

Claus Lindbjerg Andersen

List of Publications by Citations

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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.

111 papers	13,919 citations	47 h-index	117 g-index
137 ext. papers	16,540 ext. citations	9.1 avg, IF	6.07 L-index

#	Paper	IF	Citations
111	Normalization of real-time quantitative reverse transcription-PCR data: a model-based variance estimation approach to identify genes suited for normalization, applied to bladder and colon cancer data sets. <i>Cancer Research</i> , 2004 , 64, 5245-50	10.1	4870
110	Oncogene-induced senescence is part of the tumorigenesis barrier imposed by DNA damage checkpoints. <i>Nature</i> , 2006 , 444, 633-7	50.4	1495
109	Direct detection of early-stage cancers using circulating tumor DNA. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	537
108	Diagnostic and prognostic microRNAs in stage II colon cancer. <i>Cancer Research</i> , 2008 , 68, 6416-24	10.1	423
107	p53-Responsive micrnas 192 and 215 are capable of inducing cell cycle arrest. <i>Cancer Research</i> , 2008 , 68, 10094-104	10.1	385
106	Genome-wide cell-free DNA fragmentation in patients with cancer. <i>Nature</i> , 2019 , 570, 385-389	50.4	339
105	Metastasis-Associated Gene Expression Changes Predict Poor Outcomes in Patients with Dukes Stage B and C Colorectal Cancer. <i>Clinical Cancer Research</i> , 2009 , 15, 7642-7651	12.9	320
104	Genomic profiling of microRNAs in bladder cancer: miR-129 is associated with poor outcome and promotes cell death in vitro. <i>Cancer Research</i> , 2009 , 69, 4851-60	10.1	320
103	Analysis of circulating tumour DNA to monitor disease burden following colorectal cancer surgery. <i>Gut</i> , 2016 , 65, 625-34	19.2	285
102	A dual program for translation regulation in cellular proliferation and differentiation. <i>Cell</i> , 2014 , 158, 1281-1292	56.2	278
101	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017 , 4, 587-599.e4	10.6	255
100	Analysis of Plasma Cell-Free DNA by Ultradeep Sequencing in Patients With Stages I to III Colorectal Cancer. <i>JAMA Oncology</i> , 2019 , 5, 1124-1131	13.4	251
99	Next-generation sequencing of RNA and DNA isolated from paired fresh-frozen and formalin-fixed paraffin-embedded samples of human cancer and normal tissue. <i>PLoS ONE</i> , 2014 , 9, e98187	3.7	223
98	Dynamics of human DNA topoisomerases IIalpha and IIbeta in living cells. <i>Journal of Cell Biology</i> , 2002 , 157, 31-44	7.3	176
97	Alternative splicing in colon, bladder, and prostate cancer identified by exon array analysis. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1214-24	7.6	174
96	Clinical Implications of Monitoring Circulating Tumor DNA in Patients with Colorectal Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 5437-5445	12.9	147
95	SNHG5 promotes colorectal cancer cell survival by counteracting STAU1-mediated mRNA destabilization. <i>Nature Communications</i> , 2016 , 7, 13875	17.4	143

