SÃ-lvia BeÃ

List of Publications by Year
in descending order

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149
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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.	1.7	18
2	Insights into the mechanisms underlying aberrant SOX11 oncogene expression in mantle cell lymphoma. Leukemia, 2022, 36, 583-587.	3.3	5
3	Balanced and unbalanced translocations in a multicentric series of 2843 patients with chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2022, 61, 37-43.	1.5	10
4	Clinicoâ€•biological features and outcome of patients with splenic marginal zone lymphoma with histological transformation. British Journal of Haematology, 2022, 196, 146-155.	1.2	17
5	Genetic and phenotypic attributes of splenic marginal zone lymphoma. Blood, 2022, 139, 732-747.	0.6	49
6	Ibrutinib in Combination With Rituximab for Indolent Clinical Forms of Mantle Cell Lymphoma (IMCL-2015): A Multicenter, Open-Label, Single-Arm, Phase II Trial. Journal of Clinical Oncology, 2022, 40, 1196-1205.	0.8	27
7	Genomic and transcriptomic profiling reveals distinct molecular subsets associated with outcomes in mantle cell lymphoma. Journal of Clinical Investigation, 2022, 132, .	3.9	30
8	PanCancer analysis of somatic mutations in repetitive regions reveals recurrent mutations in snRNA U2. Npj Genomic Medicine, 2022, 7, 19.	1.7	2
9	Serum soluble CD23 levels are an independent predictor of time to first treatment in chronic lymphocytic leukemia. Hematological Oncology, 2022, 40, 588-595.	0.8	0
10	Cell-Free DNA for Genomic Analysis in Primary Mediastinal Large B-Cell Lymphoma. Diagnostics, 2022, 12, 1575.	1.3	6
11	A Cyclin D1â€“Dependent Transcriptional Program Predicts Clinical Outcome in Mantle Cell Lymphoma. Clinical Cancer Research, 2021, 27, 213-225.	3.2	10
12	Mutational Landscape and Tumor Burden Assessed by Cell-free DNA in Diffuse Large B-Cell Lymphoma in a Population-Based Study. Clinical Cancer Research, 2021, 27, 513-521.	3.2	45
13	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. Nature Communications, 2021, 12, 651.	5.8	67
14	SOX11, CD70, and Treg cells configure the tumor immune microenvironment of aggressive mantle cell lymphoma. Blood, 2021, 138, 2202-2215.	0.6	22
15	SAMHD1 mutations in mantle cell lymphoma are recurrent and confer in vitro resistance to nucleoside analogues. Leukemia Research, 2021, 107, 106608.	0.4	6
16	<i>KMT2A-CBL</i>rearrangements in acute leukemias: clinical characteristics and genetic breakpoints. Blood Advances, 2021, 5, 5617-5620.	2.5	1
17	Molecular Pathogenesis of Mantle Cell Lymphoma. Hematology/Oncology Clinics of North America, 2020, 34, 795-807.	0.9	40
18	Cryptic insertions of the immunoglobulin light chain enhancer region near <i>CCND1</i> in t(11;14)-negative mantle cell lymphoma. Haematologica, 2020, 105, e408-e411.	1.7	13

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19	Monomorphic Epitheliotropic Intestinal T-Cell Lymphoma in Asia Frequently Shows SETD2 Alterations. Cancers, 2020, 12, 3539.	1.7	22
20	The proliferative history shapes the DNA methylome of B-cell tumors and predicts clinical outcome. Nature Cancer, 2020, 1, 1066-1081.	5.7	51
21	PI3KÎ´ inhibition reshapes follicular lymphomaâ€“immune microenvironment cross talk and unleashes the activity of venetoclax. Blood Advances, 2020, 4, 4217-4231.	2.5	23
22	FMOD expression in whole blood aids in distinguishing between chronic lymphocytic leukemia and other leukemic lymphoproliferative disorders. A pilot study. Cytometry Part B - Clinical Cytometry, 2020, 98, 421-428.	0.7	9
23	Chronic lymphocytic leukaemia and prolymphocytic leukaemia. Two coins or two sides of the same coin?. Haematologica, 2020, 105, e484.	1.7	2
24	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. Nature Communications, 2020, 11, 3390.	5.8	24
25	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. Blood, 2020, 136, 1419-1432.	0.6	131
