Karla Plevova

List of Publications by Year
in descending order

90 papers	3,243 citations	186209 28 h-index	155592 55 g-index
91 all docs	91 docs citations	91 times ranked	5297 citing authors

#	Article	IF	Citations
1	Towards error-free profiling of immune repertoires. Nature Methods, 2014, 11, 653-655.	9.0	411
2	MicroRNA isolation and stability in stored RNA samples. Biochemical and Biophysical Research Communications, 2009, 390, 1-4.	1.0	189
3	High-quality full-length immunoglobulin profiling with unique molecular barcoding. Nature Protocols, 2016, 11, 1599-1616.	5.5	179
4	Cytogenetic complexity in chronic lymphocytic leukemia: definitions, associations, and clinical impact. Blood, 2019, 133, 1205-1216.	0.6	164
5	miR-34a, miR-29c and miR-17-5p are downregulated in CLL patients with TP53 abnormalities. Leukemia, 2009, 23, 1159-1163.	3.3	162
6	Detailed analysis of therapy-driven clonal evolution of TP53 mutations in chronic lymphocytic leukemia. Leukemia, 2015, 29, 877-885.	3.3	132
7	Whole-exome sequencing in relapsing chronic lymphocytic leukemia: clinical impact of recurrent RPS15 mutations. Blood, 2016, 127, 1007-1016.	0.6	130
8	Chromosomal translocations and karyotype complexity in chronic lymphocytic leukemia: A systematic reappraisal of classic cytogenetic data. American Journal of Hematology, 2014, 89, 249-255.	2.0	113
9	MicroRNAs in chronic lymphocytic leukemia pathogenesis and disease subtypes. Leukemia and Lymphoma, 2009, 50, 506-509.	0.6	101
10	MicroRNAs Regulate p21Waf1/Cip1 Protein Expression and the DNA Damage Response in Human Embryonic Stem Cells. Stem Cells, 2012, 30, 1362-1372.	1.4	97
11	Clinical effect of stereotyped B-cell receptor immunoglobulins in chronic lymphocytic leukaemia: a retrospective multicentre study. Lancet Haematology,the, 2014, 1, e74-e84.	2.2	93
12	MicroRNA-650 expression is influenced by immunoglobulin gene rearrangement and affects the biology of chronic lymphocytic leukemia. Blood, 2012, 119, 2110-2113.	0.6	92
13	Distinct patterns of novel gene mutations in poor-prognostic stereotyped subsets of chronic lymphocytic leukemia: the case of SF3B1 and subset #2. Leukemia, 2013, 27, 2196-2199.	3.3	90
14	Functional loss of IÎºBÎµ leads to NF-ÎºB deregulation in aggressive chronic lymphocytic leukemia. Journal of Experimental Medicine, 2015, 212, 833-843.	4.2	85
15	The Planar Cell Polarity Pathway Drives Pathogenesis of Chronic Lymphocytic Leukemia by the Regulation of B-Lymphocyte Migration. Cancer Research, 2013, 73, 1491-1501.	0.4	83
16	Higher-order connections between stereotyped subsets: implications for improved patient classification in CLL. Blood, 2021, 137, 1365-1376.	0.6	72
17	Not all IGHV3-21 chronic lymphocytic leukemias are equal: prognostic considerations. Blood, 2015, 125, 856-859.	0.6	70
18	Quality control and quantification in IG/TR next-generation sequencing marker identification: protocols and bioinformatic functionalities by EuroClonality-NGS. Leukemia, 2019, 33, 2254-2265.	3.3	70

