

# 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	The biogenesis, biology and characterization of circular RNAs. <i>Nature Reviews Genetics</i> , 2019, 20, 675-691.	16.3	2,832
2	Circular RNAs in cancer: opportunities and challenges in the field. <i>Oncogene</i> , 2018, 37, 555-565.	5.9	1,102
3	The emerging roles of circRNAs in cancer and oncology. <i>Nature Reviews Clinical Oncology</i> , 2022, 19, 188-206.	27.6	387
4	Epigenetics and cancer treatment. <i>European Journal of Pharmacology</i> , 2009, 625, 131-142.	3.5	189
5	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
6	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
7	Circular RNAs are abundantly expressed and upregulated during human epidermal stem cell differentiation. <i>RNA Biology</i> , 2018, 15, 280-291.	3.1	137
8	Enzyme-free digital counting of endogenous circular RNA molecules in B-cell malignancies. <i>Laboratory Investigation</i> , 2018, 98, 1657-1669.	3.7	93
9	Predicting response to epigenetic therapy. <i>Journal of Clinical Investigation</i> , 2014, 124, 47-55.	8.2	78
10	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
11	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
12	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
13	DNA methylation, epimutations and cancer predisposition. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 34-39.	2.8	63
14	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
15	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
16	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
17	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
18	Best practice standards for circular RNA research. <i>Nature Methods</i> , 2022, 19, 1208-1220.	19.0	58

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19	Identification and validation of candidate epigenetic biomarkers in lung adenocarcinoma. Scientific Reports, 2016, 6, 35807.	3.3	54
20	Aberrant methylation of cell-free circulating DNA in plasma predicts poor outcome in diffuse large B cell lymphoma. Clinical Epigenetics, 2016, 8, 95.	4.1	47
21	High-throughput RNA sequencing from paired lesional- and non-lesional skin reveals major alterations in the psoriasis circRNAome. BMC Medical Genomics, 2019, 12, 174.	1.5	43
22	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
23	Global hypomethylation is an independent prognostic factor in diffuse large B cell lymphoma. American Journal of Hematology, 2017, 92, 689-694.	4.1	36
24	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
25	Direct Genotyping of Single Nucleotide Polymorphisms in Methyl Metabolism Genes Using Probe-Free High-Resolution Melting Analysis. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1240-1247.	2.5	34
26	Hypermethylation of DAPK1 is an independent prognostic factor predicting survival in diffuse large B-cell lymphoma. Oncotarget, 2014, 5, 9798-9810.	1.8	34
27	Increased sensitivity of KRAS mutation detection by high-resolution melting analysis of COLD-PCR products. Human Mutation, 2010, 31, 1366-1373.	2.5	33
28	Assessment of Quantitative and Allelic MGMT Methylation Patterns as a Prognostic Marker in Glioblastoma. Journal of Neuropathology and Experimental Neurology, 2016, 75, 246-255.	1.7	33
29	Long Non-Coding RNAs Guide the Fine-Tuning of Gene Regulation in B-Cell Development and Malignancy. International Journal of Molecular Sciences, 2018, 19, 2475.	4.1	33
30	Characterization of circular RNA transcriptomes in psoriasis and atopic dermatitis reveals disease-specific expression profiles. Experimental Dermatology, 2021, 30, 1187-1196.	2.9	33
31	Circular RNAs as microRNA sponges: evidence and controversies. Essays in Biochemistry, 2021, 65, 685-696.	4.7	33
32	Methylation profiling of normal individuals reveals mosaic promoter methylation of cancer-associated genes. Oncotarget, 2012, 3, 450-461.	1.8	33
33	Mutations in idiopathic cytopenia of undetermined significance assist diagnostics and correlate to dysplastic changes. American Journal of Hematology, 2016, 91, 1234-1238.	4.1	32
34	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
35	Defects in LC3B2 and ATG4A underlie HSV2 meningitis and reveal a critical role for autophagy in antiviral defense in humans. Science Immunology, 2020, 5, .	11.9	27
36	Tumor suppressor microRNAs are downregulated in myelodysplastic syndrome with spliceosome mutations. Oncotarget, 2016, 7, 9951-9963.	1.8	27

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37	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
38	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
39	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
40	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
41	Genome-Wide Circular RNA Expression Patterns Reflect Resistance to Immunomodulatory Drugs in Multiple Myeloma Cells. <i>Cancers</i> , 2021, 13, 365.	3.7	19
42	The transcriptional landscape and biomarker potential of circular RNAs in prostate cancer. <i>Genome Medicine</i> , 2022, 14, 8.	8.2	19
43	Distinct circular RNA expression profiles in pediatric ependymomas. <i>Brain Pathology</i> , 2021, 31, 387-392.	4.1	18
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	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
47	The HSP90 inhibitor RGRN-305 exhibits strong immunomodulatory effects in human keratinocytes. <i>Experimental Dermatology</i> , 2021, 30, 773-781.	2.9	15
48	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
49	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
50	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
51	<i>ELMO3</i> : A direct driver of cancer metastasis?. <i>Cell Cycle</i> , 2014, 13, 2483-2484.	2.6	11
52	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
53	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
54	Analysis of Epigenetic Modifications of DNA in Human Cells. <i>Current Protocols in Human Genetics</i> , 2013, 77, Unit20.2.	3.5	9

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55	Profiling of circRNAs using an enzyme-free digital counting method. <i>Methods</i> , 2021, 196, 11-16.	3.8	9
56	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
57	Allele-Specific DNA Methylation Detection by Pyrosequencing <sup>®</sup> . <i>Methods in Molecular Biology</i> , 2015, 1315, 271-289.	0.9	5
58	Biomarkers and Methodologies for Monitoring Epigenetic Drug Effects in Cancer. , 2016, , 91-118.		2
59	The Challenges of Comparing a Clinically Validated Test to Other Methods. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 535-537.	2.8	0