

Lise Lotte Hansen

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

3,302
citations

172457

29
h-index

149698

56
g-index

81
all docs

81
docs citations

81
times ranked

5665
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737. | 17.5 | 270 |
| 2 | Methylation-sensitive high-resolution melting. <i>Nature Protocols</i> , 2008, 3, 1903-1908. | 12.0 | 262 |
| 3 | Epigenetics and cancer treatment. <i>European Journal of Pharmacology</i> , 2009, 625, 131-142. | 3.5 | 189 |
| 4 | PCR-Based Methods for Detecting Single-Locus DNA Methylation Biomarkers in Cancer Diagnostics, Prognostics, and Response to Treatment. <i>Clinical Chemistry</i> , 2009, 55, 1471-1483. | 3.2 | 189 |
| 5 | Comprehensive Genome Methylation Analysis in Bladder Cancer: Identification and Validation of Novel Methylated Genes and Application of These as Urinary Tumor Markers. <i>Clinical Cancer Research</i> , 2011, 17, 5582-5592. | 7.0 | 183 |
| 6 | Akt-mediated phosphorylation of CDK2 regulates its dual role in cell cycle progression and apoptosis. <i>Journal of Cell Science</i> , 2008, 121, 979-988. | 2.0 | 160 |
| 7 | Identification and validation of highly frequent CpG island hypermethylation in colorectal adenomas and carcinomas. <i>International Journal of Cancer</i> , 2011, 129, 2855-2866. | 5.1 | 140 |
| 8 | Familial Cancer Associated with a Polymorphism in <i>ARLTS1</i> . <i>New England Journal of Medicine</i> , 2005, 352, 1667-1676. | 27.0 | 119 |
| 9 | A new approach to primer design for the control of PCR bias in methylation studies. <i>BMC Research Notes</i> , 2008, 1, 54. | 1.4 | 117 |
| 10 | Primer design versus PCR bias in methylation independent PCR amplifications. <i>Epigenetics</i> , 2009, 4, 231-234. | 2.7 | 91 |
| 11 | Mutations and polymorphisms in the pyruvate dehydrogenase E1 α gene. <i>Human Mutation</i> , 1992, 1, 97-102. | 2.5 | 89 |
| 12 | miR-151a induces partial EMT by regulating E-cadherin in NSCLC cells. <i>Oncogenesis</i> , 2017, 6, e366-e366. | 4.9 | 73 |
| 13 | Hypomethylation and increased expression of the putative oncogene ELMO3 are associated with lung cancer development and metastases formation. <i>Oncoscience</i> , 2014, 1, 367-374. | 2.2 | 71 |
| 14 | Evaluation of BRAF Mutation Testing Methodologies in Formalin-Fixed, Paraffin-Embedded Cutaneous Melanomas. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 70-80. | 2.8 | 68 |
| 15 | Reversal of PCR bias for improved sensitivity of the DNA methylation melting curve assay. <i>BioTechniques</i> , 2006, 41, 274-278. | 1.8 | 61 |
| 16 | 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. <i>BMC Cancer</i> , 2009, 9, 453. | 2.6 | 61 |
| 17 | Methods and biomarkers for the diagnosis and prognosis of cancer and other diseases: Towards personalized medicine. <i>Drug Resistance Updates</i> , 2006, 9, 198-210. | 14.4 | 60 |
| 18 | Limitations and advantages of MS-HRM and bisulfite sequencing for single locus methylation studies. <i>Expert Review of Molecular Diagnostics</i> , 2010, 10, 575-580. | 3.1 | 59 |