26	Reproducibility of histologic prognostic parameters for mantle cell lymphoma: cytology, Ki67, p53 and SOX11. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2020, 477, 259-267.	1.4	15
27	Minimal spatial heterogeneity in chronic lymphocytic leukemia at diagnosis. Leukemia, 2020, 34, 1929-1933.	3.3	2
28	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. Nature Communications, 2019, 10, 3615.	5.8	32
29	MULTI-OMICS LANDSCAPE OF SPLENIC MARGINAL ZONE LYMPHOMA (SMZL) - INTERIM ANALYSIS OF IELSG46 STUDY. Hematological Oncology, 2019, 37, 181-182.	0.8	0
30	Notch1 signaling in NOTCH1-mutated mantle cell lymphoma depends on Delta-Like ligand 4 and is a potential target for specific antibody therapy. Journal of Experimental and Clinical Cancer Research, 2019, 38, 446.	3.5	28
31	Increased tumour angiogenesis in SOX11â€positive mantle cell lymphoma. Histopathology, 2019, 75, 704-714.	1.6	16
32	CCND2 and CCND3 hijack immunoglobulin light-chain enhancers in cyclin D1âˆ’ mantle cell lymphoma. Blood, 2019, 133, 940-951.	0.6	77
33	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
34	Splenic Marginal Zone Lymphoma: Risk of Transformation, Clinico-Biological Features at Transformation and Prognosis. Blood, 2019, 134, 4015-4015.	0.6	0
35	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.	0.6	1
36	Igcaller: Reconstructing the Rearranged Immunoglobulin Gene in Lymphoid Neoplasms from Whole-Genome Sequencing Data. Blood, 2019, 134, 3023-3023.	0.6	0

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37	The U1 Spliceosomal RNA: A Novel Non-Coding Hotspot Driver Mutation Independently Associated with Clinical Outcome in Chronic Lymphocytic Leukemia. Blood, 2019, 134, 847-847.	0.6	0
38	Mutational Landscape, Copy Number Alterations and Tumor Burden Assessed By Cell-Free DNA in Diffuse Large B-Cell Lymphoma. Blood, 2019, 134, 4110-4110.	0.6	0
39	Clinicopathological and genomic analysis of double-hit follicular lymphoma: comparison with high-grade B-cell lymphoma with MYC and BCL2 and/or BCL6 rearrangements. Modern Pathology, 2018, 31, 313-326.	2.9	42
40	Clinical impact of the subclonal architecture and mutational complexity in chronic lymphocytic leukemia. Leukemia, 2018, 32, 645-653.	3.3	91
41	The mutational landscape of small lymphocytic lymphoma compared to non-early stage chronic lymphocytic leukemia. Leukemia and Lymphoma, 2018, 59, 2318-2326.	0.6	5
42	A gene signature that distinguishes conventional and leukemic nonnodal mantle cell lymphoma helps predict outcome. Blood, 2018, 132, 413-422.	0.6	89
43	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157
44	Cyclin D1 overexpression induces global transcriptional downregulation in lymphoid neoplasms. Journal of Clinical Investigation, 2018, 128, 4132-4147.	3.9	31
45	Molecular Subtypes of Splenic Marginal Zone Lymphoma (SMZL) Are Associated with Distinct Pathogenic Mechanisms and Outcomes - Interim Analysis of the IELSG46 Study. Blood, 2018, 132, 922-922.	0.6	2
46	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
47	Role of SOX11 and Genetic Events Cooperating with Cyclin D1 in Mantle Cell Lymphoma. Current Oncology Reports, 2017, 19, 43.	1.8	23
48	Improved classification of leukemic B-cell lymphoproliferative disorders using a transcriptional and genetic classifier. Haematologica, 2017, 102, e360-e363.	1.7	27
49	Genetic landscape and deregulated pathways in Bâ€cell lymphoid malignancies. Journal of Internal Medicine, 2017, 282, 371-394.	2.7	59
50	The Bruton tyrosine kinase inhibitor CC-292 shows activity in mantle cell lymphoma and synergizes with lenalidomide and NIK inhibitors depending on nuclear factor-ÎºB mutational status. Haematologica, 2017, 102, e447-e451.	1.7	18
51	Clinicopathological characteristics and genomic profile of primary sinonasal tract diffuse large B cell lymphoma (<scp>DLBCL</scp>) reveals gain at 1q31 and <scp>RGS</scp>1 encoding protein; high <scp>RGS</scp>1 immunohistochemical expression associates with poor overall survival in <scp>DLBCL</scp> not otherwise specified (<scp>NOS</scp>). Histopathology, 2017, 70, 595-621.	1.6	41
