

Lasse Sommer Kristensen

List of Publications by Year in Descending Order

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Version: 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

60
papers

3,861
citations

26
h-index

62
g-index

64
ext. papers

5,307
ext. citations

7.1
avg, IF

6.17
L-index

#	Paper	IF	Citations
60	The transcriptional landscape and biomarker potential of circular RNAs in prostate cancer.. <i>Genome Medicine</i> , 2022 , 14, 8	14.4	1
59	-targeting miR-agshRNAs combine efficacy with specificity and safety for retinal gene therapy.. <i>Molecular Therapy - Nucleic Acids</i> , 2022 , 28, 58-76	10.7	0
58	The emerging roles of circRNAs in cancer and oncology.. <i>Nature Reviews Clinical Oncology</i> , 2021 ,	19.4	25
57	Unravelling similarities and differences in the role of circular and linear PVT1 in cancer and human disease. <i>British Journal of Cancer</i> , 2021 ,	8.7	2
56	Characterization of circular RNA transcriptomes in psoriasis and atopic dermatitis reveals disease-specific expression profiles. <i>Experimental Dermatology</i> , 2021 , 30, 1187-1196	4	9
55	The HSP90 inhibitor RGRN-305 exhibits strong immunomodulatory effects in human keratinocytes. <i>Experimental Dermatology</i> , 2021 , 30, 773-781	4	4
54	Circular RNAs as microRNA sponges: evidence and controversies. <i>Essays in Biochemistry</i> , 2021 , 65, 685-696	6.6	5
53	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> , 2021 ,	10.7	2
52	Distinct circular RNA expression profiles in pediatric ependymomas. <i>Brain Pathology</i> , 2021 , 31, 387-392	6	5
51	Genome-Wide Circular RNA Expression Patterns Reflect Resistance to Immunomodulatory Drugs in Multiple Myeloma Cells. <i>Cancers</i> , 2021 , 13,	6.6	8
50	Profiling of circRNAs using an enzyme-free digital counting method. <i>Methods</i> , 2021 , 196, 11-16	4.6	2
49	Defects in and underlie HSV2 meningitis and reveal a critical role for autophagy in antiviral defense in humans. <i>Science Immunology</i> , 2020 , 5,	28	13
48	A comprehensive analysis of coding and non-coding transcriptomic changes in cutaneous squamous cell carcinoma. <i>Scientific Reports</i> , 2020 , 10, 3637	4.9	35
47	Spatial expression analyses of the putative oncogene ciRS-7 in cancer reshape the microRNA sponge theory. <i>Nature Communications</i> , 2020 , 11, 4551	17.4	38
46	The biogenesis, biology and characterization of circular RNAs. <i>Nature Reviews Genetics</i> , 2019 , 20, 675-693	30.1	1343
45	Identification of an IRF3 variant and defective antiviral interferon responses in a patient with severe influenza. <i>European Journal of Immunology</i> , 2019 , 49, 2111-2114	6.1	8
44	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	3.7	28

43	Circular RNAs are abundantly expressed and upregulated during human epidermal stem cell differentiation. <i>RNA Biology</i> , 2018 , 15, 280-291	4.8	96
42	Circular RNAs in cancer: opportunities and challenges in the field. <i>Oncogene</i> , 2018 , 37, 555-565	9.2	794
41	DNA Methylation Levels of the ELMO Gene Promoter CpG Islands in Human Glioblastomas. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	5
40	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,	6.3	21
39	Enzyme-free digital counting of endogenous circular RNA molecules in B-cell malignancies. <i>Laboratory Investigation</i> , 2018 , 98, 1657-1669	5.9	60
38	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	7.9	38
37	Global hypomethylation is an independent prognostic factor in diffuse large B cell lymphoma. <i>American Journal of Hematology</i> , 2017 , 92, 689-694	7.1	23
36	Epigenetic changes in myelofibrosis: Distinct methylation changes in the myeloid compartments and in cases with ASXL1 mutations. <i>Scientific Reports</i> , 2017 , 7, 6774	4.9	7
35	Mutations in idiopathic cytopenia of undetermined significance assist diagnostics and correlate to dysplastic changes. <i>American Journal of Hematology</i> , 2016 , 91, 1234-1238	7.1	25
34	Identification and validation of candidate epigenetic biomarkers in lung adenocarcinoma. <i>Scientific Reports</i> , 2016 , 6, 35807	4.9	41
33	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	7.3	12
32	Assessment of Quantitative and Allelic MGMT Methylation Patterns as a Prognostic Marker in Glioblastoma. <i>Journal of Neuropathology and Experimental Neurology</i> , 2016 , 75, 246-55	3.1	22
31	Tumor suppressor microRNAs are downregulated in myelodysplastic syndrome with spliceosome mutations. <i>Oncotarget</i> , 2016 , 7, 9951-63	3.3	19
30	Biomarkers and Methodologies for Monitoring Epigenetic Drug Effects in Cancer 2016 , 91-118		1
29	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	7.7	38
28	Allele-Specific DNA Methylation Detection by Pyrosequencing . <i>Methods in Molecular Biology</i> , 2015 , 1315, 271-89	1.4	5
27	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, 40588-97	3.3	13
26	Hypermethylation of the VTRNA1-3 Promoter is Associated with Poor Outcome in Lower Risk Myelodysplastic Syndrome Patients. <i>Genes</i> , 2015 , 6, 977-90	4.2	13

