

# Karla Plevova

## List of Publications by Year in descending order

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Version: 2024-02-01

90  
papers

3,243  
citations

186265

28  
h-index

155660

55  
g-index

91  
all docs

91  
docs citations

91  
times ranked

5297  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of TP53 abnormalities during CLL disease course is associated with telomere length changes. <i>BMC Cancer</i> , 2022, 22, 137.	2.6	2
2	Memory B-cell like chronic lymphocytic leukaemia is associated with specific methylation profile of <i>WNT5A</i> promoter and undetectable expression of <i>WNT5A</i> gene. <i>Epigenetics</i> , 2022, 17, 1628-1635.	2.7	3
3	Clonal haematopoiesis as a risk factor for therapy-related myeloid neoplasms in patients with chronic lymphocytic leukaemia treated with chemo-immunotherapy. <i>British Journal of Haematology</i> , 2022, 198, 103-113.	2.5	7
4	Higher-order connections between stereotyped subsets: implications for improved patient classification in CLL. <i>Blood</i> , 2021, 137, 1365-1376.	1.4	72
5	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
6	Low-burden TP53 mutations in CLL: clinical impact and clonal evolution within the context of different treatment options. <i>Blood</i> , 2021, 138, 2670-2685.	1.4	29
7	Identification of Clinically Relevant Subgroups of Chronic Lymphocytic Leukemia Through Discovery of Abnormal Molecular Pathways. <i>Frontiers in Genetics</i> , 2021, 12, 627964.	2.3	2
8	<i>RPS15</i> mutations rewire RNA translation in chronic lymphocytic leukemia. <i>Blood Advances</i> , 2021, 5, 2788-2792.	5.2	12
9	LYmphoid NeXt-Generation Sequencing (LYNX) Panel. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 959-974.	2.8	11
10	Chromothripsis in Chronic Lymphocytic Leukemia: A Driving Force of Genome Instability. <i>Frontiers in Oncology</i> , 2021, 11, 771664.	2.8	3
11	High-throughput sequencing of T cell receptor alpha chain clonal rearrangements at the DNA level in lymphoid malignancies. <i>British Journal of Haematology</i> , 2020, 188, 723-731.	2.5	13
12	Real-world data on efficacy and safety of obinutuzumab plus chlorambucil, rituximab plus chlorambucil, and rituximab plus bendamustine in the frontline treatment of chronic lymphocytic leukemia: The GO-CLEAR Study by the Czech CLL Study Group. <i>Hematological Oncology</i> , 2020, 38, 509-516.	1.7	7
13	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
14	Profiling of biological and environmental risk factors in immunogenetic subgroups of chronic lymphocytic leukemia - Czech national study. <i>Biomedical Papers of the Medical Faculty of the University Palacky, Olomouc, Czechoslovakia</i> , 2020, 164, 425-434.	0.6	0
15	Clinical impact of genomic analysis in children with B-acute lymphoblastic leukemia: A pilot study in Slovakia. <i>Neoplasma</i> , 2019, 66, 1009-1018.	1.6	0
16	Quality control and quantification in IG/TR next-generation sequencing marker identification: protocols and bioinformatic functionalities by EuroClonality-NGS. <i>Leukemia</i> , 2019, 33, 2254-2265.	7.2	70
17	The importance of complex karyotype in prognostication and treatment of chronic lymphocytic leukemia (CLL): a comprehensive review of the literature. <i>Leukemia and Lymphoma</i> , 2019, 60, 2348-2355.	1.3	6
18	DNA methylation profiles in chronic lymphocytic leukemia patients treated with chemoimmunotherapy. <i>Clinical Epigenetics</i> , 2019, 11, 177.	4.1	15

