

# Richard Rosenquist

## List of Publications by Year in descending order

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234  
papers

11,000  
citations

28274

55  
h-index

37204

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.	1.4	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.	1.4	350
3	Downregulation of Death-Associated Protein Kinase 1 (DAPK1) in Chronic Lymphocytic Leukemia. <i>Cell</i> , 2007, 129, 879-890.	28.9	338
4	Somatically mutated Ig VH3-21 genes characterize a new subset of chronic lymphocytic leukemia. <i>Blood</i> , 2002, 99, 2262-2264.	1.4	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.	1.4	285
6	Chronic lymphocytic leukemias utilizing the VH3-21 gene display highly restricted V $\lambda$ 2-14 gene use and homologous CDR3s: implicating recognition of a common antigen epitope. <i>Blood</i> , 2003, 101, 4952-4957.	1.4	280
7	Recurrent mutations refine prognosis in chronic lymphocytic leukemia. <i>Leukemia</i> , 2015, 29, 329-336.	7.2	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.	3.5	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.	1.4	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.	1.4	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.	21.4	223
12	ERIC recommendations on IGHV gene mutational status analysis in chronic lymphocytic leukemia. <i>Leukemia</i> , 2007, 21, 1-3.	7.2	219
13	Two main genetic pathways lead to the transformation of chronic lymphocytic leukemia to Richter syndrome. <i>Blood</i> , 2013, 122, 2673-2682.	1.4	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.	1.4	167
15	A genome-wide association study identifies multiple susceptibility loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2014, 46, 56-60.	21.4	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.	9.6	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.	1.4	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.	7.2	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.	1.5	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.	1.8	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.	1.4	130
22	Genetics and Prognostication in Splenic Marginal Zone Lymphoma: Revelations from Deep Sequencing. <i>Clinical Cancer Research</i> , 2015, 21, 4174-4183.	7.0	129
23	Differential genome-wide array-based methylation profiles in prognostic subsets of chronic lymphocytic leukemia. <i>Blood</i> , 2010, 115, 296-305.	1.4	126
24	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.	8.2	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.	1.4	122
26	Antigen receptor stereotypy in chronic lymphocytic leukemia. <i>Leukemia</i> , 2017, 31, 282-291.	7.2	122
27	T cells in chronic lymphocytic leukemia display dysregulated expression of immune checkpoints and activation markers. <i>Haematologica</i> , 2017, 102, 562-572.	3.5	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.	1.4	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.	1.4	118
30	Immunoglobulin gene sequence analysis in chronic lymphocytic leukemia: updated ERIC recommendations. <i>Leukemia</i> , 2017, 31, 1477-1481.	7.2	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.	2.8	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.	7.2	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.	7.2	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.	3.5	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.	4.6	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.	7.2	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.	3.5	87
38	DNA repair genes are selectively mutated in diffuse large B cell lymphomas. <i>Journal of Experimental Medicine</i> , 2013, 210, 1729-1742.	8.5	87
39	International prognostic score for asymptomatic early-stage chronic lymphocytic leukemia. <i>Blood</i> , 2020, 135, 1859-1869.	1.4	86
40	Functional loss of $\text{I}\kappa\text{B}\alpha$ leads to NF- $\kappa\text{B}$ deregulation in aggressive chronic lymphocytic leukemia. <i>Journal of Experimental Medicine</i> , 2015, 212, 833-843.	8.5	85
41	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. <i>Blood</i> , 2016, 128, 2666-2670.	1.4	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.	7.2	75
43	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. <i>Nature Communications</i> , 2017, 8, 14175.	12.8	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.	7.2	72
45	Higher-order connections between stereotyped subsets: implications for improved patient classification in CLL. <i>Blood</i> , 2021, 137, 1365-1376.	1.4	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.	1.4	71
47	Not all IGHV3-21 chronic lymphocytic leukemias are equal: prognostic considerations. <i>Blood</i> , 2015, 125, 856-859.	1.4	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.	7.2	69
49	Genomic disruption of the histone methyltransferase SETD2 in chronic lymphocytic leukaemia. <i>Leukemia</i> , 2016, 30, 2179-2186.	7.2	69
50	Antigens in chronic lymphocytic leukemia $\hat{\text{C}}\text{TM}$ Implications for cell origin and leukemogenesis. <i>Seminars in Cancer Biology</i> , 2010, 20, 400-409.	9.6	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.	1.4	64
52	Comprehensive characterization of IGHV3-21 $\hat{\text{C}}\text{TM}$ expressing B-cell chronic lymphocytic leukemia: an Italian multicenter study. <i>Blood</i> , 2007, 109, 2989-2998.	1.4	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.	7.2	62
54	NF- $\kappa\text{B}$ 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.	9.6	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.	7.2	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.	1.3	59
57	Genetic landscape and deregulated pathways in B-cell lymphoid malignancies. <i>Journal of Internal Medicine</i> , 2017, 282, 371-394.	6.0	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.	3.5	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.	3.5	57
60	Deciphering the molecular landscape in chronic lymphocytic leukemia: time frame of disease evolution. <i>Haematologica</i> , 2015, 100, 7-16.	3.5	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.	4.6	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.	1.8	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, .	12.4	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.	7.2	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.	6.0	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.	3.5	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.	3.5	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.	6.4	47
69	Immunogenetic Studies of Chronic Lymphocytic Leukemia: Revelations and Speculations about Ontogeny and Clinical Evolution. <i>Cancer Research</i> , 2014, 74, 4211-4216.	0.9	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.	3.5	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.	6.0	46
72	EGR2 mutations define a new clinically aggressive subgroup of chronic lymphocytic leukemia. <i>Leukemia</i> , 2017, 31, 1547-1554.	7.2	46