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|----|--|-----|-----------|
| 19 | Identification and validation of candidate epigenetic biomarkers in lung adenocarcinoma. <i>Scientific Reports</i> , 2016, 6, 35807. | 3.3 | 54 |
| 20 | Germline Mutation in RNASEL Predicts Increased Risk of Head and Neck, Uterine Cervix and Breast Cancer. <i>PLoS ONE</i> , 2008, 3, e2492. | 2.5 | 54 |
| 21 | X-linked pyruvate dehydrogenase E1 α subunit deficiency in heterozygous females: Variable manifestation of the same mutation. <i>Journal of Inherited Metabolic Disease</i> , 1992, 15, 835-847. | 3.6 | 46 |
| 22 | miRNA profiling identifies deregulated miRNAs associated with osteosarcoma development and time to metastasis in two large cohorts. <i>Molecular Oncology</i> , 2018, 12, 114-131. | 4.6 | 46 |
| 23 | Characterization of the mutations in three patients with pyruvate dehydrogenase E1 α deficiency. <i>Journal of Inherited Metabolic Disease</i> , 1991, 14, 140-151. | 3.6 | 44 |
| 24 | 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. <i>Lung Cancer</i> , 2013, 81, 180-186. | 2.0 | 38 |
| 25 | 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. <i>Lung Cancer</i> , 2011, 71, 130-136. | 2.0 | 35 |
| 26 | Increased sensitivity of KRAS mutation detection by high-resolution melting analysis of COLD-PCR products. <i>Human Mutation</i> , 2010, 31, 1366-1373. | 2.5 | 33 |
| 27 | The association between miR-34 dysregulation and distant metastases formation in lung adenocarcinoma. <i>Experimental and Molecular Pathology</i> , 2017, 102, 484-491. | 2.1 | 33 |
| 28 | The effect of genetic variability on drug response in conventional breast cancer treatment. <i>European Journal of Pharmacology</i> , 2009, 625, 122-130. | 3.5 | 32 |
| 29 | Allelic imbalance in selected chromosomal regions in ovarian cancer. <i>Cancer Genetics and Cytogenetics</i> , 2002, 139, 1-8. | 1.0 | 31 |
| 30 | Investigation of MGMT and DAPK1 methylation patterns in diffuse large B-cell lymphoma using allelic MSP-pyrosequencing. <i>Scientific Reports</i> , 2013, 3, 2789. | 3.3 | 30 |
| 31 | A fragile site within the HPC1 region at 1q25.3 affecting <i>RGS16</i> , <i>RGSL1</i> , and <i>RGSL2</i> in human breast carcinomas. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 766-780. | 2.8 | 26 |
| 32 | Small RNA sequencing reveals metastasis-related microRNAs in lung adenocarcinoma. <i>Oncotarget</i> , 2017, 8, 27047-27061. | 1.8 | 26 |
| 33 | Identification and characterization of locus-specific methylation patterns within novel loci undergoing hypermethylation during breast cancer pathogenesis. <i>Breast Cancer Research</i> , 2014, 16, R17. | 5.0 | 24 |
| 34 | Methylation-Sensitive High Resolution Melting (MS-HRM). <i>Methods in Molecular Biology</i> , 2018, 1708, 551-571. | 0.9 | 24 |
| 35 | Techniques Used in Studies of Age-Related DNA Methylation Changes. <i>Annals of the New York Academy of Sciences</i> , 2006, 1067, 479-487. | 3.8 | 23 |
| 36 | Strategies for Integrated Analysis of Genetic, Epigenetic, and Gene Expression Variation in Cancer: Addressing the Challenges. <i>Frontiers in Genetics</i> , 2016, 7, 2. | 2.3 | 23 |