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19	CLL cells cumulate genetic aberrations prior to the first therapy even in outwardly inactive disease phase. <i>Leukemia</i> , 2019, 33, 518-558.	7.2	15
20	Cytogenetic complexity in chronic lymphocytic leukemia: definitions, associations, and clinical impact. <i>Blood</i> , 2019, 133, 1205-1216.	1.4	164
21	Integrated epigenomic and transcriptomic analysis reveals <i>TP63</i> as a novel player in clinically aggressive chronic lymphocytic leukemia. <i>International Journal of Cancer</i> , 2019, 144, 2695-2706.	5.1	24
22	Tailored approaches grounded on immunogenetic features for refined prognostication in chronic lymphocytic leukemia. <i>Haematologica</i> , 2019, 104, 360-369.	3.5	42
23	Chromothripsis – Extensive Chromosomal Rearrangements and Their Significance in Cancer. <i>Klinická Onkologie</i> , 2019, 32, 101-108.	0.3	2
24	Telomere dynamics in adult hematological malignancies. <i>Biomedical Papers of the Medical Faculty of the University Palacký, Olomouc, Czechoslovakia</i> , 2019, 163, 1-7.	0.6	3
25	Bioinformatic pipelines for whole transcriptome sequencing data exploitation in leukemia patients with complex structural variants. <i>PeerJ</i> , 2019, 7, e7071.	2.0	1
26	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
27	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
28	Casein kinase 1 is a therapeutic target in chronic lymphocytic leukemia. <i>Blood</i> , 2018, 131, 1206-1218.	1.4	39
29	Low-burden TP53 mutations in chronic phase of myeloproliferative neoplasms: association with age, hydroxyurea administration, disease type and JAK2 mutational status. <i>Leukemia</i> , 2018, 32, 450-461.	7.2	54
30	Expression of COBL1 encoding novel ROR1 binding partner is robust predictor of survival in chronic lymphocytic leukemia. <i>Haematologica</i> , 2018, 103, 313-324.	3.5	16
31	C-terminal RUNX1 mutation in familial platelet disorder with predisposition to myeloid malignancies. <i>International Journal of Hematology</i> , 2018, 108, 652-657.	1.6	8
32	Multiple productive IGH rearrangements denote oligoclonality even in immunophenotypically monoclonal CLL. <i>Leukemia</i> , 2018, 32, 234-236.	7.2	18
33	COBL1, LPL and ZAP70 expression defines prognostic subgroups of chronic lymphocytic leukemia patients with high accuracy and correlates with IGHV mutational status. <i>Leukemia and Lymphoma</i> , 2017, 58, 70-79.	1.3	14
34	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
35	Chromosome 6q deletion correlates with poor prognosis and low relative expression of <i>FOXO3</i> in chronic lymphocytic leukemia patients. <i>American Journal of Hematology</i> , 2017, 92, E604-E607.	4.1	13
36	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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37	Single cell analysis revealed a coexistence of <i>NOTCH1</i> and <i>TP53</i> mutations within the same cancer cells in chronic lymphocytic leukaemia patients. <i>British Journal of Haematology</i> , 2017, 178, 979-982.	2.5	5
38	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
39	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
40	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
41	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
42	Whole-exome sequencing in relapsing chronic lymphocytic leukemia: clinical impact of recurrent RPS15 mutations. <i>Blood</i> , 2016, 127, 1007-1016.	1.4	130
43	High-quality full-length immunoglobulin profiling with unique molecular barcoding. <i>Nature Protocols</i> , 2016, 11, 1599-1616.	12.0	179
44	Flow-based immunomagnetic protocol allows efficient separation of CLL and healthy B cells. <i>British Journal of Haematology</i> , 2016, 175, 339-342.	2.5	6
45	Decreased <i>WNT3</i> expression in chronic lymphocytic leukaemia is a hallmark of disease progression and identifies patients with worse prognosis in the subgroup with mutated <i>IGHV</i> . <i>British Journal of Haematology</i> , 2016, 175, 851-859.	2.5	13
46	Autocrine Signaling by Wnt-5a Deregulates Chemotaxis of Leukemic Cells and Predicts Clinical Outcome in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2016, 22, 459-469.	7.0	47
47	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
48	Tailored Approaches for Refined Prognostication in Chronic Lymphocytic Leukemia Patients with Mutated Versus Unmutated Immunoglobulin Receptors. <i>Blood</i> , 2016, 128, 3199-3199.	1.4	0
49	Low-Burden TP53 Mutations Occur in Chronic Phase of Myeloproliferative Neoplasms Regardless of Hydroxyurea Administration, Disease Type, and JAK2 Status. <i>Blood</i> , 2016, 128, 4284-4284.	1.4	0
50	Analysis of Clonal Evolution in Chronic Lymphocytic Leukemia from Inactive to Symptomatic Disease Prior Treatment Using Whole-Exome Sequencing. <i>Blood</i> , 2016, 128, 3206-3206.	1.4	0
51	Not all IGHV3-21 chronic lymphocytic leukemias are equal: prognostic considerations. <i>Blood</i> , 2015, 125, 856-859.	1.4	70
52	Functional loss of $\mu$ leads to NF- $\kappa$ B deregulation in aggressive chronic lymphocytic leukemia. <i>Journal of Experimental Medicine</i> , 2015, 212, 833-843.	8.5	85
53	TP53 mutation analysis in chronic lymphocytic leukemia: comparison of different detection methods. <i>Tumor Biology</i> , 2015, 36, 3371-3380.	1.8	10
54	Ofatumumab added to dexamethasone in patients with relapsed or refractory chronic lymphocytic leukemia: Results from a phase II study. <i>American Journal of Hematology</i> , 2015, 90, 417-421.	4.1	18

