

# Lasse Sommer Kristensen

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

6,683  
citations

159585

30  
h-index

138484

58  
g-index

64  
all docs

64  
docs citations

64  
times ranked

8241  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Expression patterns and prognostic potential of circular RNAs in mantle cell lymphoma: a study of younger patients from the MCL2 and MCL3 clinical trials. <i>Leukemia</i> , 2022, 36, 177-188. | 7.2  | 11        |
| 2  | Unravelling similarities and differences in the role of circular and linear PVT1 in cancer and human disease. <i>British Journal of Cancer</i> , 2022, 126, 835-850.                            | 6.4  | 24        |
| 3  | The transcriptional landscape and biomarker potential of circular RNAs in prostate cancer. <i>Genome Medicine</i> , 2022, 14, 8.  | 8.2  | 19        |
| 4  | The emerging roles of circRNAs in cancer and oncology. <i>Nature Reviews Clinical Oncology</i> , 2022, 19, 188-206.   | 27.6 | 387       |
| 5  | VEGFA-targeting miR-agshRNAs combine efficacy with specificity and safety for retinal gene therapy. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 28, 58-76.                                 | 5.1  | 6         |
| 6  | Best practice standards for circular RNA research. <i>Nature Methods</i> , 2022, 19, 1208-1220.   | 19.0 | 58        |
| 7  | Characterization of circular RNA transcriptomes in psoriasis and atopic dermatitis reveals disease-specific expression profiles. <i>Experimental Dermatology</i> , 2021, 30, 1187-1196.         | 2.9  | 33        |
| 8  | Distinct circular RNA expression profiles in pediatric ependymomas. <i>Brain Pathology</i> , 2021, 31, 387-392.   | 4.1  | 18        |
| 9  | Genome-Wide Circular RNA Expression Patterns Reflect Resistance to Immunomodulatory Drugs in Multiple Myeloma Cells. <i>Cancers</i> , 2021, 13, 365.  | 3.7  | 19        |
| 10 | Profiling of circRNAs using an enzyme-free digital counting method. <i>Methods</i> , 2021, 196, 11-16.  | 3.8  | 9         |
| 11 | The HSP90 inhibitor RGRN-305 exhibits strong immunomodulatory effects in human keratinocytes. <i>Experimental Dermatology</i> , 2021, 30, 773-781.  | 2.9  | 15        |
| 12 | Circular RNAs as microRNA sponges: evidence and controversies. <i>Essays in Biochemistry</i> , 2021, 65, 685-696.   | 4.7  | 33        |
| 13 | Spatial expression analyses of the putative oncogene ciRS-7 in cancer reshape the microRNA sponge theory. <i>Nature Communications</i> , 2020, 11, 4551.  | 12.8 | 72        |
| 14 | Defects in <i>LC3B2</i> and <i>ATG4A</i> underlie HSV2 meningitis and reveal a critical role for autophagy in antiviral defense in humans. <i>Science Immunology</i> , 2020, 5, .               | 11.9 | 27        |
| 15 | A comprehensive analysis of coding and non-coding transcriptomic changes in cutaneous squamous cell carcinoma. <i>Scientific Reports</i> , 2020, 10, 3637.                                      | 3.3  | 60        |
| 16 | The biogenesis, biology and characterization of circular RNAs. <i>Nature Reviews Genetics</i> , 2019, 20, 675-691.  | 16.3 | 2,832     |
| 17 | Identification of an <i>IRF3</i> variant and defective antiviral interferon responses in a patient with severe influenza. <i>European Journal of Immunology</i> , 2019, 49, 2111-2114.          | 2.9  | 13        |
| 18 | High-throughput RNA sequencing from paired lesional- and non-lesional skin reveals major alterations in the psoriasis circRNAome. <i>BMC Medical Genomics</i> , 2019, 12, 174.                  | 1.5  | 43        |

