Lise Lotte Hansen

List of Publications by Year
in descending order

80	3,302	172457	149698
papers	citations	29 h-index	56 g-index

81	81	81	5665
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	IGHV-associated methylation signatures more accurately predict clinical outcomes of chronic lymphocytic leukemia patients than IGHV mutation load. Haematologica, 2022, 107, 877-886.	3.5	5
2	Bortezomib induces methylation changes in neuroblastoma cells that appear to play a significant role in resistance development to this compound. Scientific Reports, 2021, 11, 9846.	3.3	7
3	miR-151a enhances Slug dependent angiogenesis. Oncotarget, 2020, 11, 2160-2171.	1.8	8
4	The polymorphic insertion of the luteinizing hormone receptor â€œinsLQâ€•show a negative association to LHR gene expression and to the follicular fluid hormonal profile in human small antral follicles. Molecular and Cellular Endocrinology, 2018, 460, 57-62.	3.2	4
5	Methylation-Sensitive High Resolution Melting (MS-HRM). Methods in Molecular Biology, 2018, 1708, 551-571.	0.9	24
6	mi<scp>RNA</scp> profiling identifies deregulated mi<scp>RNA</scp>s associated with osteosarcoma development and time to metastasis in two large cohorts. Molecular Oncology, 2018, 12, 114-131.	4.6	46
7	Chronic lymphocytic leukemia patients with heterogeneously or fully methylated LPL promotor display longer time to treatment. Epigenomics, 2018, 10, 1155-1166.	2.1	7
8	The association between miR-34 dysregulation and distant metastases formation in lung adenocarcinoma. Experimental and Molecular Pathology, 2017, 102, 484-491.	2.1	33
9	Epigenetic changes in myelofibrosis: Distinct methylation changes in the myeloid compartments and in cases with ASXL1 mutations. Scientific Reports, 2017, 7, 6774.	3.3	16
10	miR-151a induces partial EMT by regulating E-cadherin in NSCLC cells. Oncogenesis, 2017, 6, e366-e366.	4.9	73
11	The Common Follicle-Stimulating Hormone Receptor (FSHR) Promoter Polymorphism FSHR â^'29Gâ€‰›â€‰A Affects Androgen Production in Normal Human Small Antral Follicles. Frontiers in Endocrinology, 2017, 8, 122.	3.5	8
12	Small RNA sequencing reveals metastasis-related microRNAs in lung adenocarcinoma. Oncotarget, 2017, 8, 27047-27061.	1.8	26
13	Strategies for Integrated Analysis of Genetic, Epigenetic, and Gene Expression Variation in Cancer: Addressing the Challenges. Frontiers in Genetics, 2016, 7, 2.	2.3	23
14	Identification and validation of candidate epigenetic biomarkers in lung adenocarcinoma. Scientific Reports, 2016, 6, 35807.	3.3	54
15	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	17.5	270
16	Size matters: Associations between the androgen receptor CAG repeat length and the intrafollicular hormone milieu. Molecular and Cellular Endocrinology, 2016, 419, 12-17.	3.2	15
17	Effect of the FSH receptor single nucleotide polymorphisms (FSHR 307/680) on the follicular fluid hormone profile and the granulosa cell gene expression in human small antral follicles. Molecular Human Reproduction, 2015, 21, 255-261.	2.8	18
18	The influence of DNA degradation in formalin-fixed, paraffin-embedded (FFPE) tissue on locus-specific methylation assessment by MS-HRM. Experimental and Molecular Pathology, 2015, 99, 632-640.	2.1	22

