

Richard Rosenquist

List of Publications by Year in descending order

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234
papers

11,000
citations

28190
55
h-index

37111
96
g-index

235
all docs

235
docs citations

235
times ranked

11786
citing authors

#	ARTICLE	IF	CITATIONS
1	SF3B1 mutation identifies a distinct subset of myelodysplastic syndrome with ring sideroblasts. <i>Blood</i> , 2015, 126, 233-241.	0.6	361
2	Stereotyped B-cell receptors in one-third of chronic lymphocytic leukemia: a molecular classification with implications for targeted therapies. <i>Blood</i> , 2012, 119, 4467-4475.	0.6	350
3	Downregulation of Death-Associated Protein Kinase 1 (DAPK1) in Chronic Lymphocytic Leukemia. <i>Cell</i> , 2007, 129, 879-890.	13.5	338
4	Somatically mutated Ig VH3-21 genes characterize a new subset of chronic lymphocytic leukemia. <i>Blood</i> , 2002, 99, 2262-2264.	0.6	289
5	Stereotyped patterns of somatic hypermutation in subsets of patients with chronic lymphocytic leukemia: implications for the role of antigen selection in leukemogenesis. <i>Blood</i> , 2008, 111, 1524-1533.	0.6	285
6	Chronic lymphocytic leukemias utilizing the VH3-21 gene display highly restricted V λ 2-14 gene use and homologous CDR3s: implicating recognition of a common antigen epitope. <i>Blood</i> , 2003, 101, 4952-4957.	0.6	280
7	Recurrent mutations refine prognosis in chronic lymphocytic leukemia. <i>Leukemia</i> , 2015, 29, 329-336.	3.3	253
8	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003212.	1.5	244
9	Subsets with restricted immunoglobulin gene rearrangement features indicate a role for antigen selection in the development of chronic lymphocytic leukemia. <i>Blood</i> , 2004, 104, 2879-2885.	0.6	241
10	A new perspective: molecular motifs on oxidized LDL, apoptotic cells, and bacteria are targets for chronic lymphocytic leukemia antibodies. <i>Blood</i> , 2008, 111, 3838-3848.	0.6	236
11	Common variants at 2q37.3, 8q24.21, 15q21.3 and 16q24.1 influence chronic lymphocytic leukemia risk. <i>Nature Genetics</i> , 2010, 42, 132-136.	9.4	223
12	ERIC recommendations on IGHV gene mutational status analysis in chronic lymphocytic leukemia. <i>Leukemia</i> , 2007, 21, 1-3.	3.3	219
13	Two main genetic pathways lead to the transformation of chronic lymphocytic leukemia to Richter syndrome. <i>Blood</i> , 2013, 122, 2673-2682.	0.6	208
14	Strikingly homologous immunoglobulin gene rearrangements and poor outcome in VH3-21-using chronic lymphocytic leukemia patients independent of geographic origin and mutational status. <i>Blood</i> , 2006, 107, 2889-2894.	0.6	167
15	A genome-wide association study identifies multiple susceptibility loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2014, 46, 56-60.	9.4	166
16	Lymphoma development in patients with autoimmune and inflammatory disorders – What are the driving forces?. <i>Seminars in Cancer Biology</i> , 2014, 24, 61-70.	4.3	150
17	Is there a role for antigen selection in mantle cell lymphoma? Immunogenetic support from a series of 807 cases. <i>Blood</i> , 2011, 118, 3088-3095.	0.6	149
18	ERIC recommendations for TP53 mutation analysis in chronic lymphocytic leukemia – update on methodological approaches and results interpretation. <i>Leukemia</i> , 2018, 32, 1070-1080.	3.3	149

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19	Reproducible diagnosis of chronic lymphocytic leukemia by flow cytometry: An European Research Initiative on CLL (ERIC) & European Society for Clinical Cell Analysis (ESCCA) Harmonisation project. <i>Cytometry Part B - Clinical Cytometry</i> , 2018, 94, 121-128.	0.7	133
20	Genetic heterogeneity in primary and relapsed mantle cell lymphomas: Impact of recurrent <i>CARD11</i> mutations. <i>Oncotarget</i> , 2016, 7, 38180-38190.	0.8	130
21	Whole-exome sequencing in relapsing chronic lymphocytic leukemia: clinical impact of recurrent <i>RPS15</i> mutations. <i>Blood</i> , 2016, 127, 1007-1016.	0.6	130
22	Genetics and Prognostication in Splenic Marginal Zone Lymphoma: Revelations from Deep Sequencing. <i>Clinical Cancer Research</i> , 2015, 21, 4174-4183.	3.2	129
23	Differential genome-wide array-based methylation profiles in prognostic subsets of chronic lymphocytic leukemia. <i>Blood</i> , 2010, 115, 296-305.	0.6	126
24	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.	3.9	124
25	Short telomeres are associated with genetic complexity, high-risk genomic aberrations, and short survival in chronic lymphocytic leukemia. <i>Blood</i> , 2008, 111, 2246-2252.	0.6	122
26	Antigen receptor stereotypy in chronic lymphocytic leukemia. <i>Leukemia</i> , 2017, 31, 282-291.	3.3	122
27	T cells in chronic lymphocytic leukemia display dysregulated expression of immune checkpoints and activation markers. <i>Haematologica</i> , 2017, 102, 562-572.	1.7	121
28	CD38 expression is a poor predictor for VH gene mutational status and prognosis in chronic lymphocytic leukemia. <i>Blood</i> , 2001, 97, 1892-1894.	0.6	119
29	Telomere length as a prognostic parameter in chronic lymphocytic leukemia with special reference to VH gene mutation status. <i>Blood</i> , 2005, 105, 4807-4812.	0.6	118
30	Immunoglobulin gene sequence analysis in chronic lymphocytic leukemia: updated ERIC recommendations. <i>Leukemia</i> , 2017, 31, 1477-1481.	3.3	118
31	Screening for copy number alterations and loss of heterozygosity in chronic lymphocytic leukemia—A comparative study of four differently designed, high resolution microarray platforms. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 697-711.	1.5	111
32	A different ontogenesis for chronic lymphocytic leukemia cases carrying stereotyped antigen receptors: molecular and computational evidence. <i>Leukemia</i> , 2010, 24, 125-132.	3.3	109
33	450K-array analysis of chronic lymphocytic leukemia cells reveals global DNA methylation to be relatively stable over time and similar in resting and proliferative compartments. <i>Leukemia</i> , 2013, 27, 150-158.	3.3	95
34	<i>TP53</i> aberrations in chronic lymphocytic leukemia: an overview of the clinical implications of improved diagnostics. <i>Haematologica</i> , 2018, 103, 1956-1968.	1.7	94
35	Clinical effect of stereotyped B-cell receptor immunoglobulins in chronic lymphocytic leukaemia: a retrospective multicentre study. <i>Lancet Haematology</i> , 2014, 1, e74-e84.	2.2	93
36	Distinct patterns of novel gene mutations in poor-prognostic stereotyped subsets of chronic lymphocytic leukemia: the case of <i>SF3B1</i> and subset #2. <i>Leukemia</i> , 2013, 27, 2196-2199.	3.3	90

