

Daniel Mertens

List of Publications by Year in descending order

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120
papers

6,284
citations

70961

41
h-index

69108

77
g-index

122
all docs

122
docs citations

122
times ranked

8894
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutations driving CLL and their evolution in progression and relapse. <i>Nature</i> , 2015, 526, 525-530.	13.7	868
2	From pathogenesis to treatment of chronic lymphocytic leukaemia. <i>Nature Reviews Cancer</i> , 2010, 10, 37-50.	12.8	503
3	Gene mutations and treatment outcome in chronic lymphocytic leukemia: results from the CLL8 trial. <i>Blood</i> , 2014, 123, 3247-3254.	0.6	428
4	miR-34a as part of the resistance network in chronic lymphocytic leukemia. <i>Blood</i> , 2009, 113, 3801-3808.	0.6	258
5	DNA methylation dynamics during B cell maturation underlie a continuum of disease phenotypes in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2016, 48, 253-264.	9.4	254
6	Detailed analysis of p53 pathway defects in fludarabine-refractory chronic lymphocytic leukemia (CLL): dissecting the contribution of 17p deletion, TP53 mutation, p53-p21 dysfunction, and miR34a in a prospective clinical trial. <i>Blood</i> , 2009, 114, 2589-2597.	0.6	253
7	High-resolution genomic profiling of chronic lymphocytic leukemia reveals new recurrent genomic alterations. <i>Blood</i> , 2012, 120, 4783-4794.	0.6	179
8	Venetoclax resistance and acquired <i>BCL2</i> mutations in chronic lymphocytic leukemia. <i>Haematologica</i> , 2019, 104, e434-e437.	1.7	144
9	Evolution of DNA Methylation Is Linked to Genetic Aberrations in Chronic Lymphocytic Leukemia. <i>Cancer Discovery</i> , 2014, 4, 348-361.	7.7	135
10	Epigenetic Upregulation of lncRNAs at 13q14.3 in Leukemia Is Linked to the In Cis Downregulation of a Gene Cluster That Targets NF- κ B. <i>PLoS Genetics</i> , 2013, 9, e1003373.	1.5	134
11	Impact of serum storage conditions on microRNA stability. <i>Leukemia</i> , 2012, 26, 2414-2416.	3.3	133
12	Evidence for distinct pathomechanisms in B-cell chronic lymphocytic leukemia and mantle cell lymphoma by quantitative expression analysis of cell cycle and apoptosis-associated genes. <i>Blood</i> , 2002, 99, 4554-4561.	0.6	125
13	Quantitative DNA Methylation Analysis Identifies a Single CpG Dinucleotide Important for ZAP-70 Expression and Predictive of Prognosis in Chronic Lymphocytic Leukemia. <i>Journal of Clinical Oncology</i> , 2012, 30, 2483-2491.	0.8	120
14	Circulating microRNAs in hematological diseases: principles, challenges, and perspectives. <i>Blood</i> , 2013, 121, 4977-4984.	0.6	118
15	Down-regulation of candidate tumor suppressor genes within chromosome band 13q14.3 is independent of the DNA methylation pattern in B-cell chronic lymphocytic leukemia. <i>Blood</i> , 2002, 99, 4116-4121.	0.6	91
16	Prognostic and predictive impact of genetic markers in patients with CLL treated with obinutuzumab and venetoclax. <i>Blood</i> , 2020, 135, 2402-2412.	0.6	83
17	B-cell neoplasia associated gene with multiple splicing (BCMS): the candidate B-CLL gene on 13q14 comprises more than 560 kb covering all critical regions. <i>Human Molecular Genetics</i> , 2001, 10, 1275-1285.	1.4	81
18	Expression analysis of imbalanced genes in prostate carcinoma using tissue microarrays. <i>British Journal of Cancer</i> , 2007, 96, 82-88.	2.9	77

