Sarka Pospisilova

List of Publications by Year
in descending order

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250 papers	8,069 citations	47006 47 h-index	62596 80 g-index
253 all docs	253 docs citations	253 times ranked	10596 citing authors

#	ARTICLE	IF	CITATIONS
1	A GP1BA Variant in a Czech Family with Monoallelic Bernard-Soulier Syndrome. International Journal of Molecular Sciences, 2022, 23, 885.	4.1	1
2	Evolution of TP53 abnormalities during CLL disease course is associated with telomere length changes. BMC Cancer, 2022, 22, 137.	2.6	2
3	Lyn Phosphorylates and Controls ROR1 Surface Dynamics During Chemotaxis of CLL Cells. Frontiers in Cell and Developmental Biology, 2022, 10, 838871.	3.7	4
4	Very rare nearâ€haploid acute lymphoblastic leukemia resistant to immunotherapy and CARâ€T therapy in 19â€yearâ€old male patient. Clinical Case Reports (discontinued), 2022, 10, e05545.	0.5	2
5	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.	2.7	3
6	The EHA Research Roadmap: Malignant Lymphoid Diseases. HemaSphere, 2022, 6, e726.	2.7	1
7	Comparative analysis of targeted next-generation sequencing panels for the detection of gene mutations in chronic lymphocytic leukemia: an ERIC multi-center study. Haematologica, 2021, 106, 682-691.	3.5	10
8	Whole Exome Sequencing reveals NOTCH1 mutations in anaplastic large cell lymphoma and points to Notch both as a key pathway and a potential therapeutic target. Haematologica, 2021, 106, 1693-1704.	3.5	40
9	Thyroid and androgen receptor signaling are antagonized by Î¼â€Crystallin in prostate cancer. International Journal of Cancer, 2021, 148, 731-747.	5.1	17
10	Higher-order connections between stereotyped subsets: implications for improved patient classification in CLL. Blood, 2021, 137, 1365-1376.	1.4	72
11	Higher-order immunoglobulin repertoire restrictions in CLL: the illustrative case of stereotyped subsets 2 and 169. Blood, 2021, 137, 1895-1904.	1.4	21
12	STAT3 and TP53 mutations associate with poor prognosis in anaplastic large cell lymphoma. Leukemia, 2021, 35, 1500-1505.	7.2	29
13	Identification and functional characterization of new missense SNPs in the coding region of the TP53 gene. Cell Death and Differentiation, 2021, 28, 1477-1492.	11.2	26
14	<i>miR-29</i>modulates CD40 signaling in chronic lymphocytic leukemia by targeting TRAF4: an axis affected by BCR inhibitors. Blood, 2021, 137, 2481-2494.	1.4	37
15	RGDS-Modified Superporous Poly(2-Hydroxyethyl Methacrylate)-Based Scaffolds as 3D In Vitro Leukemia Model. International Journal of Molecular Sciences, 2021, 22, 2376.	4.1	10
16	Bioinformatic strategies for the analysis of genomic aberrations detected by targeted NGS panels with clinical application. PeerJ, 2021, 9, e10897.	2.0	4
17	Genomic landscape of B-other acute lymphoblastic leukemia in an adult retrospective cohort with a focus on <i>BCR-ABL1</i>-like subtype. Acta OncolÃ³gica, 2021, 60, 760-770.	1.8	2
18	FoxO1-GAB1 axis regulates homing capacity and tonic AKT activity in chronic lymphocytic leukemia. Blood, 2021, 138, 758-772.	1.4	19

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19	Two Novel Mutations in the JAG1 Gene in Pediatric Patients with Alagille Syndrome: The First Case Series in Czech Republic. Diagnostics, 2021, 11, 983.	2.6	2
20	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.	1.4	29
21	Dynamic miRNA changes during the process of epileptogenesis in an infantile and adult-onset model. Scientific Reports, 2021, 11, 9649.	3.3	12
22	Identification of Clinically Relevant Subgroups of Chronic Lymphocytic Leukemia Through Discovery of Abnormal Molecular Pathways. Frontiers in Genetics, 2021, 12, 627964.	2.3	2
23	IL4-STAT6 signaling induces CD20 in chronic lymphocytic leukemia and this axis is repressed by PI3KÎ´ inhibitor idelalisib. Haematologica, 2021, 106, 2995-2999.	3.5	14
24	<i>RPS15</i> mutations rewire RNA translation in chronic lymphocytic leukemia. Blood Advances, 2021, 5, 2788-2792.	5.2	12
25	Hypermethylation of CD19 promoter enables antigen-negative escape to CART-19 in vivo and in vitro. , 2021, 9, e002352.		14
26	Distribution of SARS-CoV-2 Lineages in the Czech Republic, Analysis of Data from the First Year of the Pandemic. Microorganisms, 2021, 9, 1671.	3.6	7
27	LYmphoid NeXt-Generation Sequencing (LYNX) Panel. Journal of Molecular Diagnostics, 2021, 23, 959-974.	2.8	11
28	Super-enhancer-based identification of a BATF3/IL-2Râˆ'module reveals vulnerabilities in anaplastic large cell lymphoma. Nature Communications, 2021, 12, 5577.	12.8	21
29	High activation of STAT5A drives peripheral T-cell lymphoma and leukemia. Haematologica, 2020, 105, 435-447.	3.5	27
30	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.	2.5	13
31	Epilepsy miRNA Profile Depends on the Age of Onset in Humans and Rats. Frontiers in Neuroscience, 2020, 14, 924.	2.8	14
32	Functional analysis of germline ETV6 W380R mutation causing inherited thrombocytopenia and secondary acute lymphoblastic leukemia or essential thrombocythemia. Platelets, 2020, 32, 1-4.	2.3	2
33	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.	1.7	7
34	International prognostic score for asymptomatic early-stage chronic lymphocytic leukemia. Blood, 2020, 135, 1859-1869.	1.4	86
35	IL10RA Modulates Crizotinib Sensitivity in NPM1-ALK-positive Anaplastic Large Cell Lymphoma. Blood, 2020, 136, 1657-1669.	1.4	22
36	Nuclear inclusions of pathogenic ataxin-1 induce oxidative stress and perturb the protein synthesis machinery. Redox Biology, 2020, 32, 101458.	9.0	14

