

Anders Jacobsen

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

87,600
citations

50276

46
h-index

71685

76
g-index

88
all docs

88
docs citations

88
times ranked

91681
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulatory enhancer profiling of mesenchymal-type gastric cancer reveals subtype-specific epigenomic landscapes and targetable vulnerabilities. <i>Gut</i> , 2023, 72, 226-241.	12.1	6
2	Epigenetic promoter alterations in GI tumour immune-editing and resistance to immune checkpoint inhibition. <i>Gut</i> , 2022, 71, 1277-1288.	12.1	23
3	Dynamic phenotypic heterogeneity and the evolution of multiple RNA subtypes in hepatocellular carcinoma: the PLANET study. <i>National Science Review</i> , 2022, 9, nwab192.	9.5	15
4	Obtaining spatially resolved tumor purity maps using deep multiple instance learning in a pan-cancer study. <i>Patterns</i> , 2022, 3, 100399.	5.9	6
5	A phase 1b study of <scp>OXIRI</scp> in pancreatic adenocarcinoma patients and its immunomodulatory effects. <i>International Journal of Cancer</i> , 2022, , .	5.1	0
6	A pan-cancer metabolic atlas of the tumor microenvironment. <i>Cell Reports</i> , 2022, 39, 110800.	6.4	19
7	Deficiency of the splicing factor RBM10 limits EGFR inhibitor response in EGFR-mutant lung cancer. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	15
8	Single-cell and bulk transcriptome sequencing identifies two epithelial tumor cell states and refines the consensus molecular classification of colorectal cancer. <i>Nature Genetics</i> , 2022, 54, 963-975.	21.4	106
9	A chemical genetic screen identifies Aurora kinases as a therapeutic target in EGFR T790M negative, gefitinib-resistant head and neck squamous cell carcinoma (HNSCC). <i>EBioMedicine</i> , 2021, 64, 103220.	6.1	10
10	Pan-Cancer Analysis of Ligandâ€“Receptor Cross-talk in the Tumor Microenvironment. <i>Cancer Research</i> , 2021, 81, 1802-1812.	0.9	41
11	Targeting the developmental origins of cancer. <i>Nature Cancer</i> , 2021, 2, 256-257.	13.2	2
12	The long non-coding RNA MIR31HG regulates the senescence associated secretory phenotype. <i>Nature Communications</i> , 2021, 12, 2459.	12.8	27
13	Tissue-specific cell-free DNA degradation quantifies circulating tumor DNA burden. <i>Nature Communications</i> , 2021, 12, 2229.	12.8	49
14	Individualized Molecular Profiling for Allocation to Clinical Trials Singapore Studyâ€“An Asian Tertiary Cancer Center Experience. <i>JCO Precision Oncology</i> , 2021, 5, 859-875.	3.0	4
15	Integrative Profiling of T790M-Negative EGFR-Mutated NSCLC Reveals Pervasive Lineage Transition and Therapeutic Opportunities. <i>Clinical Cancer Research</i> , 2021, 27, 5939-5950.	7.0	21
16	Integrative epigenomic and high-throughput functional enhancer profiling reveals determinants of enhancer heterogeneity in gastric cancer. <i>Genome Medicine</i> , 2021, 13, 158.	8.2	7
17	Association of Clinicopathologic and Molecular Tumor Features With Recurrence in Resected Early-Stage Epidermal Growth Factor Receptorâ€“Positive Nonâ€“Small Cell Lung Cancer. <i>JAMA Network Open</i> , 2021, 4, e2131892.	5.9	25
18	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent <i>CCNE1</i> and <i>IGF2</i> enhancer hijacking in primary gastric adenocarcinoma. <i>Gut</i> , 2020, 69, 1039-1052.	12.1	36

