

Anders Jacobsen

List of Publications by Year in descending order

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80
papers

87,600
citations

57681

46
h-index

81351

76
g-index

88
all docs

88
docs citations

88
times ranked

98993
citing authors

#	ARTICLE	IF	CITATIONS
1	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. <i>Cancer Discovery</i> , 2012, 2, 401-404.	7.7	12,801
2	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. <i>Science Signaling</i> , 2013, 6, pl1.	1.6	11,344
3	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	13.7	10,282
4	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	13.7	7,168
5	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	9.4	6,265
6	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014, 513, 202-209.	13.7	5,055
7	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
8	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	3,979
9	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012, 489, 519-525.	13.7	3,483
10	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015, 517, 576-582.	13.7	3,209
11	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	13.7	2,839
12	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
13	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
14	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.	13.7	2,496
15	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
16	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	1,242
17	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.	1.6	1,001
18	Genome-wide analysis of noncoding regulatory mutations in cancer. <i>Nature Genetics</i> , 2014, 46, 1160-1165.	9.4	469

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19	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	9.4	408
20	Genomic landscape of lung adenocarcinoma in East Asians. <i>Nature Genetics</i> , 2020, 52, 177-186.	9.4	281
21	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.	3.0	231
22	miR-449 inhibits cell proliferation and is down-regulated in gastric cancer. <i>Molecular Cancer</i> , 2011, 10, 29.	7.9	206
23	Analysis of microRNA-target interactions across diverse cancer types. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1325-1332.	3.6	184
24	Body Mass Index and Metastatic Renal Cell Carcinoma: Clinical and Biological Correlations. <i>Journal of Clinical Oncology</i> , 2016, 34, 3655-3663.	0.8	174
25	The lncRNA MIR31HG regulates p16INK4A expression to modulate senescence. <i>Nature Communications</i> , 2015, 6, 6967.	5.8	161
26	MicroRNA-145 Targets YES and STAT1 in Colon Cancer Cells. <i>PLoS ONE</i> , 2010, 5, e8836.	1.1	150
27	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.	15.2	141
28	Molecular analysis of aggressive renal cell carcinoma with unclassified histology reveals distinct subsets. <i>Nature Communications</i> , 2016, 7, 13131.	5.8	140
29	SQSTM1 Is a Pathogenic Target of 5q Copy Number Gains in Kidney Cancer. <i>Cancer Cell</i> , 2013, 24, 738-750.	7.7	135
30	MicroRNA-143 down-regulates Hexokinase 2 in colon cancer cells. <i>BMC Cancer</i> , 2012, 12, 232.	1.1	128
31	TCEB1-mutated renal cell carcinoma: a distinct genomic and morphological subtype. <i>Modern Pathology</i> , 2015, 28, 845-853.	2.9	127
32	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , 2013, 141, 409-420.	1.1	120
33	Mutation hotspots at CTCF binding sites coupled to chromosomal instability in gastrointestinal cancers. <i>Nature Communications</i> , 2018, 9, 1520.	5.8	109
34	Small RNA Sequencing and Functional Characterization Reveals MicroRNA-143 Tumor Suppressor Activity in Liposarcoma. <i>Cancer Research</i> , 2011, 71, 5659-5669.	0.4	106
35	miR-34a Repression in Proneural Malignant Gliomas Upregulates Expression of Its Target PDGFRA and Promotes Tumorigenesis. <i>PLoS ONE</i> , 2012, 7, e33844.	1.1	106
36	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.	9.4	106

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37	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. <i>PLoS ONE</i> , 2012, 7, e34546.	1.1	104
38	Signatures of RNA binding proteins globally coupled to effective microRNA target sites. <i>Genome Research</i> , 2010, 20, 1010-1019.	2.4	102
39	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.	7.9	91
40	Comprehensive Analysis of Long Non-Coding RNAs in Ovarian Cancer Reveals Global Patterns and Targeted DNA Amplification. <i>PLoS ONE</i> , 2013, 8, e80306.	1.1	90
41	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.	8.0	78
42	miR-339-5p regulates the p53 tumor-suppressor pathway by targeting MDM2. <i>Oncogene</i> , 2015, 34, 1908-1918.	2.6	72
43	MicroRNA transfection and AGO-bound CLIP-seq data sets reveal distinct determinants of miRNA action. <i>Rna</i> , 2011, 17, 820-834.	1.6	63
44	β -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.	2.9	61
45	Intragenomic Matching Reveals a Huge Potential for miRNA-Mediated Regulation in Plants. <i>PLoS Computational Biology</i> , 2007, 3, e238.	1.5	59
46	Down-Regulation of miR-129-5p and the let-7 Family in Neuroendocrine Tumors and Metastases Leads to Up-Regulation of Their Targets Egr1, G3bp1, Hmga2 and Bach1. <i>Genes</i> , 2015, 6, 1-21.	1.0	53
47	Tissue-specific cell-free DNA degradation quantifies circulating tumor DNA burden. <i>Nature Communications</i> , 2021, 12, 2229.	5.8	49
48	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. <i>Nature Communications</i> , 2019, 10, 3682.	5.8	48
49	Pan-Cancer Analysis of Ligand- \times Receptor Cross-talk in the Tumor Microenvironment. <i>Cancer Research</i> , 2021, 81, 1802-1812.	0.4	41
50	Identification and analysis of miRNAs in human breast cancer and teratoma samples using deep sequencing. <i>BMC Medical Genomics</i> , 2009, 2, 35.	0.7	40
51	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent CCNE1 and IGF2 enhancer hijacking in primary gastric adenocarcinoma. <i>Gut</i> , 2020, 69, 1039-1052.	6.1	36
52	cWords - systematic microRNA regulatory motif discovery from mRNA expression data. <i>Silence: A Journal of RNA Regulation</i> , 2013, 4, 2.	8.0	35
53	Molecular Subtypes of Uterine Leiomyosarcoma and Correlation with Clinical Outcome. <i>Neoplasia</i> , 2015, 17, 183-189.	2.3	33
54	Whole-genome noncoding sequence analysis in T-cell acute lymphoblastic leukemia identifies oncogene enhancer mutations. <i>Blood</i> , 2017, 129, 3264-3268.	0.6	32