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37	CD20 is dispensable for B-cell receptor signaling but is required for proper actin polymerization, adhesion and migration of malignant B cells. PLoS ONE, 2020, 15, e0229170.	2.5	15
38	Performance of anti-CD19 chimeric antigen receptor T cells in genetically defined classes of chronic lymphocytic leukemia. , 2020, 8, e000471.		8
39	Diagnosis of Bloom Syndrome in a Patient with Short Stature, Recurrence of Malignant Lymphoma, and Consanguineous Origin. Molecular Syndromology, 2020, 11, 73-82.	0.8	2
40	The Effect of SF3B1 Mutation on the DNA Damage Response and Nonsense-Mediated mRNA Decay in Cancer. Frontiers in Oncology, 2020, 10, 609409.	2.8	15
41	Genomic arrays identify high-risk chronic lymphocytic leukemia with genomic complexity: a multi-center study. Haematologica, 2020, 106, 87-97.	3.5	43
42	Abstract 4715: Characterization of potential co-drivers of pathogenesis in ALK positive ALCL. , 2020, , .		0
43	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 Palacky&#x0301;, Olomouc, Czechoslovakia, 2020, 164, 425-434.	0.6	0
44	MicroRNA miR-34a downregulates FOXP1 during DNA damage response to limit BCR signalling in chronic lymphocytic leukaemia B cells. Leukemia, 2019, 33, 403-414.	7.2	46
45	Novel genetic variant of HPS1 gene in Hermansky-Pudlak syndrome with fulminant progression of pulmonary fibrosis: a case report. BMC Pulmonary Medicine, 2019, 19, 178.	2.0	7
46	Deficiency and haploinsufficiency of histone macroH2A1.1 in mice recapitulate hematopoietic defects of human myelodysplastic syndrome. Clinical Epigenetics, 2019, 11, 121.	4.1	21
47	International Prognostic Score (IPS-A) for Patients with Early Stage Chronic Lymphocytic Leukemia. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, S278.	0.4	1
48	Different time-dependent changes of risk for evolution in chronic lymphocytic leukemia with mutated or unmutated antigen B cell receptors. Leukemia, 2019, 33, 1801-1805.	7.2	5
49	Detection of a deletion at 22q11 locus involving <i>ZNF280A/ZNF280B/PRAME/GGTLC2</i> in Bâ€cell malignancies: simply a consequence of an immunoglobulin lambda light chain rearrangement. British Journal of Haematology, 2019, 186, e91-e94.	2.5	3
50	Impact of gene mutations and chromosomal aberrations on progression-free survival in chronic lymphocytic leukemia patients treated with front-line chemoimmunotherapy: Clinical practice experience. Leukemia Research, 2019, 81, 75-81.	0.8	8
51	A novel germline mutation of the SFTPA1 gene in familial interstitial pneumonia. Human Genome Variation, 2019, 6, 12.	0.7	15
52	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.	1.3	6
53	DNA methylation profiles in chronic lymphocytic leukemia patients treated with chemoimmunotherapy. Clinical Epigenetics, 2019, 11, 177.	4.1	15
54	CLL cells cumulate genetic aberrations prior to the first therapy even in outwardly inactive disease phase. Leukemia, 2019, 33, 518-558.	7.2	15

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55	Cytogenetic complexity in chronic lymphocytic leukemia: definitions, associations, and clinical impact. Blood, 2019, 133, 1205-1216.	1.4	164
56	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.	5.1	24
57	Activation-induced deaminase and its splice variants associate with trisomy 12 in chronic lymphocytic leukemia. Annals of Hematology, 2019, 98, 423-435.	1.8	2
58	Diseaseâ€biased and shared characteristics of the immunoglobulin gene repertoires in marginal zone B cell lymphoproliferations. Journal of Pathology, 2019, 247, 416-421.	4.5	25
59	Tailored approaches grounded on immunogenetic features for refined prognostication in chronic lymphocytic leukemia. Haematologica, 2019, 104, 360-369.	3.5	42
60	Analysis of Mutational Landscape in Systemic Anaplastic Large Cell Lymphoma Identifies Novel Prognostic Markers. Blood, 2019, 134, 1490-1490.	1.4	2
61	MicroRNA-210 expression during childbirth and postpartum as a potential biomarker of acute fetal hypoxia. Biomedical Papers of the Medical Faculty of the University Palacky&#x0301;, Olomouc, Czechoslovakia, 2019, 163, 259-264.	0.6	5
62	Telomere dynamics in adult hematological malignancies. Biomedical Papers of the Medical Faculty of the University Palacky&#x0301;, Olomouc, Czechoslovakia, 2019, 163, 1-7.	0.6	3
63	Bioinformatic pipelines for whole transcriptome sequencing data exploitation in leukemia patients with complex structural variants. PeerJ, 2019, 7, e7071.	2.0	1
64	Characterization of Pathogenic Variants Associated with Hereditary Thrombocytopenias in Families from the Czech Republic. Blood, 2019, 134, 2343-2343.	1.4	0
65	Higher Order Restrictions of the Immunoglobulin Repertoire in CLL: The Illustrative Case of Stereotyped Subsets #2 and #169. Blood, 2019, 134, 5453-5453.	1.4	1
66	ERIC recommendations for TP53 mutation analysis in chronic lymphocytic leukemiaâ€"update on methodological approaches and results interpretation. Leukemia, 2018, 32, 1070-1080.	7.2	149
67	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.	3.5	16
68	Casein kinase 1 is a therapeutic target in chronic lymphocytic leukemia. Blood, 2018, 131, 1206-1218.	1.4	39
69	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.	7.2	54
70	Transcription factor YY1 can control AIDâ€mediated mutagenesis in mice. European Journal of Immunology, 2018, 48, 273-282.	2.9	5
71	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. Cytometry Part B - Clinical Cytometry, 2018, 94, 121-128.	1.5	133
72	Expression of COBLL1 encoding novel ROR1 binding partner is robust predictor of survival in chronic lymphocytic leukemia. Haematologica, 2018, 103, 313-324.	3.5	16