94	Early Detection of Metastatic Relapse and Monitoring of Therapeutic Efficacy by Ultra-Deep Sequencing of Plasma Cell-Free DNA in Patients With Urothelial Bladder Carcinoma. <i>Journal of Clinical Oncology</i> , 2019 , 37, 1547-1557	2.2	138
93	Evaluation of two commercial global miRNA expression profiling platforms for detection of less abundant miRNAs. <i>BMC Genomics</i> , 2011 , 12, 435	4.5	127
92	Identification and validation of highly frequent CpG island hypermethylation in colorectal adenomas and carcinomas. <i>International Journal of Cancer</i> , 2011 , 129, 2855-66	7.5	123
91	Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , 2014 , 512, 87-90	50.4	115
90	Circulating U2 small nuclear RNA fragments as a novel diagnostic biomarker for pancreatic and colorectal adenocarcinoma. <i>International Journal of Cancer</i> , 2013 , 132, E48-57	7.5	108
89	SNHG16 is regulated by the Wnt pathway in colorectal cancer and affects genes involved in lipid metabolism. <i>Molecular Oncology</i> , 2016 , 10, 1266-82	7.9	107
88	The splicing factor SRSF6 is amplified and is an oncoprotein in lung and colon cancers. <i>Journal of Pathology</i> , 2013 , 229, 630-9	9.4	95
87	Frequent occurrence of uniparental disomy in colorectal cancer. <i>Carcinogenesis</i> , 2007 , 28, 38-48	4.6	93
86	Dysregulation of the transcription factors SOX4, CBFB and SMARCC1 correlates with outcome of colorectal cancer. <i>British Journal of Cancer</i> , 2009 , 100, 511-23	8.7	88
85	MiRNA-362-3p induces cell cycle arrest through targeting of E2F1, USF2 and PTPN1 and is associated with recurrence of colorectal cancer. <i>International Journal of Cancer</i> , 2013 , 133, 67-78	7.5	81
84	Role of activating fibroblast growth factor receptor 3 mutations in the development of bladder tumors. <i>Clinical Cancer Research</i> , 2005 , 11, 7709-19	12.9	80
83	A DERL3-associated defect in the degradation of SLC2A1 mediates the Warburg effect. <i>Nature Communications</i> , 2014 , 5, 3608	17.4	77
82	Repression of KIAA1199 attenuates Wnt-signalling and decreases the proliferation of colon cancer cells. <i>British Journal of Cancer</i> , 2011 , 105, 552-61	8.7	72
81	High expression of microRNA-625-3p is associated with poor response to first-line oxaliplatin based treatment of metastatic colorectal cancer. <i>Molecular Oncology</i> , 2013 , 7, 637-46	7.9	71
80	Mnk2 alternative splicing modulates the p38-MAPK pathway and impacts Ras-induced transformation. <i>Cell Reports</i> , 2014 , 7, 501-513	10.6	68
79	DNA copy-number alterations underlie gene expression differences between microsatellite stable and unstable colorectal cancers. <i>Clinical Cancer Research</i> , 2008 , 14, 8061-9	12.9	67
78	Attenuation of the beta-catenin/TCF4 complex in colorectal cancer cells induces several growth-suppressive microRNAs that target cancer promoting genes. <i>Oncogene</i> , 2012 , 31, 2750-60	9.2	63
77	miRNA profiling of circulating EpCAM(+) extracellular vesicles: promising biomarkers of colorectal cancer. <i>Journal of Extracellular Vesicles</i> , 2016 , 5, 31488	16.4	63

