Ole Christian Lingjærde

List of Publications by Year
in descending order

86 papers	6,842 citations	117625 34 h-index	66911 78 g-index
94 all docs	94 docs citations	94 times ranked	14902 citing authors

#	Article	IF	Citations
1	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
2	Allele-specific copy number analysis of tumors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16910-16915.	7.1	979
3	Principles and methods of integrative genomic analyses in cancer. Nature Reviews Cancer, 2014, 14, 299-313.	28.4	337
4	CGH-Explorer: a program for analysis of array-CGH data. Bioinformatics, 2005, 21, 821-822.	4.1	291
5	Copynumber: Efficient algorithms for single- and multi-track copy number segmentation. BMC Genomics, 2012, 13, 591.	2.8	251
6	Breast Cancer Molecular Stratification. American Journal of Pathology, 2017, 187, 2152-2162.	3.8	198
7	Breast cancer quantitative proteome and proteogenomic landscape. Nature Communications, 2019, 10, 1600.	12.8	152
8	Glycan gene expression signatures in normal and malignant breast tissue; possible role in diagnosis and progression. Molecular Oncology, 2010, 4, 98-118.	4.6	147
9	Genomic Architecture Characterizes Tumor Progression Paths and Fate in Breast Cancer Patients. Science Translational Medicine, 2010, 2, 38ra47.	12.4	138
10	Plasma microRNAs predicting clinical outcome in metastatic colorectal cancer patients receiving first‐line oxaliplatin‐based treatment. Molecular Oncology, 2014, 8, 59-67.	4.6	132
11	Presence of bone marrow micrometastasis is associated with different recurrence risk within molecular subtypes of breast cancer. Molecular Oncology, 2007, 1, 160-171.	4.6	128
12	Human ectoparasites and the spread of plague in Europe during the Second Pandemic. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1304-1309.	7.1	110
13	Merging transcriptomics and metabolomics - advances in breast cancer profiling. BMC Cancer, 2010, 10, 628.	2.6	101
14	Integrative clustering reveals a novel split in the luminal A subtype of breast cancer with impact on outcome. Breast Cancer Research, 2017, 19, 44.	5.0	85
15	Individual and combined effects of DNA methylation and copy number alterations on miRNA expression in breast tumors. Genome Biology, 2013, 14, R126.	9.6	80
16	Influence of DNA copy number and mRNA levels on the expression of breast cancer related proteins. Molecular Oncology, 2013, 7, 704-718.	4.6	77
17	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. Nature Communications, 2017, 8, 1221.	12.8	75
18	T Cells Expressing Checkpoint Receptor TIGIT Are Enriched in Follicular Lymphoma Tumors and Characterized by Reversible Suppression of T-cell Receptor Signaling. Clinical Cancer Research, 2018, 24, 870-881.	7.0	75

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19	Intratumor heterogeneity defines treatmentâ€resistant <scp>HER</scp>2+ breast tumors. Molecular Oncology, 2018, 12, 1838-1855.	4.6	74
20	Snow conditions may create an invisible barrier for lynx. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10632-10634.	7.1	71
21	Intra-patient Inter-metastatic Genetic Heterogeneity in Colorectal Cancer as a Key Determinant of Survival after Curative Liver Resection. PLoS Genetics, 2016, 12, e1006225.	3.5	64
22	Neutral tumor evolution?. Nature Genetics, 2018, 50, 1630-1633.	21.4	59
23	Genomic alterations reveal potential for higher grade transformation in follicular lymphoma and confirm parallel evolution of tumor cell clones. Blood, 2010, 116, 1489-1497.	1.4	58
24	The immune microenvironment in nonâ€small cell lung cancer is predictive of prognosis after surgery. Molecular Oncology, 2019, 13, 1166-1179.	4.6	57
25	The tumour microenvironment influences survival and time to transformation in follicular lymphoma in the rituximab era. British Journal of Haematology, 2016, 175, 102-114.	2.5	56
26	Identifying In-Trans Process Associated Genes in Breast Cancer by Integrated Analysis of Copy Number and Expression Data. PLoS ONE, 2013, 8, e53014.	2.5	54
27	ESR1 gene amplification in breast cancer: a common phenomenon?. Nature Genetics, 2008, 40, 807-808.	21.4	53
28	From The Cover: The effect of climatic forcing on population synchrony and genetic structuring of the Canadian lynx. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6056-6061.	7.1	50
29	Whole-genome integrative analysis reveals expression signatures predicting transformation in follicular lymphoma. Blood, 2014, 123, 1051-1054.	1.4	49
30	Highâ€resolution analyses of copy number changes in disseminated tumor cells of patients with breast cancer. International Journal of Cancer, 2012, 131, E405-15.	5.1	48
31	Statistical dissection of genetic pathways involved in prostate carcinogenesis. Genes Chromosomes and Cancer, 2006, 45, 154-163.	2.8	44
32	The importance of gene-centring microarray data. Lancet Oncology, The, 2010, 11, 719-720.	10.7	42
33	Combining Gene Signatures Improves Prediction of Breast Cancer Survival. PLoS ONE, 2011, 6, e17845.	2.5	38
34	Gene expression profiles of breast biopsies from healthy women identify a group with claudin-low features. BMC Medical Genomics, 2011, 4, 77.	1.5	38
35	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. Molecular Oncology, 2015, 9, 115-127.	4.6	38
36	Expression levels of uridine 5'-diphospho-glucuronosyltransferase genes in breast tissue from healthy women are associated with mammographic density. Breast Cancer Research, 2010, 12, R65.	5.0	37