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37	Array-based genomic screening at diagnosis and during follow-up in chronic lymphocytic leukemia. <i>Haematologica</i> , 2011, 96, 1161-1169.	1.7	87
38	DNA repair genes are selectively mutated in diffuse large B cell lymphomas. <i>Journal of Experimental Medicine</i> , 2013, 210, 1729-1742.	4.2	87
39	International prognostic score for asymptomatic early-stage chronic lymphocytic leukemia. <i>Blood</i> , 2020, 135, 1859-1869.	0.6	86
40	Functional loss of $\text{I}\kappa\text{B}\alpha$ leads to NF- κB deregulation in aggressive chronic lymphocytic leukemia. <i>Journal of Experimental Medicine</i> , 2015, 212, 833-843.	4.2	85
41	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. <i>Blood</i> , 2016, 128, 2666-2670.	0.6	82
42	Immunoglobulin sequence analysis and prognostication in CLL: guidelines from the ERIC review board for reliable interpretation of problematic cases. <i>Leukemia</i> , 2011, 25, 979-984.	3.3	75
43	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. <i>Nature Communications</i> , 2017, 8, 14175.	5.8	75
44	Large but not small copy-number alterations correlate to high-risk genomic aberrations and survival in chronic lymphocytic leukemia: a high-resolution genomic screening of newly diagnosed patients. <i>Leukemia</i> , 2010, 24, 211-215.	3.3	72
45	Higher-order connections between stereotyped subsets: implications for improved patient classification in CLL. <i>Blood</i> , 2021, 137, 1365-1376.	0.6	72
46	Evidence for the significant role of immunoglobulin light chains in antigen recognition and selection in chronic lymphocytic leukemia. <i>Blood</i> , 2009, 113, 403-411.	0.6	71
47	Not all IGHV3-21 chronic lymphocytic leukemias are equal: prognostic considerations. <i>Blood</i> , 2015, 125, 856-859.	0.6	70
48	On the way towards a $\hat{\text{C}}\text{LL}$ prognostic index $\hat{\text{C}}\text{TM}$: focus on TP53, BIRC3, SF3B1, NOTCH1 and MYD88 in a population-based cohort. <i>Leukemia</i> , 2014, 28, 710-713.	3.3	69
49	Genomic disruption of the histone methyltransferase SETD2 in chronic lymphocytic leukaemia. <i>Leukemia</i> , 2016, 30, 2179-2186.	3.3	69
50	Antigens in chronic lymphocytic leukemia $\hat{\text{C}}$ Implications for cell origin and leukemogenesis. <i>Seminars in Cancer Biology</i> , 2010, 20, 400-409.	4.3	68
51	Extensive intraclonal diversification in a subgroup of chronic lymphocytic leukemia patients with stereotyped IGHV4-34 receptors: implications for ongoing interactions with antigen. <i>Blood</i> , 2009, 114, 4460-4468.	0.6	64
52	Comprehensive characterization of IGHV3-21 $\hat{\text{C}}$ expressing B-cell chronic lymphocytic leukemia: an Italian multicenter study. <i>Blood</i> , 2007, 109, 2989-2998.	0.6	62
53	NOTCH1 and SF3B1 mutations can be added to the hierarchical prognostic classification in chronic lymphocytic leukemia. <i>Leukemia</i> , 2013, 27, 512-514.	3.3	62
54	NF- κB activation in chronic lymphocytic leukemia: A point of convergence of external triggers and intrinsic lesions. <i>Seminars in Cancer Biology</i> , 2016, 39, 40-48.	4.3	60