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73	<i>TP53</i> aberrations in chronic lymphocytic leukemia: an overview of the clinical implications of improved diagnostics. Haematologica, 2018, 103, 1956-1968.	3.5	94
74	A novel germline mutation in <i>GP1BA</i> gene N-terminal domain in monoallelic Bernard-Soulier syndrome. Platelets, 2018, 29, 827-833.	2.3	8
75	ToTem: a tool for variant calling pipeline optimization. BMC Bioinformatics, 2018, 19, 243.	2.6	2
76	The Role of Oncogenic Tyrosine Kinase NPM-ALK in Genomic Instability. Cancers, 2018, 10, 64.	3.7	10
77	Rituximab primarily targets an intra-clonal BCR signaling proficient CLL subpopulation characterized by high CD20 levels. Leukemia, 2018, 32, 2028-2031.	7.2	26
78	C-terminal RUNX1 mutation in familial platelet disorder with predisposition to myeloid malignancies. International Journal of Hematology, 2018, 108, 652-657.	1.6	8
79	Multiple productive IGH rearrangements denote oligoclonality even in immunophenotypically monoclonal CLL. Leukemia, 2018, 32, 234-236.	7.2	18
80	A Prognostic Tool for the Identification of Patients with Early Stage Chronic Lymphocytic Leukemia at Risk of Progression. Blood, 2018, 132, 1834-1834.	1.4	1
81	Abstract 1012: CD20 supports BCR signaling in an intra-clonal aggressive chronic lymphocytic leukemia subpopulation of cells and rituximab primarily targets these BCR-proficient B cells in vivo. , 2018, , .		0
82	Abstract 1417: Investigating the functional impacts of single-nucleotide variants in anaplastic large cell lymphoma. , 2018, , .		0
83	Epigenetic Drug Screen on Resistant CLL Cells Reveals Aurora Kinase Inhibitors As Enhancers of CD20 Expression and Sensitizers to Treatment with CD20 Monoclonal Antibodies. Blood, 2018, 132, 4407-4407.	1.4	0
84	Gene Aberrations in Adult Patients with Ph-Negative ALL in the Czech Republic. Blood, 2018, 132, 4090-4090.	1.4	0
85	Ability to downregulate the level of cyclin-dependent kinase inhibitor p27^{Kip1} after DNA damage is retained in chronic lymphocytic leukemia cells with functional ATM/p53 signaling pathway. Leukemia and Lymphoma, 2017, 58, 199-203.	1.3	2
86	COBLL1,LPLandZAP70expression defines prognostic subgroups of chronic lymphocytic leukemia patients with high accuracy and correlates withIGHVmutational status. Leukemia and Lymphoma, 2017, 58, 70-79.	1.3	14
87	Chronic lymphocytic leukemia: A prognostic model comprising only two biomarkers (<scp><i>IGHV</i></scp> mutational status and <scp>FISH</scp> cytogenetics) separates patients with different outcome and simplifies the <scp>CLLâ€IPI</scp>. American Journal of Hematology, 2017, 92, 375-380.	4.1	79
88	Recommended Guidelines for Validation, Quality Control, and Reporting of <i>TP53</i> Variants in Clinical Practice. Cancer Research, 2017, 77, 1250-1260.	0.9	68
89	Restrictions in the T-cell repertoire of chronic lymphocytic leukemia: high-throughput immunoprofiling supports selection by shared antigenic elements. Leukemia, 2017, 31, 1555-1561.	7.2	47
90	Chronic Lymphocytic Leukemia with Mutated IGHV4-34 Receptors: Shared and Distinct Immunogenetic Features and Clinical Outcomes. Clinical Cancer Research, 2017, 23, 5292-5301.	7.0	27