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37	Molecular signatures of mRNAs and miRNAs as prognostic biomarkers in pancreatobiliary and intestinal types of periampullary adenocarcinomas. Molecular Oncology, 2015, 9, 758-771.	4.6	35
38	Analyzing Cancer Samples with SNP Arrays. Methods in Molecular Biology, 2012, 802, 57-72.	0.9	34
39	Systematic assessment of prognostic gene signatures for breast cancer shows distinct influence of time and ER status. BMC Cancer, 2014, 14, 211.	2.6	34
40	Integrated analysis reveals microRNA networks coordinately expressed with key proteins in breast cancer. Genome Medicine, 2015, 7, 21.	8.2	34
41	Identifying clusters in genomics data by recursive partitioning. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 637-52.	0.6	33
42	The Genomic Landscape of Pancreatic and Periampullary Adenocarcinoma. Cancer Research, 2016, 76, 5092-5102.	0.9	33
43	Linear and non-linear dependencies between copy number aberrations and mRNA expression reveal distinct molecular pathways in breast cancer. BMC Bioinformatics, 2011, 12, 197.	2.6	32
44	The Longitudinal Transcriptional Response to Neoadjuvant Chemotherapy with and without Bevacizumab in Breast Cancer. Clinical Cancer Research, 2017, 23, 4662-4670.	7.0	31
45	miRNA expression changes during the course of neoadjuvant bevacizumab and chemotherapy treatment in breast cancer. Molecular Oncology, 2019, 13, 2278-2296.	4.6	30
46	Ischemia caused by time to freezing induces systematic microRNA and mRNA responses in cancer tissue. Molecular Oncology, 2011, 5, 564-576.	4.6	29
47	Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 2028-2029.	27.0	28
48	Canine Mammary Tumours Are Affected by Frequent Copy Number Aberrations, including Amplification of MYC and Loss of PTEN. PLoS ONE, 2015, 10, e0126371.	2.5	28
49	Partial least squares Cox regression for genome-wide data. Lifetime Data Analysis, 2008, 14, 179-195.	0.9	27
50	Subtypeâ€specific response to bevacizumab is reflected in the metabolome and transcriptome of breast cancer xenografts. Molecular Oncology, 2013, 7, 130-142.	4.6	26
51	Tumor expression, plasma levels and genetic polymorphisms of the coagulation inhibitor TFPI are associated with clinicopathological parameters and survival in breast cancer, in contrast to the coagulation initiator TF. Breast Cancer Research, 2015, 17, 44.	5.0	24
52	*N*â€glycan signatures identified in tumor interstitial fluid and serum of breast cancer patients: association with tumor biology and clinical outcome. Molecular Oncology, 2018, 12, 972-990.	4.6	24
53	Contrasting DCIS and invasive breast cancer by subtype suggests basal-like DCIS as distinct lesions. Npj Breast Cancer, 2020, 6, 26.	5.2	24
54	High Levels of Genomic Aberrations in Serous Ovarian Cancers Are Associated with Better Survival. PLoS ONE, 2013, 8, e54356.	2.5	22

