Iver Nordentoft

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2,669 36 24 33 h-index g-index citations papers 36 3,729 4.39 9.1 L-index ext. citations avg, IF ext. papers

#	Paper	IF	Citations
33	Comprehensive Transcriptional Analysis of Early-Stage Urothelial Carcinoma. <i>Cancer Cell</i> , 2016 , 30, 27-4	1224.3	325
32	Analysis of circulating tumour DNA to monitor disease burden following colorectal cancer surgery. <i>Gut</i> , 2016 , 65, 625-34	19.2	285
31	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
30	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
29	Cellular disposal of miR23b by RAB27-dependent exosome release is linked to acquisition of metastatic properties. <i>Cancer Research</i> , 2014 , 74, 5758-71	10.1	195
28	Clinical Implications of Monitoring Circulating Tumor DNA in Patients with Colorectal Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 5437-5445	12.9	147
27	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
26	Genomic Alterations in Liquid Biopsies from Patients with Bladder Cancer. <i>European Urology</i> , 2016 , 70, 75-82	10.2	123
25	Liquid Biopsy Analysis of FGFR3 and PIK3CA Hotspot Mutations for Disease Surveillance in Bladder Cancer. <i>European Urology</i> , 2017 , 71, 961-969	10.2	100
24	Mutational context and diverse clonal development in early and late bladder cancer. <i>Cell Reports</i> , 2014 , 7, 1649-1663	10.6	94
23	Profiling of long non-coding RNAs identifies LINC00958 and LINC01296 as candidate oncogenes in bladder cancer. <i>Scientific Reports</i> , 2017 , 7, 395	4.9	82
22	miRNAs associated with chemo-sensitivity in cell lines and in advanced bladder cancer. <i>BMC Medical Genomics</i> , 2012 , 5, 40	3.7	77
21	Comprehensive multiregional analysis of molecular heterogeneity in bladder cancer. <i>Scientific Reports</i> , 2017 , 7, 11702	4.9	76
20	Pervasive chromosomal instability and karyotype order in tumour evolution. <i>Nature</i> , 2020 , 587, 126-132	2 50.4	67
19	Monitoring Treatment Response and Metastatic Relapse in Advanced Bladder Cancer by Liquid Biopsy Analysis. <i>European Urology</i> , 2018 , 73, 535-540	10.2	65
18	Paired Exome Analysis Reveals Clonal Evolution and Potential Therapeutic Targets in Urothelial Carcinoma. <i>Cancer Research</i> , 2016 , 76, 5894-5906	10.1	65
17	Widespread DNA hypomethylation and differential gene expression in Turner syndrome. <i>Scientific Reports</i> , 2016 , 6, 34220	4.9	60

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16	Altered gene expression and repressed markers of autophagy in skeletal muscle of insulin resistant patients with type 2 diabetes. <i>Scientific Reports</i> , 2017 , 7, 43775	4.9	41
15	Molecular correlates of cisplatin-based chemotherapy response in muscle invasive bladder cancer by integrated multi-omics analysis. <i>Nature Communications</i> , 2020 , 11, 4858	17.4	41
14	Spatial and temporal clonal evolution during development of metastatic urothelial carcinoma. <i>Molecular Oncology</i> , 2016 , 10, 1450-1460	7.9	32
13	Optimized targeted sequencing of cell-free plasma DNA from bladder cancer patients. <i>Scientific Reports</i> , 2018 , 8, 1917	4.9	31
12	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
11	Increased expression of transcription factor TFAP2lborrelates with chemosensitivity in advanced bladder cancer. <i>BMC Cancer</i> , 2011 , 11, 135	4.8	24
10	An integrated multi-omics analysis identifies prognostic molecular subtypes of non-muscle-invasive bladder cancer. <i>Nature Communications</i> , 2021 , 12, 2301	17.4	24
9	Discordant molecular subtype classification in the basal-squamous subtype of bladder tumors and matched lymph-node metastases. <i>Modern Pathology</i> , 2018 , 31, 1869-1881	9.8	22
8	RHCG and TCAF1 promoter hypermethylation predicts biochemical recurrence in prostate cancer patients treated by radical prostatectomy. <i>Oncotarget</i> , 2017 , 8, 5774-5788	3.3	20
7	Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. <i>Cell Reports</i> , 2020 , 31, 107550	10.6	19
6	Epigenetic and transcriptomic consequences of excess X-chromosome material in 47,XXX syndrome-A comparison with Turner syndrome and 46,XX females. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics,</i> 2020 , 184, 279-293	3.1	7
5	Abstract 913: 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 2019 ,		3
4	Mutational Analysis of Field Cancerization in Bladder Cancer. <i>Bladder Cancer</i> , 2020 , 6, 253-264	1	3
3	, , Mutation Status and APOBEC Mutation Signatures are Predictive of Mitomycin C Response in Non-muscle-invasive Bladder Cancer <i>European Urology Open Science</i> , 2021 , 34, 59-67	0.9	O
2	Expression Analysis of cPLA2 Alpha Interacting TIP60 in Diabetic KKAy and Non-Diabetic C57BL Wild-Type Mice: No Impact of Transient and Stable TIP60 Overexpression on Glucose-Stimulated Insulin Secretion in Pancreatic Beta-Cells. <i>Review of Diabetic Studies</i> , 2007 , 4, 147-58	3.6	
1	Genome-wide circulating tumor DNA monitoring for bladder cancer treatment management and organ preservation <i>Journal of Clinical Oncology</i> , 2021 , 39, e16527-e16527	2.2	