Ulrich Lehmann

List of Publications by Year
in descending order

121 papers	5,092 citations	101543 36 h-index	95266 68 g-index
129 all docs	129 docs citations	129 times ranked	8600 citing authors

#	Article	IF	Citations
1	LEF-1 is crucial for neutrophil granulocytopoiesis and its expression is severely reduced in congenital neutropenia. Nature Medicine, 2006, 12, 1191-1197.	30.7	1,015
2	Real-Time PCR Analysis of DNA and RNA Extracted from Formalin-Fixed and Paraffin-Embedded Biopsies. Methods, 2001, 25, 409-418.	3.8	336
3	Quantitative Assessment of Promoter Hypermethylation during Breast Cancer Development. American Journal of Pathology, 2002, 160, 605-612.	3.8	210
4	Plexiform Lesions in Pulmonary Arterial Hypertension. American Journal of Pathology, 2011, 179, 167-179.	3.8	144
5	Detection of Gene Amplification in Archival Breast Cancer Specimens by Laser-Assisted Microdissection and Quantitative Real-Time Polymerase Chain Reaction. American Journal of Pathology, 2000, 156, 1855-1864.	3.8	138
6	Transposable Elements in Human Cancer: Causes and Consequences of Deregulation. International Journal of Molecular Sciences, 2017, 18, 974.	4.1	128
7	Identification of differentially expressed microRNAs in human male breast cancer. BMC Cancer, 2010, 10, 109.	2.6	119
8	Loss of Imprinting and Allelic Switching at the DLK1-MEG3 Locus in Human Hepatocellular Carcinoma. PLoS ONE, 2012, 7, e49462.	2.5	119
9	MicroRNA profiles of healthy basal and luminal mammary epithelial cells are distinct and reflected in different breast cancer subtypes. Breast Cancer Research and Treatment, 2011, 130, 735-745.	2.5	117
10	Impact of Molecular Genetics on Outcome in Myelofibrosis Patients after Allogeneic Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2017, 23, 1095-1101.	2.0	89
11	High-Resolution Genomic Profiling Reveals Association of Chromosomal Aberrations on 1q and 16p with Histologic and Genetic Subgroups of Invasive Breast Cancer. Clinical Cancer Research, 2006, 12, 345-352.	7.0	85
12	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	5.1	76
13	Common and epithelioid variants of hepatic angiomyolipoma exhibit clonal growth and share a distinctive immunophenotype. Hepatology, 2000, 32, 213-217.	7.3	74
14	DNA methylation, microRNAs, and their crosstalk as potential biomarkers in hepatocellular carcinoma. World Journal of Gastroenterology, 2014, 20, 7894.	3.3	74
15	Quantitative High-Resolution CpG Island Mapping with Pyrosequencingâ„¢ Reveals Disease-Specific Methylation Patterns of the CDKN2B Gene in Myelodysplastic Syndrome and Myeloid Leukemia. Clinical Chemistry, 2007, 53, 17-23.	3.2	69
16	Concordant hypermethylation of intergenic microRNA genes in human hepatocellular carcinoma as new diagnostic and prognostic marker. International Journal of Cancer, 2013, 133, 660-670.	5.1	68
17	Testing the importance of p27 degradation by the SCFskp2 pathway in murine models of lung and colon cancer. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14009-14014.	7.1	62
18	Distinct Methylation Patterns of Benign and Malignant Liver Tumors Revealed by Quantitative Methylation Profiling. Clinical Cancer Research, 2005, 11, 3654-3660.	7.0	60