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19	Different spectra of recurrent gene mutations in subsets of chronic lymphocytic leukemia harboring stereotyped B-cell receptors. Haematologica, 2016, 101, 959-967.	1.7	57
20	Low-burden TP53 mutations in chronic phase of myeloproliferative neoplasms: association with age, hydroxyurea administration, disease type and JAK2 mutational status. Leukemia, 2018, 32, 450-461.	3.3	54
21	Autocrine Signaling by Wnt-5a Deregulates Chemotaxis of Leukemic Cells and Predicts Clinical Outcome in Chronic Lymphocytic Leukemia. Clinical Cancer Research, 2016, 22, 459-469.	3.2	47
22	EGR2 mutations define a new clinically aggressive subgroup of chronic lymphocytic leukemia. Leukemia, 2017, 31, 1547-1554.	3.3	46
23	Genomic arrays identify high-risk chronic lymphocytic leukemia with genomic complexity: a multi-center study. Haematologica, 2020, 106, 87-97.	1.7	43
24	Tailored approaches grounded on immunogenetic features for refined prognostication in chronic lymphocytic leukemia. Haematologica, 2019, 104, 360-369.	1.7	42
25	Casein kinase 1 is a therapeutic target in chronic lymphocytic leukemia. Blood, 2018, 131, 1206-1218.	0.6	39
26	Multiple productive immunoglobulin heavy chain gene rearrangements in chronic lymphocytic leukemia are mostly derived from independent clones. Haematologica, 2014, 99, 329-338.	1.7	37
27	Additional trisomies amongst patients with chronic lymphocytic leukemia carrying trisomy 12: the accompanying chromosome makes a difference. Haematologica, 2016, 101, e299-e302.	1.7	35
28	Postâ€translational modifications regulate signalling by Ror1. Acta Physiologica, 2011, 203, 351-362.	1.8	33
29	Low-burden <i>TP53</i> mutations in CLL: clinical impact and clonal evolution within the context of different treatment options. Blood, 2021, 138, 2670-2685.	0.6	29
30	Chronic Lymphocytic Leukemia with Mutated IGHV4-34 Receptors: Shared and Distinct Immunogenetic Features and Clinical Outcomes. Clinical Cancer Research, 2017, 23, 5292-5301.	3.2	27
31	Integrated epigenomic and transcriptomic analysis reveals <i>TP63</i> as a novel player in clinically aggressive chronic lymphocytic leukemia. International Journal of Cancer, 2019, 144, 2695-2706.	2.3	24
32	Higher-order immunoglobulin repertoire restrictions in CLL: the illustrative case of stereotyped subsets 2 and 169. Blood, 2021, 137, 1895-1904.	0.6	21
33	Epigenetic silencing of miR-26A1 in chronic lymphocytic leukemia and mantle cell lymphoma: Impact on EZH2 expression. Epigenetics, 2016, 11, 335-343.	1.3	20
34	Identification of novel sequence variations in microRNAs in chronic lymphocytic leukemia. Carcinogenesis, 2014, 35, 992-1002.	1.3	18
35	Ofatumumab added to dexamethasone in patients with relapsed or refractory chronic lymphocytic leukemia: Results from a phase II study. American Journal of Hematology, 2015, 90, 417-421.	2.0	18
36	Multiple productive IGH rearrangements denote oligoclonality even in immunophenotypically monoclonal CLL. Leukemia, 2018, 32, 234-236.	3.3	18

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37	The origin of deletion 22q11 in chronic lymphocytic leukemia is related to the rearrangement of immunoglobulin lambda light chain locus. Leukemia Research, 2013, 37, 802-808.	0.4	17
38	The frequency of <i><scp>TP</scp>53</i> gene defects differs between chronic lymphocytic leukaemia subgroups harbouring distinct antigen receptors. British Journal of Haematology, 2014, 166, 621-625.	1.2	17
39	ATM mutations in major stereotyped subsets of chronic lymphocytic leukemia: enrichment in subset #2 is associated with markedly short telomeres. Haematologica, 2016, 101, e369-e373.	1.7	16
40	No improvement in long-term survival over time for chronic lymphocytic leukemia patients in stereotyped subsets #1 and #2 treated with chemo(immuno)therapy. Haematologica, 2018, 103, e158-e161.	1.7	16
41	Expression of COBLL1 encoding novel ROR1 binding partner is robust predictor of survival in chronic lymphocytic leukemia. Haematologica, 2018, 103, 313-324.	1.7	16
42	DNA methylation profiles in chronic lymphocytic leukemia patients treated with chemoimmunotherapy. Clinical Epigenetics, 2019, 11, 177.	1.8	15
43	CLL cells cumulate genetic aberrations prior to the first therapy even in outwardly inactive disease phase. Leukemia, 2019, 33, 518-558.	3.3	15
44	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. Blood, 2013, 122, 2877-2877.	0.6	15
45	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. Leukemia Research, 2014, 38, 170-175.	0.4	14
46	COBLL1,LPLandZAP70expression defines prognostic subgroups of chronic lymphocytic leukemia patients with high accuracy and correlates withIGHVmutational status. Leukemia and Lymphoma, 2017, 58, 70-79.	0.6	14
47	Decreased <i><scp>WNT</scp>3</i> expression in chronic lymphocytic leukaemia is a hallmark of disease progression and identifies patients with worse prognosis in the subgroup with mutated <i><scp>IGHV</scp></i>. British Journal of Haematology, 2016, 175, 851-859.	1.2	13
48	Chromosome 6q deletion correlates with poor prognosis and low relative expression of <i>FOXO3</i> in chronic lymphocytic leukemia patients. American Journal of Hematology, 2017, 92, E604-E607.	2.0	13
49	Highâ€throughput sequencing of Tâ€cell receptor alpha chain clonal rearrangements at the DNA level in lymphoid malignancies. British Journal of Haematology, 2020, 188, 723-731.	1.2	13
50	<i>RPS15</i> mutations rewire RNA translation in chronic lymphocytic leukemia. Blood Advances, 2021, 5, 2788-2792.	2.5	12
51	LYmphoid NeXt-Generation Sequencing (LYNX) Panel. Journal of Molecular Diagnostics, 2021, 23, 959-974.	1.2	11
52	TP53 mutation analysis in chronic lymphocytic leukemia: comparison of different detection methods. Tumor Biology, 2015, 36, 3371-3380.	0.8	10
53	C-terminal RUNX1 mutation in familial platelet disorder with predisposition to myeloid malignancies. International Journal of Hematology, 2018, 108, 652-657.	0.7	8
54	Realâ€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 <scp>GOâ€CLLEAR</scp> Study by the Czech <scp>CLL</scp> Study Group. Hematological Oncology, 2020, 38, 509-516.	0.8	7

