

Jan Budczies

List of Publications by Year in descending order

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86
papers

5,856
citations

117625

34
h-index

82547

72
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87
all docs

87
docs citations

87
times ranked

10077
citing authors

#	ARTICLE	IF	CITATIONS
1	Artificial intelligence and pathology: From principles to practice and future applications in histomorphology and molecular profiling. <i>Seminars in Cancer Biology</i> , 2022, 84, 129-143.	9.6	41
2	Deciphering the immunosuppressive tumor microenvironment in ALK- and EGFR-positive lung adenocarcinoma. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 251-265.	4.2	22
3	Mutations in TP53 or DNA damage repair genes define poor prognostic subgroups in primary prostate cancer. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2022, 40, 8.e11-8.e18.	1.6	8
4	Assigning evidence to actionability: An introduction to variant interpretation in precision cancer medicine. <i>Genes Chromosomes and Cancer</i> , 2022, 61, 303-313.	2.8	15
5	The Different Immune Profiles of Normal Colonic Mucosa in Cancer-Free Lynch Syndrome Carriers and Lynch Syndrome Colorectal Cancer Patients. <i>Gastroenterology</i> , 2022, 162, 907-919.e10.	1.3	27
6	<scp>Homologous recombination deficiency</scp> is inversely correlated with <scp>microsatellite instability</scp> and identifies immunologically cold tumors in most cancer types. <i>Journal of Pathology: Clinical Research</i> , 2022, 8, 371-382.	3.0	10
7	LINC00152 Drives a Competing Endogenous RNA Network in Human Hepatocellular Carcinoma. <i>Cells</i> , 2022, 11, 1528.	4.1	6
8	The impact of TP53 co-mutations and immunologic microenvironment on outcome of lung cancer with EGFR exon 20 insertions. <i>European Journal of Cancer</i> , 2022, 170, 106-118.	2.8	15
9	Serum Response Factor (SRF) Drives the Transcriptional Upregulation of the MDM4 Oncogene in HCC. <i>Cancers</i> , 2021, 13, 199.	3.7	8
10	A gene expression signature associated with B cells predicts benefit from immune checkpoint blockade in lung adenocarcinoma. <i>Onc Immunology</i> , 2021, 10, 1860586.	4.6	40
11	Reconstructing tumor history in breast cancer: signatures of mutational processes and response to neoadjuvant chemotherapy. <i>Annals of Oncology</i> , 2021, 32, 500-511.	1.2	9
12	Targeting rare and non-canonical driver variants in NSCLC – An uncharted clinical field. <i>Lung Cancer</i> , 2021, 154, 131-141.	2.0	8
13	Conventional and semi-automatic histopathological analysis of tumor cell content for multigene sequencing of lung adenocarcinoma. <i>Translational Lung Cancer Research</i> , 2021, 10, 1666-1678.	2.8	6
14	The journey of tumor-infiltrating lymphocytes as a biomarker in breast cancer: clinical utility in an era of checkpoint inhibition. <i>Annals of Oncology</i> , 2021, 32, 1236-1244.	1.2	109
15	The immune microenvironment in EGFR- and ERBB2-mutated lung adenocarcinoma. <i>ESMO Open</i> , 2021, 6, 100253.	4.5	17
16	Decoding and targeting the molecular basis of MACC1-driven metastatic spread: Lessons from big data mining and clinical-experimental approaches. <i>Seminars in Cancer Biology</i> , 2020, 60, 365-379.	9.6	24
17	PARP-1 expression as a prognostic factor in Desmoid-type fibromatosis. <i>Annals of Diagnostic Pathology</i> , 2020, 44, 151442.	1.3	6
18	Updating the risk profile of fatal head trauma: an autopsy study with focus on age- and sex-dependent differences. <i>International Journal of Legal Medicine</i> , 2020, 134, 295-307.	2.2	4