#	Article	IF	Citations
19	Promoter hypermethylation of the death-associated protein kinase gene in breast cancer is associated with the invasive lobular subtype. Cancer Research, 2002, 62, 6634-8.	0.9	58
20	Hypermethylation of the suppressor of cytokine signalling-1 (SOCS-1) in myelodysplastic syndrome. British Journal of Haematology, 2005, 130, 209-217.	2.5	57
21	MicroRNAs: Emerging Novel Clinical Biomarkers for Hepatocellular Carcinomas. Journal of Clinical Medicine, 2015, 4, 1631-1650.	2.4	53
22	A novel germline POLE mutation causes an early onset cancer prone syndrome mimicking constitutional mismatch repair deficiency. Familial Cancer, 2017, 16, 67-71.	1.9	52
23	The prognostic role of IDH mutations in homogeneously treated patients with anaplastic astrocytomas and glioblastomas. Acta Neuropathologica Communications, 2019, 7, 156.	5.2	47
24	Quantitative Analysis of Promoter Hypermethylation in Laser-Microdissected Archival Specimens. Laboratory Investigation, 2001, 81, 635-637.	3.7	45
25	Epigenetic defects of hepatocellular carcinoma are already found in non-neoplastic liver cells from patients with hereditary haemochromatosis. Human Molecular Genetics, 2007, 16, 1335-1342.	2.9	45
26	Infratentorial IDH-mutant astrocytoma is a distinct subtype. Acta Neuropathologica, 2020, 140, 569-581.	7.7	45
27	One-Step Extraction of RNA from Archival Biopsies. Analytical Biochemistry, 2001, 295, 116-117.	2.4	44
28	Reliable microRNA profiling in routinely processed formalin-fixed paraffin-embedded breast cancer specimens using fluorescence labelled bead technology. BMC Biotechnology, 2008, 8, 90.	3.3	43
29	Testosterone-receptor positive hepatocellular carcinoma in a 29-year old bodybuilder with a history of anabolic androgenic steroid abuse: a case report. BMC Gastroenterology, 2015, 15, 60.	2.0	42
30	Routine clinical mutation profiling using next generation sequencing and a customized gene panel improves diagnostic precision in myeloid neoplasms. Oncotarget, 2016, 7, 30084-30093.	1.8	42
31	Quantitative Molecular Analysis of Laser-Microdissected Paraffin- Embedded Human Tissues. Pathobiology, 2000, 68, 202-208.	3.8	41
32	Up-regulation of DNA methyltransferases DNMT1, 3A, and 3B in myelodysplastic syndrome. Leukemia Research, 2005, 29, 325-329.	0.8	40
33	Absence of p21CIP1, p27KIP1 and p57KIP2 methylation in MDS and AML. Leukemia Research, 2005, 29, 1357-1360.	0.8	39
34	Systematic cross-validation of 454 sequencing and pyrosequencing for the exact quantification of DNA methylation patterns with single CpG resolution. BMC Biotechnology, 2011, 11, 6.	3.3	39
35	Deregulation of <scp>RB1</scp> expression by loss of imprinting in human hepatocellular carcinoma. Journal of Pathology, 2014, 233, 392-401.	4.5	38
36	Molecular Analysis of Circulating Cell-Free DNA from Lung Cancer Patients in Routine Laboratory Practice. Journal of Molecular Diagnostics, 2017, 19, 722-732.	2.8	37

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37	Oncogenic PIK3CA mutations in lobular breast cancer progression. Genes Chromosomes and Cancer, 2013, 52, 69-80.	2.8	36
38	Amplification of Growth Regulatory Genes in Intraductal Breast Cancer Is Associated with Higher Nuclear Grade but Not with the Progression to Invasiveness. Laboratory Investigation, 2001, 81, 565-571.	3.7	35
39	Role of epigenetic changes in hematological malignancies. Annals of Hematology, 2004, 83, 137-152.	1.8	35
40	High intrahepatic HHV-6 virus loads but neither CMV nor EBV are associated with decreased graft survival after diagnosis of graft hepatitis. Journal of Hepatology, 2012, 56, 1063-1069.	3.7	35
41	Absence of MGMT promoter methylation in diffuse midline glioma, H3 K27M-mutant. Acta Neuropathologica Communications, 2017, 5, 98.	5.2	35
42	Frequent and Distinct Aberrations of DNA Methylation Patterns in Fibrolamellar Carcinoma of the Liver. PLoS ONE, 2010, 5, e13688.	2.5	34
43	KAI1/CD82 is a novel target of estrogen receptorâ€mediated gene repression and downregulated in primary human breast cancer. International Journal of Cancer, 2008, 123, 2239-2246.	5.1	33
44	FGFR inhibitors in cholangiocarcinoma: whatâ€™s now and whatâ€™s next?. Therapeutic Advances in Medical Oncology, 2020, 12, 175883592095329.	3.2	33
45	Comprehensive genetic and functional characterization of IPHâ€926: a novel CDH1â€null tumour cell line from human lobular breast cancer. Journal of Pathology, 2009, 217, 620-632.	4.5	32
46	Regulation of Cellular Heterogeneity and Rates of Symmetric and Asymmetric Divisions in Triple-Negative Breast Cancer. Cell Reports, 2018, 24, 3237-3250.	6.4	31
47	Persistence of Occult Hepatitis B after Removal of the Hepatitis B Virusâ€“Infected Liver. Journal of Infectious Diseases, 2008, 197, 355-360.	4.0	30
48	Epigenetic inactivation of tumour suppressor gene KLF11 in myelodysplastic syndromes*. European Journal of Haematology, 2010, 84, 298-303.	2.2	30
49	Breast Cancer Anti-Estrogen Resistance 4 (BCAR4) Drives Proliferation of IPH-926 lobular Carcinoma Cells. PLoS ONE, 2015, 10, e0136845.	2.5	30
50	EGFR T790M mutation testing of non-small cell lung cancer tissue and blood samples artificially spiked with circulating cell-free tumor DNA: results of a round robin trial. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2017, 471, 509-520.	2.8	29
51	Estrogen receptor (ESR1) mutation in bone metastases from breast cancer. Modern Pathology, 2018, 31, 56-61.	5.5	29
52	CDKN2A loss and PIK3CA mutation in myoepithelialâ€like metaplastic breast cancer. Journal of Pathology, 2018, 245, 373-383.	4.5	28
53	ERBB2 mutation frequency in lobular breast cancer with pleomorphic histology or highâ€risk characteristics by molecular expression profiling. Genes Chromosomes and Cancer, 2019, 58, 175-185.	2.8	27
54	Mutations associated with age-related clonal hematopoiesis in PMF patients with rapid progression to myelofibrosis. Leukemia, 2020, 34, 1364-1372.	7.2	27

