

Richard Rosenquist

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	Clinical utility of whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 32-39.	9.6	35
3	Analytical demands to use whole-genome sequencing in precision oncology. <i>Seminars in Cancer Biology</i> , 2022, 84, 16-22.	9.6	22
4	Precision diagnostics in lymphomas – Recent developments and future directions. <i>Seminars in Cancer Biology</i> , 2022, 84, 170-183.	9.6	13
5	Transcriptome sequencing of archived lymphoma specimens is feasible and clinically relevant using exome capture technology. <i>Genes Chromosomes and Cancer</i> , 2022, 61, 27-36.	2.8	2
6	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.	2.2	5
7	Towards precision medicine in lymphoid malignancies. <i>Journal of Internal Medicine</i> , 2022, 292, 221-242.	6.0	9
8	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.	2.5	6
9	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
10	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
11	Precision medicine in cancer: A paradigm shift. <i>Seminars in Cancer Biology</i> , 2022, 84, 1-2.	9.6	5
12	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.	3.5	10
13	Higher-order connections between stereotyped subsets: implications for improved patient classification in CLL. <i>Blood</i> , 2021, 137, 1365-1376.	1.4	72
14	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
15	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
16	Assessing Patients' Knowledge on Chronic Lymphocytic Leukemia: Validation of the ERIC CLL Knowledge Questionnaire in Greece. <i>HemaSphere</i> , 2021, 5, e546.	2.7	0
17	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.	3.0	1
18	Molecular diagnostics and reporting in lymphoid malignancies: Current status and beyond. <i>Hematological Oncology</i> , 2021, 39, 73-77.	1.7	1

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19	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.	1.3	1
20	<i>RPS15</i> mutations rewire RNA translation in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2021, 5, 2788-2792.	5.2	12
21	Technological readiness and implementation of genomic-driven precision medicine for complex diseases. <i>Journal of Internal Medicine</i> , 2021, 290, 602-620.	6.0	18
22	Consistent B Cell Receptor Immunoglobulin Features Between Siblings in Familial Chronic Lymphocytic Leukemia. <i>Frontiers in Oncology</i> , 2021, 11, 740083.	2.8	5
23	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.	1.9	8
24	Specific T Cell Receptor Gene Repertoire Profiles in Subgroups of CLL Patients with Distinct Genomic Aberrations. <i>Blood</i> , 2021, 138, 3749-3749.	1.4	0
25	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.	1.4	1
26	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
27	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
28	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.	2.5	6
29	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.	2.2	1
30	International prognostic score for asymptomatic early-stage chronic lymphocytic leukemia. <i>Blood</i> , 2020, 135, 1859-1869.	1.4	86
31	Immunoglobulin gene analysis in chronic lymphocytic leukemia in the era of next generation sequencing. <i>Leukemia</i> , 2020, 34, 2545-2551.	7.2	29
32	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
33	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
34	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.	1.4	0
35	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
36	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.	7.2	5

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37	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
38	INTERNATIONAL PROGNOSTIC SCORE FOR EARLY STAGE CHRONIC LYMPHOCYtic LEUKEMIA (IPS-A). <i>Hematological Oncology</i> , 2019, 37, 81-82.	1.7	1
39	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
40	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
41	Expression of GNAZ , encoding the G α z protein, predicts survival in mantle cell lymphoma. <i>British Journal of Haematology</i> , 2019, 185, 708-712.	2.5	4
42	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
43	Inhibition of EZH2 and immune signaling exerts synergistic antitumor effects in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2019, 3, 1891-1896.	5.2	10
44	Genome-wide promoter methylation of hairy cell leukemia. <i>Blood Advances</i> , 2019, 3, 384-396.	5.2	16
45	p66Shc deficiency sets the scene for clinically aggressive chronic lymphocytic leukemia. <i>Haematologica</i> , 2019, 104, 1914-1916.	3.5	1
46	DNA methylation profiles in chronic lymphocytic leukemia patients treated with chemoimmunotherapy. <i>Clinical Epigenetics</i> , 2019, 11, 177.	4.1	15
47	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
48	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
49	Immunoglobulin Gene Analysis in Chronic Lymphocytic Leukemia. <i>Methods in Molecular Biology</i> , 2019, 1881, 51-62.	0.9	2
50	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
51	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
52	Tailored approaches grounded on immunogenetic features for refined prognostication in chronic lymphocytic leukemia. <i>Haematologica</i> , 2019, 104, 360-369.	3.5	42
53	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.	1.4	1
54	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