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19	MutSpot: detection of non-coding mutation hotspots in cancer genomes. <i>Npj Genomic Medicine</i> , 2020, 5, 26.	3.8	12
20	Genomic landscape of lung adenocarcinoma in East Asians. <i>Nature Genetics</i> , 2020, 52, 177-186.	21.4	281
21	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 3005-3020.	8.2	12
22	Ensemble-Based Somatic Mutation Calling in Cancer Genomes. <i>Methods in Molecular Biology</i> , 2020, 2120, 37-46.	0.9	1
23	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. <i>Nature Communications</i> , 2019, 10, 3682.	12.8	48
24	SMuRF: portable and accurate ensemble prediction of somatic mutations. <i>Bioinformatics</i> , 2019, 35, 3157-3159.	4.1	19
25	Mutation hotspots at CTCF binding sites coupled to chromosomal instability in gastrointestinal cancers. <i>Nature Communications</i> , 2018, 9, 1520.	12.8	109
26	Advances in genomic hepatocellular carcinoma research. <i>GigaScience</i> , 2018, 7, .	6.4	25
27	Obstructive sleep apnea and Fuhrman grade in patients with clear cell renal cell carcinoma treated surgically. <i>World Journal of Urology</i> , 2017, 35, 51-56.	2.2	13
28	Whole-genome noncoding sequence analysis in T-cell acute lymphoblastic leukemia identifies oncogene enhancer mutations. <i>Blood</i> , 2017, 129, 3264-3268.	1.4	32
29	Long noncoding RNA EGFR-AS1 mediates epidermal growth factor receptor addiction and modulates treatment response in squamous cell carcinoma. <i>Nature Medicine</i> , 2017, 23, 1167-1175.	30.7	141
30	Np63 Inhibits Oxidative Stress-Induced Cell Death, Including Ferroptosis, and Cooperates with the BCL-2 Family to Promote Clonogenic Survival. <i>Cell Reports</i> , 2017, 21, 2926-2939.	6.4	61
31	Genomic differences between black and white patients implicate a distinct immune response to papillary renal cell carcinoma. <i>Oncotarget</i> , 2017, 8, 5196-5205.	1.8	22
32	Validation and genomic interrogation of the <i>MET</i> variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma. <i>Cancer</i> , 2016, 122, 402-410.	4.1	18
33	Body Mass Index and Metastatic Renal Cell Carcinoma: Clinical and Biological Correlations. <i>Journal of Clinical Oncology</i> , 2016, 34, 3655-3663.	1.6	174
34	Molecular analysis of aggressive renal cell carcinoma with unclassified histology reveals distinct subsets. <i>Nature Communications</i> , 2016, 7, 13131.	12.8	140
35	Down-Regulation of miR-129-5p and the let-7 Family in Neuroendocrine Tumors and Metastases Leads to Up-Regulation of Their Targets <i>Egr1</i> , <i>G3bp1</i> , <i>Hmga2</i> and <i>Bach1</i> . <i>Genes</i> , 2015, 6, 1-21.	2.4	53
36	TCEB1-mutated renal cell carcinoma: a distinct genomic and morphological subtype. <i>Modern Pathology</i> , 2015, 28, 845-853.	5.5	127

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37	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015, 517, 576-582.	27.8	3,209
38	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	28.9	2,562
39	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	27.0	2,582
40	The lncRNA MIR31HG regulates p16INK4A expression to modulate senescence. <i>Nature Communications</i> , 2015, 6, 6967.	12.8	161
41	Molecular Subtypes of Uterine Leiomyosarcoma and Correlation with Clinical Outcome. <i>Neoplasia</i> , 2015, 17, 183-189.	5.3	33
42	miR-339-5p regulates the p53 tumor-suppressor pathway by targeting MDM2. <i>Oncogene</i> , 2015, 34, 1908-1918.	5.9	72
43	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	28.9	2,318
44	MP36-02 VALIDATION AND GENOMIC INTERROGATION OF THE MET VARIANT RS11762213 AS A PREDICTOR OF ADVERSE OUTCOMES IN CLEAR CELL RENAL CELL CARCINOMA. <i>Journal of Urology</i> , 2014, 191, .	0.4	0
45	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.	27.8	2,496
46	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014, 513, 202-209.	27.8	5,055
47	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	28.9	1,242
48	Genome-wide analysis of noncoding regulatory mutations in cancer. <i>Nature Genetics</i> , 2014, 46, 1160-1165.	21.4	469
49	Validation and genomic interrogation of the MET variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma.. <i>Journal of Clinical Oncology</i> , 2014, 32, 395-395.	1.6	1
50	Integrated analysis of metastatic disease in clear cell renal cell carcinoma: A collaborative TCGA analysis.. <i>Journal of Clinical Oncology</i> , 2014, 32, 432-432.	1.6	0
51	cWords - systematic microRNA regulatory motif discovery from mRNA expression data. <i>Silence: A Journal of RNA Regulation</i> , 2013, 4, 2.	8.1	35
52	Analysis of microRNA-target interactions across diverse cancer types. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1325-1332.	8.2	184
53	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	28.9	3,979
54	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 409-420.	2.5	120