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55	Antigen receptor stereotypy across B-cell lymphoproliferations: the case of IGHV4-59/IGKV3-20 receptors with rheumatoid factor activity. <i>Leukemia</i> , 2012, 26, 1127-1131.	3.3	59
56	Prognostic markers and their clinical applicability in chronic lymphocytic leukemia: where do we stand?. <i>Leukemia and Lymphoma</i> , 2013, 54, 2351-2364.	0.6	59
57	Genetic landscape and deregulated pathways in B-cell lymphoid malignancies. <i>Journal of Internal Medicine</i> , 2017, 282, 371-394.	2.7	59
58	Targeted next-generation sequencing in chronic lymphocytic leukemia: a high-throughput yet tailored approach will facilitate implementation in a clinical setting. <i>Haematologica</i> , 2015, 100, 370-376.	1.7	57
59	Different spectra of recurrent gene mutations in subsets of chronic lymphocytic leukemia harboring stereotyped B-cell receptors. <i>Haematologica</i> , 2016, 101, 959-967.	1.7	57
60	Deciphering the molecular landscape in chronic lymphocytic leukemia: time frame of disease evolution. <i>Haematologica</i> , 2015, 100, 7-16.	1.7	54
61	Lymphoblastoid cell line with B1 cell characteristics established from a chronic lymphocytic leukemia clone by in vitro EBV infection. <i>Onc Immunology</i> , 2012, 1, 18-27.	2.1	53
62	U-CAN: a prospective longitudinal collection of biomaterials and clinical information from adult cancer patients in Sweden. <i>Acta Oncologica</i> , 2018, 57, 187-194.	0.8	52
63	Targetable genetic alterations of <i>TCF4</i> (<i>E2-2</i>) drive immunoglobulin expression in diffuse large B cell lymphoma. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	51
64	Intraclonal diversification of immunoglobulin light chains in a subset of chronic lymphocytic leukemia alludes to antigen-driven clonal evolution. <i>Leukemia</i> , 2010, 24, 1317-1324.	3.3	50
65	Cell-free tumour DNA testing for early detection of cancer – a potential future tool. <i>Journal of Internal Medicine</i> , 2019, 286, 118-136.	2.7	50
66	Long-term real-world results of ibrutinib therapy in patients with relapsed or refractory chronic lymphocytic leukemia: 30-month follow up of the Swedish compassionate use cohort. <i>Haematologica</i> , 2019, 104, e208-e210.	1.7	50
67	LPL is the strongest prognostic factor in a comparative analysis of RNA-based markers in early chronic lymphocytic leukemia. <i>Haematologica</i> , 2011, 96, 1153-1160.	1.7	49
68	Association between telomere length and VH gene mutation status in chronic lymphocytic leukaemia: clinical and biological implications. <i>British Journal of Cancer</i> , 2003, 88, 593-598.	2.9	47
69	Immunogenetic Studies of Chronic Lymphocytic Leukemia: Revelations and Speculations about Ontogeny and Clinical Evolution. <i>Cancer Research</i> , 2014, 74, 4211-4216.	0.4	47
70	Highly similar genomic landscapes in monoclonal B-cell lymphocytosis and ultra-stable chronic lymphocytic leukemia with low frequency of driver mutations. <i>Haematologica</i> , 2018, 103, 865-873.	1.7	47
71	Prognostic indices in chronic lymphocytic leukaemia: where do we stand how do we proceed?. <i>Journal of Internal Medicine</i> , 2016, 279, 347-357.	2.7	46
72	EGR2 mutations define a new clinically aggressive subgroup of chronic lymphocytic leukemia. <i>Leukemia</i> , 2017, 31, 1547-1554.	3.3	46

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73	Uncovering the DNA methylome in chronic lymphocytic leukemia. <i>Epigenetics</i> , 2013, 8, 138-148.	1.3	44
74	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , 2016, 7, 13182.	5.8	44
75	Prognostic impact of prevalent chronic lymphocytic leukemia stereotyped subsets: analysis within prospective clinical trials of the German CLL Study Group (GCLLSG). <i>Haematologica</i> , 2020, 105, 2598-2607.	1.7	44
76	High-density screening reveals a different spectrum of genomic aberrations in chronic lymphocytic leukemia patients with 'stereotyped' IGHV3-21 and IGHV4-34 B-cell receptors. <i>Haematologica</i> , 2010, 95, 1519-1525.	1.7	43
77	<i>microRNA-34b/c</i> on chromosome 11q23 is aberrantly methylated in chronic lymphocytic leukemia. <i>Epigenetics</i> , 2014, 9, 910-917.	1.3	43
78	Clinical impact of recurrently mutated genes on lymphoma diagnostics: state-of-the-art and beyond. <i>Haematologica</i> , 2016, 101, 1002-1009.	1.7	43
79	Antigen Selection Shapes the T-cell Repertoire in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2016, 22, 167-174.	3.2	43
80	Genomic arrays identify high-risk chronic lymphocytic leukemia with genomic complexity: a multi-center study. <i>Haematologica</i> , 2020, 106, 87-97.	1.7	43
81	Distinctive gene expression pattern in VH3-21 utilizing B-cell chronic lymphocytic leukemia. <i>Blood</i> , 2005, 106, 681-689.	0.6	42
82	Clonal rearrangements in childhood and adult precursor B acute lymphoblastic leukemia: a comparative polymerase chain reaction study using multiple sets of primers. <i>European Journal of Haematology</i> , 1999, 63, 211-218.	1.1	42
83	A key role for EZH2 in epigenetic silencing of HOX genes in mantle cell lymphoma. <i>Epigenetics</i> , 2013, 8, 1280-1288.	1.3	42
84	Tailored approaches grounded on immunogenetic features for refined prognostication in chronic lymphocytic leukemia. <i>Haematologica</i> , 2019, 104, 360-369.	1.7	42
85	The complex interplay between cell-intrinsic and cell-extrinsic factors driving the evolution of chronic lymphocytic leukemia. <i>Seminars in Cancer Biology</i> , 2015, 34, 22-35.	4.3	40
86	Epigenetic deregulation in chronic lymphocytic leukemia: Clinical and biological impact. <i>Seminars in Cancer Biology</i> , 2018, 51, 1-11.	4.3	40
87	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. <i>Blood Cancer Journal</i> , 2019, 9, 1.	2.8	40
88	Triggering interferon signaling in T cells with avadomide sensitizes CLL to anti-PD-L1/PD-1 immunotherapy. <i>Blood</i> , 2021, 137, 216-231.	0.6	40
89	TP53 Mutations are infrequent in newly diagnosed chronic lymphocytic leukemia. <i>Leukemia Research</i> , 2011, 35, 272-274.	0.4	38
90	Antigen selection in B-cell lymphomas—Tracing the evidence. <i>Seminars in Cancer Biology</i> , 2013, 23, 399-409.	4.3	38