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55	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
56	Epigenetic deregulation in chronic lymphocytic leukemia: Clinical and biological impact. <i>Seminars in Cancer Biology</i> , 2018, 51, 1-11.	9.6	40
57	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
58	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
59	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
60	<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
61	Automated shape-based clustering of 3D immunoglobulin protein structures in chronic lymphocytic leukemia. <i>BMC Bioinformatics</i> , 2018, 19, 414.	2.6	9
62	Immunoglobulin Gene Sequence Analysis In Chronic Lymphocytic Leukemia: From Patient Material To Sequence Interpretation. <i>Journal of Visualized Experiments</i> , 2018, , .	0.3	6
63	Clinical and functional impact of recurrent S1PR1 mutations in mantle cell lymphoma. <i>Blood Advances</i> , 2018, 2, 621-625.	5.2	10
64	Introduction: Epigenetics in cancer. <i>Seminars in Cancer Biology</i> , 2018, 51, iv-v.	9.6	6
65	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.	1.8	8
66	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. <i>Nature Communications</i> , 2017, 8, 14175.	12.8	75
67	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
68	Numerous Ontogenetic Roads to Mantle Cell Lymphoma. <i>American Journal of Pathology</i> , 2017, 187, 1454-1458.	3.8	11
69	Immunoglobulin gene sequence analysis in chronic lymphocytic leukemia: updated ERIC recommendations. <i>Leukemia</i> , 2017, 31, 1477-1481.	7.2	118
70	Genetic landscape and deregulated pathways in B-cell lymphoid malignancies. <i>Journal of Internal Medicine</i> , 2017, 282, 371-394.	6.0	59
71	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
72	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

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73	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.	3.4	10
74	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
75	Introduction to the symposium "Targeted therapy in B-cell malignancies". <i>Journal of Internal Medicine</i> , 2017, 282, 358-359.	6.0	0
76	DRUG PERTURBATION BASED STRATIFICATION OF LYMPHOPROLIFERATIVE DISORDERS. <i>Hematological Oncology</i> , 2017, 35, 56-56.	1.7	2
77	Identification and gene expression analysis of the side population subclone in mantle cell lymphoma. <i>Hematological Oncology</i> , 2017, 35, 284-284.	1.7	0
78	Antigen receptor stereotypy in chronic lymphocytic leukemia. <i>Leukemia</i> , 2017, 31, 282-291.	7.2	122
79	EGR2 mutations define a new clinically aggressive subgroup of chronic lymphocytic leukemia. <i>Leukemia</i> , 2017, 31, 1547-1554.	7.2	46
80	Drug-perturbation-based stratification of blood cancer. <i>Journal of Clinical Investigation</i> , 2017, 128, 427-445.	8.2	124
81	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
82	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
83	Frequent NFKBIE deletions are associated with poor outcome in primary mediastinal B-cell lymphoma. <i>Blood</i> , 2016, 128, 2666-2670.	1.4	82
84	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
85	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
86	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
87	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
88	Prognostic impact of epigenetic classification in chronic lymphocytic leukemia: The case of subset #2. <i>Epigenetics</i> , 2016, 11, 449-455.	2.7	21
89	Whole-exome sequencing in relapsing chronic lymphocytic leukemia: clinical impact of recurrent RPS15 mutations. <i>Blood</i> , 2016, 127, 1007-1016.	1.4	130
90	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

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91	NF- κ 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
92	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
93	B-cell malignancies: All roads lead to NF- κ B activation. <i>Seminars in Cancer Biology</i> , 2016, 39, 1-2.	9.6	4
94	Massive and parallel expression profiling using microarrayed single-cell sequencing. <i>Nature Communications</i> , 2016, 7, 13182.	12.8	44
95	Unraveling the DNA Methylome in Mantle Cell Lymphoma: New Insights into the Cellular Origin. <i>Cancer Cell</i> , 2016, 30, 665-667.	16.8	0
96	Genomic disruption of the histone methyltransferase SETD2 in chronic lymphocytic leukaemia. <i>Leukemia</i> , 2016, 30, 2179-2186.	7.2	69
97	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
98	Transposon Mutagenesis Reveals Fludarabine Resistance Mechanisms in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2016, 22, 6217-6227.	7.0	26
99	Antigen Selection Shapes the T-cell Repertoire in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2016, 22, 167-174.	7.0	43
100	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.	1.4	1
101	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
102	Reappraising Immunoglobulin Repertoire Restrictions in Chronic Lymphocytic Leukemia: Focus on Major Stereotyped Subsets and Closely Related Satellites. <i>Blood</i> , 2016, 128, 4376-4376.	1.4	1
103	The histone methyltransferase EZH2 as a novel prosurvival factor in clinically aggressive chronic lymphocytic leukemia. <i>Oncotarget</i> , 2016, 7, 35946-35959.	1.8	29
104	Not all IGHV3-21 chronic lymphocytic leukemias are equal: prognostic considerations. <i>Blood</i> , 2015, 125, 856-859.	1.4	70
105	Prognostic relevance of MYD88 mutations in CLL: the jury is still out. <i>Blood</i> , 2015, 126, 1043-1044.	1.4	32
106	Deciphering the molecular landscape in chronic lymphocytic leukemia: time frame of disease evolution. <i>Haematologica</i> , 2015, 100, 7-16.	3.5	54
107	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
108	Functional loss of β 2-microglobulin leads to NF- κ B deregulation in aggressive chronic lymphocytic leukemia. <i>Journal of Experimental Medicine</i> , 2015, 212, 833-843.	8.5	85