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55	Clonal haematopoiesis as a risk factor for therapyâ€related myeloid neoplasms in patients with chronic lymphocytic leukaemia treated with chemoâ€(immuno)therapy. British Journal of Haematology, 2022, 198, 103-113.	1.2	7
56	<scp>ROR</scp>1â€based immunomagnetic protocol allows efficient separation of <scp>CLL</scp> and healthy B cells. British Journal of Haematology, 2016, 175, 339-342.	1.2	6
57	The importance of complex karyotype in prognostication and treatment of chronic lymphocytic leukemia (CLL): a comprehensive review of the literature. Leukemia and Lymphoma, 2019, 60, 2348-2355.	0.6	6
58	Subset-Specific Spectra of Recurrent Gene Mutations in Chronic Lymphocytic Leukemia with Stereotyped B-Cell Receptors. Blood, 2014, 124, 3320-3320.	0.6	6
59	Single cell analysis revealed a coexistence of <i><scp>NOTCH</scp>1</i> and <i><scp>TP</scp>53</i> mutations within the same cancer cells in chronic lymphocytic leukaemia patients. British Journal of Haematology, 2017, 178, 979-982.	1.2	5
60	Specific p53 mutations do not impact results of alemtuzumab therapy among patients with chronic lymphocytic leukemia. Leukemia and Lymphoma, 2012, 53, 1817-1819.	0.6	4
61	Analysis of Prognostic Significance of Merkel Cell Polyomavirus in Chronic Lymphocytic Leukemia. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, 439-442.	0.2	4
62	Telomere dynamics in adult hematological malignancies. Biomedical Papers of the Medical Faculty of the University Palacký, Olomouc, Czechoslovakia, 2019, 163, 1-7.	0.2	3
63	Chromothripsis in Chronic Lymphocytic Leukemia: A Driving Force of Genome Instability. Frontiers in Oncology, 2021, 11, 771664.	1.3	3
64	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. Epigenetics, 2022, 17, 1628-1635.	1.3	3
65	Identification of Clinically Relevant Subgroups of Chronic Lymphocytic Leukemia Through Discovery of Abnormal Molecular Pathways. Frontiers in Genetics, 2021, 12, 627964.	1.1	2
66	Chromothripsis â€“ Extensive Chromosomal Rearrangements and Their Significance in Cancer. Klinicka Onkologie, 2019, 32, 101-108.	0.1	2
67	Evolution of TP53 abnormalities during CLL disease course is associated with telomere length changes. BMC Cancer, 2022, 22, 137.	1.1	2
68	Differential Distribution Of Recurrent Gene Mutations In Subsets Of Chronic Lymphocytic Leukemia Patients With Stereotyped B-Cell Receptors: Results From A Multicenter Project Of The European Research Initiative On CLL In A Series Of 2482 Cases. Blood, 2013, 122, 4113-4113.	0.6	1
69	Reappraising Immunoglobulin Repertoire Restrictions in Chronic Lymphocytic Leukemia: Focus on Major Stereotyped Subsets and Closely Related Satellites. Blood, 2016, 128, 4376-4376.	0.6	1
70	Bioinformatic pipelines for whole transcriptome sequencing data exploitation in leukemia patients with complex structural variants. PeerJ, 2019, 7, e7071.	0.9	1
71	Higher Order Restrictions of the Immunoglobulin Repertoire in CLL: The Illustrative Case of Stereotyped Subsets #2 and #169. Blood, 2019, 134, 5453-5453.	0.6	1
72	Duplication of 8q24 in Chronic Lymphocytic Leukemia: Cytogenetic and Molecular Biologic Analysis of MYC Aberrations. Frontiers in Oncology, 0, 12, .	1.3	1

