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List of Publications by Year in descending order

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Version: 2024-02-01

76 papers	8,325 citations	134610 34 h-index	111975 67 g-index
77 all docs	77 docs citations	77 times ranked	11035 citing authors

#	Article	IF	Citations
1	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
2	CD5-negative mantle cell lymphoma: clinicopathologic features of an indolent variant that confers a survival advantage. Leukemia and Lymphoma, 2022, 63, 911-917.	0.6	2
3	Higher-order connections between stereotyped subsets: implications for improved patient classification in CLL. Blood, 2021, 137, 1365-1376.	0.6	72
4	A Cyclin D1â€“Dependent Transcriptional Program Predicts Clinical Outcome in Mantle Cell Lymphoma. Clinical Cancer Research, 2021, 27, 213-225.	3.2	10
5	IGLV3-21R110 identifies an aggressive biological subtype of chronic lymphocytic leukemia with intermediate epigenetics. Blood, 2021, 137, 2935-2946.	0.6	49
6	SOX11, CD70, and Treg cells configure the tumor immune microenvironment of aggressive mantle cell lymphoma. Blood, 2021, 138, 2202-2215.	0.6	22
7	Molecular Pathogenesis of Mantle Cell Lymphoma. Hematology/Oncology Clinics of North America, 2020, 34, 795-807.	0.9	40
8	Cryptic insertions of the immunoglobulin light chain enhancer region near CCND1 in t(11;14)-negative mantle cell lymphoma. Haematologica, 2020, 105, e408-e411.	1.7	13
9	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. Nature Communications, 2020, 11, 3390.	5.8	24
10	Genomic and epigenomic insights into the origin, pathogenesis, and clinical behavior of mantle cell lymphoma subtypes. Blood, 2020, 136, 1419-1432.	0.6	131
11	Increased tumour angiogenesis in SOX11â€positive mantle cell lymphoma. Histopathology, 2019, 75, 704-714.	1.6	16
12	CCND2 and CCND3 hijack immunoglobulin light-chain enhancers in cyclin D1â^' mantle cell lymphoma. Blood, 2019, 133, 940-951.	0.6	77
13	Tailored approaches grounded on immunogenetic features for refined prognostication in chronic lymphocytic leukemia. Haematologica, 2019, 104, 360-369.	1.7	42
14	Analysis of criteria for treatment initiation in patients with progressive chronic lymphocytic leukemia. Blood Cancer Journal, 2018, 8, 10.	2.8	6
15	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
16	A gene signature that distinguishes conventional and leukemic nonnodal mantle cell lymphoma helps predict outcome. Blood, 2018, 132, 413-422.	0.6	89
17	Numerous Ontogenetic Roads to Mantle Cell Lymphoma. American Journal of Pathology, 2017, 187, 1454-1458.	1.9	11
18	Improved classification of leukemic B-cell lymphoproliferative disorders using a transcriptional and genetic classifier. Haematologica, 2017, 102, e360-e363.	1.7	27

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19	Mutations of MAP2K1 are frequent in pediatric-type follicular lymphoma and result in ERK pathway activation. Blood, 2017, 130, 323-327.	0.6	69
20	Chronic Lymphocytic Leukemia with Mutated IGHV4-34 Receptors: Shared and Distinct Immunogenetic Features and Clinical Outcomes. Clinical Cancer Research, 2017, 23, 5292-5301.	3.2	27
21	The Bruton tyrosine kinase inhibitor CC-292 shows activity in mantle cell lymphoma and synergizes with lenalidomide and NIK inhibitors depending on nuclear factor-Î¹B mutational status. Haematologica, 2017, 102, e447-e451.	1.7	18
22	Different spectra of recurrent gene mutations in subsets of chronic lymphocytic leukemia harboring stereotyped B-cell receptors. Haematologica, 2016, 101, 959-967.	1.7	57
23	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
24	Pathogenic role of B-cell receptor signaling and canonical NF-Î¹B activation in mantle cell lymphoma. Blood, 2016, 128, 82-92.	0.6	141
25	Clinical impact of MYD88 mutations in chronic lymphocytic leukemia. Blood, 2016, 127, 1611-1613.	0.6	8
26	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
27	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
28	Reappraising Immunoglobulin Repertoire Restrictions in Chronic Lymphocytic Leukemia: Focus on Major Stereotyped Subsets and Closely Related Satellites. Blood, 2016, 128, 4376-4376.	0.6	1
29	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
30	Mutations in CHD2 cause defective association with active chromatin in chronic lymphocytic leukemia. Blood, 2015, 126, 195-202.	0.6	50
31	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2015, 526, 519-524.	13.7	749
32	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
33	A B-cell epigenetic signature defines three biologic subgroups of chronic lymphocytic leukemia with clinical impact. Leukemia, 2015, 29, 598-605.	3.3	129
34	Recurrent mutations refine prognosis in chronic lymphocytic leukemia. Leukemia, 2015, 29, 329-336.	3.3	253
35	CLL with Mutated IGHV4-34 Antigen Receptors Is Clinically Heterogeneous: Antigen Receptor Stereotypy Makes the Difference. Blood, 2015, 126, 5263-5263.	0.6	0
36	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