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55	Analysis of Prognostic Significance of Merkel Cell Polyomavirus in Chronic Lymphocytic Leukemia. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2015, 15, 439-442.	0.4	4
56	Detailed analysis of therapy-driven clonal evolution of TP53 mutations in chronic lymphocytic leukemia. <i>Leukemia</i> , 2015, 29, 877-885.	7.2	132
57	Abstract 3084: MicroRNA involvement in DNA damage response and BCR signaling in malignant B cells. , 2015, , .		0
58	Single Cell Analysis Proves the Coexistence of NOTCH1 and TP53 Mutations within the Same Cancer Cells in Patients with Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 2913-2913.	1.4	0
59	ATM Mutations in Major Stereotyped CLL Subsets: Enrichment in Subset #2 is Associated with Unfavourable Outcome. <i>Blood</i> , 2015, 126, 1712-1712.	1.4	0
60	Single Cell Analysis of IG Genes in CLL: Cases with Multiple IGH Rearrangements Are Constituted of Several Independent Clones Even When Indistinguishable By Flow Cytometry. <i>Blood</i> , 2015, 126, 4139-4139.	1.4	0
61	EGR2 Mutations in Chronic Lymphocytic Leukemia: A New Bad Player. <i>Blood</i> , 2015, 126, 4126-4126.	1.4	0
62	CLL with Mutated IGHV4-34 Antigen Receptors Is Clinically Heterogeneous: Antigen Receptor Stereotypy Makes the Difference. <i>Blood</i> , 2015, 126, 5263-5263.	1.4	0
63	Multiple productive immunoglobulin heavy chain gene rearrangements in chronic lymphocytic leukemia are mostly derived from independent clones. <i>Haematologica</i> , 2014, 99, 329-338.	3.5	37
64	Chromosomal translocations and karyotype complexity in chronic lymphocytic leukemia: A systematic reappraisal of classic cytogenetic data. <i>American Journal of Hematology</i> , 2014, 89, 249-255.	4.1	113
65	Towards error-free profiling of immune repertoires. <i>Nature Methods</i> , 2014, 11, 653-655.	19.0	411
66	Clonal evolution in chronic lymphocytic leukemia detected by fluorescence in situ hybridization and conventional cytogenetics after stimulation with CpG oligonucleotides and interleukin-2: A prospective analysis. <i>Leukemia Research</i> , 2014, 38, 170-175.	0.8	14
67	Identification of novel sequence variations in microRNAs in chronic lymphocytic leukemia. <i>Carcinogenesis</i> , 2014, 35, 992-1002.	2.8	18
68	Clinical effect of stereotyped B-cell receptor immunoglobulins in chronic lymphocytic leukaemia: a retrospective multicentre study. <i>Lancet Haematology</i> , the, 2014, 1, e74-e84.	4.6	93
69	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
70	Abstract 5198: Identification of microRNAs involved in DNA damage response in malignant B cells and their biological and clinical relevance. , 2014, , .		0
71	Prognostic Impact of NOTCH1 Hotspot Mutation in TP53-Mutated Patients with Chronic Lymphocytic Leukemia. <i>Blood</i> , 2014, 124, 3283-3283.	1.4	0
72	Charting Unique Signatures of Somatic Hypermutation Amongst Chronic Lymphocytic Leukemia Patients Expressing IGHV4-34 Clonotypic B Cell Receptors. <i>Blood</i> , 2014, 124, 1969-1969.	1.4	0