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|----|--|-----|-----------|
| 37 | Molecular genetic analysis of easily accessible breast tumour DNA, purified from tissue left over from hormone receptor measurement. <i>Apmis</i> , 1998, 106, 371-377. | 2.0 | 22 |
| 38 | The influence of DNA degradation in formalin-fixed, paraffin-embedded (FFPE) tissue on locus-specific methylation assessment by MS-HRM. <i>Experimental and Molecular Pathology</i> , 2015, 99, 632-640. | 2.1 | 22 |
| 39 | Copy number variations alter methylation and parallel IGF2 overexpression in adrenal tumors. <i>Endocrine-Related Cancer</i> , 2015, 22, 953-967. | 3.1 | 21 |
| 40 | No difference in the frequency of locus-specific methylation in the peripheral blood DNA of women diagnosed with breast cancer and age-matched controls. <i>Future Oncology</i> , 2011, 7, 1451-1455. | 2.4 | 19 |
| 41 | LOH rather than genotypes of TP53 codon 72 is associated with disease-free survival in primary breast cancer. <i>Acta Oncologica</i> , 2006, 45, 602-609. | 1.8 | 18 |
| 42 | 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. <i>Molecular Human Reproduction</i> , 2015, 21, 255-261. | 2.8 | 18 |
| 43 | Methylation of cancer related genes in tumor and peripheral blood DNA from the same breast cancer patient as two independent events. <i>Diagnostic Pathology</i> , 2011, 6, 116. | 2.0 | 17 |
| 44 | Competitive amplification of differentially melting amplicons (CADMA) enables sensitive and direct detection of all mutation types by high-resolution melting analysis. <i>Human Mutation</i> , 2012, 33, 264-271. | 2.5 | 17 |
| 45 | A role for immunohistochemical detection of BRAF V600E prior to BRAF-inhibitor treatment of malignant melanoma?. <i>Journal of Clinical Pathology</i> , 2013, 66, 723-725. | 2.0 | 17 |
| 46 | Improved reproducibility in genome-wide DNA methylation analysis for PAXgene-fixed samples compared with restored formalin-fixed and paraffin-embedded DNA. <i>Analytical Biochemistry</i> , 2015, 468, 50-58. | 2.4 | 17 |
| 47 | Polymorphisms in the human X-linked pyruvate dehydrogenase E1 γ gene. <i>Human Genetics</i> , 1991, 87, 49-53. | 3.8 | 16 |
| 48 | Pyruvate dehydrogenase deficiency caused by a 5 base pair duplication in the E1 α subunit. <i>Human Molecular Genetics</i> , 1993, 2, 805-807. | 2.9 | 16 |
| 49 | Epigenetic changes in myelofibrosis: Distinct methylation changes in the myeloid compartments and in cases with ASXL1 mutations. <i>Scientific Reports</i> , 2017, 7, 6774. | 3.3 | 16 |
| 50 | Pyruvate dehydrogenase deficiency caused by a 33 base pair duplication in the PDH E1 α subunit. <i>Human Molecular Genetics</i> , 1994, 3, 1021-1022. | 2.9 | 15 |
| 51 | Size matters: Associations between the androgen receptor CAG repeat length and the intrafollicular hormone milieu. <i>Molecular and Cellular Endocrinology</i> , 2016, 419, 12-17. | 3.2 | 15 |
| 52 | Sensitive and fast mutation detection by solid phase chemical cleavage. , 1996, 7, 256-263. | | 13 |
| 53 | High-Resolution Melting Analysis for Mutation Screening of RGS11, RGS16, and RGS8 in Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 397-407. | 2.5 | 12 |
| 54 | Deconstructing PTI-1: PTI-1 is a truncated, but not mutated, form of translation elongation factor 1A1, eEF1A1. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2005, 1727, 116-124. | 2.4 | 11 |

