 in patients with an epimutation and a deletion of the imprintedDLK1/GTL2gene cluster. Human Mutation, 2008, 29, 1141-1146.	1.1	68
103	Microarrayâ€based DNA methylation analysis of imprinted loci in a patient with transient neonatal diabetes mellitus. American Journal of Medical Genetics, Part A, 2008, 146A, 3227-3229.	0.7	11
104	Identification of candidate tumour suppressor gene loci for Hodgkin and Reedâ€Sternberg cells by characterisation of homozygous deletions in classical Hodgkin lymphoma cell lines. British Journal of Haematology, 2008, 142, 916-924.	1.2	34
105	Characterization of homozygous deletions in laryngeal squamous cell carcinoma cell lines. Cancer Genetics and Cytogenetics, 2008, 184, 38-43.	1.0	15
106	BCL2 and BCL3 are recurrent translocation partners of the IGH locus. Cancer Genetics and Cytogenetics, 2008, 186, 110-114.	1.0	24
107	Epigenetic Inactivation of the Groucho Homologue Gene TLE1 in Hematologic Malignancies. Cancer Research, 2008, 68, 4116-4122.	0.4	50
108	Detection of genomic imbalances in microdissected Hodgkin and Reed-Sternberg cells of classical Hodgkin's lymphoma by array-based comparative genomic hybridization. Haematologica, 2008, 93, 1318-1326.	1.7	97

#	Article	IF	Citations
109	Recurrent loss of the Y chromosome and homozygous deletions within the pseudoautosomal region 1: association with male predominance in mantle cell lymphoma. Haematologica, 2008, 93, 949-950.	1.7	17
110	The pattern of genomic gains in salivary gland MALT lymphomas. Haematologica, 2007, 92, 921-927.	1.7	25
111	Pulmonary mucosa-associated lymphoid tissue lymphoma with strong nuclear B-cell CLL/lymphoma 10 (BCL10) expression and novel translocation t(1;2)(p22;p12)/immunoglobulin Â chain-BCL10. Journal of Clinical Pathology, 2007, 60, 727-728.	1.0	19
112	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.	0.6	188
113	Transcriptional Profiling of the Nuclear Factor-ÎºB Pathway Identifies a Subgroup of Primary Lymphoma of the Central Nervous System With Low BCL10 Expression. Journal of Neuropathology and Experimental Neurology, 2007, 66, 230-237.	0.9	44
114	Gains ofREL in primary mediastinal B-cell lymphoma coincide with nuclear accumulation of REL protein. Genes Chromosomes and Cancer, 2007, 46, 406-415.	1.5	77
115	PVRL2 is translocated to the TRA@ locus in t(14;19)(q11;q13)â€positive peripheral Tâ€cell lymphomas. Genes Chromosomes and Cancer, 2007, 46, 1011-1018.	1.5	28
116	High expression of several tyrosine kinases and activation of the PI3K/AKT pathway in mediastinal large B cell lymphoma reveals further similarities to Hodgkin lymphoma. Leukemia, 2007, 21, 780-787.	3.3	61
117	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.	3.3	85
118	Combined single nucleotide polymorphism-based genomic mapping and global gene expression profiling identifies novel chromosomal imbalances, mechanisms and candidate genes important in the pathogenesis of T-cell prolymphocytic leukemia with inv(14)(q11q32). Leukemia, 2007, 21, 2153-2163.	3.3	93
119	Trisomy 19 is associated with trisomy 12 and mutatedIGHVgenes in B-chronic lymphocytic leukaemia. British Journal of Haematology, 2007, 138, 217-220.	1.2	40
120	Combining arrayâ€based approaches for the identification of candidate tumor suppressor loci in mature lymphoid neoplasms. Apmis, 2007, 115, 1107-1134.	0.9	17
121	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
122	FISH Analysis for the Detection of Lymphoma-Associated Chromosomal Abnormalities in Routine Paraffin-Embedded Tissue. Journal of Molecular Diagnostics, 2006, 8, 141-151.	1.2	263
123	A Biologic Definition of Burkitt's Lymphoma from Transcriptional and Genomic Profiling. New England Journal of Medicine, 2006, 354, 2419-2430.	13.9	915
124	Chromosomal Breakpoints Affecting Immunoglobulin Loci Are Recurrent in Hodgkin and Reed-Sternberg Cells of Classical Hodgkin Lymphoma. Cancer Research, 2006, 66, 10332-10338.	0.4	85
125	Aberrant Expression of ID2, a Suppressor of B-Cell-Specific Gene Expression, in Hodgkin's Lymphoma. American Journal of Pathology, 2006, 169, 655-664.	1.9	72
126	BCL6 alternative breakpoint region break and homozygous deletion of 17q24 in the nodular lymphocyte predominance type of Hodgkin's lymphomaâ€"derived cell line DEV. Human Pathology, 2006, 37, 675-683.	1.1	29