52	Genomic and immunohistochemical profiles of enteropathy-associated T-cell lymphoma in Japan. Pathology, 2016, 48, S159-S160.	0.3	0
53	Clinical impact of clonal and subclonal TP53, SF3B1, BIRC3, NOTCH1, and ATM mutations in chronic lymphocytic leukemia. Blood, 2016, 127, 2122-2130.	0.6	260
54	Genetic Predisposition to Chronic Lymphocytic Leukemia Is Mediated by a BMF Super-Enhancer Polymorphism. Cell Reports, 2016, 16, 2061-2067.	2.9	58

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55	Pathogenic role of B-cell receptor signaling and canonical NF-ÎºB activation in mantle cell lymphoma. Blood, 2016, 128, 82-92.	0.6	141
56	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
57	NOTCH1, TP53, and MAP2K1 Mutations in Splenic Diffuse Red Pulp Small B-cell Lymphoma Are Associated With Progressive Disease. American Journal of Surgical Pathology, 2016, 40, 192-201.	2.1	40
58	Clinical Impact of the Quantitative Subclonal Architecture in Chronic Lymphocytic Leukemia. Blood, 2016, 128, 2024-2024.	0.6	0
59	Aberrant Expression of the SOX11 Oncogene in Mantle Cell Lymphoma Is Associated with Activation and De Novo 3D Looping of a Distant Enhancer Element. Blood, 2016, 128, 459-459.	0.6	0
60	Detection of chromothripsisâ€like patterns with a custom array platform for chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2015, 54, 668-680.	1.5	23
61	Is <scp>TCL</scp>1 overexpression a good or a bad player in mantle cell lymphoma?. European Journal of Haematology, 2015, 95, 487-488.	1.1	1
62	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2015, 526, 519-524.	13.7	749
63	Genomic and immunohistochemical profiles of enteropathy-associated T-cell lymphoma in Japan. Modern Pathology, 2015, 28, 1286-1296.	2.9	58
64	Plasma cell and terminal B-cell differentiation in mantle cell lymphoma mainly occur in the SOX11-negative subtype. Modern Pathology, 2015, 28, 1435-1447.	2.9	35
65	A B-cell epigenetic signature defines three biologic subgroups of chronic lymphocytic leukemia with clinical impact. Leukemia, 2015, 29, 598-605.	3.3	129
66	Clinical Impact of Clonal and Subclonal TP53, SF3B1, BIRC3, and ATM Mutations in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 4138-4138.	0.6	1
67	Checkâ€™-ing DLBCL. Oncoscience, 2015, 2, 71-72.	0.9	1
68	Gene Expression Profiling Signatures Allow the Identification of Unclassifiable Leukemic B-Cell Lymphoid Neoplasms. Blood, 2015, 126, 3902-3902.	0.6	0
69	The prognostic impact of minimal residual disease in patients with chronic lymphocytic leukemia requiring first-line therapy. Haematologica, 2014, 99, 873-880.	1.7	32
70	Assessment of SOX11 Expression in Routine Lymphoma Tissue Sections. American Journal of Surgical Pathology, 2014, 38, 86-93.	2.1	58
71	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. Nature Biotechnology, 2014, 32, 1106-1112.	9.4	74
72	Genomic complexity and IGHV mutational status are key predictors of outcome of chronic lymphocytic leukemia patients with TP53 disruption. Haematologica, 2014, 99, e231-e234.	1.7	33

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73	Cyclin D1 transcriptional activation in MCL. Blood, 2014, 123, 1979-1980.	0.6	5
74	Synergistic anti-tumor activity of acadesine (AICAR) in combination with the anti-CD20 monoclonal antibody rituximab in <i>in vivo</i> and <i>in vitro</i> models of mantle cell lymphoma. Oncotarget, 2014, 5, 726-739.	0.8	25
75	Dual PI3K/mTOR inhibition is required to effectively impair microenvironment survival signals in mantle cell lymphoma. Oncotarget, 2014, 5, 6788-6800.	0.8	32
76	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.	0.6	4
77	Whole-Genome DNA Methylation Analysis of Mantle Cell Lymphoma: Biological and Clinical Implications. Blood, 2014, 124, 3563-3563.	0.6	0