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91	Immunoglobulin genes in chronic lymphocytic leukemia: key to understanding the disease and improving risk stratification. Haematologica, 2017, 102, 968-971.	3.5	28
92	Micro<scp>RNA</scp> and mesial temporal lobe epilepsy with hippocampal sclerosis: Whole mi<scp>RN</scp>ome profiling of human hippocampus. Epilepsia, 2017, 58, 1782-1793.	5.1	41
93	GLASS: assisted and standardized assessment of gene variations from Sanger sequence trace data. Bioinformatics, 2017, 33, 3802-3804.	4.1	4
94	Fragment analysis represents a suitable approach for the detection of hotspot c.7541_7542delCT NOTCH1 mutation in chronic lymphocytic leukemia. Leukemia Research, 2017, 60, 145-150.	0.8	2
95	EGR2 mutations define a new clinically aggressive subgroup of chronic lymphocytic leukemia. Leukemia, 2017, 31, 1547-1554.	7.2	46
96	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.	2.5	5
97	Next-generation sequencing in chronic lymphocytic leukemia: recent findings and new horizons. Oncotarget, 2017, 8, 71234-71248.	1.8	25
98	Abstract 1479: Differential expression of microRNAs in transformation of follicular lymphoma to diffuse large B cell lymphoma. , 2017, , .		0
99	Additional trisomies amongst patients with chronic lymphocytic leukemia carrying trisomy 12: the accompanying chromosome makes a difference. Haematologica, 2016, 101, e299-e302.	3.5	35
100	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.	3.5	16
101	Clinical and pathogenic features of <i>ETV6</i> -related thrombocytopenia with predisposition to acute lymphoblastic leukemia. Haematologica, 2016, 101, 1333-1342.	3.5	92
102	Different spectra of recurrent gene mutations in subsets of chronic lymphocytic leukemia harboring stereotyped B-cell receptors. Haematologica, 2016, 101, 959-967.	3.5	57
103	Innovation in the prognostication of chronic lymphocytic leukemia: how far beyond TP53 gene analysis can we go?. Haematologica, 2016, 101, 263-265.	3.5	19
104	Epigenetic silencing of miR-26A1 in chronic lymphocytic leukemia and mantle cell lymphoma: Impact on EZH2 expression. Epigenetics, 2016, 11, 335-343.	2.7	20
105	Whole-exome sequencing in relapsing chronic lymphocytic leukemia: clinical impact of recurrent RPS15 mutations. Blood, 2016, 127, 1007-1016.	1.4	130
106	Ibrutinib inhibits CD20 upregulation on CLL B cells mediated by the CXCR4/SDF-1 axis. Blood, 2016, 128, 1609-1613.	1.4	85
107	High-quality full-length immunoglobulin profiling with unique molecular barcoding. Nature Protocols, 2016, 11, 1599-1616.	12.0	179
108	<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.	2.5	6

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109	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.	2.5	13
110	An Immunogenetic Signature of Ongoing Antigen Interactions in Splenic Marginal Zone Lymphoma Expressing IGHV1-2*04 Receptors. Clinical Cancer Research, 2016, 22, 2032-2040.	7.0	17
111	A complementary role of multiparameter flow cytometry and high-throughput sequencing for minimal residual disease detection in chronic lymphocytic leukemia: an European Research Initiative on CLL study. Leukemia, 2016, 30, 929-936.	7.2	200
112	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.	7.0	47
113	CLL: A Prognostic Model Comprising Only Two Biomarkers (IGHV Mutational Status and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 128, 3205-3205.	1.4	1
114	Reappraising Immunoglobulin Repertoire Restrictions in Chronic Lymphocytic Leukemia: Focus on Major Stereotyped Subsets and Closely Related Satellites. Blood, 2016, 128, 4376-4376.	1.4	1
115	Abstract 3291: The expression of CD20 on malignant B cells is regulated by chemokine signaling through the CXCR4/SDF-1 axis: implications for targeting the microenvironmental interactions. , 2016, , .		0
116	The Role of Microrna-150 in the Prognosis and Transformation of Follicular Lymphoma. Blood, 2016, 128, 4125-4125.	1.4	0
117	Rituximab Preferentially Eliminates BCR Signaling Proficient Chronic Lymphocytic Leukemia B Cells In Vivo. Blood, 2016, 128, 2030-2030.	1.4	0
118	Tailored Approaches for Refined Prognostication in Chronic Lymphocytic Leukemia Patients with Mutated Versus Unmutated Immunoglobulin Receptors. Blood, 2016, 128, 3199-3199.	1.4	0
119	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.	1.4	0
120	Analysis of Clonal Evolution in Chronic Lymphocytic Leukemia from Inactive to Symptomatic Disease Prior Treatment Using Whole-Exome Sequencing. Blood, 2016, 128, 3206-3206.	1.4	0
121	Not all IGHV3-21 chronic lymphocytic leukemias are equal: prognostic considerations. Blood, 2015, 125, 856-859.	1.4	70
122	Prognostic relevance of MYD88 mutations in CLL: the jury is still out. Blood, 2015, 126, 1043-1044.	1.4	32
123	Functional loss of IÎºBÎµ leads to NF-Î°B deregulation in aggressive chronic lymphocytic leukemia. Journal of Experimental Medicine, 2015, 212, 833-843.	8.5	85
124	TP53 mutation analysis in chronic lymphocytic leukemia: comparison of different detection methods. Tumor Biology, 2015, 36, 3371-3380.	1.8	10
125	Ofatumumab in poor-prognosis chronic lymphocytic leukemia: a Phase IV, non-interventional, observational study from the European Research Initiative on Chronic Lymphocytic Leukemia. Haematologica, 2015, 100, 511-516.	3.5	42
126	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.	4.1	18