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91	Short telomere length is associated with <i>NOTCH1/SF3B1/TP53</i> aberrations and poor outcome in newly diagnosed chronic lymphocytic leukemia patients. <i>American Journal of Hematology</i> , 2013, 88, 647-651.	2.0	38
92	Distinct transcriptional control in major immunogenetic subsets of chronic lymphocytic leukemia exhibiting subset-biased global DNA methylation profiles. <i>Epigenetics</i> , 2012, 7, 1435-1442.	1.3	37
93	Additional trisomies amongst patients with chronic lymphocytic leukemia carrying trisomy 12: the accompanying chromosome makes a difference. <i>Haematologica</i> , 2016, 101, e299-e302.	1.7	35
94	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 32-39.	4.3	35
95	Verification that common variation at 2q37.1, 6p25.3, 11q24.1, 15q23, and 19q13.32 influences chronic lymphocytic leukaemia risk. <i>British Journal of Haematology</i> , 2010, 150, 473-479.	1.2	34
96	Immunoglobulin gene sequence analysis in chronic lymphocytic leukemia: the 2022 update of the recommendations by ERIC, the European Research Initiative on CLL. <i>Leukemia</i> , 2022, 36, 1961-1968.	3.3	34
97	Distinct gene expression profiles in subsets of chronic lymphocytic leukemia expressing stereotyped IGHV4-34 B-cell receptors. <i>Haematologica</i> , 2010, 95, 2072-2079.	1.7	33
98	Prognostic relevance of MYD88 mutations in CLL: the jury is still out. <i>Blood</i> , 2015, 126, 1043-1044.	0.6	32
99	Lipoprotein lipase is differentially expressed in prognostic subsets of chronic lymphocytic leukemia but displays invariably low catalytical activity. <i>Leukemia Research</i> , 2010, 34, 301-306.	0.4	30
100	<i>ANGPT2</i> promoter methylation is strongly associated with gene expression and prognosis in chronic lymphocytic leukemia. <i>Epigenetics</i> , 2013, 8, 720-729.	1.3	30
101	A Systematic Search Into The Role Of IGHV Gene Replacement In Shaping The Immunoglobulin Repertoire Of Chronic Lymphocytic Leukemia. <i>Blood</i> , 2013, 122, 4129-4129.	0.6	30
102	Clonal evolution as judged by immunoglobulin heavy chain gene rearrangements in relapsing precursor $\alpha\beta$ acute lymphoblastic leukemia. <i>European Journal of Haematology</i> , 1999, 63, 171-179.	1.1	29
103	High-resolution genomic screening in mantle cell lymphoma-specific changes correlate with genomic complexity, the proliferation signature and survival. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 113-121.	1.5	29
104	Immunoglobulin gene analysis in chronic lymphocytic leukemia in the era of next generation sequencing. <i>Leukemia</i> , 2020, 34, 2545-2551.	3.3	29
105	The histone methyltransferase EZH2 as a novel pro-survival factor in clinically aggressive chronic lymphocytic leukemia. <i>Oncotarget</i> , 2016, 7, 35946-35959.	0.8	29
106	Immunoglobulin genes in chronic lymphocytic leukemia: key to understanding the disease and improving risk stratification. <i>Haematologica</i> , 2017, 102, 968-971.	1.7	28
107	Chronic Lymphocytic Leukemia with Mutated IGHV4-34 Receptors: Shared and Distinct Immunogenetic Features and Clinical Outcomes. <i>Clinical Cancer Research</i> , 2017, 23, 5292-5301.	3.2	27
108	Cell-of-origin determined by both gene expression profiling and immunohistochemistry is the strongest predictor of survival in patients with diffuse large B-cell lymphoma. <i>American Journal of Hematology</i> , 2020, 95, 57-67.	2.0	27

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109	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2015, 17, 61.	2.2	26
110	Transposon Mutagenesis Reveals Fludarabine Resistance Mechanisms in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2016, 22, 6217-6227.	3.2	26
111	Whole-Exome Sequencing Revealed No Recurrent Mutations within the PI3K Pathway in Relapsed Chronic Lymphocytic Leukemia Patients Progressing Under Idelalisib Treatment. <i>Blood</i> , 2016, 128, 2770-2770.	0.6	26
112	Patients with chronic lymphocytic leukemia with mutated VH genes presenting with Binet stage B or C form a subgroup with a poor outcome. <i>Haematologica</i> , 2005, 90, 465-9.	1.7	26
113	Inhibition of SYK or BTK augments venetoclax sensitivity in SHP1-negative/BCL-2-positive diffuse large B-cell lymphoma. <i>Leukemia</i> , 2019, 33, 2416-2428.	3.3	25
114	Clinical significance of DNA methylation in chronic lymphocytic leukemia patients: results from 3 UK clinical trials. <i>Blood Advances</i> , 2019, 3, 2474-2481.	2.5	25
115	Disease-biased and shared characteristics of the immunoglobulin gene repertoires in marginal zone B cell lymphoproliferations. <i>Journal of Pathology</i> , 2019, 247, 416-421.	2.1	25
116	Common variation at 12q24.13 (OAS3) influences chronic lymphocytic leukemia risk. <i>Leukemia</i> , 2015, 29, 748-751.	3.3	24
117	EZH2 upregulates the PI3K/AKT pathway through IGF1R and MYC in clinically aggressive chronic lymphocytic leukaemia. <i>Epigenetics</i> , 2019, 14, 1125-1140.	1.3	24
118	Integrated epigenomic and transcriptomic analysis reveals TP63 as a novel player in clinically aggressive chronic lymphocytic leukemia. <i>International Journal of Cancer</i> , 2019, 144, 2695-2706.	2.3	24
119	Next generation RNA-sequencing in prognostic subsets of chronic lymphocytic leukemia. <i>American Journal of Hematology</i> , 2012, 87, 737-740.	2.0	23
120	Surface antigen expression and correlation with variable heavy-chain gene mutation status in chronic lymphocytic leukemia. <i>European Journal of Haematology</i> , 2003, 70, 53-59.	1.1	22
121	Trailblazing precision medicine in Europe: A joint view by Genomic Medicine Sweden and the Centers for Personalized Medicine, ZPM, in Germany. <i>Seminars in Cancer Biology</i> , 2022, 84, 242-254.	4.3	22
122	Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 16-22.	4.3	22
123	The novel NF- κ B inhibitor IMD-0354 induces apoptosis in chronic lymphocytic leukemia. <i>Blood Cancer Journal</i> , 2011, 1, e12-e12.	2.8	21
124	Coexistence of trisomies of chromosomes 12 and 19 in chronic lymphocytic leukemia occurs exclusively in the rare IgG-positive variant. <i>Leukemia</i> , 2012, 26, 170-172.	3.3	21
125	Prognostic impact of epigenetic classification in chronic lymphocytic leukemia: The case of subset #2. <i>Epigenetics</i> , 2016, 11, 449-455.	1.3	21
126	Higher-order immunoglobulin repertoire restrictions in CLL: the illustrative case of stereotyped subsets 2 and 169. <i>Blood</i> , 2021, 137, 1895-1904.	0.6	21