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19	Off-target effects of siRNA specific for GFP. <i>BMC Molecular Biology</i> , 2008, 9, 60.	3.0	76
20	Importance of genetics in chronic lymphocytic leukemia. <i>Blood Reviews</i> , 2011, 25, 131-137.	2.8	75
21	NOTCH1, SF3B1, and TP53 mutations in fludarabine-refractory CLL patients treated with alemtuzumab: results from the CLL2H trial of the GCLLSG. <i>Blood</i> , 2013, 122, 1266-1270.	0.6	68
22	Programmed Death-1 and Its Ligand Are Novel Immunotolerant Molecules Expressed on Leukemic B Cells in Chronic Lymphocytic Leukemia. <i>PLoS ONE</i> , 2012, 7, e35178.	1.1	68
23	Reduced Expression of CAMTA1 Correlates with Adverse Outcome in Neuroblastoma Patients. <i>Clinical Cancer Research</i> , 2006, 12, 131-138.	3.2	67
24	Evidence for Distinct Pathomechanisms in Genetic Subgroups of Chronic Lymphocytic Leukemia Revealed by Quantitative Expression Analysis of Cell Cycle, Activation, and Apoptosis-Associated Genes. <i>Journal of Clinical Oncology</i> , 2005, 23, 3780-3792.	0.8	66
25	Defective DROSHA processing contributes to downregulation of MiR-15/-16 in chronic lymphocytic leukemia. <i>Leukemia</i> , 2014, 28, 98-107.	3.3	64
26	Analysis of 11q22-q23 deletion target genes in B-cell chronic lymphocytic leukaemia: Evidence for a pathogenic role of NPAT, CUL5, and PPP2R1B. <i>European Journal of Cancer</i> , 2007, 43, 1328-1335.	1.3	62
27	FBXW7 mutations reduce binding of NOTCH1, leading to cleaved NOTCH1 accumulation and target gene activation in CLL. <i>Blood</i> , 2019, 133, 830-839.	0.6	56
28	Functional screening for proapoptotic genes by reverse transfection cell array technology. <i>Genomics</i> , 2006, 87, 665-672.	1.3	55
29	A Novel Paradigm to Trigger Apoptosis in Chronic Lymphocytic Leukemia. <i>Cancer Research</i> , 2009, 69, 8977-8986.	0.4	55
30	Lenalidomide treatment of chronic lymphocytic leukaemia patients reduces regulatory T cells and induces Th17 T helper cells. <i>British Journal of Haematology</i> , 2010, 148, 948-950.	1.2	55
31	Moving from prognostic to predictive factors in chronic lymphocytic leukaemia (CLL). <i>Best Practice and Research in Clinical Haematology</i> , 2010, 23, 71-84.	0.7	55
32	From Biology to Therapy: The CLL Success Story. <i>HemaSphere</i> , 2019, 3, e175.	1.2	55
33	Efficiency of the algorithms for the calculation of Slater molecular integrals in polyatomic molecules. <i>Journal of Computational Chemistry</i> , 2004, 25, 1987-1994.	1.5	54
34	Distinct gene expression patterns in chronic lymphocytic leukemia defined by usage of specific VH genes. <i>Blood</i> , 2006, 107, 2090-2093.	0.6	54
35	Allelic silencing at the tumor-suppressor locus 13q14.3 suggests an epigenetic tumor-suppressor mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 7741-7746.	3.3	54
36	Frequent amplifications and abundant expression of TRIO, NKD2, and IRX2 in soft tissue sarcomas. <i>Genes Chromosomes and Cancer</i> , 2006, 45, 829-838.	1.5	52