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19	Improved reproducibility in genome-wide DNA methylation analysis for PAXgene-fixed samples compared with restored formalin-fixed and paraffin-embedded DNA. Analytical Biochemistry, 2015, 468, 50-58.	2.4	17
20	Copy number variations alter methylation and parallel IGF2 overexpression in adrenal tumors. Endocrine-Related Cancer, 2015, 22, 953-967.	3.1	21
21	Abstract LB-159: Methylation of BRCA1 gene in blood is not inherited via maternal germ line and may predispose to triple-negative or medullary breast cancer. , 2015, , .		0
22	Genotyping common FSHR polymorphisms based on competitive amplification of differentially melting amplicons (CADMA).. Journal of Assisted Reproduction and Genetics, 2014, 31, 1427-1436.	2.5	10
23	ELMO3: A direct driver of cancer metastasis?. Cell Cycle, 2014, 13, 2483-2484.	2.6	11
24	Identification and characterization of locus-specific methylation patterns within novel loci undergoing hypermethylation during breast cancer pathogenesis. Breast Cancer Research, 2014, 16, R17.	5.0	24
25	Hypomethylation and increased expression of the putative oncogene ELMO3 are associated with lung cancer development and metastases formation. Oncoscience, 2014, 1, 367-374.	2.2	71
26	Abstract 2308: Heterogeneous and low-level methylation of novel biomarker candidates for breast cancer clinical management. , 2014, , .		0
27	Chromosome 1q25.3 copy number alterations in primary breast cancers detected by multiplex ligation-dependent probe amplification and allelic imbalance assays and its comparison with fluorescent in situ hybridization assays. Cellular Oncology (Dordrecht), 2013, 36, 113-120.	4.4	8
28	Identification of accurate reference genes for RT-qPCR analysis of formalin-fixed paraffin-embedded tissue from primary Non-Small Cell Lung Cancers and brain and lymph node metastases. Lung Cancer, 2013, 81, 180-186.	2.0	38
29	Evaluation of BRAF Mutation Testing Methodologies in Formalin-Fixed, Paraffin-Embedded Cutaneous Melanomas. Journal of Molecular Diagnostics, 2013, 15, 70-80.	2.8	68
30	The Challenges of Comparing a Clinically Validated Test to Other Methods. Journal of Molecular Diagnostics, 2013, 15, 535-537.	2.8	0
31	Investigation of MGMT and DAPK1 methylation patterns in diffuse large B-cell lymphoma using allelic MSP-pyrosequencing. Scientific Reports, 2013, 3, 2789.	3.3	30
32	A role for immunohistochemical detection of BRAF V600E prior to BRAF-inhibitor treatment of malignant melanoma?. Journal of Clinical Pathology, 2013, 66, 723-725.	2.0	17
33	Abstract B28: Investigation of MGMT methylation patterns in diffuse large B-cell lymphoma using a novel allelic methylation-specific PCR pyrosequencing assay. , 2013, , .		0
34	Author's reply: To PMID 23159593. Journal of Molecular Diagnostics, 2013, 15, 536-7.	2.8	0
35	Competitive amplification of differentially melting amplicons (CADMA) improves KRAS hotspot mutation testing in colorectal cancer. BMC Cancer, 2012, 12, 548.	2.6	11
36	Competitive amplification of differentially melting amplicons (CADMA) enables sensitive and direct detection of all mutation types by high-resolution melting analysis. Human Mutation, 2012, 33, 264-271.	2.5	17

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37	Abstract 1703: Discovery and validation of 20 novel breast cancer methylation biomarkers: A new workflow for methylation biomarker development. , 2012, , .		0
38	Comprehensive Genome Methylation Analysis in Bladder Cancer: Identification and Validation of Novel Methylated Genes and Application of These as Urinary Tumor Markers. Clinical Cancer Research, 2011, 17, 5582-5592.	7.0	183
39	Methylation of MGMT in malignant pleural mesothelioma occurs in a subset of patients and is associated with the T allele of the rs16906252 MGMT promoter SNP. Lung Cancer, 2011, 71, 130-136.	2.0	35
40	Identification and validation of highly frequent CpG island hypermethylation in colorectal adenomas and carcinomas. International Journal of Cancer, 2011, 129, 2855-2866.	5.1	140
41	Methylation of cancer related genes in tumor and peripheral blood DNA from the same breast cancer patient as two independent events. Diagnostic Pathology, 2011, 6, 116.	2.0	17
42	No difference in the frequency of locus-specific methylation in the peripheral blood DNA of women diagnosed with breast cancer and age-matched controls. Future Oncology, 2011, 7, 1451-1455.	2.4	19
43	High-Resolution Melting Analysis for Mutation Screening of RGSL1, RGS16, and RGS8 in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 397-407.	2.5	12
44	A simple way to evaluate self-designed probes for tumor specific Multiplex Ligation-dependent Probe Amplification (MLPA). BMC Research Notes, 2010, 3, 179.	1.4	2
45	Increased sensitivity of KRAS mutation detection by high-resolution melting analysis of COLD-PCR products. Human Mutation, 2010, 31, 1366-1373.	2.5	33
46	Limitations and advantages of MS-HRM and bisulfite sequencing for single locus methylation studies. Expert Review of Molecular Diagnostics, 2010, 10, 575-580.	3.1	59
47	Primer design versus PCR bias in methylation independent PCR amplifications. Epigenetics, 2009, 4, 231-234.	2.7	91
48	Quality assessment of DNA derived from up to 30 years old formalin fixed paraffin embedded (FFPE) tissue for PCR-based methylation analysis using SMART-MSP and MS-HRM. BMC Cancer, 2009, 9, 453.	2.6	61
49	The effect of genetic variability on drug response in conventional breast cancer treatment. European Journal of Pharmacology, 2009, 625, 122-130.	3.5	32
50	Epigenetics and cancer treatment. European Journal of Pharmacology, 2009, 625, 131-142.	3.5	189
51	PCR-Based Methods for Detecting Single-Locus DNA Methylation Biomarkers in Cancer Diagnostics, Prognostics, and Response to Treatment. Clinical Chemistry, 2009, 55, 1471-1483.	3.2	189
52	A fragile site within the HPC1 region at 1q25.3 affecting RGS16, RGSL1, and RGSL2 in human breast carcinomas. Genes Chromosomes and Cancer, 2008, 47, 766-780.	2.8	26
53	Methylation-sensitive high-resolution melting. Nature Protocols, 2008, 3, 1903-1908.	12.0	262
54	A new approach to primer design for the control of PCR bias in methylation studies. BMC Research Notes, 2008, 1, 54.	1.4	117