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127	Epigenetic silencing of miR-26A1 in chronic lymphocytic leukemia and mantle cell lymphoma: Impact on EZH2 expression. <i>Epigenetics</i> , 2016, 11, 335-343.	1.3	20
128	Innovation in the prognostication of chronic lymphocytic leukemia: how far beyond TP53 gene analysis can we go?. <i>Haematologica</i> , 2016, 101, 263-265.	1.7	19
129	Technological readiness and implementation of genomicâ€driven precision medicine for complex diseases. <i>Journal of Internal Medicine</i> , 2021, 290, 602-620.	2.7	18
130	A comprehensive evaluation of the role of genetic variation in follicular lymphoma survival. <i>BMC Medical Genetics</i> , 2014, 15, 113.	2.1	17
131	The frequency of <i>TP53</i> gene defects differs between chronic lymphocytic leukaemia subgroups harbouring distinct antigen receptors. <i>British Journal of Haematology</i> , 2014, 166, 621-625.	1.2	17
132	An Immunogenetic Signature of Ongoing Antigen Interactions in Splenic Marginal Zone Lymphoma Expressing IGHV1-2*04 Receptors. <i>Clinical Cancer Research</i> , 2016, 22, 2032-2040.	3.2	17
133	Unlocking the secrets of immunoglobulin receptors in mantle cell lymphoma: Implications for the origin and selection of the malignant cells. <i>Seminars in Cancer Biology</i> , 2011, 21, 299-307.	4.3	16
134	The microenvironment in lymphomas â€“ Dissecting the complex crosstalk between tumor cells and â€by-standerâ€™ cells. <i>Seminars in Cancer Biology</i> , 2014, 24, 1-2.	4.3	16
135	ATM mutations in major stereotyped subsets of chronic lymphocytic leukemia: enrichment in subset #2 is associated with markedly short telomeres. <i>Haematologica</i> , 2016, 101, e369-e373.	1.7	16
136	No improvement in long-term survival over time for chronic lymphocytic leukemia patients in stereotyped subsets #1 and #2 treated with chemo(immuno)therapy. <i>Haematologica</i> , 2018, 103, e158-e161.	1.7	16
137	Genome-wide promoter methylation of hairy cell leukemia. <i>Blood Advances</i> , 2019, 3, 384-396.	2.5	16
138	DNA methylation profiles in chronic lymphocytic leukemia patients treated with chemoimmunotherapy. <i>Clinical Epigenetics</i> , 2019, 11, 177.	1.8	15
139	A Study Protocol for Validation and Implementation of Whole-Genome and -Transcriptome Sequencing as a Comprehensive Precision Diagnostic Test in Acute Leukemias. <i>Frontiers in Medicine</i> , 2022, 9, 842507.	1.2	15
140	Identification of B-cell lymphoma subsets by plasma protein profiling using recombinant antibody microarrays. <i>Leukemia Research</i> , 2014, 38, 682-690.	0.4	14
141	Mantle cell lymphoma displays a homogenous methylation profile: A comparative analysis with chronic lymphocytic leukemia. <i>American Journal of Hematology</i> , 2012, 87, 361-367.	2.0	13
142	Molecular Evidence for Antigen Drive in the Natural History of Mantle Cell Lymphoma. <i>American Journal of Pathology</i> , 2015, 185, 1740-1748.	1.9	13
143	Flow Cytometric Measurement of Blood Cells with BCR-ABL1 Fusion Protein in Chronic Myeloid Leukemia. <i>Scientific Reports</i> , 2017, 7, 623.	1.6	13
144	The Number of Signaling Pathways Altered by Driver Mutations in Chronic Lymphocytic Leukemia Impacts Disease Outcome. <i>Clinical Cancer Research</i> , 2020, 26, 1507-1515.	3.2	13