76	Gene expression signatures for colorectal cancer microsatellite status and HNPCC. <i>British Journal of Cancer</i> , 2005 , 92, 2240-8	8.7	62
75	High-throughput copy number analysis of 17q23 in 3520 tissue specimens by fluorescence in situ hybridization to tissue microarrays. <i>American Journal of Pathology</i> , 2002 , 161, 73-9	5.8	61
74	Long-range epigenetic silencing of chromosome 5q31 protocadherins is involved in early and late stages of colorectal tumorigenesis through modulation of oncogenic pathways. <i>Oncogene</i> , 2012 , 31, 4409-19	9.2	60
73	Alternative splicing of SLC39A14 in colorectal cancer is regulated by the Wnt pathway. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.002998	7.6	58
72	Establishment and characterization of models of chemotherapy resistance in colorectal cancer: Towards a predictive signature of chemoresistance. <i>Molecular Oncology</i> , 2015 , 9, 1169-85	7.9	57
71	Non-CpG island promoter hypomethylation and miR-149 regulate the expression of SRPX2 in colorectal cancer. <i>International Journal of Cancer</i> , 2013 , 132, 2303-15	7.5	57
70	Molecular-Subtype-Specific Biomarkers Improve Prediction of Prognosis in Colorectal Cancer. <i>Cell Reports</i> , 2017 , 19, 1268-1280	10.6	55
69	Improved procedure for fluorescence in situ hybridization on tissue microarrays. <i>Cytometry</i> , 2001 , 45, 83-6		55
68	miR-625-3p regulates oxaliplatin resistance by targeting MAP2K6-p38 signalling in human colorectal adenocarcinoma cells. <i>Nature Communications</i> , 2016 , 7, 12436	17.4	52
67	Differential expression of DHHC9 in microsatellite stable and instable human colorectal cancer subgroups. <i>British Journal of Cancer</i> , 2007 , 96, 1896-903	8.7	52
66	Clusterin expression in normal mucosa and colorectal cancer. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1039-48	7.6	51
65	The DNA damage checkpoint precedes activation of ARF in response to escalating oncogenic stress during tumorigenesis. <i>Cell Death and Differentiation</i> , 2013 , 20, 1485-97	12.7	50
64	Genome-wide analysis of allelic imbalance in prostate cancer using the Affymetrix 50K SNP mapping array. <i>British Journal of Cancer</i> , 2007 , 96, 499-506	8.7	47
63	Novel DNA methylation biomarkers show high sensitivity and specificity for blood-based detection of colorectal cancer-a clinical biomarker discovery and validation study. <i>Clinical Epigenetics</i> , 2019 , 11, 158	7.7	47
62	Blockage of receptor for advanced glycation end products prevents development of cardiac dysfunction in db/db type 2 diabetic mice. <i>European Journal of Heart Failure</i> , 2009 , 11, 638-47	12.3	46
61	Functional screening identifies miRNAs influencing apoptosis and proliferation in colorectal cancer. <i>PLoS ONE</i> , 2014 , 9, e96767	3.7	45
60	Tumor-specific usage of alternative transcription start sites in colorectal cancer identified by genome-wide exon array analysis. <i>BMC Genomics</i> , 2011 , 12, 505	4.5	43
59	Translocation t(2;7)(p12;q21-22) with dysregulation of the CDK6 gene mapping to 7q21-22 in a non-Hodgkin's lymphoma with leukemia. <i>Haematologica</i> , 2002 , 87, 357-62	6.6	41

58	Comparative analysis of 12 different kits for bisulfite conversion of circulating cell-free DNA. <i>Epigenetics</i> , 2017 , 12, 626-636	5.7	40
57	Are microRNAs located in genomic regions associated with cancer?. <i>British Journal of Cancer</i> , 2006 , 95, 1415-8	8.7	36
56	The non-coding variant rs1800734 enhances DCLK3 expression through long-range interaction and promotes colorectal cancer progression. <i>Nature Communications</i> , 2017 , 8, 14418	17.4	34
55	Performance of the colorectal cancer screening marker Sept9 is influenced by age, diabetes and arthritis: a nested case-control study. <i>BMC Cancer</i> , 2015 , 15, 819	4.8	34
54	The effect of surgical trauma on circulating free DNA levels in cancer patients-implications for studies of circulating tumor DNA. <i>Molecular Oncology</i> , 2020 , 14, 1670-1679	7.9	32
53	A narrow deletion of 7q is common to HCL, and SMZL, but not CLL. <i>European Journal of Haematology</i> , 2004 , 72, 390-402	3.8	32
52	Clusterin expression can be modulated by changes in TCF1-mediated Wnt signaling. <i>Journal of Molecular Signaling</i> , 2007 , 2, 6	1	30
51	Frequent genomic loss at chr16p13.2 is associated with poor prognosis in colorectal cancer. <i>International Journal of Cancer</i> , 2011 , 129, 1848-58	7.5	27
50	Characterization of genetic intratumor heterogeneity in colorectal cancer and matching patient-derived spheroid cultures. <i>Molecular Oncology</i> , 2018 , 12, 132-147	7.9	25
49	Identification of 33 candidate oncogenes by screening for base-specific mutations. <i>British Journal of Cancer</i> , 2014 , 111, 1657-62	8.7	24
48	Elevated microRNA-126 is associated with high vascular endothelial growth factor receptor 2 expression levels and high microvessel density in colorectal cancer. <i>Oncology Letters</i> , 2011 , 2, 1101-1106 ^{2.6}		23
47	A Hidden Markov Model to estimate population mixture and allelic copy-numbers in cancers using Affymetrix SNP arrays. <i>BMC Bioinformatics</i> , 2007 , 8, 434	3.6	23
46	Active, but not inactive, human centromeres display topoisomerase II activity in vivo. <i>Chromosome Research</i> , 2002 , 10, 305-12	4.4	23
45	A genetically inducible porcine model of intestinal cancer. <i>Molecular Oncology</i> , 2017 , 11, 1616-1629	7.9	22
44	CpG islands detected by self-primed in situ labeling (SPRINS). <i>Chromosoma</i> , 1998 , 107, 260-6	2.8	22
43	Recurrent genomic imbalances in B-cell splenic marginal-zone lymphoma revealed by comparative genomic hybridization. <i>Cancer Genetics and Cytogenetics</i> , 2005 , 156, 122-8		22
42	Detection and characterization of lung cancer using cell-free DNA fragmentomes. <i>Nature Communications</i> , 2021 , 12, 5060	17.4	21
41	Genotyping and annotation of Affymetrix SNP arrays. <i>Nucleic Acids Research</i> , 2006 , 34, e100	20.1	17