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|----|--|-----|-----------|
| 19 | Circular RNAs are abundantly expressed and upregulated during human epidermal stem cell differentiation. <i>RNA Biology</i> , 2018, 15, 280-291.   | 3.1 | 137       |
| 20 | Circular RNAs in cancer: opportunities and challenges in the field. <i>Oncogene</i> , 2018, 37, 555-565.   | 5.9 | 1,102     |
| 21 | Dual inhibition of DNMTs and EZH2 can overcome both intrinsic and acquired resistance of myeloma cells to IMiDs in a cereblon-independent manner. <i>Molecular Oncology</i> , 2018, 12, 180-195.                     | 4.6 | 62        |
| 22 | DNA Methylation Levels of the ELMO Gene Promoter CpG Islands in Human Glioblastomas. <i>International Journal of Molecular Sciences</i> , 2018, 19, 679.   | 4.1 | 19        |
| 23 | Long Non-Coding RNAs Guide the Fine-Tuning of Gene Regulation in B-Cell Development and Malignancy. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2475.   | 4.1 | 33        |
| 24 | Enzyme-free digital counting of endogenous circular RNA molecules in B-cell malignancies. <i>Laboratory Investigation</i> , 2018, 98, 1657-1669.   | 3.7 | 93        |
| 25 | Global hypomethylation is an independent prognostic factor in diffuse large B cell lymphoma. <i>American Journal of Hematology</i> , 2017, 92, 689-694.  | 4.1 | 36        |
| 26 | 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        |
| 27 | Aberrant methylation of cell-free circulating DNA in plasma predicts poor outcome in diffuse large B cell lymphoma. <i>Clinical Epigenetics</i> , 2016, 8, 95.   | 4.1 | 47        |
| 28 | Mutations in idiopathic cytopenia of undetermined significance assist diagnostics and correlate to dysplastic changes. <i>American Journal of Hematology</i> , 2016, 91, 1234-1238.                                  | 4.1 | 32        |
| 29 | Identification and validation of candidate epigenetic biomarkers in lung adenocarcinoma. <i>Scientific Reports</i> , 2016, 6, 35807.   | 3.3 | 54        |
| 30 | TP53 hotspot mutations are predictive of survival in primary central nervous system lymphoma patients treated with combination chemotherapy. <i>Acta Neuropathologica Communications</i> , 2016, 4, 40.              | 5.2 | 19        |
| 31 | Assessment of Quantitative and Allelic MGMT Methylation Patterns as a Prognostic Marker in Glioblastoma. <i>Journal of Neuropathology and Experimental Neurology</i> , 2016, 75, 246-255.                            | 1.7 | 33        |
| 32 | Biomarkers and Methodologies for Monitoring Epigenetic Drug Effects in Cancer. , 2016, , 91-118.   |     | 2         |
| 33 | Tumor suppressor microRNAs are downregulated in myelodysplastic syndrome with spliceosome mutations. <i>Oncotarget</i> , 2016, 7, 9951-9963.   | 1.8 | 27        |
| 34 | Whole-exome sequencing and genome-wide methylation analyses identify novel disease associated mutations and methylation patterns in idiopathic hypereosinophilic syndrome. <i>Oncotarget</i> , 2015, 6, 40588-40597. | 1.8 | 14        |
| 35 | Hypermethylation of the VTRNA1-3 Promoter is Associated with Poor Outcome in Lower Risk Myelodysplastic Syndrome Patients. <i>Genes</i> , 2015, 6, 977-990.  | 2.4 | 19        |
| 36 | Allele-Specific DNA Methylation Detection by Pyrosequencing®. <i>Methods in Molecular Biology</i> , 2015, 1315, 271-289.   | 0.9 | 5         |

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|----|--|-----|-----------|
| 37 | 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        |
| 38 | <i>ELMO3</i>: A direct driver of cancer metastasis?. Cell Cycle, 2014, 13, 2483-2484.  | 2.6 | 11        |
| 39 | Predicting response to epigenetic therapy. Journal of Clinical Investigation, 2014, 124, 47-55.  | 8.2 | 78        |
| 40 | 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        |
| 41 | Hypermethylation of DAPK1 is an independent prognostic factor predicting survival in diffuse large B-cell lymphoma. Oncotarget, 2014, 5, 9798-9810.  | 1.8 | 34        |
| 42 | 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        |
| 43 | Evaluation of BRAF Mutation Testing Methodologies in Formalin-Fixed, Paraffin-Embedded Cutaneous Melanomas. Journal of Molecular Diagnostics, 2013, 15, 70-80.   | 2.8 | 68        |
| 44 | The Challenges of Comparing a Clinically Validated Test to Other Methods. Journal of Molecular Diagnostics, 2013, 15, 535-537.   | 2.8 | 0         |
| 45 | Analysis of Epigenetic Modifications of DNA in Human Cells. Current Protocols in Human Genetics, 2013, 77, Unit20.2.   | 3.5 | 9         |
| 46 | 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        |
| 47 | 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        |
| 48 | Competitive amplification of differentially melting amplicons (CADMA) improves KRAS hotspot mutation testing in colorectal cancer. BMC Cancer, 2012, 12, 548.  | 2.6 | 11        |
| 49 | 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        |
| 50 | Methylation profiling of normal individuals reveals mosaic promoter methylation of cancer-associated genes. Oncotarget, 2012, 3, 450-461.  | 1.8 | 33        |
| 51 | 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        |
| 52 | Increased sensitivity of KRAS mutation detection by high-resolution melting analysis of COLD-PCR products. Human Mutation, 2010, 31, 1366-1373.  | 2.5 | 33        |
| 53 | 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        |
| 54 | 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        |

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|----|--|------|-----------|
| 55 | Epigenetics and cancer treatment. <i>European Journal of Pharmacology</i> , 2009, 625, 131-142.  | 3.5  | 189       |
| 56 | DNA methylation, epimutations and cancer predisposition. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 34-39.  | 2.8  | 63        |
| 57 | 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       |
| 58 | Direct Genotyping of Single Nucleotide Polymorphisms in Methyl Metabolism Genes Using Probe-Free High-Resolution Melting Analysis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 1240-1247. | 2.5  | 34        |
| 59 | Sensitive Melting Analysis after Real Time- Methylation Specific PCR (SMART-MSP): high-throughput and probe-free quantitative DNA methylation detection. <i>Nucleic Acids Research</i> , 2008, 36, e42-e42.    | 14.5 | 159       |