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37	Initial Clinico-Biological Characteristics and Follow-up Data of Elderly Patients With Chronic Lymphocytic Leukemia (CLL): A Retrospective Analysis of a Series of 364 Cases. Clinical Lymphoma, Myeloma and Leukemia, 2014, 14, S129-S130.	0.2	0
38	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. Nature Biotechnology, 2014, 32, 1106-1112.	9.4	74
39	Recurrent mutations ofNOTCHgenes in follicular lymphoma identify a distinctive subset of tumours. Journal of Pathology, 2014, 234, 423-430.	2.1	59
40	Mutations in TLR/MYD88 pathway identify a subset of young chronic lymphocytic leukemia patients with favorable outcome. Blood, 2014, 123, 3790-3796.	0.6	97
41	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
42	Chronic lymphocytic leukemia in the elderly: clinico-biological features, outcomes, and proposal of a prognostic model. Haematologica, 2014, 99, 1599-1604.	1.7	56
43	Subset-Specific Spectra of Recurrent Gene Mutations in Chronic Lymphocytic Leukemia with Stereotyped B-Cell Receptors. Blood, 2014, 124, 3320-3320.	0.6	6
44	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
45	Whole-Genome DNA Methylation Analysis of Mantle Cell Lymphoma: Biological and Clinical Implications. Blood, 2014, 124, 3563-3563.	0.6	0
46	Clonal evolution in chronic lymphocytic leukemia: Analysis of correlations with IGHV mutational status, NOTCH1 mutations and clinical significance. Genes Chromosomes and Cancer, 2013, 52, 920-927.	1.5	15
47	Sorafenib Inhibits Cell Migration and Stroma-Mediated Bortezomib Resistance by Interfering B-cell Receptor Signaling and Protein Translation in Mantle Cell Lymphoma. Clinical Cancer Research, 2013, 19, 586-597.	3.2	24
48	microRNA Expression Profiles Identify Subtypes of Mantle Cell Lymphoma with Different Clinicobiological Characteristics. Clinical Cancer Research, 2013, 19, 3121-3129.	3.2	35
49	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
50	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
51	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
52	Sporadic and reversible chromothripsis in chronic lymphocytic leukemia revealed by longitudinal genomic analysis. Leukemia, 2013, 27, 2376-2379.	3.3	29
53	SOX11 regulates PAX5 expression and blocks terminal B-cell differentiation in aggressive mantle cell lymphoma. Blood, 2013, 121, 2175-2185.	0.6	129
54	CCND2 rearrangements are the most frequent genetic events in cyclin D1â˜ mantle cell lymphoma. Blood, 2013, 121, 1394-1402.	0.6	183

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55	Differential Distribution Of Recurrent Gene Mutations In Subsets Of Chronic Lymphocytic Leukemia Patients With Stereotyped B-Cell Receptors: Results From A Multicenter Project Of The European Research Initiative On CLL In A Series Of 2482 Cases. Blood, 2013, 122, 4113-4113.	0.6	1
56	Novel Gene Mutations In Chronic Lymphocytic Leukemia: Prevalence and Clinical Implications In A Series Of 3185 Cases - Initial Results From The European Research Initiative On CLL. Blood, 2013, 122, 1614-1614.	0.6	0
57	Clinical Monoclonal B Lymphocytosis (cMBL), Chronic Lymphocytic Leukemia (CLL) and Small Lymphocytic Lymphoma (SLL): Diagnostic Criteria, Features At Diagnosis and Natural History. Blood, 2013, 122, 5273-5273.	0.6	0
58	Initial Characteristics, Treatment and Prognosis Of Elderly (â‰¥ 70 years) Patients With Chronic Lymphocytic Leukemia (CLL): An Analysis Of a Series Of 367 Cases. Blood, 2013, 122, 4155-4155.	0.6	0
59	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.	0.4	231
60	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
61	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	9.4	525
62	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
63	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 47-52.	9.4	893
64	Different distribution of NOTCH1 mutations in chronic lymphocytic leukemia with isolated trisomy 12 or associated with other chromosomal alterations. Genes Chromosomes and Cancer, 2012, 51, 881-889.	1.5	57
65	NOTCH1 mutations in chronic lymphocytic leukemia with trisomy 12. Genes Chromosomes and Cancer, 2012, 51, 1064-1065.	1.5	0
66	A new genetic abnormality leading to TP53 gene deletion in chronic lymphocytic leukaemia. British Journal of Haematology, 2012, 156, 612-618.	1.2	7
67	High Expression of Activation-Induced Cytidine Deaminase and in Vivo Class Switch Recombination in Mantle Cell Lymphoma: Further Support for Antigen Involvement in Lymphomagenesis. Blood, 2012, 120, 1538-1538.	0.6	0
68	The Multi-Kinase Inhibitor Sorafenib Blocks Migration, BCR Survival Signals, Protein Translation and Stroma-Mediated Bortezomib Resistance in Mantle Cell Lymphoma. Blood, 2012, 120, 1647-1647.	0.6	5
69	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
70	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	13.7	1,364
71	Molecular Pathogenesis of Mantle Cell Lymphoma: New Perspectives and Challenges With Clinical Implications. Seminars in Hematology, 2011, 48, 155-165.	1.8	16
72	Identification of Methylated Genes Associated with Aggressive Clinicopathological Features in Mantle Cell Lymphoma. PLoS ONE, 2011, 6, e19736.	1.1	32

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73	Genomic and Gene Expression Profiling Defines Indolent Forms of Mantle Cell Lymphoma. Cancer Research, 2010, 70, 1408-1418.	0.4	429
74	MicroRNA Expression, Chromosomal Alterations, and Immunoglobulin Variable Heavy Chain Hypermutations in Mantle Cell Lymphomas. Cancer Research, 2009, 69, 7071-7078.	0.4	78
75	EML4-ALK Rearrangement in Non-Small Cell Lung Cancer and Non-Tumor Lung Tissues. American Journal of Pathology, 2009, 174, 661-670.	1.9	301
76	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