40	DAPK1 loss triggers tumor invasion in colorectal tumor cells. <i>Cell Death and Disease</i> , 2019 , 10, 895	9.8	17
39	Determinants of recurrence after intended curative resection for colorectal cancer. <i>Scandinavian Journal of Gastroenterology</i> , 2014 , 49, 1399-408	2.4	15
38	The association between genetic variants in hMLH1 and hMSH2 and the development of sporadic colorectal cancer in the Danish population. <i>BMC Medical Genetics</i> , 2008 , 9, 52	2.1	14
37	Circulating Tumor DNA in Stage III Colorectal Cancer, beyond Minimal Residual Disease Detection, toward Assessment of Adjuvant Therapy Efficacy and Clinical Behavior of Recurrences. <i>Clinical Cancer Research</i> , 2021 ,	12.9	14
36	Correlation between early dynamics in circulating tumour DNA and outcome from FOLFIRI treatment in metastatic colorectal cancer. <i>Scientific Reports</i> , 2019 , 9, 11542	4.9	13
35	Validation of computational determination of microsatellite status using whole exome sequencing data from colorectal cancer patients. <i>BMC Cancer</i> , 2019 , 19, 971	4.8	12
34	The potential role of Alu Y in the development of resistance to SN38 (Irinotecan) or oxaliplatin in colorectal cancer. <i>BMC Genomics</i> , 2015 , 16, 404	4.5	11
33	Contribution of allelic imbalance to colorectal cancer. <i>Nature Communications</i> , 2018 , 9, 3664	17.4	11
32	IMPROVE-IT2: implementing noninvasive circulating tumor DNA analysis to optimize the operative and postoperative treatment for patients with colorectal cancer - intervention trial 2. Study protocol. <i>Acta Oncologica</i> , 2020 , 59, 336-341	3.2	10
31	A beta-mixture model for dimensionality reduction, sample classification and analysis. <i>BMC Bioinformatics</i> , 2011 , 12, 215	3.6	9
30	Characterization of three hairy cell leukemia- derived cell lines (ESKOL, JOK-1, and hair-M) by multiplex-FISH, comparative genomic hybridization, FISH, PRINS, and dideoxyPRINS. <i>Cytogenetic and Genome Research</i> , 2000 , 90, 30-9	1.9	8
29	Circulating tumor DNA analysis for assessment of recurrence risk, benefit of adjuvant therapy, and early relapse detection after treatment in colorectal cancer patients.. <i>Journal of Clinical Oncology</i> , 2021 , 39, 11-11	2.2	8
28	Functional characterization of rare missense mutations in MLH1 and MSH2 identified in Danish colorectal cancer patients. <i>Familial Cancer</i> , 2009 , 8, 489-500	3	7
27	Trisomy 10 survival: a literature review and presentation of seven new cases. <i>Cancer Genetics and Cytogenetics</i> , 1998 , 103, 130-2		7
26	Recurrent imbalances involving chromosome 5 and 7q22-q35 in hairy cell leukemia: A comparative genomic hybridization study. <i>Genes Chromosomes and Cancer</i> , 2001 , 30, 218-219	5	7
25	Enhanced Performance of DNA Methylation Markers by Simultaneous Measurement of Sense and Antisense DNA Strands after Cytosine Conversion. <i>Clinical Chemistry</i> , 2020 , 66, 925-933	5.5	6
24	Gel-Based Proteomics of Clinical Samples Identifies Potential Serological Biomarkers for Early Detection of Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	6
23	Development of blood-based biomarker tests for early detection of colorectal neoplasia: Influence of blood collection timing and handling procedures. <i>Clinica Chimica Acta</i> , 2020 , 507, 39-53	6.2	5