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127	Molecular Evidence for Antigen Drive in the Natural History of Mantle Cell Lymphoma. American Journal of Pathology, 2015, 185, 1740-1748.	3.8	13
128	NOD/SCID IL2RÎ³-null mouse xenograft model of human p53-mutated chronic lymphocytic leukemia and ATM-mutated mantle cell lymphoma using permanent cell lines. Leukemia and Lymphoma, 2015, 56, 3198-3206.	1.3	6
129	Analysis of Prognostic Significance of Merkel Cell Polyomavirus in Chronic Lymphocytic Leukemia. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, 439-442.	0.4	4
130	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
131	Immunoglobulin heavy variable (IGHV) genes and alleles: new entities, new names and implications for research and prognostication in chronic lymphocytic leukaemia. Immunogenetics, 2015, 67, 61-66.	2.4	20
132	The impact of SF3B1 mutations in CLL on the DNA-damage response. Leukemia, 2015, 29, 1133-1142.	7.2	74
133	Detailed analysis of therapy-driven clonal evolution of TP53 mutations in chronic lymphocytic leukemia. Leukemia, 2015, 29, 877-885.	7.2	132
134	Recurrent mutations refine prognosis in chronic lymphocytic leukemia. Leukemia, 2015, 29, 329-336.	7.2	253
135	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
136	Next Generation Sequence Immunoprofiling of the T-Cell Repertoire in Chronic Lymphocytic Leukemia Supports Selection By Shared Antigenic Elements. Blood, 2015, 126, 618-618.	1.4	1
137	Histone H1 Differentially Inhibits DNA Bending by Reduced and Oxidized HMGB1 Protein. PLoS ONE, 2015, 10, e0138774.	2.5	19
138	Oxidative stress as a therapeutic perspective for ATM-deficient chronic lymphocytic leukemia patients. Haematologica, 2015, 100, 994-6.	3.5	6
139	Abstract 3084: MicroRNA involvement in DNA damage response and BCR signaling in malignant B cells. , 2015, , .		0
140	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.	1.4	0
141	Clustering Adult ACUTE Lymphoblastic Leukemia (ALL) Philadelphia Negative (Ph-) By Whole Exome Sequencing (WES) Analysis. Blood, 2015, 126, 2623-2623.	1.4	0
142	ATM Mutations in Major Stereotyped CLL Subsets: Enrichment in Subset #2 is Associated with Unfavourable Outcome. Blood, 2015, 126, 1712-1712.	1.4	0
143	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.	1.4	0
144	EGR2 Mutations in Chronic Lymphocytic Leukemia: A New Bad Player. Blood, 2015, 126, 4126-4126.	1.4	0

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145	Personalized Modeling of Disease Evolution in CLL: Does Statistical Significance Translate into Predictive Accuracy?. Blood, 2015, 126, 2921-2921.	1.4	0
146	Microenvironmental Interactions up-Regulate CD20 Expression in CLL B Cells through the CXCR4/SDF-1 Axis: Implications for CD20-Targeting Antibodies and the Use of BCR-Inhibitors in Combination. Blood, 2015, 126, 4124-4124.	1.4	0
147	CLL with Mutated IGHV4-34 Antigen Receptors Is Clinically Heterogeneous: Antigen Receptor Stereotypy Makes the Difference. Blood, 2015, 126, 5263-5263.	1.4	0
148	Transmission of t(11;14)-positive cells by allogeneic stem cell transplant: 10-year journey to mantle cell lymphoma. Leukemia and Lymphoma, 2014, 55, 1935-1938.	1.3	6
149	Multiple productive immunoglobulin heavy chain gene rearrangements in chronic lymphocytic leukemia are mostly derived from independent clones. Haematologica, 2014, 99, 329-338.	3.5	37
150	TP53 Mutation Analysis in Clinical Practice: Lessons From Chronic Lymphocytic Leukemia. Human Mutation, 2014, 35, 663-671.	2.5	24
151	Assessment of <scp>TP</scp>53 functionality in chronic lymphocytic leukaemia by different assays; an <scp>ERIC</scp>â€wide approach. British Journal of Haematology, 2014, 167, 565-569.	2.5	7
152	Detecting minimal residual disease in patients with chronic lymphocytic leukemia using 8â€color flow cytometry protocol in routine hematological practice. International Journal of Laboratory Hematology, 2014, 36, 165-171.	1.3	15
153	TaqMan based real time PCR assay targeting EML4-ALK fusion transcripts in NSCLC. Lung Cancer, 2014, 85, 25-30.	2.0	12
154	Chromosomal translocations and karyotype complexity in chronic lymphocytic leukemia: A systematic reappraisal of classic cytogenetic data. American Journal of Hematology, 2014, 89, 249-255.	4.1	113
155	Towards error-free profiling of immune repertoires. Nature Methods, 2014, 11, 653-655.	19.0	411
156	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.	0.8	14
157	Identification of novel sequence variations in microRNAs in chronic lymphocytic leukemia. Carcinogenesis, 2014, 35, 992-1002.	2.8	18
158	Clinical effect of stereotyped B-cell receptor immunoglobulins in chronic lymphocytic leukaemia: a retrospective multicentre study. Lancet Haematology,the, 2014, 1, e74-e84.	4.6	93
159	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.	2.5	17
160	Distinct inÂvitro sensitivity of p53-mutated and ATM-mutated chronic lymphocytic leukemia cells to ofatumumab and rituximab. Experimental Hematology, 2014, 42, 867-874.e1.	0.4	10
161	MDM2 promotor polymorphism and disease characteristics in chronic lymphocytic leukemia: results of an individual patient data-based meta-analysis. Haematologica, 2014, 99, 1285-1291.	3.5	2
162	High-Throughput Profiling of the T-Cell Receptor Gene Repertoire Supports Antigen Drive in the Pathogenesis of Chronic Idiopathic Neutropenia. Blood, 2014, 124, 2731-2731.	1.4	1