78	PRDM1/BLIMP1 is commonly inactivated in anaplastic large T-cell lymphoma. Blood, 2013, 122, 2683-2693.	0.6	98
79	Update on the molecular pathogenesis and clinical treatment of mantle cell lymphoma: report of the 11th annual conference of the European Mantle Cell Lymphoma Network. Leukemia and Lymphoma, 2013, 54, 699-707.	0.6	37
80	microRNA Expression Profiles Identify Subtypes of Mantle Cell Lymphoma with Different Clinicobiological Characteristics. Clinical Cancer Research, 2013, 19, 3121-3129.	3.2	35
81	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	9.4	179
82	NOTCH1 mutations identify a genetic subgroup of chronic lymphocytic leukemia patients with high risk of transformation and poor outcome. Leukemia, 2013, 27, 1100-1106.	3.3	167
83	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
84	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
85	Sporadic and reversible chromothripsis in chronic lymphocytic leukemia revealed by longitudinal genomic analysis. Leukemia, 2013, 27, 2376-2379.	3.3	29
86	SOX11 regulates PAX5 expression and blocks terminal B-cell differentiation in aggressive mantle cell lymphoma. Blood, 2013, 121, 2175-2185.	0.6	129
87	CCND2 rearrangements are the most frequent genetic events in cyclin D1âˆ’ mantle cell lymphoma. Blood, 2013, 121, 1394-1402.	0.6	183
88	Molecular Subsets of Mantle Cell Lymphoma Defined by the <i>IGHV</i> Mutational Status and SOX11 Expression Have Distinct Biologic and Clinical Features. Cancer Research, 2012, 72, 5307-5316.	0.4	231
89	Increased tumor cell proliferation in mantle cell lymphoma is associated with elevated insulin-like growth factor 2 mRNA-binding protein 3 expression. Modern Pathology, 2012, 25, 1227-1235.	2.9	21
90	SNP-based mapping arrays reveal high genomic complexity in monoclonal gammopathies, from MGUS to myeloma status. Leukemia, 2012, 26, 2521-2529.	3.3	100

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91	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	9.4	525
92	Non-nodal type of mantle cell lymphoma is a specific biological and clinical subgroup of the disease. Leukemia, 2012, 26, 1895-1898.	3.3	141
93	Estimation of Copy Number Alterations from Exome Sequencing Data. PLoS ONE, 2012, 7, e51422.	1.1	18
94	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 47-52.	9.4	893
95	Detailed Molecular Analysis of Patients with Chronic Lymphocytic Leukemia Carrying 17p Deletions Reveals Concurrent Abnormalities with Prognostic Impact. Blood, 2012, 120, 4577-4577.	0.6	0
96	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	13.7	1,364
97	Identification of Methylated Genes Associated with Aggressive Clinicopathological Features in Mantle Cell Lymphoma. PLoS ONE, 2011, 6, e19736.	1.1	32
98	Epigenetic Activation of SOX11 in Lymphoid Neoplasms by Histone Modifications. PLoS ONE, 2011, 6, e21382.	1.1	38
99	The complex landscape of genetic alterations in mantle cell lymphoma. Seminars in Cancer Biology, 2011, 21, 322-334.	4.3	100
100	Update on the molecular pathogenesis and clinical treatment of mantle cell lymphoma: report of the 10th annual conference of the European Mantle Cell Lymphoma Network. Leukemia and Lymphoma, 2011, 52, 2226-2236.	0.6	29
101	BLIMP1 Is Commonly Inactivated In Anaplastic Large T-Cell Lymphomas (ALCL). Blood, 2011, 118, 2634-2634.	0.6	0
102	Pathway discovery in mantle cell lymphoma by integrated analysis of high-resolution gene expression and copy number profiling. Blood, 2010, 116, 953-961.	0.6	122
103	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
104	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
105	Amplifications and target genes in diffuse large B-cell lymphoma: real targets or consequences of structural features of the genome?. Leukemia and Lymphoma, 2010, 51, 743-744.	0.6	2
106	Update on the molecular pathogenesis and clinical treatment of Mantle Cell Lymphoma (MCL): minutes of the 9th European MCL Network conference. Leukemia and Lymphoma, 2010, 51, 1612-1622.	0.6	21