22	The monosomy 7 clone in interphase and metaphase cell population: a combined chromosome and primed in situ labeling study. <i>Acta Haematologica</i> , 1997 , 97, 216-21	2.7	5
21	Transcriptomic and proteomic intra-tumor heterogeneity of colorectal cancer varies depending on tumor location within the colorectum. <i>PLoS ONE</i> , 2020 , 15, e0241148	3.7	5
20	Triage for selection to colonoscopy?. <i>European Journal of Surgical Oncology</i> , 2018 , 44, 1539-1541	3.6	5
19	Rseg--an R package to optimize segmentation of SNP array data. <i>Bioinformatics</i> , 2011 , 27, 419-20	7.2	3
18	SNPTools: a software tool for visualization and analysis of microarray data. <i>Bioinformatics</i> , 2007 , 23, 1550-2	3	
17	Extensive cytogenetic analysis of a stable dicentric isochromosome 21, idic(21), formed by fusion of the terminal long arms. <i>Cytogenetic and Genome Research</i> , 2002 , 97, 145-8	1.9	3
16	Tumour-agnostic circulating tumour DNA analysis for improved recurrence surveillance after resection of colorectal liver metastases: A prospective cohort study.. <i>European Journal of Cancer</i> , 2022 , 163, 163-176	7.5	3
15	Circulating tumor DNA to detect minimal residual disease, response to adjuvant therapy, and identify patients at high risk of recurrence in patients with stage I-III CRC.. <i>Journal of Clinical Oncology</i> , 2020 , 38, 4009-4009	2.2	3
14	MethCORR modelling of methylomes from formalin-fixed paraffin-embedded tissue enables characterization and prognostication of colorectal cancer. <i>Nature Communications</i> , 2020 , 11, 2025	17.4	2
13	3RUTR poly(T/U) repeat of EWSR1 is altered in microsatellite unstable colorectal cancer with nearly perfect sensitivity. <i>Familial Cancer</i> , 2015 , 14, 449-53	3	2
12	Early detection of lung cancer using cfDNA fragmentation.. <i>Journal of Clinical Oncology</i> , 2021 , 39, 8519-8519	2	
11	Age-stratified reference intervals unlock the clinical potential of circulating cell-free DNA as a biomarker of poor outcome for healthy individuals and patients with colorectal cancer. <i>International Journal of Cancer</i> , 2021 , 148, 1665-1675	7.5	2
10	DNA Microarrays and Genetic Testing 2010 , 247-265		1
9	Serial circulating tumor DNA analysis to assess recurrence risk, benefit of adjuvant therapy, growth rate and early relapse detection in stage III colorectal cancer patients.. <i>Journal of Clinical Oncology</i> , 2021 , 39, 3540-3540	2.2	0
8	Are CIMP and chr16p13.2 copy-number status independent prognostic markers in stages II and III colorectal cancer?. <i>International Journal of Cancer</i> , 2012 , 130, 243	7.5	
7	Plasma-only ctDNA-Guided MRD Detection in Patients with CRC-Letter. <i>Clinical Cancer Research</i> , 2021 , 27, 6613	12.9	
6	Genome-wide cell-free DNA fragmentation profiling for early cancer detection.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 3018-3018	2.2	
5	MethCORR infers gene expression from DNA methylation and allows molecular analysis of ten common cancer types using fresh-frozen and formalin-fixed paraffin-embedded tumor samples. <i>Clinical Epigenetics</i> , 2021 , 13, 20	7.7	

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