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145	Precision diagnostics in lymphomas – Recent developments and future directions. <i>Seminars in Cancer Biology</i> , 2022, 84, 170-183.	4.3	13
146	<i>RPS15</i> mutations rewire RNA translation in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2021, 5, 2788-2792.	2.5	12
147	Immunoglobulin VH gene replacements in a T-cell lymphoblastic lymphoma. <i>Molecular Immunology</i> , 1997, 34, 305-313.	1.0	11
148	Temporal Dynamics of Clonal Evolution in Chronic Lymphocytic Leukemia with Stereotyped IGHV4-34/IGKV2-30 Antigen Receptors: Longitudinal Immunogenetic Evidence. <i>Molecular Medicine</i> , 2013, 19, 230-236.	1.9	11
149	Numerous Ontogenetic Roads to Mantle Cell Lymphoma. <i>American Journal of Pathology</i> , 2017, 187, 1454-1458.	1.9	11
150	RNA-based markers as prognostic factors in chronic lymphocytic leukemia. <i>Expert Review of Hematology</i> , 2012, 5, 69-79.	1.0	10
151	Possible Interaction Between Cigarette Smoking and HLA-DRB1 Variation in the Risk of Follicular Lymphoma. <i>American Journal of Epidemiology</i> , 2017, 185, 681-687.	1.6	10
152	Clinical and functional impact of recurrent S1PR1 mutations in mantle cell lymphoma. <i>Blood Advances</i> , 2018, 2, 621-625.	2.5	10
153	Inhibition of EZH2 and immune signaling exerts synergistic antitumor effects in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2019, 3, 1891-1896.	2.5	10
154	Comparative analysis of targeted next-generation sequencing panels for the detection of gene mutations in chronic lymphocytic leukemia: an ERIC multi-center study. <i>Haematologica</i> , 2021, 106, 682-691.	1.7	10
155	The international Prognostic Index for patients with CLL (CLL-IPI): An international meta-analysis.. <i>Journal of Clinical Oncology</i> , 2015, 33, 7002-7002.	0.8	10
156	Exploring the genetic landscape in chronic lymphocytic leukemia using high-resolution technologies. <i>Leukemia and Lymphoma</i> , 2013, 54, 1583-1590.	0.6	9
157	Feasibility of targeted next-generation sequencing of the TP53 and ATM genes in chronic lymphocytic leukemia. <i>Leukemia</i> , 2014, 28, 694-696.	3.3	9
158	Silenced B-cell receptor response to autoantigen in a poor-prognostic subset of chronic lymphocytic leukemia. <i>Haematologica</i> , 2014, 99, 1722-1730.	1.7	9
159	Automated shape-based clustering of 3D immunoglobulin protein structures in chronic lymphocytic leukemia. <i>BMC Bioinformatics</i> , 2018, 19, 414.	1.2	9
160	Towards precision medicine in lymphoid malignancies. <i>Journal of Internal Medicine</i> , 2022, 292, 221-242.	2.7	9
161	Patient-Specific Assays Based on Whole-Genome Sequencing Data to Measure Residual Disease in Children With Acute Lymphoblastic Leukemia: A Proof of Concept Study. <i>Frontiers in Oncology</i> , 0, 12, .	1.3	9
162	A novel ex vivo high-throughput assay reveals antiproliferative effects of idelalisib and ibrutinib in chronic lymphocytic leukemia. <i>Oncotarget</i> , 2018, 9, 26019-26031.	0.8	8

#	ARTICLE	IF	CITATIONS
163	MyPal ADULT study protocol: a randomised clinical trial of the MyPal ePRO-based early palliative care system in adult patients with haematological malignancies. <i>BMJ Open</i> , 2021, 11, e050256.	0.8	8
164	Response: high ERG gene expression is an unfavorable prognostic marker in pediatric acute myeloid leukemia. <i>Blood</i> , 2012, 119, 1087-1088.	0.6	7
165	Antigens in lymphoma development—Current knowledge and future directions. <i>Seminars in Cancer Biology</i> , 2013, 23, 397-398.	4.3	6
166	Clonal evolution in chronic lymphocytic leukemia: impact of subclonality on disease progression. <i>Expert Review of Hematology</i> , 2015, 8, 71-78.	1.0	6
167	Immunoglobulin Gene Sequence Analysis In Chronic Lymphocytic Leukemia: From Patient Material To Sequence Interpretation. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	6
168	Introduction: Epigenetics in cancer. <i>Seminars in Cancer Biology</i> , 2018, 51, iv-v.	4.3	6
169	Risk-adapted bendamustine+Rituximab is a tolerable treatment alternative for elderly patients with chronic lymphocytic leukaemia: a regional real-world report on 141 consecutive Swedish patients. <i>British Journal of Haematology</i> , 2020, 191, 426-432.	1.2	6
170	T Cell Receptor Gene Repertoire Restriction in Chronic Lymphocytic Leukemia with Stereotyped IGHV4-34/IGKV2-30 Antigen Receptors. <i>Blood</i> , 2012, 120, 3908-3908.	0.6	6
171	Strikingly Homologous Immunoglobulin Gene Rearrangements and Poor Outcome in VH3-21-Utilizing Chronic Lymphocytic Leukemia Independent of Geographical Origin and Mutational Status.. <i>Blood</i> , 2005, 106, 175-175.	0.6	6
172	International validation of the <sc>EORTC QLQ-CLL17</sc> questionnaire for assessment of health-related quality of life for patients with chronic lymphocytic leukaemia. <i>British Journal of Haematology</i> , 2022, 197, 431-441.	1.2	6
173	Introduction: the role of inflammation, autoimmune disease and infectious agents in development of leukaemia and lymphoma. <i>Journal of Internal Medicine</i> , 2008, 264, 512-513.	2.7	5
174	Different time-dependent changes of risk for evolution in chronic lymphocytic leukemia with mutated or unmutated antigen B cell receptors. <i>Leukemia</i> , 2019, 33, 1801-1805.	3.3	5
175	Consistent B Cell Receptor Immunoglobulin Features Between Siblings in Familial Chronic Lymphocytic Leukemia. <i>Frontiers in Oncology</i> , 2021, 11, 740083.	1.3	5
176	Identifying patients with chronic lymphocytic leukemia without need of treatment: End of endless watch and wait?. <i>European Journal of Haematology</i> , 2022, 108, 369-378.	1.1	5
177	Precision medicine in cancer: A paradigm shift. <i>Seminars in Cancer Biology</i> , 2022, 84, 1-2.	4.3	5
178	Alterations of the Immunoglobulin Heavy Chain Locus in Progressive B-cell Lymphomas. <i>Acta Oncologica</i> , 1998, 37, 193-200.	0.8	4
179	An Entity Evolving into a Community: Defining the Common Ancestor and Evolutionary Trajectory of Chronic Lymphocytic Leukemia Stereotyped Subset #4. <i>Molecular Medicine</i> , 2014, 20, 720-728.	1.9	4
180	B-cell malignancies: All roads lead to NF- κ B activation. <i>Seminars in Cancer Biology</i> , 2016, 39, 1-2.	4.3	4