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55	Megakaryocytes from chronic myeloproliferative disorders show enhanced nuclear bFGF expression. Blood, 2002, 100, 2274-2275.	1.4	26
56	Recipient-Derived Neoangiogenesis of Arterioles and Lymphatics in Quilty Lesions of Cardiac Allografts. Transplantation, 2007, 84, 1335-1342.	1.0	26
57	IPH-926 lobular breast cancer cells harbor a p53 mutant with temperature-sensitive functional activity and allow for profiling of p53-responsive genes. Laboratory Investigation, 2012, 92, 1635-1647.	3.7	26
58	The CpG island methylator phenotype in breast cancer is associated with the lobular subtype. Epigenomics, 2015, 7, 187-199.	2.1	26
59	E-cadherin to P-cadherin switching in lobular breast cancer with tubular elements. Modern Pathology, 2020, 33, 2483-2498.	5.5	26
60	Quantitative Intra-Individual Monitoring of BCR-ABL Transcript Levels in Archival Bone Marrow Trephines of Patients with Chronic Myeloid Leukemia. Journal of Molecular Diagnostics, 2003, 5, 54-60.	2.8	24
61	Bone marrow infiltration pattern in B-cell chronic lymphocytic leukemia is related to immunoglobulin heavy-chain variable region mutation status and expression of 70-kd Î¶-associated protein (ZAP-70). Human Pathology, 2006, 37, 1153-1161.	2.0	24
62	NGS-based BRCA1/2 mutation testing of high-grade serous ovarian cancer tissue: results and conclusions of the first international round robin trial. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2016, 468, 697-705.	2.8	24
63	Lobular carcinoma in situ and invasive lobular breast cancer are characterized by enhanced expression of transcription factor AP-2Î². Laboratory Investigation, 2018, 98, 117-129.	3.7	24
64	Aberrant DNA methylation of microRNA genes in human breast cancer â€“ a critical appraisal. Cell and Tissue Research, 2014, 356, 657-664.	2.9	23
65	A child with Liâ€“Fraumeni syndrome: Modes to inactivate the second allele of TP53 in three different malignancies. Pediatric Blood and Cancer, 2015, 62, 1481-1484.	1.5	22
66	Cerebellar glioblastoma: a clinical series with contemporary molecular analysis. Acta Neurochirurgica, 2018, 160, 2237-2248.	1.7	22
67	Overexpression of delta-like (Dlk) in a subset of myelodysplastic syndrome bone marrow trephines. Leukemia Research, 2004, 28, 1081-1083.	0.8	20
68	Demonstration of Light Chain Restricted Clonal B-Lymphoid Infiltrates in Archival Bone Marrow Trephines by Quantitative Real-Time Polymerase Chain Reaction. American Journal of Pathology, 2001, 159, 2023-2029.	3.8	19
69	Comprehensive mutation profiling and mRNA expression analysis in atypical chronic myeloid leukemia in comparison with chronic myelomonocytic leukemia. Cancer Medicine, 2019, 8, 742-750.	2.8	19
70	Interâ€observer agreement for the histological diagnosis of invasive lobular breast carcinoma. Journal of Pathology: Clinical Research, 2022, 8, 191-205.	3.0	19
71	hsa-mir-183 is frequently methylated and related to poor survival in human hepatocellular carcinoma. World Journal of Gastroenterology, 2017, 23, 1568.	3.3	17
72	Down-regulation of the IGF-2/H19 locus during normal and malignant hematopoiesis is independent of the imprinting pattern. International Journal of Oncology, 2005, 26, 499-507.	3.3	16