#	ARTICLE	IF	CITATIONS
163	Binding of Histone H1 to DNA Is Differentially Modulated by Redox State of HMGB1. PLoS ONE, 2014, 9, e89070.	2.5	27
164	Abstract 5198: Identification of microRNAs involved in DNA damage response in malignant B cells and their biological and clinical relevance. , 2014, , .		0
165	Tracing the Ontogeny of IgG-Switched CLL: High-Throughput Immunogenetic Evidence. Blood, 2014, 124, 3285-3285.	1.4	0
166	Prognostic Impact of NOTCH1 Hotspot Mutation in TP53-Mutated Patients with Chronic Lymphocytic Leukemia. Blood, 2014, 124, 3283-3283.	1.4	0
167	Charting Unique Signatures of Somatic Hypermutation Amongst Chronic Lymphocytic Leukemia Patients Expressing IGHV4-34 Clonotypic B Cell Receptors. Blood, 2014, 124, 1969-1969.	1.4	0
168	A Complementary Role of High Throughput Sequencing and Multiparameter Cytometry for Minimal Residual Disease (MRD) Detection in Chronic Lymphocytic Leukemia (CLL):an European Research Initiative (ERIC) Study. Blood, 2014, 124, 1976-1976.	1.4	2
169	Subset-Specific Spectra of Recurrent Gene Mutations in Chronic Lymphocytic Leukemia with Stereotyped B-Cell Receptors. Blood, 2014, 124, 3320-3320.	1.4	6
170	High-Throughput T-Cell Receptor Gene Repertoire Profiling in Chronic Lymphocytic Leukemia Reveals a Molecular Signature of Antigen Selection. Blood, 2014, 124, 1950-1950.	1.4	0
171	The<i>BCRâ€“ABL1</i>T315I mutation and additional genomic aberrations are dominant genetic lesions associated with disease progression in patients with chronic myelogenous leukemia resistant to tyrosine kinase inhibitor therapy. Leukemia and Lymphoma, 2013, 54, 2083-2087.	1.3	1
172	Combination of fludarabine, amsacrine, and cytarabine followed by reduced-intensity conditioning and allogeneic hematopoietic stem cell transplantation in patients with high-risk acute myeloid leukemia. Annals of Hematology, 2013, 92, 1397-1403.	1.8	16
173	Fludarabine with cytarabine followed by reduced-intensity conditioning and allogeneic hematopoietic stem cell transplantation in patients with poor-risk chronic lymphocytic leukemia. Annals of Hematology, 2013, 92, 249-254.	1.8	6
174	Mesalamine modulates intercellular adhesion through inhibition of p-21 activated kinase-1. Biochemical Pharmacology, 2013, 85, 234-244.	4.4	38
175	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.	0.8	17
176	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.	7.2	90
177	Overview of available p53 function tests in relation toTP53andATMgene alterations and chemoresistance in chronic lymphocytic leukemia. Leukemia and Lymphoma, 2013, 54, 1849-1853.	1.3	15
178	ATM mutations uniformly lead to ATM dysfunction in chronic lymphocytic leukemia: application of functional test using doxorubicin. Haematologica, 2013, 98, 1124-1131.	3.5	35
179	The Planar Cell Polarity Pathway Drives Pathogenesis of Chronic Lymphocytic Leukemia by the Regulation of B-Lymphocyte Migration. Cancer Research, 2013, 73, 1491-1501.	0.9	83
180	The outcome of chronic lymphocytic leukemia patients who relapsed after fludarabine, cyclophosphamide, and rituximab. European Journal of Haematology, 2013, 90, 479-485.	2.2	11

#	ARTICLE	IF	CITATIONS
181	A Multicenter, Phase IV Observational Study Of Ofatumumab In Chronic Lymphocytic Leukemia (CLL): A European Research Initiative On CLL (ERIC) Study. Blood, 2013, 122, 1645-1645.	1.4	2
182	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.	1.4	15
183	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.	1.4	1
184	The Interlaboratory Robustness Of Next-Generation Sequencing (IRON) Study Phase II: Deep-Sequencing Analyses Of Hematological Malignancies Performed In 8,867 Cases By An International Network Involving 27 Laboratories. Blood, 2013, 122, 743-743.	1.4	6
185	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.	1.4	0
186	SF3B1 Mutations Frequently Occur With Both ATM Mutations and TP53 Mutations In CLL Patients. Blood, 2013, 122, 2868-2868.	1.4	0
187	Detection and Measurement of Fungal Burden in a Guinea Pig Model of Invasive Pulmonary Aspergillosis by Novel Quantitative Nested Real-Time PCR Compared with Galactomannan and (1,3)-Â-D-Glucan Detection. Journal of Clinical Microbiology, 2012, 50, 602-608.	3.9	28
188	Antigen receptor stereotypy across B-cell lymphoproliferations: the case of IGHV4-59/IGKV3-20 receptors with rheumatoid factor activity. Leukemia, 2012, 26, 1127-1131.	7.2	59
189	MicroRNA-650 expression is influenced by immunoglobulin gene rearrangement and affects the biology of chronic lymphocytic leukemia. Blood, 2012, 119, 2110-2113.	1.4	92
190	613 Clonal Selection of TP53 Mutations in Chronic Lymphocytic Leukaemia Detected by Ultra-deep Pyrosequencing. European Journal of Cancer, 2012, 48, S146.	2.8	0
191	885 P53 Mutations Affecting DNA-binding Have Prominent Impact on Survival in Chronic Lymphocytic Leukemia. European Journal of Cancer, 2012, 48, S214.	2.8	0
192	Gene expression profiling of acute graft-vs-host disease after hematopoietic stem cell transplantation. Experimental Hematology, 2012, 40, 899-905.e5.	0.4	7
193	Specific p53 mutations do not impact results of alemtuzumab therapy among patients with chronic lymphocytic leukemia. Leukemia and Lymphoma, 2012, 53, 1817-1819.	1.3	4
194	Stereotyped B-cell receptors in one-third of chronic lymphocytic leukemia: a molecular classification with implications for targeted therapies. Blood, 2012, 119, 4467-4475.	1.4	350
195	Potential biomarkers for early detection of acute graftâ€versusâ€host disease. Proteomics - Clinical Applications, 2012, 6, 351-363.	1.6	4
196	MicroRNAs in chronic lymphocytic leukemia: from causality to associations and back. Expert Review of Hematology, 2012, 5, 579-581.	2.2	52
197	MicroRNAs Regulate p21Waf1/Cip1 Protein Expression and the DNA Damage Response in Human Embryonic Stem Cells. Stem Cells, 2012, 30, 1362-1372.	3.2	97
198	ERIC recommendations on TP53 mutation analysis in chronic lymphocytic leukemia. Leukemia, 2012, 26, 1458-1461.	7.2	182