#	ARTICLE	IF	CITATIONS
181	Expression of GNAZ , encoding the G α z protein, predicts survival in mantle cell lymphoma. British Journal of Haematology, 2019, 185, 708-712.	1.2	4
182	Screening for Copy Number Alterations and Loss of Heterozygosity in Chronic Lymphocytic Leukemia - A Comparative Study of Four Differently Designed, High Resolution Microarray Platforms.. Blood, 2007, 110, 2084-2084.	0.6	4
183	LPL Is the Strongest Prognostic Factor in a Comparative Study of RNA-Based Markers in Chronic Lymphocytic Leukemia.. Blood, 2009, 114, 1254-1254.	0.6	4
184	Chronic Lymphocytic Leukemia Patients with IGHV Genes Carrying Only Silent Mutations Have A Longer Time From Diagnosis to Initial Therapy Than Patients Expressing B-Cell Receptors with No Somatic Mutations. Blood, 2011, 118, 288-288.	0.6	3
185	Genome-Wide Methylation Arrays Reveal Distinct Methylation Profiles in Prognostic Subsets of Chronic Lymphocytic Leukemia.. Blood, 2009, 114, 364-364.	0.6	3
186	Low rate of somatic hypermutations characterize progressive Bâ€cell lymphomas. European Journal of Haematology, 1998, 61, 164-172.	1.1	2
187	New insights into the pathobiology of chronic lymphocytic leukemia. Journal of Hematopathology, 2011, 4, 149-163.	0.2	2
188	MDM2 promotor polymorphism and disease characteristics in chronic lymphocytic leukemia: results of an individual patient data-based meta-analysis. Haematologica, 2014, 99, 1285-1291.	1.7	2
189	DRUG PERTURBATION BASED STRATIFICATION OF LYMPHOPROLIFERATIVE DISORDERS. Hematological Oncology, 2017, 35, 56-56.	0.8	2
190	Immunoglobulin Gene Analysis in Chronic Lymphocytic Leukemia. Methods in Molecular Biology, 2019, 1881, 51-62.	0.4	2
191	Sequence-Based Evidence for Antigen Selection in Mantle Cell Lymphoma: Remarkable Immunoglobulin Gene Repertoire Biases, Stereotyped Antigen-Binding Sites and Recurrent Hypermutations in Certain Subsets.. Blood, 2009, 114, 1933-1933.	0.6	2
192	The Composition of the B Cell Receptor Repertoire In 7428 Cases of Chronic Lymphocytic Leukemia: One Third Stereotyped, Two Thirds Heterogeneous - What Does This Mean?. Blood, 2010, 116, 43-43.	0.6	2
193	Diffuse Large B-Cell Lymphoma (DLBCL) Tumor Cells Reprogram Lymphatic Fibroblasts into Cancer-Associated Fibroblasts (CAFs) That Contribute to Tumor Microenvironment (TME)-Driven Immune Privilege. Blood, 2015, 126, 1474-1474.	0.6	2
194	Unique Versus Common: Disease-Biased Immunoglobulin Gene Repertoires Along with Public Antigen Receptor Stereotypes in Marginal Zone B-Cell Lymphoproliferations. Blood, 2015, 126, 1479-1479.	0.6	2
195	Reproducible Diagnosis of Chronic Lymphocytic Leukemia (CLL) By Flow Cytometry: An European Research Initiative on CLL (ERIC) & European Society for Clinical Cell Analysis (ESCCA) Harmonisation Project. Blood, 2015, 126, 4146-4146.	0.6	2
196	Transcriptome sequencing of archived lymphoma specimens is feasible and clinically relevant using exome capture technology. Genes Chromosomes and Cancer, 2022, 61, 27-36.	1.5	2
197	INTERNATIONAL PROGNOSTIC SCORE FOR EARLY STAGE CHRONIC LYMPHOCYTIC LEUKEMIA (IPS-A). Hematological Oncology, 2019, 37, 81-82.	0.8	1
198	p66Shc deficiency sets the scene for clinically aggressive chronic lymphocytic leukemia. Haematologica, 2019, 104, 1914-1916.	1.7	1

#	ARTICLE	IF	CITATIONS
199	Concordance in survival among first-degree relatives diagnosed with indolent lymphoid malignancies including chronic lymphocytic leukemia. <i>European Journal of Haematology</i> , 2020, 105, 779-785.	1.1	1
200	Discordant Reporting of a Previously Undescribed Pathogenic Germline BRCA2 Variant in Blood and Tumor Tissue in a Patient With Pancreatic Adenocarcinoma. <i>JCO Precision Oncology</i> , 2021, 5, 974-980.	1.5	1
201	Molecular diagnostics and reporting in lymphoid malignancies: Current status and beyond. <i>Hematological Oncology</i> , 2021, 39, 73-77.	0.8	1
202	Mutations known from B-cell lymphoid malignancies are not found in CD34 ⁺ stem cells from patients with lymphoma. <i>Leukemia and Lymphoma</i> , 2021, 62, 2808-2811.	0.6	1
203	DNA Copy Number Gains of TCF4 (E2-2) Are Associated with Poor Outcome in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016, 128, 2686-2686.	0.6	1
204	Reappraising Immunoglobulin Repertoire Restrictions in Chronic Lymphocytic Leukemia: Focus on Major Stereotyped Subsets and Closely Related Satellites. <i>Blood</i> , 2016, 128, 4376-4376.	0.6	1
205	SNP-Arrays Provide New Insights Into the Pathogenesis of Richter Syndrome (RS). <i>Blood</i> , 2011, 118, 263-263.	0.6	1
206	Prognostic Assessment In Patients With Chronic Lymphocytic Leukemia (CLL) In Clinical Practice: A European Research Initiative On CLL (ERIC) Survey. <i>Blood</i> , 2013, 122, 4156-4156.	0.6	1
207	Higher Order Restrictions of the Immunoglobulin Repertoire in CLL: The Illustrative Case of Stereotyped Subsets #2 and #169. <i>Blood</i> , 2019, 134, 5453-5453.	0.6	1
208	Different Prognostic Impact of Recurrent Gene Mutations in IGHV-Mutated and IGHV-Unmutated Chronic Lymphocytic Leukemia: A Retrospective, Multi-Center Cohort Study By Eric, the European Research Initiative on CLL, in Harmony. <i>Blood</i> , 2021, 138, 2617-2617.	0.6	1
209	A new piece to the stereotypy "puzzle" in chronic lymphocytic leukemia. <i>Leukemia and Lymphoma</i> , 2015, 56, 3008-3009.	0.6	0
210	Unraveling the DNA Methylome in Mantle Cell Lymphoma: New Insights into the Cellular Origin. <i>Cancer Cell</i> , 2016, 30, 665-667.	7.7	0
211	Introduction to the symposium "Targeted therapy in B-cell malignancies". <i>Journal of Internal Medicine</i> , 2017, 282, 358-359.	2.7	0
212	Identification and gene expression analysis of the side population subclone in mantle cell lymphoma. <i>Hematological Oncology</i> , 2017, 35, 284-284.	0.8	0
213	Assessing Patients' Knowledge on Chronic Lymphocytic Leukemia: Validation of the ERIC CLL Knowledge Questionnaire in Greece. <i>HemaSphere</i> , 2021, 5, e546.	1.2	0
214	Telomere Length as a Prognostic Parameter in Chronic Lymphocytic Leukemia with Reference to IGV(H) Gene Mutation Status.. <i>Blood</i> , 2004, 104, 4795-4795.	0.6	0
215	Short Telomeres Are Associated with Genetic Instability and the Occurrence of High Risk Genomic Aberrations in Chronic Lymphocytic Leukemia.. <i>Blood</i> , 2005, 106, 1178-1178.	0.6	0
216	Stereotyped Patterns of Somatic Hypermutation (SHM) in Subsets of Patients with Chronic Lymphocytic Leukemia (CLL): Implications for the Role of Antigen Selection in Leukemogenesis.. <i>Blood</i> , 2007, 110, 744-744.	0.6	0