25	Predicting response to epigenetic therapy. <i>Journal of Clinical Investigation</i> , 2014 , 124, 47-55	15.9	56
24	Genotyping common FSHR polymorphisms based on competitive amplification of differentially melting amplicons (CADMA). <i>Journal of Assisted Reproduction and Genetics</i> , 2014 , 31, 1427-36	3.4	9
23	Hypomethylation and increased expression of the putative oncogene ELMO3 are associated with lung cancer development and metastases formation. <i>Oncoscience</i> , 2014 , 1, 367-74	0.8	57
22	Hypermethylation of DAPK1 is an independent prognostic factor predicting survival in diffuse large B-cell lymphoma. <i>Oncotarget</i> , 2014 , 5, 9798-810	3.3	32
21	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, 180-6	5.9	33
20	Evaluation of BRAF mutation testing methodologies in formalin-fixed, paraffin-embedded cutaneous melanomas. <i>Journal of Molecular Diagnostics</i> , 2013 , 15, 70-80	5.1	61
19	The challenges of comparing a clinically validated test to other methods. <i>Journal of Molecular Diagnostics</i> , 2013 , 15, 535-7	5.1	
18	Analysis of epigenetic modifications of DNA in human cells. <i>Current Protocols in Human Genetics</i> , 2013 , Chapter 20, Unit20.2	3.2	8
17	Investigation of MGMT and DAPK1 methylation patterns in diffuse large B-cell lymphoma using allelic MSP-pyrosequencing. <i>Scientific Reports</i> , 2013 , 3, 2789	4.9	27
16	A role for immunohistochemical detection of BRAF V600E prior to BRAF-inhibitor treatment of malignant melanoma?. <i>Journal of Clinical Pathology</i> , 2013 , 66, 723-5	3.9	11
15	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, 264-71	4.7	17
14	Competitive amplification of differentially melting amplicons (CADMA) improves KRAS hotspot mutation testing in colorectal cancer. <i>BMC Cancer</i> , 2012 , 12, 548	4.8	11
13	Methylation profiling of normal individuals reveals mosaic promoter methylation of cancer-associated genes. <i>Oncotarget</i> , 2012 , 3, 450-61	3.3	28
12	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, 130-6	5.9	31
11	Limitations and advantages of MS-HRM and bisulfite sequencing for single locus methylation studies. <i>Expert Review of Molecular Diagnostics</i> , 2010 , 10, 575-80	3.8	50
10	Increased sensitivity of KRAS mutation detection by high-resolution melting analysis of COLD-PCR products. <i>Human Mutation</i> , 2010 , 31, 1366-73	4.7	31
9	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	4.8	56
8	Epigenetics and cancer treatment. <i>European Journal of Pharmacology</i> , 2009 , 625, 131-42	5.3	167

7	DNA methylation, epimutations and cancer predisposition. <i>International Journal of Biochemistry and Cell Biology</i> , 2009 , 41, 34-9	5.6	56
6	PCR-based methods for detecting single-locus DNA methylation biomarkers in cancer diagnostics, prognostics, and response to treatment. <i>Clinical Chemistry</i> , 2009 , 55, 1471-83	5.5	167
5	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, 1240-7	4	32
4	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	20.1	144
3	Circular RNA expression profiles in pediatric ependymomas		1
2	High-throughput RNA sequencing from paired lesional- and non-lesional skin reveals major alterations in the psoriasis circRNAome		2
1	Best practice standards for circular RNA research. <i>Nature Methods</i> ,	21.6	1