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|----|---|-----|-----------|
| 55 | Competitive amplification of differentially melting amplicons (CADMA) improves KRAS hotspot mutation testing in colorectal cancer. <i>BMC Cancer</i> , 2012, 12, 548. | 2.6 | 11 |
| 56 | <i>ELMO3</i>: A direct driver of cancer metastasis?. <i>Cell Cycle</i> , 2014, 13, 2483-2484. | 2.6 | 11 |
| 57 | Genotyping common FSHR polymorphisms based on competitive amplification of differentially melting amplicons (CADMA).. <i>Journal of Assisted Reproduction and Genetics</i> , 2014, 31, 1427-1436. | 2.5 | 10 |
| 58 | Structure of the human CpG-island-containing lung Kruppel-like factor (LKLf) gene and its location in chromosome 19p13.11-13 locus. <i>FEBS Letters</i> , 1999, 448, 149-152. | 2.8 | 8 |
| 59 | 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. <i>Cellular Oncology (Dordrecht)</i> , 2013, 36, 113-120. | 4.4 | 8 |
| 60 | The Common Follicle-Stimulating Hormone Receptor (FSHR) Promoter Polymorphism FSHR $\hat{\sim}29G\hat{\epsilon}\%o>\hat{\epsilon}\%oA$ Affects Androgen Production in Normal Human Small Antral Follicles. <i>Frontiers in Endocrinology</i> , 2017, 8, 122. | 3.5 | 8 |
| 61 | miR-151a enhances Slug dependent angiogenesis. <i>Oncotarget</i> , 2020, 11, 2160-2171. | 1.8 | 8 |
| 62 | Assignment<footref rid="foot01"> ¹</footref> of the human mitochondrial tryptophanyl-tRNA synthetase (WARS2) to 1p13.3 $\hat{\text{a}}\hat{\text{t}}\hat{\text{p}}13.1$ by radiation hybrid mapping. <i>Cytogenetic and Genome Research</i> , 1998, 83, 249-250. | 1.1 | 7 |
| 63 | Chronic lymphocytic leukemia patients with heterogeneously or fully methylated <i>LPL</i> promotor display longer time to treatment. <i>Epigenomics</i> , 2018, 10, 1155-1166. | 2.1 | 7 |
| 64 | Bortezomib induces methylation changes in neuroblastoma cells that appear to play a significant role in resistance development to this compound. <i>Scientific Reports</i> , 2021, 11, 9846. | 3.3 | 7 |
| 65 | Refined localization of the pyruvate dehydrogenase E1 $\hat{\pm}$ gene (PDHA1) by linkage analysis. <i>Human Genetics</i> , 1996, 99, 80-82. | 3.8 | 6 |
| 66 | Assignment<footref rid="foot01"> ¹</footref> of the human peptide chain release factor 3 (GSPT2) to Xp11.23 $\hat{\text{a}}\hat{\text{t}}\hat{\text{p}}11.21$ and of the distal marker DXS1039 by radiation hybrid mapping. <i>Cytogenetic and Genome Research</i> , 1999, 86, 250-251. | 1.1 | 6 |
| 67 | A nine-nucleotide deletion and splice variation in the coding region of the interferon induced ISG12 gene. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2003, 1638, 227-234. | 3.8 | 5 |
| 68 | IGHV-associated methylation signatures more accurately predict clinical outcomes of chronic lymphocytic leukemia patients than IGHV mutation load. <i>Haematologica</i> , 2022, 107, 877-886. | 3.5 | 5 |
| 69 | The polymorphic insertion of the luteinizing hormone receptor $\hat{\text{a}}\hat{\text{e}}\hat{\text{ins}}LQ\hat{\text{a}}\hat{\text{e}}\hat{\text{.}}$ show a negative association to LHR gene expression and to the follicular fluid hormonal profile in human small antral follicles. <i>Molecular and Cellular Endocrinology</i> , 2018, 460, 57-62. | 3.2 | 4 |
| 70 | Conflicting results in SNP genotype assessment. <i>BioTechniques</i> , 2007, 43, 756-762. | 1.8 | 2 |
| 71 | A simple way to evaluate self-designed probes for tumor specific Multiplex Ligation-dependent Probe Amplification (MLPA). <i>BMC Research Notes</i> , 2010, 3, 179. | 1.4 | 2 |
| 72 | 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. <i>Cytogenetic and Genome Research</i> , 1999, 87, 256-257. | 1.1 | 0 |

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|----|---|-----|-----------|
| 73 | Assignment<footref rid="foot01">¹</footref> of the human postmeiotic segregation increased <i>(S. cerevisiae)</i> 1 (PMS1) to chromosome 2q31.1 by radiation hybrid mapping. Cytogenetic and Genome Research, 2000, 88, 200-201. | 1.1 | 0 |
| 74 | Molecular Diagnosis of Breast Cancer. , 2006, , 201-233. | | 0 |
| 75 | The Challenges of Comparing a Clinically Validated Test to Other Methods. Journal of Molecular Diagnostics, 2013, 15, 535-537. | 2.8 | 0 |
| 76 | Abstract 1703: Discovery and validation of 20 novel breast cancer methylation biomarkers: A new workflow for methylation biomarker development. , 2012, , . | | 0 |
| 77 | Abstract B28: Investigation of MGMT methylation patterns in diffuse large B-cell lymphoma using a novel allelic methylation-specific PCR pyrosequencing assay. , 2013, , . | | 0 |
| 78 | Abstract 2308: Heterogeneous and low-level methylation of novel biomarker candidates for breast cancer clinical management. , 2014, , . | | 0 |
| 79 | 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 |
| 80 | Author's reply: To PMID 23159593. Journal of Molecular Diagnostics, 2013, 15, 536-7. | 2.8 | 0 |