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55	Akt-mediated phosphorylation of CDK2 regulates its dual role in cell cycle progression and apoptosis. Journal of Cell Science, 2008, 121, 979-988.	2.0	160
56	Germline Mutation in RNASEL Predicts Increased Risk of Head and Neck, Uterine Cervix and Breast Cancer. PLoS ONE, 2008, 3, e2492.	2.5	54
57	Conflicting results in SNP genotype assessment. BioTechniques, 2007, 43, 756-762.	1.8	2
58	Methods and biomarkers for the diagnosis and prognosis of cancer and other diseases: Towards personalized medicine. Drug Resistance Updates, 2006, 9, 198-210.	14.4	60
59	Reversal of PCR bias for improved sensitivity of the DNA methylation melting curve assay. BioTechniques, 2006, 41, 274-278.	1.8	61
60	Techniques Used in Studies of Age-Related DNA Methylation Changes. Annals of the New York Academy of Sciences, 2006, 1067, 479-487.	3.8	23
61	LOH rather than genotypes ofTP53codon 72 is associated with disease-free survival in primary breast cancer. Acta OncolÃ³gica, 2006, 45, 602-609.	1.8	18
62	Molecular Diagnosis of Breast Cancer. , 2006, , 201-233.		0
63	Deconstructing PTI-1: PT1-1 is a truncated, but not mutated, form of translation elongation factor 1A1, eEF1A1. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2005, 1727, 116-124.	2.4	11
64	Familial Cancer Associated with a Polymorphism inARLTS1. New England Journal of Medicine, 2005, 352, 1667-1676.	27.0	119
65	A nine-nucleotide deletion and splice variation in the coding region of the interferon induced ISG12 gene. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2003, 1638, 227-234.	3.8	5
66	Allelic imbalance in selected chromosomal regions in ovarian cancer. Cancer Genetics and Cytogenetics, 2002, 139, 1-8.	1.0	31
67	Assignment<footref rid="foot01">¹</footref> of the human postmeiotic segregation increased (S. cerevisiae) 1 (PMS1) to chromosome 2q31.1 by radiation hybrid mapping. Cytogenetic and Genome Research, 2000, 88, 200-201.	1.1	0
68	Assignment<footref rid="foot01">¹</footref> of the human peptide chain release factor 3 (GSPT2) to Xp11.23â†'p11.21 and of the distal marker DXS1039 by radiation hybrid mapping. Cytogenetic and Genome Research, 1999, 86, 250-251.	1.1	6
69	Assignment<footref rid="foot01">¹</footref> of the human translation termination factor 1 (ETF1) to 5q31.1 and of the proximal marker D5S1995 by radiation hybrid mapping. Cytogenetic and Genome Research, 1999, 87, 256-257.	1.1	0
70	Structure of the human CpG-island-containing lung Kruppel-like factor (LKLF) gene and its location in chromosome 19p13.11-13 locus. FEBS Letters, 1999, 448, 149-152.	2.8	8
71	Molecular genetic analysis of easily accessible breast tumour DNA, purified from tissue left over from hormone receptor measurement. Apmis, 1998, 106, 371-377.	2.0	22
72	Assignment<footref rid="foot01">¹</footref> of the human mitochondrial tryptophanyl-tRNA synthetase (WARS2) to 1p13.3â†'p13.1 by radiation hybrid mapping. Cytogenetic and Genome Research, 1998, 83, 249-250.	1.1	7

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73	Refined localization of the pyruvate dehydrogenase E1Î± gene (PDHA1) by linkage analysis. Human Genetics, 1996, 99, 80-82.	3.8	6
74	Sensitive and fast mutation detection by solid phase chemical cleavage. , 1996, 7, 256-263.		13
75	Pyruvate dehydrogenase deficiency caused by a 33 base pair duplication in the PDH E1Î± subunit. Human Molecular Genetics, 1994, 3, 1021-1022.	2.9	15
76	Pyruvate dehydrogenase deficiency caused by a 5 base pair duplication in the E1Î± subunit. Human Molecular Genetics, 1993, 2, 805-807.	2.9	16
77	X-linked pyruvate dehydrogenase E1Î± subunit deficiency in heterozygous females: Variable manifestation of the same mutation. Journal of Inherited Metabolic Disease, 1992, 15, 835-847.	3.6	46
78	Mutations and polymorphisms in the pyruvate dehydrogenase E1Î± gene. Human Mutation, 1992, 1, 97-102.	2.5	89
79	Characterization of the mutations in three patients with pyruvate dehydrogenase E1Î± deficiency. Journal of Inherited Metabolic Disease, 1991, 14, 140-151.	3.6	44
80	Polymorphisms in the human X-linked pyruvate dehydrogenase E1? gene. Human Genetics, 1991, 87, 49-53.	3.8	16