#	ARTICLE	IF	CITATIONS
217	Evidence for the Significant Role of Immunoglobulin Light Chains in Antigen Recognition and Selection in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2008, 112, 780-780.	0.6	0
218	A Different Ontogenesis for CLL Cases Carrying Stereotyped Antigen Receptors: Molecular and Computational Evidence. <i>Blood</i> , 2008, 112, 777-777.	0.6	0
219	High Resolution Screening of Copy-Number Alterations in Chronic Lymphocytic Leukemia Using Affymetrix 250K SNP-Arrays Reveals a Higher Complexity of Genomic Alterations in Patients with Unmutated IGHV Genes. <i>Blood</i> , 2008, 112, 3133-3133.	0.6	0
220	Lymphomas in Rheumatoid Arthritis Patients Treated with Anti-TNF Therapy: A Report from the Swedish Biologics Register (ARTIS) and the ARTIS Study Group 1998-2006. <i>Blood</i> , 2008, 112, 3754-3754.	0.6	0
221	Apoptosis Gene Expression Profiling in Chronic Lymphocytic Leukemia Using Multiplex Ligation-Dependent Probe Amplification. <i>Blood</i> , 2009, 114, 3457-3457.	0.6	0
222	Implications On Drug Resistance and Survival of ABCB1 Single Nucleotide Polymorphisms in Normal Karyotype De Novo AML. <i>Blood</i> , 2009, 114, 2648-2648.	0.6	0
223	Relapsed Childhood High Hyperdiploid Acute Lymphoblastic Leukemia: Genome-Wide Screening Reveals the Presence of Preleukemic Ancestral Clones and the Secondary Nature of Microdeletions and RTK-RAS Mutations. <i>Blood</i> , 2009, 114, 2591-2591.	0.6	0
224	Chronic Lymphocytic Leukemia with Stereotyped IGHV4-59/IGKV3-20 B Cell Receptors: Another Manifestation of Hepatitis C Virus-Associated B Cell Lymphoproliferation?. <i>Blood</i> , 2009, 114, 2331-2331.	0.6	0
225	Extensive Intracлонаl Diversification in a Subgroup of Chronic Lymphocytic Leukemia Patients with Stereotyped IGHV4-34/IGKV2-30 B cell Receptors: Implications for Ongoing Interactions with Antigen. <i>Blood</i> , 2009, 114, 2337-2337.	0.6	0
226	Genome-Wide Array-Based Methylation Profiling Reveals Preferential Methylation of Homeobox Transcription Factor Genes In Mantle Cell Lymphoma and Pro-Apoptotic Genes In Chronic Lymphocytic Leukemia. <i>Blood</i> , 2010, 116, 536-536.	0.6	0
227	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. <i>Blood</i> , 2013, 122, 1614-1614.	0.6	0
228	An Innovative High-Throughput Ex Vivo Drug Assay Incorporating the Native Microenvironment Reveals a Novel Mechanism of Action of Idelalisib in CLL. <i>Blood</i> , 2015, 126, 2485-2485.	0.6	0
229	ATM Mutations in Major Stereotyped CLL Subsets: Enrichment in Subset #2 is Associated with Unfavourable Outcome. <i>Blood</i> , 2015, 126, 1712-1712.	0.6	0
230	Genomic Disruption of the Histone Methyltransferase SETD2 in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 365-365.	0.6	0
231	Personalized Modeling of Disease Evolution in CLL: Does Statistical Significance Translate into Predictive Accuracy?. <i>Blood</i> , 2015, 126, 2921-2921.	0.6	0
232	CLL with Mutated IGHV4-34 Antigen Receptors Is Clinically Heterogeneous: Antigen Receptor Stereotypy Makes the Difference. <i>Blood</i> , 2015, 126, 5263-5263.	0.6	0
233	Specific T Cell Receptor Gene Repertoire Profiles in Subgroups of CLL Patients with Distinct Genomic Aberrations. <i>Blood</i> , 2021, 138, 3749-3749.	0.6	0
234	Proteogenomic Subtyping of Chronic Lymphocytic Leukemia Identifies a Novel Poor Outcome Subgroup with a Distinct Drug Response Profile. <i>Blood</i> , 2020, 136, 10-11.	0.6	0