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73	Subset-Specific Spectra of Recurrent Gene Mutations in Chronic Lymphocytic Leukemia with Stereotyped B-Cell Receptors. <i>Blood</i> , 2014, 124, 3320-3320.	1.4	6
74	The origin of deletion 22q11 in chronic lymphocytic leukemia is related to the rearrangement of immunoglobulin lambda light chain locus. <i>Leukemia Research</i> , 2013, 37, 802-808.	0.8	17
75	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
76	The Planar Cell Polarity Pathway Drives Pathogenesis of Chronic Lymphocytic Leukemia by the Regulation of B-Lymphocyte Migration. <i>Cancer Research</i> , 2013, 73, 1491-1501.	0.9	83
77	Ofatumumab Added To Dexamethasone In Patients With Relapsed Or Refractory Chronic Lymphocytic Leukemia. Results From a Phase II Study Of The Czech Leukemia Study Group For Life. <i>Blood</i> , 2013, 122, 2877-2877.	1.4	15
78	Differential Distribution Of Recurrent Gene Mutations In Subsets Of Chronic Lymphocytic Leukemia Patients With Stereotyped B-Cell Receptors: Results From A Multicenter Project Of The European Research Initiative On CLL In A Series Of 2482 Cases. <i>Blood</i> , 2013, 122, 4113-4113.	1.4	1
79	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.	1.4	0
80	SF3B1 Mutations Frequently Occur With Both ATM Mutations and TP53 Mutations In CLL Patients. <i>Blood</i> , 2013, 122, 2868-2868.	1.4	0
81	MicroRNA-650 expression is influenced by immunoglobulin gene rearrangement and affects the biology of chronic lymphocytic leukemia. <i>Blood</i> , 2012, 119, 2110-2113.	1.4	92
82	Specific p53 mutations do not impact results of alemtuzumab therapy among patients with chronic lymphocytic leukemia. <i>Leukemia and Lymphoma</i> , 2012, 53, 1817-1819.	1.3	4
83	MicroRNAs Regulate p21Waf1/Cip1 Protein Expression and the DNA Damage Response in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2012, 30, 1362-1372.	3.2	97
84	Post-translational modifications regulate signalling by Ror1. <i>Acta Physiologica</i> , 2011, 203, 351-362.	3.8	33
85	Mutational Analysis of Mir-29 Family Members in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2011, 118, 1770-1770.	1.4	0
86	Clonal Evolution of Malignant Populations In Potentially Biclinal Chronic Lymphocytic Leukemia Patients. <i>Blood</i> , 2010, 116, 2412-2412.	1.4	0
87	MicroRNAs in chronic lymphocytic leukemia pathogenesis and disease subtypes. <i>Leukemia and Lymphoma</i> , 2009, 50, 506-509.	1.3	101
88	MicroRNA isolation and stability in stored RNA samples. <i>Biochemical and Biophysical Research Communications</i> , 2009, 390, 1-4.	2.1	189
89	miR-34a, miR-29c and miR-17-5p are downregulated in CLL patients with TP53 abnormalities. <i>Leukemia</i> , 2009, 23, 1159-1163.	7.2	162
90	Duplication of 8q24 in Chronic Lymphocytic Leukemia: Cytogenetic and Molecular Biologic Analysis of MYC Aberrations. <i>Frontiers in Oncology</i> , 0, 12, .	2.8	1