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109	Clonal evolution in chronic lymphocytic leukemia: impact of subclonality on disease progression. Expert Review of Hematology, 2015, 8, 71-78.	2.2	6
110	Molecular Evidence for Antigen Drive in the Natural History of Mantle Cell Lymphoma. American Journal of Pathology, 2015, 185, 1740-1748.	3.8	13
111	A new piece to the stereotypy "puzzle" in chronic lymphocytic leukemia. Leukemia and Lymphoma, 2015, 56, 3008-3009.	1.3	0
112	Genetics and Prognostication in Splenic Marginal Zone Lymphoma: Revelations from Deep Sequencing. Clinical Cancer Research, 2015, 21, 4174-4183.	7.0	129
113	SF3B1 mutation identifies a distinct subset of myelodysplastic syndrome with ring sideroblasts. Blood, 2015, 126, 233-241.	1.4	361
114	The complex interplay between cell-intrinsic and cell-extrinsic factors driving the evolution of chronic lymphocytic leukemia. Seminars in Cancer Biology, 2015, 34, 22-35.	9.6	40
115	Targeted next-generation sequencing in chronic lymphocytic leukemia: a high-throughput yet tailored approach will facilitate implementation in a clinical setting. Haematologica, 2015, 100, 370-376.	3.5	57
116	Common variation at 12q24.13 (OAS3) influences chronic lymphocytic leukemia risk. Leukemia, 2015, 29, 748-751.	7.2	24
117	Recurrent mutations refine prognosis in chronic lymphocytic leukemia. Leukemia, 2015, 29, 329-336.	7.2	253
118	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.	1.4	2
119	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.	1.4	2
120	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.	1.4	2
121	The international Prognostic Index for patients with CLL (CLL-IPI): An international meta-analysis.. Journal of Clinical Oncology, 2015, 33, 7002-7002.	1.6	10
122	An Innovative High-Throughput Ex Vivo Drug Assay Incorporating the Native Microenvironment Reveals a Novel Mechanism of Action of Idelalisib in CLL. Blood, 2015, 126, 2485-2485.	1.4	0
123	ATM Mutations in Major Stereotyped CLL Subsets: Enrichment in Subset #2 is Associated with Unfavourable Outcome. Blood, 2015, 126, 1712-1712.	1.4	0
124	Genomic Disruption of the Histone Methyltransferase SETD2 in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 365-365.	1.4	0
125	Personalized Modeling of Disease Evolution in CLL: Does Statistical Significance Translate into Predictive Accuracy?. Blood, 2015, 126, 2921-2921.	1.4	0
126	CLL with Mutated IGHV4-34 Antigen Receptors Is Clinically Heterogeneous: Antigen Receptor Stereotypy Makes the Difference. Blood, 2015, 126, 5263-5263.	1.4	0

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127	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.	4.4	4
128	<i>microRNA-34b</i> on chromosome 11q23 is aberrantly methylated in chronic lymphocytic leukemia. <i>Epigenetics</i> , 2014, 9, 910-917.	2.7	43
129	A comprehensive evaluation of the role of genetic variation in follicular lymphoma survival. <i>BMC Medical Genetics</i> , 2014, 15, 113.	2.1	17
130	The microenvironment in lymphomas – Dissecting the complex crosstalk between tumor cells and “by-stander” cells. <i>Seminars in Cancer Biology</i> , 2014, 24, 1-2.	9.6	16
131	Feasibility of targeted next-generation sequencing of the TP53 and ATM genes in chronic lymphocytic leukemia. <i>Leukemia</i> , 2014, 28, 694-696.	7.2	9
132	A genome-wide association study identifies multiple susceptibility loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2014, 46, 56-60.	21.4	166
133	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
134	The frequency of TP53 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
135	On the way towards a CLL prognostic index™: focus on TP53, BIRC3, SF3B1, NOTCH1 and MYD88 in a population-based cohort. <i>Leukemia</i> , 2014, 28, 710-713.	7.2	69
136	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
137	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
138	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
139	MDM2 promotor polymorphism and disease characteristics in chronic lymphocytic leukemia: results of an individual patient data-based meta-analysis. <i>Haematologica</i> , 2014, 99, 1285-1291.	3.5	2
140	Silenced B-cell receptor response to autoantigen in a poor-prognostic subset of chronic lymphocytic leukemia. <i>Haematologica</i> , 2014, 99, 1722-1730.	3.5	9
141	Antigen selection in B-cell lymphomas – Tracing the evidence. <i>Seminars in Cancer Biology</i> , 2013, 23, 399-409.	9.6	38
142	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
143	Antigens in lymphoma development – Current knowledge and future directions. <i>Seminars in Cancer Biology</i> , 2013, 23, 397-398.	9.6	6
144	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

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145	Exploring the genetic landscape in chronic lymphocytic leukemia using high-resolution technologies. <i>Leukemia and Lymphoma</i> , 2013, 54, 1583-1590.	1.3	9
146	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
147	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
148	Distinct patterns of novel gene mutations in poor-prognostic stereotyped subsets of chronic lymphocytic leukemia: the case of SF3B1 and subset #2. <i>Leukemia</i> , 2013, 27, 2196-2199.	7.2	90
149	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
150	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
151	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
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