107	Genomic and Gene Expression Profiling Defines Indolent Forms of Mantle Cell Lymphoma. Cancer Research, 2010, 70, 1408-1418.	0.4	429
108	MicroRNA Expression, Chromosomal Alterations, and Immunoglobulin Variable Heavy Chain Hypermutations in Mantle Cell Lymphomas. Cancer Research, 2009, 69, 7071-7078.	0.4	78

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109	Follicular lymphomas with and without translocation t(14;18) differ in gene expression profiles and genetic alterations. Blood, 2009, 114, 826-834.	0.6	177
110	Uniparental disomies, homozygous deletions, amplifications, and target genes in mantle cell lymphoma revealed by integrative high-resolution whole-genome profiling. Blood, 2009, 113, 3059-3069.	0.6	162
111	Multiple recurrent chromosomal breakpoints in mantle cell lymphoma revealed by a combination of molecular cytogenetic techniques. Genes Chromosomes and Cancer, 2008, 47, 1086-1097.	1.5	28
112	Genomic profiling reveals different genetic aberrations in systemic ALKâ€positive and ALKâ€negative anaplastic large cell lymphomas. British Journal of Haematology, 2008, 140, 516-526.	1.2	145
113	Integrated genomic and expression profiling in mantle cell lymphoma: identification of geneâ€dosage regulated candidate genes. British Journal of Haematology, 2008, 143, 210-221.	1.2	27
114	Chromosomal alterations detected by comparative genomic hybridization in subgroups of gene expression-defined Burkitt's lymphoma. Haematologica, 2008, 93, 1327-1334.	1.7	80
115	Gene expression profile and genomic changes in disease progression of early-stage chronic lymphocytic leukemia. Haematologica, 2008, 93, 132-136.	1.7	17
116	Secondary genomic alterations in non-Hodgkin's lymphomas: tumor-specific profiles with impact on clinical behavior. Haematologica, 2008, 93, 641-645.	1.7	16
117	Specific Secondary Genetic Alterations in Mantle Cell Lymphoma Provide Prognostic Information Independent of the Gene Expressionâ€“Based Proliferation Signature. Journal of Clinical Oncology, 2007, 25, 1216-1222.	0.8	166
118	Inactivation of RB1 in mantle-cell lymphoma detected by nonsense-mediated mRNA decay pathway inhibition and microarray analysis. Blood, 2007, 109, 5422-5429.	0.6	76
119	Leukemic involvement is a common feature in mantle cell lymphoma. Cancer, 2007, 109, 2473-2480.	2.0	82
120	Follicular Lymphomas with and without Translocation t(14;18) Differ in Gene Expression Profiles and Genetic Alterations.. Blood, 2007, 110, 360-360.	0.6	7
121	SNP Array Analysis Reveals Copy Number Alterations and Uniparental Disomy in Mantle Cell Lymphomas at High Resolution.. Blood, 2007, 110, 1585-1585.	0.6	0
122	Genomic imbalances and patterns of karyotypic variability in mantle-cell lymphoma cell lines. Leukemia Research, 2006, 30, 923-934.	0.4	45
123	Analysis ofAurora-A andhMPS1 mitotic kinases in mantle cell lymphoma. International Journal of Cancer, 2006, 118, 357-363.	2.3	28
124	Unbalanced expression of licensing DNA replication factors occurs in a subset of mantle cell lymphomas with genomic instability. International Journal of Cancer, 2006, 119, 2768-2774.	2.3	32
125	Integrated CGH- and Epression Array Profiling of Mantle Cell Lymphoma.. Blood, 2006, 108, 2252-2252.	0.6	0
126	Loss of major histocompatibility class II expression in non-immune-privileged site diffuse large B-cell lymphoma is highly coordinated and not due to chromosomal deletions. Blood, 2005, 107, 1101-1107.	0.6	68

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127	Checkpoint kinase 1 (CHK1) protein and mRNA expression is downregulated in aggressive variants of human lymphoid neoplasms. Leukemia, 2005, 19, 112-117.	3.3	42
128	CDK4 and MDM2 Gene Alterations Mainly Occur in Highly Proliferative and Aggressive Mantle Cell Lymphomas with Wild-type INK4a/ARF Locus. Cancer Research, 2005, 65, 2199-2206.	0.4	93