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37	Epigenetic silencing of miR-708 enhances NF- κ B signaling in chronic lymphocytic leukemia. <i>International Journal of Cancer</i> , 2015, 137, 1352-1361.	2.3	52
38	IGF1R as druggable target mediating PI3K- γ inhibitor resistance in a murine model of chronic lymphocytic leukemia. <i>Blood</i> , 2019, 134, 534-547.	0.6	51
39	CDX2-driven leukemogenesis involves KLF4 repression and deregulated PPAR γ signaling. <i>Journal of Clinical Investigation</i> , 2013, 123, 299-314.	3.9	47
40	Prognostic and Predictive Factors in Patients With Chronic Lymphocytic Leukemia: Relevant in the Era of Novel Treatment Approaches?. <i>Journal of Clinical Oncology</i> , 2014, 32, 869-872.	0.8	45
41	Ala228 variant of trail receptor 1 affecting the ligand binding site is associated with chronic lymphocytic leukemia, mantle cell lymphoma, prostate cancer, head and neck squamous cell carcinoma and bladder cancer. <i>International Journal of Cancer</i> , 2006, 118, 1831-1835.	2.3	43
42	Chronic lymphocytic leukemia and 13q14: miRs and more. <i>Leukemia and Lymphoma</i> , 2009, 50, 502-505.	0.6	42
43	The Phospholipase C β 2 Mutants R665W and L845F Identified in Ibrutinib-resistant Chronic Lymphocytic Leukemia Patients Are Hypersensitive to the Rho GTPase Rac2 Protein. <i>Journal of Biological Chemistry</i> , 2016, 291, 22136-22148.	1.6	42
44	Discovery of Candidate DNA Methylation Cancer Driver Genes. <i>Cancer Discovery</i> , 2021, 11, 2266-2281.	7.7	42
45	Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. <i>Molecular Systems Biology</i> , 2019, 15, e8339.	3.2	39
46	Molecular diagnostics in chronic lymphocytic leukemia – Pathogenetic and clinical implications. <i>Leukemia and Lymphoma</i> , 2008, 49, 864-873.	0.6	37
47	Treatment resistance in chronic lymphocytic leukemia – the role of the p53 pathway. <i>Leukemia and Lymphoma</i> , 2009, 50, 510-513.	0.6	35
48	DNA damage – induced transcriptional program in CLL: biological and diagnostic implications for functional p53 testing. <i>Blood</i> , 2011, 117, 1622-1632.	0.6	35
49	Translocation t(X;11)(q13;q23) in B-cell chronic lymphocytic leukemia disrupts two novel genes. <i>Genes Chromosomes and Cancer</i> , 2005, 42, 128-143.	1.5	34
50	NFATC1 activation by DNA hypomethylation in chronic lymphocytic leukemia correlates with clinical staging and can be inhibited by ibrutinib. <i>International Journal of Cancer</i> , 2018, 142, 322-333.	2.3	33
51	Nurse-like cells show deregulated expression of genes involved in immunocompetence. <i>British Journal of Haematology</i> , 2011, 154, 349-356.	1.2	32
52	The candidate immunotherapeutical target, the receptor for hyaluronic acid-mediated motility, is associated with proliferation and shows prognostic value in B-cell chronic lymphocytic leukemia. <i>Leukemia</i> , 2009, 23, 519-527.	3.3	31
53	HDAC3 functions as a positive regulator in Notch signal transduction. <i>Nucleic Acids Research</i> , 2020, 48, 3496-3512.	6.5	31
54	Prognostic and predictive role of gene mutations in chronic lymphocytic leukemia: results from the pivotal phase III study COMPLEMENT1. <i>Haematologica</i> , 2020, 105, 2440-2447.	1.7	31