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73	Uncovering the DNA methylome in chronic lymphocytic leukemia. <i>Epigenetics</i> , 2013, 8, 138-148.	2.7	44
74	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , 2016, 7, 13182.	12.8	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.	3.5	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.	3.5	43
77	<i>microRNA-34b/c</i> on chromosome 11q23 is aberrantly methylated in chronic lymphocytic leukemia. <i>Epigenetics</i> , 2014, 9, 910-917.	2.7	43
78	Clinical impact of recurrently mutated genes on lymphoma diagnostics: state-of-the-art and beyond. <i>Haematologica</i> , 2016, 101, 1002-1009.	3.5	43
79	Antigen Selection Shapes the T-cell Repertoire in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2016, 22, 167-174.	7.0	43
80	Genomic arrays identify high-risk chronic lymphocytic leukemia with genomic complexity: a multi-center study. <i>Haematologica</i> , 2020, 106, 87-97.	3.5	43
81	Distinctive gene expression pattern in VH3-21 utilizing B-cell chronic lymphocytic leukemia. <i>Blood</i> , 2005, 106, 681-689.	1.4	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.	2.2	42
83	A key role for EZH2 in epigenetic silencing of HOX genes in mantle cell lymphoma. <i>Epigenetics</i> , 2013, 8, 1280-1288.	2.7	42
84	Tailored approaches grounded on immunogenetic features for refined prognostication in chronic lymphocytic leukemia. <i>Haematologica</i> , 2019, 104, 360-369.	3.5	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.	9.6	40
86	Epigenetic deregulation in chronic lymphocytic leukemia: Clinical and biological impact. <i>Seminars in Cancer Biology</i> , 2018, 51, 1-11.	9.6	40
87	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. <i>Blood Cancer Journal</i> , 2019, 9, 1.	6.2	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.	1.4	40
89	TP53 Mutations are infrequent in newly diagnosed chronic lymphocytic leukemia. <i>Leukemia Research</i> , 2011, 35, 272-274.	0.8	38
90	Antigen selection in B-cell lymphomas—Tracing the evidence. <i>Seminars in Cancer Biology</i> , 2013, 23, 399-409.	9.6	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.	4.1	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.	2.7	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.	3.5	35
94	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 32-39.	9.6	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.	2.5	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.	7.2	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.	3.5	33
98	Prognostic relevance of MYD88 mutations in CLL: the jury is still out. <i>Blood</i> , 2015, 126, 1043-1044.	1.4	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.	0.8	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.	2.7	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.	1.4	30
102	Clonal evolution as judged by immunoglobulin heavy chain gene rearrangements in relapsing precursor acute lymphoblastic leukemia. <i>European Journal of Haematology</i> , 1999, 63, 171-179.	2.2	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.	2.8	29
104	Immunoglobulin gene analysis in chronic lymphocytic leukemia in the era of next generation sequencing. <i>Leukemia</i> , 2020, 34, 2545-2551.	7.2	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.	1.8	29
106	Immunoglobulin genes in chronic lymphocytic leukemia: key to understanding the disease and improving risk stratification. <i>Haematologica</i> , 2017, 102, 968-971.	3.5	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.	7.0	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.	4.1	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.	5.0	26
110	Transposon Mutagenesis Reveals Fludarabine Resistance Mechanisms in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2016, 22, 6217-6227.	7.0	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.	1.4	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.	3.5	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.	7.2	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.	5.2	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.	4.5	25
116	Common variation at 12q24.13 (OAS3) influences chronic lymphocytic leukemia risk. <i>Leukemia</i> , 2015, 29, 748-751.	7.2	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.	2.7	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.	5.1	24
119	Next generation RNA-sequencing in prognostic subsets of chronic lymphocytic leukemia. <i>American Journal of Hematology</i> , 2012, 87, 737-740.	4.1	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.	2.2	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.	9.6	22
122	Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 16-22.	9.6	22
123	The novel NF- $\kappa$ B inhibitor IMD-0354 induces apoptosis in chronic lymphocytic leukemia. <i>Blood Cancer Journal</i> , 2011, 1, e12-e12.	6.2	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.	7.2	21
125	Prognostic impact of epigenetic classification in chronic lymphocytic leukemia: The case of subset #2. <i>Epigenetics</i> , 2016, 11, 449-455.	2.7	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.	1.4	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.	2.7	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.	3.5	19
129	Technological readiness and implementation of genomicâ€driven precision medicine for complex diseases. <i>Journal of Internal Medicine</i> , 2021, 290, 602-620.	6.0	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.	2.5	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.	7.0	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.	9.6	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.	9.6	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.	3.5	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.	3.5	16
137	Genome-wide promoter methylation of hairy cell leukemia. <i>Blood Advances</i> , 2019, 3, 384-396.	5.2	16
138	DNA methylation profiles in chronic lymphocytic leukemia patients treated with chemoimmunotherapy. <i>Clinical Epigenetics</i> , 2019, 11, 177.	4.1	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.	2.6	15
140	Identification of B-cell lymphoma subsets by plasma protein profiling using recombinant antibody microarrays. <i>Leukemia Research</i> , 2014, 38, 682-690.	0.8	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.	4.1	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.	3.8	13
143	Flow Cytometric Measurement of Blood Cells with BCR-ABL1 Fusion Protein in Chronic Myeloid Leukemia. <i>Scientific Reports</i> , 2017, 7, 623.	3.3	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.	7.0	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.	9.6	13
146	<i>RPS15</i> mutations rewire RNA translation in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2021, 5, 2788-2792.	5.2	12
147	Immunoglobulin VH gene replacements in a T-cell lymphoblastic lymphoma. <i>Molecular Immunology</i> , 1997, 34, 305-313.	2.2	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.	4.4	11
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