#	Article	IF	Citations
199	A real-time (PCR) for a real lifeâ€¦? Quantitative evaluation of BCL2/IGH in follicular lymphoma and its implications for clinical practice. Experimental Hematology, 2012, 40, 528-539.e4.	0.4	3
200	Assessment of p53 Functionality in Chronic Lymphocytic Leukemia by Different Assays; An Eric-Wide Approach.. Blood, 2012, 120, 2872-2872.	1.4	1
201	High Expression of Activation-Induced Cytidine Deaminase and in Vivo Class Switch Recombination in Mantle Cell Lymphoma: Further Support for Antigen Involvement in Lymphomagenesis. Blood, 2012, 120, 1538-1538.	1.4	0
202	The Fate of Chronic Lymphocytic Leukemia Patients After Failure of Fludarabine, Cyclophosphamide, and Rituximab Regimen. Blood, 2012, 120, 4603-4603.	1.4	0
203	Inhibition of PAK-1 by Mesalazine Increases Cell Adhesion in Colorectal Cancer Cells. Gastroenterology, 2011, 140, S-402.	1.3	0
204	Missense Mutations Located in Structural p53 DNA-Binding Motifs Are Associated With Extremely Poor Survival in Chronic Lymphocytic Leukemia. Journal of Clinical Oncology, 2011, 29, 2703-2708.	1.6	77
205	Long-term results of allogeneic hematopoietic stem cell transplantation after reduced-intensity conditioning with busulfan, fludarabine, and antithymocyte globulin. Neoplasma, 2011, 58, 406-414.	1.6	4
206	MYB transcriptionally regulates the miR-155 host gene in chronic lymphocytic leukemia. Blood, 2011, 117, 3816-3825.	1.4	128
207	Bone marrow stromal cells protect lymphoma Bâ€cells from rituximabâ€induced apoptosis and targeting integrin Î±â€4â€Î²â€1 (VLAâ€4) with natalizumab can overcome this resistance. British Journal of Haematology, 2011, 155, 53-64.	2.5	99
208	Postâ€translational modifications regulate signalling by Ror1. Acta Physiologica, 2011, 203, 351-362.	3.8	33
209	Modern and conventional prognostic markers of chronic lymphocytic leukaemia in the everyday haematological practice. European Journal of Haematology, 2011, 87, 130-137.	2.2	15
210	Gene expression profiling in follicular lymphoma and its implication for clinical practice. Leukemia and Lymphoma, 2011, 52, 59-68.	1.3	13
211	Mutational Analysis of Mir-29 Family Members in Chronic Lymphocytic Leukemia. Blood, 2011, 118, 1770-1770.	1.4	0
212	Human Embryonic Stem Cells Are Capable of Executing G1/S Checkpoint Activation. Stem Cells, 2010, 28, 1143-1152.	3.2	69
213	Rapid Detection and Identification of Mucormycetes from Culture and Tissue Samples by Use of High-Resolution Melt Analysis. Journal of Clinical Microbiology, 2010, 48, 3392-3394.	3.9	49
214	Analysis of the DNA-binding activity of p53 mutants using functional protein microarrays and its relationship to transcriptional activation. Biological Chemistry, 2010, 391, 197-205.	2.5	17
215	666 Analysis of microRNAs associated with aggressive subtype of chronic lymphocytic leukaemia harbouring inactivated p53. European Journal of Cancer, Supplement, 2010, 8, 168.	2.2	0
216	High Expression of Lymphocyte-Activation Gene 3 (LAG3) in Chronic Lymphocytic Leukemia Cells Is Associated with Unmutated Immunoglobulin Variable Heavy Chain Region (IGHV) Gene and Reduced Treatment-Free Survival. Journal of Molecular Diagnostics, 2010, 12, 328-334.	2.8	38