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55	Matrix-Dependent Regulation of AKT in Hepsin-Overexpressing PC3 Prostate Cancer Cells. <i>Neoplasia</i> , 2011, 13, 579-IN2.	2.3	27
56	Kruppel-like factor 4 (KLF4) inactivation in chronic lymphocytic leukemia correlates with promoter DNA-methylation and can be reversed by inhibition of NOTCH signaling. <i>Haematologica</i> , 2016, 101, e249-e253.	1.7	26
57	High-throughput detection of nuclear factor- κ B activity using a sensitive oligo-based chemiluminescent enzyme-linked immunosorbent assay. <i>International Journal of Cancer</i> , 2010, 127, 404-411.	2.3	25
58	Germline Allele-Specific Expression of DAPK1 in Chronic Lymphocytic Leukemia. <i>PLoS ONE</i> , 2013, 8, e55261.	1.1	24
59	Genomic alterations in high-risk chronic lymphocytic leukemia frequently affect cell cycle key regulators and NOTCH1-regulated transcription. <i>Haematologica</i> , 2020, 105, 1379-1390.	1.7	24
60	Oxidative stress as candidate therapeutic target to overcome microenvironmental protection of CLL. <i>Leukemia</i> , 2020, 34, 115-127.	3.3	23
61	In-vivo quantification of primary microRNA processing by Drosha with a luciferase based system. <i>Biochemical and Biophysical Research Communications</i> , 2011, 406, 501-505.	1.0	21
62	Treating chronic lymphocytic leukemia with thalidomide and lenalidomide. <i>Expert Opinion on Pharmacotherapy</i> , 2011, 12, 2857-2864.	0.9	19
63	Telomere length in mantle cell lymphoma. <i>Blood</i> , 2013, 121, 1184-1187.	0.6	19
64	Short telomeres are associated with inferior outcome, genomic complexity, and clonal evolution in chronic lymphocytic leukemia. <i>Leukemia</i> , 2019, 33, 2183-2194.	3.3	19
65	Targeting inhibitor of apoptosis proteins by scp mimetic elicits cell death in poor prognostic subgroups of chronic lymphocytic leukemia. <i>International Journal of Cancer</i> , 2015, 137, 2959-2970.	2.3	17
66	Evaluation of vecabrutinib as a model for noncovalent BTK/ITK inhibition for treatment of chronic lymphocytic leukemia. <i>Blood</i> , 2022, 139, 859-875.	0.6	16
67	BCMSUN, a candidate gene for B-cell chronic lymphocytic leukemia and mantle-cell lymphoma, has an independently expressed homolog on 1p22-p31, BCMSUN-like. <i>International Journal of Cancer</i> , 2000, 88, 692-697.	2.3	15
68	Blocking distinct interactions between Glioblastoma cells and their tissue microenvironment: A novel multi-targeted therapeutic approach. <i>Scientific Reports</i> , 2018, 8, 5527.	1.6	15
69	Methylome-based cell-of-origin modeling (Methyl-COOM) identifies aberrant expression of immune regulatory molecules in CLL. <i>Genome Medicine</i> , 2020, 12, 29.	3.6	15
70	Multi-platform profiling characterizes molecular subgroups and resistance networks in chronic lymphocytic leukemia. <i>Nature Communications</i> , 2021, 12, 5395.	5.8	15
71	BCL10 is not the gene inactivated by mutation in the 1p22 deletion region in mantle cell lymphoma. <i>Leukemia</i> , 2000, 14, 1490-1492.	3.3	14
72	Non-malignant B cells and chronic lymphocytic leukemia cells induce a pro-survival phenotype in CD14+ cells from peripheral blood. <i>Leukemia</i> , 2011, 25, 722-726.	3.3	13