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55	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	21.4	6,265
56	SQSTM1 Is a Pathogenic Target of 5q Copy Number Gains in Kidney Cancer. <i>Cancer Cell</i> , 2013, 24, 738-750.	16.8	135
57	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	27.8	4,075
58	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. <i>Science Signaling</i> , 2013, 6, p1.	3.6	11,344
59	An Epidemiologic and Genomic Investigation Into the Obesity Paradox in Renal Cell Carcinoma. <i>Journal of the National Cancer Institute</i> , 2013, 105, 1862-1870.	6.3	231
60	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	27.8	2,839
61	Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. <i>PLoS ONE</i> , 2013, 8, e80306.	2.5	90
62	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. <i>Cancer Discovery</i> , 2012, 2, 401-404.	9.4	12,801
63	MicroRNA-143 down-regulates Hexokinase 2 in colon cancer cells. <i>BMC Cancer</i> , 2012, 12, 232.	2.6	128
64	microRNA-146a inhibits G protein-coupled receptor-mediated activation of NF- κ B by targeting CARD10 and COPS8 in gastric cancer. <i>Molecular Cancer</i> , 2012, 11, 71.	19.2	91
65	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	27.8	7,168
66	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	27.8	10,282
67	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012, 489, 519-525.	27.8	3,483
68	miR-34a Repression in Proneural Malignant Gliomas Upregulates Expression of Its Target PDGFRA and Promotes Tumorigenesis. <i>PLoS ONE</i> , 2012, 7, e33844.	2.5	106
69	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. <i>PLoS ONE</i> , 2012, 7, e34546.	2.5	104
70	Small RNA Sequencing and Functional Characterization Reveals MicroRNA-143 Tumor Suppressor Activity in Liposarcoma. <i>Cancer Research</i> , 2011, 71, 5659-5669.	0.9	106
71	miR-449 inhibits cell proliferation and is down-regulated in gastric cancer. <i>Molecular Cancer</i> , 2011, 10, 29.	19.2	206
72	Off-target effects dominate a large-scale RNAi screen for modulators of the TGF- β 2 pathway and reveal microRNA regulation of TGFBR2. <i>Silence: A Journal of RNA Regulation</i> , 2011, 2, 3.	8.1	78

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73	MicroRNA transfection and AGO-bound CLIP-seq data sets reveal distinct determinants of miRNA action. <i>Rna</i> , 2011, 17, 820-834.	3.5	63
74	miRMaid: a unified programming interface for microRNA data resources. <i>BMC Bioinformatics</i> , 2010, 11, 29.	2.6	15
75	Signatures of RNA binding proteins globally coupled to effective microRNA target sites. <i>Genome Research</i> , 2010, 20, 1010-1019.	5.5	102
76	MicroRNA-145 Targets YES and STAT1 in Colon Cancer Cells. <i>PLoS ONE</i> , 2010, 5, e8836.	2.5	150
77	Identification and analysis of miRNAs in human breast cancer and teratoma samples using deep sequencing. <i>BMC Medical Genomics</i> , 2009, 2, 35.	1.5	40
78	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
79	Programmed Cell Death 4 (PDCD4) Is an Important Functional Target of the MicroRNA miR-21 in Breast Cancer Cells. <i>Journal of Biological Chemistry</i> , 2008, 283, 1026-1033.	3.4	1,001
80	Intragenomic Matching Reveals a Huge Potential for miRNA-Mediated Regulation in Plants. <i>PLoS Computational Biology</i> , 2007, 3, e238.	3.2	59