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73	Loss of DNA methylation at imprinted loci is a frequent event in hepatocellular carcinoma and identifies patients with shortened survival. Clinical Epigenetics, 2015, 7, 110.	4.1	14
74	Molecular defects in BRAF wild-type ameloblastomas and craniopharyngiomasâ€"differences in mutation profiles in epithelial-derived oropharyngeal neoplasms. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2018, 472, 1055-1059.	2.8	14
75	Activating human epidermal growth factor receptor 2 (HER2) gene mutation in bone metastases from breast cancer. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2018, 473, 577-582.	2.8	14
76	Diffuse midline gliomas, H3 K27M-mutant are associated with less peritumoral edema and contrast enhancement in comparison to glioblastomas, H3 K27M-wildtype of midline structures. PLoS ONE, 2021, 16, e0249647.	2.5	14
77	Comprehensive Molecular Profiling of Archival Bone Marrow Trephines Using a Commercially Available Leukemia Panel and Semiconductor-Based Targeted Resequencing. PLoS ONE, 2015, 10, e0133930.	2.5	14
78	TP53 mutations are associated with primary endocrine resistance in luminal early breast cancer. Cancer Medicine, 2021, 10, 8581-8594.	2.8	14
79	Low level of DAP-kinase DNA methylation in myelodysplastic syndrome. Blood, 2004, 104, 1586-1588.	1.4	13
80	Real-Time PCR-Based Assay for Quantitative Determination of Methylation Status. , 2004, 287, 207-218.		12
81	Prognostic factors in the myoepithelial-like spindle cell type of metaplastic breast cancer. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2016, 469, 191-201.	2.8	12
82	Rare ADAR and RNASEH2B variants and a type I interferon signature in glioma and prostate carcinoma risk and tumorigenesis. Acta Neuropathologica, 2017, 134, 905-922.	7.7	12
83	LINE-1 hypomethylation in human hepatocellular carcinomas correlates with shorter overall survival and CIMP phenotype. PLoS ONE, 2019, 14, e0216374.	2.5	12
84	Quantitative DNA Methylation Analysis by PyrosequencingÂ®. Methods in Molecular Biology, 2015, 1315, 175-188.	0.9	12
85	MicroRNA-Profiling in Formalin-Fixed Paraffin-Embedded Specimens. Methods in Molecular Biology, 2010, 667, 113-125.	0.9	11
86	Analysis of Mutational Hotspots in Routinely Processed Bone Marrow Trephines by PyrosequencingÂ®. Methods in Molecular Biology, 2015, 1315, 103-114.	0.9	11
87	Precise ERBB2 copy number assessment in breast cancer by means of molecular inversion probe array analysis. Oncotarget, 2016, 7, 82733-82740.	1.8	11
88	Lobular breast cancer - the most common special subtype or a most special common subtype?. Breast Cancer Research, 2015, 17, 99.	5.0	10
89	BH3-only protein expression determines hepatocellular carcinoma response to sorafenib-based treatment. Cell Death and Disease, 2021, 12, 736.	6.3	10
90	microRNA Expression Profiling in Archival Tissue Specimens: Methods and Data Processing. Molecular Biotechnology, 2012, 50, 159-169.	2.4	9