129	Diffuse Large B-Cell Lymphoma: Clinical and Biological Characterization and Outcome According to the Nodal or Extranodal Primary Origin. Journal of Clinical Oncology, 2005, 23, 2797-2804.	0.8	253
130	Diffuse large B-cell lymphoma subgroups have distinct genetic profiles that influence tumor biology and improve gene-expression-based survival prediction. Blood, 2005, 106, 3183-3190.	0.6	348
131	Clinicopathologic Significance and Prognostic Value of Chromosomal Imbalances in Diffuse Large B-Cell Lymphomas. Journal of Clinical Oncology, 2004, 22, 3498-3506.	0.8	87
132	Chromosomal Imbalances in Germinal Center B-Cell-Like and Activated B-Cell-Like Diffuse Large B-Cell Lymphoma Influence Gene Expression Signatures and Improve Gene Expression-Based Survival Prediction(the First Two Authors Contributed Equally to This Work).. Blood, 2004, 104, 415-415.	0.6	1
133	Frequent polymorphic changes but not mutations of TRAIL receptors DR4 and DR5 in mantle cell lymphoma and other B-cell lymphoid neoplasms. Haematologica, 2004, 89, 1322-31.	1.7	19
134	Multiple cell cycle regulator alterations in Richter's transformation of chronic lymphocytic leukemia. Leukemia, 2002, 16, 1028-1034.	3.3	34
135	ATM gene inactivation in mantle cell lymphoma mainly occurs by truncating mutations and missense mutations involving the phosphatidylinositol-3 kinase domain and is associated with increasing numbers of chromosomal imbalances. Blood, 2002, 99, 238-244.	0.6	151
136	CHK2-decreased protein expression and infrequent genetic alterations mainly occur in aggressive types of non-Hodgkin lymphomas. Blood, 2002, 100, 4602-4608.	0.6	67
137	Diversity of Genomic Breakpoints in TFG-ALK Translocations in Anaplastic Large Cell Lymphomas. American Journal of Pathology, 2002, 160, 1487-1494.	1.9	102
138	Genetic Imbalances in Progressed B-Cell Chronic Lymphocytic Leukemia and Transformed Large-Cell Lymphoma (Richter's Syndrome). American Journal of Pathology, 2002, 161, 957-968.	1.9	86
139	Differential Expression of cdc25 Cell-Cycleâ€“Activating Phosphatases in Human Colorectal Carcinoma. Laboratory Investigation, 2001, 81, 465-473.	1.7	74
140	BMI-1 gene amplification and overexpression in hematological malignancies occur mainly in mantle cell lymphomas. Cancer Research, 2001, 61, 2409-12.	0.4	221
141	cdc25a and the splicing variant cdc25b2, but not cdc25B1, -B3 or -C, are over-expressed in aggressive human non-Hodgkin's lymphomas. , 2000, 89, 148-152.		56
142	INK4a/ARFLocus Alterations in Human Non-Hodgkin's Lymphomas Mainly Occur in Tumors with Wild-Type p53 Gene. American Journal of Pathology, 2000, 156, 1987-1996.	1.9	83
143	c-myc mRNA expression and genomic alterations in mantle cell lymphomas and other nodal non-Hodgkinâ€™s lymphomas. Leukemia, 1999, 13, 2087-2093.	3.3	44
144	Disregulation of p16MTS1/CDK4I protein and mRNA expression is associated with gene alterations in squamous-cell carcinoma of the larynx. , 1999, 81, 705-711.		19

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145	Increased number of chromosomal imbalances and high-level DNA amplifications in mantle cell lymphoma are associated with blastoid variants. Blood, 1999, 93, 4365-74.	0.6	218
146	TRK-fused gene (TFG) is a new partner of ALK in anaplastic large cell lymphoma producing two structurally different TFG-ALK translocations. Blood, 1999, 94, 3265-8.	0.6	127
147	p16INK4a Gene Inactivation by Deletions, Mutations, and Hypermethylation Is Associated With Transformed and Aggressive Variants of Non-Hodgkin's Lymphomas. Blood, 1998, 91, 2977-2984.	0.6	266
148	p16(INK4a) gene inactivation by deletions, mutations, and hypermethylation is associated with transformed and aggressive variants of non-Hodgkin's lymphomas. Blood, 1998, 91, 2977-84.	0.6	64
149	cdc25 cell cycle-activating phosphatases and c-myc expression in human non-Hodgkin's lymphomas. Cancer Research, 1998, 58, 1762-7.	0.4	54