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55	Pathway based analysis of SNPs with relevance to 5â€FU therapy: Relation to intratumoral mRNA expression and survival. International Journal of Cancer, 2008, 123, 577-585.	5.1	20
56	Differential expression of miRNAs in pancreatobiliary type of periampullary adenocarcinoma and its associated stroma. Molecular Oncology, 2016, 10, 303-316.	4.6	17
57	Time series analysis of neoadjuvant chemotherapy and bevacizumab-treated breast carcinomas reveals a systemic shift in genomic aberrations. Genome Medicine, 2018, 10, 92.	8.2	17
58	AGXT and ERCC2 polymorphisms are associated with clinical outcome in metastatic colorectal cancer patients treated with 5-FU/oxaliplatin. Pharmacogenomics Journal, 2016, 16, 272-279.	2.0	16
59	A systematic comparison of copy number alterations in four types of female cancer. BMC Cancer, 2016, 16, 913.	2.6	13
60	Immune phenotype of tumor microenvironment predicts response to bevacizumab in neoadjuvant treatment of <scp>ER</scp>â€positive breast cancer. International Journal of Cancer, 2020, 147, 2515-2525.	5.1	13
61	Richness dependence and climatic forcing as regulating processes of coastal fish-species richness. Ecology Letters, 2003, 6, 428-439.	6.4	11
62	Severity of illness and the use of paracetamol in febrile preschool children; a case simulation study of parents' assessments. Family Practice, 2006, 23, 618-623.	1.9	10
63	Serum <i>N</i>-Glycome Characterization in Patients with Resectable Periampullary Adenocarcinoma. Journal of Proteome Research, 2015, 14, 5144-5156.	3.7	10
64	Clinicopathological factors associated with tumourâ€specific mutation detection in plasma of patients with <scp><i>RAS</i></scp>â€mutated or <scp><i>BRAF</i></scp>â€mutated metastatic colorectal cancer. International Journal of Cancer, 2021, 149, 1385-1397.	5.1	10
65	Sample Preparation Approach Influences PAM50 Risk of Recurrence Score in Early Breast Cancer. Cancers, 2021, 13, 6118.	3.7	10
66	Convergence of risk prediction models in follicular lymphoma. Haematologica, 2019, 104, e252-e255.	3.5	9
67	DNA copy number motifs are strong and independent predictors of survival in breast cancer. Communications Biology, 2020, 3, 153.	4.4	9
68	Implementing precision cancer medicine in the public health services of Norway: the diagnostic infrastructure and a cost estimate. ESMO Open, 2017, 2, e000158.	4.5	8
69	Molecularly matched therapy in the context of sensitivity, resistance, and safety; patient outcomes in end-stage cancer â€" the MetAction study. Acta OncolÃ³gica, 2020, 59, 733-740.	1.8	8
70	NRF2 drives an oxidative stress response predictive of breast cancer. Free Radical Biology and Medicine, 2022, 184, 170-184.	2.9	8
71	Mutational dynamics and immune evasion in diffuse large B-cell lymphoma explored in a relapse-enriched patient series. Blood Advances, 2020, 4, 1859-1866.	5.2	7
72	Multilocus analysis of SNP and metabolic data within a given pathway. BMC Genomics, 2006, 7, 5.	2.8	6

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73	Patterns of constitutively phosphorylated kinases in B cells are associated with disease severity in common variable immunodeficiency. Clinical Immunology, 2017, 175, 69-74.	3.2	6
74	Spatio-temporal variability of richness estimators: coastal marine fish communities as examples. Oecologia, 2005, 144, 308-317.	2.0	5
75	A clinico-molecular predictor identifies follicular lymphoma patients at risk of early transformation after first-line immunotherapy. Haematologica, 2019, 104, e460-e464.	3.5	5
76	Protein Signature Predicts Response to Neoadjuvant Treatment With Chemotherapy and Bevacizumab in HER2-Negative Breast Cancers. JCO Precision Oncology, 2021, 5, 286-306.	3.0	5
77	Adaptive weighted least squares method for the estimation of DNA fragment lengths from agarose gels. Electrophoresis, 2002, 23, 176-181.	2.4	4
78	Whole genome copy number analyses reveal a highly aberrant genome in TP53 mutant lung adenocarcinoma tumors. BMC Cancer, 2021, 21, 1089.	2.6	3
79	Abstract P1-08-09: High mid-treatment RNA disruption in patients with HER2-negative breast cancer predicts survival benefit after neoadjuvant chemotherapy. Cancer Research, 2022, 82, P1-08-09-P1-08-09.	0.9	3
80	Prognostic Significance of the Loss of Heterozygosity of KRAS in Early-Stage Lung Adenocarcinoma. Frontiers in Oncology, 2022, 12, 873532.	2.8	3
81	PathTracer: High-sensitivity detection of differential pathway activity in tumours. Scientific Reports, 2019, 9, 16332.	3.3	2
82	miRNA normalization enables joint analysis of several datasets to increase sensitivity and to reveal novel miRNAs differentially expressed in breast cancer. PLoS Computational Biology, 2021, 17, e1008608.	3.2	1
83	Proteome Analysis of Pancreatic Tumors Implicates Extracellular Matrix in Patient Outcome. Cancer Research Communications, 2022, 2, 434-446.	1.7	1
84	Corrigendum to â€œPresence of bone marrow micrometastasis is associated with different recurrence risk within molecular subtypes of breast cancerâ€•[Mol. Oncol. 1 (2007) 160â€"171]. Molecular Oncology, 2010, 4, 169-169.	4.6	0
85	Reply to Park et al.: Human ectoparasite transmission of plague during the Second Pandemic is still plausible. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7894-E7895.	7.1	0
86	A Systemic Protein Deviation Score Linked to PD-1+ CD8+ T Cell Expansion That Predicts Overall Survival in Diffuse Large B Cell Lymphoma. Med, 2021, 2, 180-195.e5.	4.4	0