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91	Archival bone marrow trephines are suitable for high-throughput mutation analysis using next generation sequencing technology. Haematologica, 2013, 98, e115-e116.	3.5	9
92	Expression of Olig2, Nestin, NogoA and AQP4 have no impact on overall survival in IDH-wildtype glioblastoma. PLoS ONE, 2020, 15, e0229274.	2.5	9
93	The detection of BKPyV genotypes II and IV after renal transplantation as a simple tool for risk assessment for PyVAN and transplant outcome already at early stages of BKPyV reactivation. Journal of Clinical Virology, 2019, 113, 14-19.	3.1	8
94	Down-regulation of the IGF-2/H19 locus during normal and malignant hematopoiesis is independent of the imprinting pattern. International Journal of Oncology, 2005, 26, 499.	3.3	7
95	Next-Generation Sequencing Analysis of Laser-Microdissected Formalin-Fixed and Paraffin-Embedded (FFPE) Tissue Specimens. Methods in Molecular Biology, 2018, 1723, 111-118.	0.9	6
96	Quantitative Validation and Quality Control of PyrosequencingÂ® Assays. Methods in Molecular Biology, 2015, 1315, 39-46.	0.9	6
97	MicroRNA Profiling Using Fluorescence-Labeled Beads: Data Acquisition and Processing. Methods in Molecular Biology, 2011, 676, 253-268.	0.9	6
98	Differences in the MRI Signature and ADC Values of Diffuse Midline Gliomas with H3 K27M Mutation Compared to Midline Glioblastomas. Cancers, 2022, 14, 1397.	3.7	6
99	Laser-Assisted Microdissection and Isolation of DNA and RNA. , 2006, 120, 65-76.		5
100	Limited Value of KAI1/CD82 Protein Expression as a Prognostic Marker in Human Gastric Cancer. Disease Markers, 2012, 32, 337-342.	1.3	5
101	Detection of Aberrant DNA Methylation Patterns in the RB1 Gene. Methods in Molecular Biology, 2018, 1726, 35-47.	0.9	5
102	ERBB2 mutation is associated with sustained tumor cell proliferation after short-term preoperative endocrine therapy in early lobular breast cancer. Modern Pathology, 2022, 35, 1804-1811.	5.5	4
103	A liver nodule in a patient transplanted for primary sclerosing cholangitis: an interdisciplinary diagnostic approach. Zeitschrift Fur Gastroenterologie, 2017, 55, 56-62.	0.5	3
104	Chromosome 2q gain and epigenetic silencing of <scp>GATA3</scp> in microglandular adenosis of the breast. Journal of Pathology: Clinical Research, 2021, 7, 220-232.	3.0	3
105	Combined laser-assisted microdissection and short tandem repeat analysis for detection of in situ microchimerism after solid organ transplantation. Methods in Molecular Biology, 2005, 293, 113-23.	0.9	3
106	Positive Display of Methylated Sites: A Novel Method for the Detection of Promoter Methylation. Diagnostic Molecular Pathology, 2000, 9, 165-171.	2.1	2
107	Complete cytogenetic remission after decitabine treatment in a patient with secondary AML harbouring high p15 INK4b gene methylation and high global DNA methylation. Annals of Hematology, 2009, 88, 275-277.	1.8	2
108	Hotspot mutations in cancer genes may be missed in routine diagnostics due to neighbouring sequence variants. Experimental and Molecular Pathology, 2018, 105, 37-40.	2.1	2

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109	Coincidence of lymphomatoid granulomatosis, chronic myelomonocytic leukemia, and anaplastic T cell lymphoma after methotrexate therapy for rheumatoid arthritis. Annals of Hematology, 2019, 98, 515-517.	1.8	2
110	Feasibility of Combined Detection of Gene Mutations and Fusion Transcripts in Bone Marrow Trephines from Leukemic Neoplasms. Journal of Molecular Diagnostics, 2020, 22, 591-598.	2.8	2
111	Tissue Procurement for Molecular Studies Using Laser-Assisted Microdissection. Methods in Molecular Biology, 2009, 506, 299-310.	0.9	2
112	Impact of Molecular Genetics on Disease-Free Survival in Myelofibrosis Patients Following Allogeneic Stem Cell Transplantation. Blood, 2015, 126, 352-352.	1.4	2
113	Discordancy for a Villous Maturation Defect in a Dizygotic Twin Placenta. Fetal and Pediatric Pathology, 2019, 38, 432-436.	0.7	1
114	Choledochal Cysts Resected during Childhood Show No Mutations of KRAS and BRAF as Early Markers of Malignancy in Cholangiocytes. European Journal of Pediatric Surgery, 2021, 31, 020-024.	1.3	1
115	The Hannover Unified Biobank (HUB) â€“ Centralized Standardised Biobanking at Hannover Medical School. Open Journal of Bioresources, 2021, 8, .	1.5	1
116	Genome-wide DNA methylation profiling is able to identify prefibrotic PMF cases at risk for progression to myelofibrosis. Clinical Epigenetics, 2021, 13, 28.	4.1	1
117	Molecular diagnostics and therapies for gastrointestinal tumors: a real-world experience. Journal of Cancer Research and Clinical Oncology, 2022, 148, 2137-2144.	2.5	1
118	Prognostic Impact of Splicing Factor Mutations in Patients with Myelofibrosis Undergoing Allogeneic Hematopoietic Stem Cell Transplantation. Blood, 2014, 124, 3171-3171.	1.4	1
119	High-Resolution Quantitative Methylation Analysis of MicroRNA Genes Using Pyrosequencingâ„¢. Methods in Molecular Biology, 2012, 878, 229-240.	0.9	1
120	Re: Rahner et al. Coexisting somatic promoter hypermethylation and pathogenic MLH1 germline mutation in Lynch syndrome. J Pathol 2008; 214: 10â€“16. Journal of Pathology, 2008, 215, 97-97.	4.5	0
121	Polymerase chain reactionâ€“based analyses of nucleic acids from archival material. , 0, , 254-261.		0