#	ARTICLE	IF	CITATIONS
217	TP53 mutation profile in chronic lymphocytic leukemia: evidence for a disease specific profile from a comprehensive analysis of 268 mutations. Leukemia, 2010, 24, 2072-2079.	7.2	134
218	The Mystery of FDG-PET Avidity In Follicular Lymphoma. Does Microenvironment Play the Key Role?. Blood, 2010, 116, 4138-4138.	1.4	2
219	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.	1.4	2
220	Clonal Evolution of Malignant Populations In Potentially Biclonal Chronic Lymphocytic Leukemia Patients. Blood, 2010, 116, 2412-2412.	1.4	0
221	Intracoronary Delivery of Bone Marrow Cells to the Acutely Infarcted Myocardium. Cardiology, 2009, 112, 98-106.	1.4	8
222	HMGB1 and HMGB2 proteins up-regulate cellular expression of human topoisomerase IIÂ. Nucleic Acids Research, 2009, 37, 2070-2086.	14.5	45
223	Presence of heterozygous ATM deletion may not be critical in the primary response of chronic lymphocytic leukemia cells to fludarabine. European Journal of Haematology, 2009, 82, 133-142.	2.2	11
224	Inactivation of p53 and amplification of MYCN gene in a terminal lymphoblastic relapse in a chronic lymphocytic leukemia patient. Cancer Genetics and Cytogenetics, 2009, 189, 53-58.	1.0	7
225	A Complex Role for FGF-2 in Self-Renewal, Survival, and Adhesion of Human Embryonic Stem Cells. Stem Cells, 2009, 27, 1847-1857.	3.2	184
226	MicroRNAs in chronic lymphocytic leukemia pathogenesis and disease subtypes. Leukemia and Lymphoma, 2009, 50, 506-509.	1.3	101
227	MicroRNA isolation and stability in stored RNA samples. Biochemical and Biophysical Research Communications, 2009, 390, 1-4.	2.1	189
228	Monoallelic and biallelic inactivation of TP53 gene in chronic lymphocytic leukemia: selection, impact on survival, and response to DNA damage. Blood, 2009, 114, 5307-5314.	1.4	164
229	miR-34a, miR-29c and miR-17-5p are downregulated in CLL patients with TP53 abnormalities. Leukemia, 2009, 23, 1159-1163.	7.2	162
230	Identification of somatic hypermutations in the TP53 gene in B-cell chronic lymphocytic leukemia. Molecular Immunology, 2008, 45, 1525-1529.	2.2	13
231	Chimerism Status as a Possible Marker of Incipient Disease Relapse in Patients with AML.. Blood, 2007, 110, 5028-5028.	1.4	0
232	Effect of procathepsin D activation peptide on gene expression of breast cancer cells. Cancer Letters, 2006, 239, 46-54.	7.2	15
233	Inactivation of p53 and deletion of ATM in B-CLL patients in relation to IgVH mutation status and previous treatment. Leukemia, 2006, 20, 1159-1161.	7.2	27
234	MicroRNA BIOGENESIS, FUNCTIONALITY AND CANCER RELEVANCE. Biomedical Papers of the Medical Faculty of the University Palacky&#x0301;, Olomouc, Czechoslovakia, 2006, 150, 205-215.	0.6	132

#	Article	IF	Citations
235	High-Affinity Binding of Tumor-Suppressor Protein p53 and HMGB1 to Hemicatenated DNA Loopsâ€. Biochemistry, 2004, 43, 7215-7225.	2.5	70
236	Activation of the DNA-binding ability of latent p53 protein by protein kinase C is abolished by protein kinase CK2. Biochemical Journal, 2004, 378, 939-947.	3.7	33
237	Potentials for RNAi in sarcoma research and therapy: Ewingâ€™s sarcoma as a model. Seminars in Cancer Biology, 2003, 13, 275-281.	9.6	45
238	Recognition of DNA modified by antitumor cisplatin by â€œlatentâ€•and â€œactiveâ€•protein p53. Biochemical Pharmacology, 2003, 65, 1305-1316.	4.4	22
239	Response of Ewing tumor cells to forced and activated p53 expression. Oncogene, 2003, 22, 3193-3204.	5.9	24
240	New ELISA technique for analysis of p53 protein/DNA binding properties. Journal of Immunological Methods, 2002, 267, 227-235.	1.4	56
241	Crosslinking of the complementary strands of DNA by UV light: dependence on the oligonucleotide composition of the UV irradiated DNA. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2001, 1517, 365-375.	2.4	16
242	Stoichiometric Phosphorylation of Human p53 at Ser315Stimulates p53-dependent Transcription. Journal of Biological Chemistry, 2001, 276, 4699-4708.	3.4	84
243	Different Recognition of DNA Modified by Antitumor Cisplatin and Its Clinically Ineffective trans Isomer by Tumor Suppressor Protein p53. Journal of Biological Chemistry, 2001, 276, 16064-16069.	3.4	30
244	Precise characterisation of monoclonal antibodies to the C-terminal region of p53 protein using the PEPSCAN ELISA technique and a new non-radioactive gel shift assay. Journal of Immunological Methods, 2000, 237, 51-64.	1.4	21
245	Effects of Oxidation Agents and Metal Ions on Binding of p53 to Supercoiled DNA. Journal of Biomolecular Structure and Dynamics, 2000, 17, 177-183.	3.5	4
246	Specific Modulation of p53 Binding to Consensus Sequence within Supercoiled DNA by Monoclonal Antibodies. Biochemical and Biophysical Research Communications, 2000, 267, 934-939.	2.1	29
247	UV Light-induced Duplex-to-duplex Crosslinking of DNA Molecules in Aqueous Ethanol Solutions. Photochemistry and Photobiology, 1998, 67, 386.	2.5	7
248	UV Lightâ€induced Crosslinking of the Complementary Strands of Plasmid pUC19 DNA Restriction Fragments. Photochemistry and Photobiology, 1997, 65, 945-948.	2.5	16
249	UV Light-Induced Crosslinking of the Strands of Poly(dA-dT) and Related Alternating Purine-Pyrimidine DNAs. Journal of Biomolecular Structure and Dynamics, 1994, 11, 1225-1236.	3.5	9
250	Impact of the Types and Relative Quantities of IGHV Gene Mutations in Predicting Prognosis of Patients With Chronic Lymphocytic Leukemia. Frontiers in Oncology, 0, 12, .	2.8	2