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73	Advances in treating chronic lymphocytic leukemia. F1000prime Reports, 2014, 6, 65.	5.9	13
74	<i>SYK</i> carries no activating point mutations in patients with chronic lymphocytic leukaemia (CLL). British Journal of Haematology, 2010, 150, 633-636.	1.2	12
75	Thalidomide Regulation of NF- κ B Proteins Limits Tregs Activity in Chronic Lymphocytic Leukemia. Advances in Clinical and Experimental Medicine, 2014, 23, 25-32.	0.6	12
76	Biological diversity and risk-adapted treatment of chronic lymphocytic leukemia. Haematologica, 2010, 95, 1441-1443.	1.7	11
77	Loss of cooperativity of secreted CD40L and increased dose-response to IL4 on CLL cell viability correlates with enhanced activation of NF- κ B and STAT6. International Journal of Cancer, 2015, 136, 65-73.	2.3	11
78	Clonal evolution in chronic lymphocytic leukemia is scant in relapsed but accelerated in refractory cases after chemo(immune) therapy. Haematologica, 2022, 107, 604-614.	1.7	11
79	Genetics of Chronic Lymphocytic Leukemia. Clinics in Laboratory Medicine, 2011, 31, 649-658.	0.7	7
80	CLL and deletion 13q14: merely the miRs?. Blood, 2012, 119, 2974-2975.	0.6	7
81	Gene Mutations and Treatment Outcome in Chronic Lymphocytic Leukemia: Results From the CLL8 Trial. Blood, 2012, 120, 433-433.	0.6	7
82	In Vivo modeling of Resistance to PI3K \hat{I} Inhibitor Treatment Using E $\hat{\mu}$ TCL1-Tg Tumor Transfer Model. Blood, 2016, 128, 190-190.	0.6	7
83	Chronic lymphocytic leukemia - genomics lead the way. Haematologica, 2011, 96, 1402-1405.	1.7	6
84	DNA methylation of chronic lymphocytic leukemia with differential response to chemotherapy. Scientific Data, 2020, 7, 133.	2.4	6
85	Protein expression analysis of chronic lymphocytic leukemia defines the effect of genetic aberrations and uncovers a correlation of CDK4, P27 and P53 with hierarchical risk. Haematologica, 2010, 95, 1880-1888.	1.7	5
86	TCL1A and ATM are co-expressed in chronic lymphocytic leukemia cells without deletion of 11q. Haematologica, 2013, 98, 269-273.	1.7	5
87	Genomic Features: Impact on Pathogenesis and Treatment of Chronic Lymphocytic Leukemia. Oncology Research and Treatment, 2016, 39, 34-40.	0.8	5
88	Ibrutinib-resistant CLL: unwanted and unwonted!. Blood, 2017, 129, 1407-1409.	0.6	5
89	Hydroxylation of the NOTCH1 intracellular domain regulates Notch signaling dynamics. Cell Death and Disease, 2022, 13, .	2.7	5
90	In Vivo Processing Assay Based on a Dual-Luciferase Reporter System to Evaluate DROSHA Enzymatic Activity. Methods in Molecular Biology, 2014, 1095, 87-93.	0.4	4

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91	Quantitative Clonal Dynamics Define Mechanisms of CLL Evolution in Response to Combination Chemotherapy. <i>Blood</i> , 2015, 126, 362-362.	0.6	4
92	Telomere Length and Treatment Outcome In Chronic Lymphocytic Leukemia: Results From The CLL8 Trial. <i>Blood</i> , 2013, 122, 671-671.	0.6	3
93	Rapid detection of ATM/p53 function with p27Kip FACS analysis: a novel diagnostic tool for chronic lymphocytic leukemia?. <i>Leukemia and Lymphoma</i> , 2017, 58, 6-7.	0.6	2
94	Integrative prognostic models predict long-term survival after immunochemotherapy in chronic lymphocytic leukemia patients. <i>Haematologica</i> , 2021, , .	1.7	2
95	Immune modulatory agents in hematopoietic malignancies. <i>Cancer Treatment Reviews</i> , 2011, 37, S2-S7.	3.4	1
96	Toward chemotherapy-free treatment of CLL. <i>Blood</i> , 2011, 118, 3451-3452.	0.6	1
97	331 The Microenvironment Regulates Responses to Hepsin Overexpression in Prostate Cancer Cells. <i>European Journal of Cancer</i> , 2012, 48, S81.	1.3	1
98	Comprehensive microRNA expression profiling in cerebrospinal fluid distinguishes between neurological disease classes. <i>Neuropathology and Applied Neurobiology</i> , 2019, 45, 318-323.	1.8	1
99	Triggering T-cell activity in CLL. <i>Blood</i> , 2021, 137, 150-151.	0.6	1
100	NOTCH1 Signaling Is Activated in CLL By Mutations of FBXW7 and Low Expression of USP28 at 11q23. <i>Blood</i> , 2018, 132, 946-946.	0.6	1
101	NOTCH1, SF3B1 and TP53 Mutations in Fludarabine-Refractory CLL Patients Treated with Alemtuzumab: Results From the CLL2H Trial of the Gclsg. <i>Blood</i> , 2012, 120, 710-710.	0.6	1
102	Progressive Epigenetic Programming during B Cell Maturation Is Reflected in a Continuum of Epigenetic Disease Phenotypes in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 2436-2436.	0.6	1
103	Mir-34a as Part of the Chemotherapy Resistance Network in Chronic Lymphocytic Leukemia.. <i>Blood</i> , 2008, 112, 1209-1209.	0.6	1
104	ADARB1 Is Involved In a Reduced Maturation Of The miR15a/Mir-16-1 Family In Chronic Lymphocytic Leukemia. <i>Blood</i> , 2013, 122, 1252-1252.	0.6	1
105	Missing the notch in NOTCH1. <i>Leukemia and Lymphoma</i> , 2013, 54, 1579-1580.	0.6	0
106	High ZAP-70 and Differential Expression of B-Cell Receptor Related Genes in Chronic Lymphocytic Leukemia with V3-21 Gene Usage.. <i>Blood</i> , 2004, 104, 773-773.	0.6	0
107	The Response to DNA Damage in CLL Cells Is Partly Determined by the Type of TP53 Mutation and Genomic Aberrations. <i>Blood</i> , 2008, 112, 3119-3119.	0.6	0
108	Epimutation of the Tumor Suppressor Mechanism in 13q14.3 Involves Monoallelic Expression, Non-Coding RNA Genes and Deregulation of NFkB Signalling. <i>Blood</i> , 2008, 112, 783-783.	0.6	0