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55	The long non-coding RNA MIR31HG regulates the senescence associated secretory phenotype. Nature Communications, 2021, 12, 2459.	5.8	27
56	Advances in genomic hepatocellular carcinoma research. GigaScience, 2018, 7, .	3.3	25
57	Association of Clinicopathologic and Molecular Tumor Features With Recurrence in Resected Early-Stage Epidermal Growth Factor Receptor-Positive Non-Small Cell Lung Cancer. JAMA Network Open, 2021, 4, e2131892.	2.8	25
58	Epigenetic promoter alterations in GI tumour immune-editing and resistance to immune checkpoint inhibition. Gut, 2022, 71, 1277-1288.	6.1	23
59	Genomic differences between black and white patients implicate a distinct immune response to papillary renal cell carcinoma. Oncotarget, 2017, 8, 5196-5205.	0.8	22
60	Integrative Profiling of T790M-Negative EGFR-Mutated NSCLC Reveals Pervasive Lineage Transition and Therapeutic Opportunities. Clinical Cancer Research, 2021, 27, 5939-5950.	3.2	21
61	SMuRF: portable and accurate ensemble prediction of somatic mutations. Bioinformatics, 2019, 35, 3157-3159.	1.8	19
62	A pan-cancer metabolic atlas of the tumor microenvironment. Cell Reports, 2022, 39, 110800.	2.9	19
63	Validation and genomic interrogation of the <i>MET</i> variant rs11762213 as a predictor of adverse outcomes in clear cell renal cell carcinoma. Cancer, 2016, 122, 402-410.	2.0	18
64	miRMaid: a unified programming interface for microRNA data resources. BMC Bioinformatics, 2010, 11, 29.	1.2	15
65	Dynamic phenotypic heterogeneity and the evolution of multiple RNA subtypes in hepatocellular carcinoma: the PLANET study. National Science Review, 2022, 9, nwab192.	4.6	15
66	Deficiency of the splicing factor RBM10 limits EGFR inhibitor response in EGFR-mutant lung cancer. Journal of Clinical Investigation, 2022, 132, .	3.9	15
67	Obstructive sleep apnea and Fuhrman grade in patients with clear cell renal cell carcinoma treated surgically. World Journal of Urology, 2017, 35, 51-56.	1.2	13
68	MutSpot: detection of non-coding mutation hotspots in cancer genomes. Npj Genomic Medicine, 2020, 5, 26.	1.7	12
69	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. Journal of Clinical Investigation, 2020, 130, 3005-3020.	3.9	12
70	A chemical genetic screen identifies Aurora kinases as a therapeutic target in EGFR T790M negative, gefitinib-resistant head and neck squamous cell carcinoma (HNSCC). EBioMedicine, 2021, 64, 103220.	2.7	10
71	Integrative epigenomic and high-throughput functional enhancer profiling reveals determinants of enhancer heterogeneity in gastric cancer. Genome Medicine, 2021, 13, 158.	3.6	7
72	Obtaining spatially resolved tumor purity maps using deep multiple instance learning in a pan-cancer study. Patterns, 2022, 3, 100399.	3.1	6

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73	Regulatory enhancer profiling of mesenchymal-type gastric cancer reveals subtype-specific epigenomic landscapes and targetable vulnerabilities. <i>Gut</i> , 2023, 72, 226-241.	6.1	6
74	Individualized Molecular Profiling for Allocation to Clinical Trials Singapore Study—An Asian Tertiary Cancer Center Experience. <i>JCO Precision Oncology</i> , 2021, 5, 859-875.	1.5	4
75	Targeting the developmental origins of cancer. <i>Nature Cancer</i> , 2021, 2, 256-257.	5.7	2
76	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.	0.8	1
77	Ensemble-Based Somatic Mutation Calling in Cancer Genomes. <i>Methods in Molecular Biology</i> , 2020, 2120, 37-46.	0.4	1
78	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, .	0.2	0
79	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.	0.8	0
80	A phase 1b study of <scp>OXIRI</scp> in pancreatic adenocarcinoma patients and its immunomodulatory effects. <i>International Journal of Cancer</i> , 2022, , .	2.3	0