#	Article	IF	Citations
127	Chromosomal rearrangements involving the BCL3 locus are recurrent in classical Hodgkin and peripheral T-cell lymphoma. Blood, 2006, 108, 401-403.	0.6	71
128	A chromosomal translocation in cyclin D1â€“negative/cyclin D2â€“positive mantle cell lymphoma fuses the CCND2 gene to the IGK locus. Blood, 2006, 108, 1109-1110.	0.6	86
129	Distinct comparative genomic hybridisation profiles in gastric mucosa-associated lymphoid tissue lymphomas with and without t(11;18)(q21;q21). British Journal of Haematology, 2006, 133, 35-42.	1.2	56
130	Partial uniparental disomy: a recurrent genetic mechanism alternative to chromosomal deletion in malignant lymphoma. Leukemia, 2006, 20, 904-905.	3.3	42
131	Gains of the proto-oncogene BCL11A and nuclear accumulation of BCL11AXL protein are frequent in primary mediastinal B-cell lymphoma. Leukemia, 2006, 20, 1880-1882.	3.3	60
132	Towards defining the lymphoma methylome. Leukemia, 2006, 20, 1658-1660.	3.3	8
133	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
134	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
135	Mantle-cell lymphoma genotypes identified with CGH to BAC microarrays define a leukemic subgroup of disease and predict patient outcome. Blood, 2005, 105, 4445-4454.	0.6	180
136	Disruption of the BCL11B gene through inv(14)(q11.2q32.31) results in the expression of BCL11B-TRDC fusion transcripts and is associated with the absence of wild-type BCL11B transcripts in T-ALL. Leukemia, 2005, 19, 201-208.	3.3	113
137	Expression pattern of intracellular leukocyte-associated proteins in primary mediastinal B cell lymphoma. Leukemia, 2005, 19, 856-861.	3.3	23
138	ALK-positive diffuse large B-cell lymphoma with ALK-Clathrin fusion belongs to the spectrum of pediatric lymphomas. Leukemia, 2005, 19, 1839-1840.	3.3	41
139	Amplification ofIGH/MYC fusion in clinically aggressiveIGH/BCL2-positive germinal center B-cell lymphomas. Genes Chromosomes and Cancer, 2005, 43, 414-423.	1.5	37
140	MALT lymphoma with t(14;18)(q32;q21)/IGH-MALT1 is characterized by strong cytoplasmic MALT1 and BCL10 expression. Journal of Pathology, 2005, 205, 293-301.	2.1	149
141	CD95 and TRAF2 promote invasiveness of pancreatic cancer cells. FASEB Journal, 2005, 19, 1-24.	0.2	74
142	Molecular Cytogenetic Analyses of Immunoglobulin Loci in Nodular Lymphocyte Predominant Hodgkin's Lymphoma Reveal a Recurrent IGH-BCL6 Juxtaposition. Journal of Molecular Diagnostics, 2005, 7, 352-356.	1.2	58
143	Molecular Cytogenetic Analysis of Chromosomal Breakpoints in the IGH, MYC, BCL6, and MALT1 Gene Loci in Primary Cutaneous B-cell Lymphomas. Journal of Investigative Dermatology, 2004, 123, 213-219.	0.3	105
144	Chromosomal abnormalities clustering in multiple myeloma reveals cytogenetic subgroups with nonrandom acquisition of chromosomal changes. Leukemia, 2004, 18, 654-657.	3.3	14

#	Article	IF	Citations
145	Centrosome abnormalities in ALK-positive anaplastic large-cell lymphoma. Leukemia, 2004, 18, 1910-1911.	3.3	21
146	Cytogenetic and molecular characterization of simultaneous chronic and acute myelocytic leukemia. Cancer Genetics and Cytogenetics, 2003, 142, 80-82.	1.0	3
147	Interphase cytogenetic characterization of aberrations in the long arm of chromosome 1 in B-cell lymphoid malignancies. Cancer Genetics and Cytogenetics, 2003, 144, 83-84.	1.0	5
148	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.	1.5	39
149	Hodgkin's lymphoma cell lines are characterized by frequent aberrations on chromosomes 2p and 9p includingRELandJAK2. International Journal of Cancer, 2003, 103, 489-495.	2.3	143
150	Molecular cytogenetic detection of chromosomal breakpoints in T-cell receptor gene loci. Leukemia, 2003, 17, 738-745.	3.3	66
151	Segmental chromosomal aberrations and centrosome amplifications: pathogenetic mechanisms in Hodgkin and Reedâ€“Sternberg cells of classical Hodgkin's lymphoma?. Leukemia, 2003, 17, 2214-2219.	3.3	49
152	Frequent occurrence of BCL6 rearrangements in nodular lymphocyte predominance Hodgkin lymphoma but not in classical Hodgkin lymphoma. Blood, 2003, 101, 706-710.	0.6	124
153	Variable frequencies of t(11;18)(q21;q21) in MALT lymphomas of different sites: significant association with CagA strains of H pylori in gastric MALT lymphoma. Blood, 2003, 102, 1012-1018.	0.6	321
154	ALK-positive diffuse large B-cell lymphoma is associated with Clathrin-ALK rearrangements: report of 6 cases. Blood, 2003, 102, 2568-2573.	0.6	281
155	Interphase cytogenetics of hematological neoplasms under the perspective of the novel WHO classification. Anticancer Research, 2003, 23, 1139-48.	0.5	33
156	Recurrent involvement of the REL and BCL11Aloci in classical Hodgkin lymphoma. Blood, 2002, 99, 1474-1477.	0.6	224
157	Interphase Cytogenetic Analysis of Lymphoma-Associated Chromosomal Breakpoints in Primary Diffuse Large B-Cell Lymphomas of the Central Nervous System. Journal of Neuropathology and Experimental Neurology, 2002, 61, 926-933.	0.9	70
158	Multicolor-FICTION. American Journal of Pathology, 2002, 161, 413-420.	1.9	81
159	Interphase FISH assays for the detection of translocations with breakpoints in immunoglobulin light chain loci. International Journal of Cancer, 2002, 98, 470-474.	2.3	84
160	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.	2.0	13
161	Detection of secondary genetic aberrations in follicle center cell derived lymphomas: assessment of the reliability of comparative genomic hybridization and standard chromosome analysis. Leukemia, 2001, 15, 177-183.	3.3	17
162	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

#	Article	IF	Citations
163	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
164	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