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73	Clinical impact of genomic analysis in children with B-acute lymphoblastic leukemia: A pilot study in Slovakia. Neoplasma, 2019, 66, 1009-1018.	0.7	0
74	Clonal Evolution of Malignant Populations In Potentially Biclonal Chronic Lymphocytic Leukemia Patients. Blood, 2010, 116, 2412-2412.	0.6	0
75	Mutational Analysis of Mir-29 Family Members in Chronic Lymphocytic Leukemia. Blood, 2011, 118, 1770-1770.	0.6	0
76	Novel Gene Mutations In Chronic Lymphocytic Leukemia: Prevalence and Clinical Implications In A Series Of 3185 Cases - Initial Results From The European Research Initiative On CLL. Blood, 2013, 122, 1614-1614.	0.6	0
77	SF3B1 Mutations Frequently Occur With Both ATM Mutations and TP53 Mutations In CLL Patients. Blood, 2013, 122, 2868-2868.	0.6	0
78	Abstract 5198: Identification of microRNAs involved in DNA damage response in malignant B cells and their biological and clinical relevance. , 2014, , .		0
79	Prognostic Impact of NOTCH1 Hotspot Mutation in TP53-Mutated Patients with Chronic Lymphocytic Leukemia. Blood, 2014, 124, 3283-3283.	0.6	0
80	Charting Unique Signatures of Somatic Hypermutation Amongst Chronic Lymphocytic Leukemia Patients Expressing IGHV4-34 Clonotypic B Cell Receptors. Blood, 2014, 124, 1969-1969.	0.6	0
81	Abstract 3084: MicroRNA involvement in DNA damage response and BCR signaling in malignant B cells. , 2015, , .		0
82	Single Cell Analysis Proves the Coexistence of NOTCH1 and TP53 Mutations within the Same Cancer Cells in Patients with Chronic Lymphocytic Leukemia. Blood, 2015, 126, 2913-2913.	0.6	0
83	ATM Mutations in Major Stereotyped CLL Subsets: Enrichment in Subset #2 is Associated with Unfavourable Outcome. Blood, 2015, 126, 1712-1712.	0.6	0
84	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. Blood, 2015, 126, 4139-4139.	0.6	0
85	EGR2 Mutations in Chronic Lymphocytic Leukemia: A New Bad Player. Blood, 2015, 126, 4126-4126.	0.6	0
86	CLL with Mutated IGHV4-34 Antigen Receptors Is Clinically Heterogeneous: Antigen Receptor Stereotypy Makes the Difference. Blood, 2015, 126, 5263-5263.	0.6	0
87	Tailored Approaches for Refined Prognostication in Chronic Lymphocytic Leukemia Patients with Mutated Versus Unmutated Immunoglobulin Receptors. Blood, 2016, 128, 3199-3199.	0.6	0
88	Low-Burden TP53 Mutations Occur in Chronic Phase of Myeloproliferative Neoplasms Regardless of Hydroxyurea Administration, Disease Type, and JAK2 Status. Blood, 2016, 128, 4284-4284.	0.6	0
89	Analysis of Clonal Evolution in Chronic Lymphocytic Leukemia from Inactive to Symptomatic Disease Prior Treatment Using Whole-Exome Sequencing. Blood, 2016, 128, 3206-3206.	0.6	0
90	Profiling of biological and environmental risk factors in immunogenetic subgroups of chronic lymphocytic leukemia - Czech national study. Biomedical Papers of the Medical Faculty of the University Palacký, Olomouc, Czechoslovakia, 2020, 164, 425-434.	0.2	0