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109	Comprehensive Protein Expression Analysis of Chronic Lymphocytic Leukemia Uncovers a Correlation of CDK4, P27 and P53 with Hierarchical Risk and Suggests a Dichotomy of Apoptosis and Proliferation.. Blood, 2009, 114, 1255-1255.	0.6	0
110	A Novel Paradigm to Trigger Apoptosis in Chronic Lymphocytic Leukemia.. Blood, 2009, 114, 731-731.	0.6	0
111	Detection of NF κ B Activity in Primary CLL Cells Using a Sensitive Oligo-Based Chemiluminescent ELISA.. Blood, 2009, 114, 4709-4709.	0.6	0
112	Maturation of the miR15a/miR16-1 Family Is Impaired In Chronic Lymphocytic Leukaemia. Blood, 2010, 116, 53-53.	0.6	0
113	Myeloid Leukemogenesis Driven by Aberrant CDX2 Expression Involves Transcriptional Repression of KLF4 and Deregulated PPAR γ Signaling. Blood, 2011, 118, 1355-1355.	0.6	0
114	IL4 and CD40L Prevent Apoptosis of Chronic Lymphocytic Leukemia Cells Via Intracellular pSTAT6 and NF κ B Signaling and Not Via Receptor Kinetics. Blood, 2012, 120, 3893-3893.	0.6	0
115	Microrna Expression in Fludarabine-Refractory CLL Implicates Independent Mechanisms of Resistance and Is Associated with Response and Progression Free Survival After Alemtuzumab Treatment: Results From the CLL2H Trial.. Blood, 2012, 120, 2874-2874.	0.6	0
116	Heterogeneity and Evolution Of DNA Methylation In Chronic Lymphocytic Leukemia. Blood, 2013, 122, 1626-1626.	0.6	0
117	E μ -TCL1mTerc -/- Mouse Model for Telomere Dysfunction in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 1724-1724.	0.6	0
118	Microenvironmental Stromal Cells Rescue CLL Cells from Apoptosis Via Hypoxia That Can be Targeted Therapeutically. Blood, 2015, 126, 4140-4140.	0.6	0
119	Multiplatform Profiling Characterizes Functional Networks in Genomically Stable and Unstable Chronic Lymphocytic Leukemia. Blood, 2020, 136, 12-13.	0.6	0
120	Modeling the B α cell receptor signaling on single cell level reveals a stable network circuit topology between non α malignant B cells and chronic lymphocytic leukemia cells and between untreated cells and cells treated with kinase inhibitors. International Journal of Cancer, 2022, , .	2.3	0