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19	Tumor Mutational Burden as a Predictive Biomarker in Solid Tumors. <i>Cancer Discovery</i> , 2020, 10, 1808-1825.	9.4	388
20	Immuno-oncology gene expression profiling of formalin-fixed and paraffin-embedded clear cell renal cell carcinoma: Performance comparison of the NanoString nCounter technology with targeted RNA sequencing. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 406-416.	2.8	10
21	Harmonization and Standardization of Panel-Based Tumor Mutational Burden Measurement: Real-World Results and Recommendations of the Quality in Pathology Study. <i>Journal of Thoracic Oncology</i> , 2020, 15, 1177-1189.	1.1	81
22	Quantifying potential confounders of panel-based tumor mutational burden (TMB) measurement. <i>Lung Cancer</i> , 2020, 142, 114-119.	2.0	28
23	Integrated clinicomolecular characterization identifies RAS activation and CDKN2A deletion as independent adverse prognostic factors in cancer of unknown primary. <i>International Journal of Cancer</i> , 2020, 146, 3053-3064.	5.1	14
24	TP53 Mutations Predict Sensitivity to Adjuvant Gemcitabine in Patients with Pancreatic Ductal Adenocarcinoma: Next-Generation Sequencing Results from the CONKO-001 Trial. <i>Clinical Cancer Research</i> , 2020, 26, 3732-3739.	7.0	28
25	Clinical and molecular profile of de novo vs. secondary EGFR mutated metastatic non-small-cell lung cancer. <i>Pneumologie</i> , 2020, 74, .	0.1	0
26	Elevated HOX gene expression in acute myeloid leukemia is associated with NPM1 mutations and poor survival. <i>Journal of Advanced Research</i> , 2019, 20, 105-116.	9.5	45
27	Optimizing panel-based tumor mutational burden (TMB) measurement. <i>Annals of Oncology</i> , 2019, 30, 1496-1506.	1.2	123
28	Post-neoadjuvant cellular dissociation grading based on tumour budding and cell nest size is associated with therapy response and survival in oesophageal squamous cell carcinoma. <i>British Journal of Cancer</i> , 2019, 121, 1050-1057.	6.4	11
29	Morphomolecular analysis of the immune tumor microenvironment in human head and neck cancer. <i>Cancer Immunology, Immunotherapy</i> , 2019, 68, 1443-1454.	4.2	13
30	RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. <i>Cancers</i> , 2019, 11, 1309.	3.7	32
31	Spatial and Temporal Heterogeneity of Panel-Based Tumor Mutational Burden in Pulmonary Adenocarcinoma: Separating Biology From Technical Artifacts. <i>Journal of Thoracic Oncology</i> , 2019, 14, 1935-1947.	1.1	69
32	Detection of TP53 Mutations in Tissue or Liquid Rebiopsies at Progression Identifies ALK+ Lung Cancer Patients with Poor Survival. <i>Cancers</i> , 2019, 11, 124.	3.7	36
33	Clinical and analytical validation of Ki-67 in 9069 patients from IBCSG VIII, IX, BIG1-98 and GeparTrio trial: systematic modulation of interobserver variance in a comprehensive in silico ring trial. <i>Breast Cancer Research and Treatment</i> , 2019, 176, 557-568.	2.5	10
34	Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019, 145, 2996-3010.	5.1	76
35	Mutational Diversity and Therapy Response in Breast Cancer: A Sequencing Analysis in the Neoadjuvant GeparSepto Trial. <i>Clinical Cancer Research</i> , 2019, 25, 3986-3995.	7.0	32
36	A Non-interventional Clinical Trial Assessing Immune Responses After Radiofrequency Ablation of Liver Metastases From Colorectal Cancer. <i>Frontiers in Immunology</i> , 2019, 10, 2526.	4.8	29

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37	Prognostic significance of Ki-67 levels and hormone receptor expression in low-grade serous ovarian carcinoma: an investigation of the Tumor Bank Ovarian Cancer Network. <i>Human Pathology</i> , 2019, 85, 299-308.	2.0	24
38	Measurement of tumor mutational burden (TMB) in routine molecular diagnostics: <i>in silico</i> and real-life analysis of three larger gene panels. <i>International Journal of Cancer</i> , 2019, 144, 2303-2312.	5.1	95
39	Combined targeted DNA and RNA sequencing of advanced NSCLC in routine molecular diagnostics: Analysis of the first 3,000 Heidelberg cases. <i>International Journal of Cancer</i> , 2019, 145, 649-661.	5.1	85
40	Size matters: Dissecting key parameters for panel-based tumor mutational burden analysis. <i>International Journal of Cancer</i> , 2019, 144, 848-858.	5.1	131
41	Identification of a highly lethal V3 ⁺ TP53 ⁺ subset in ALK ⁺ lung adenocarcinoma. <i>International Journal of Cancer</i> , 2019, 144, 190-199.	5.1	67
42	Defining molecular risk in ALK+ NSCLC. <i>Oncotarget</i> , 2019, 10, 3093-3103.	1.8	35
43	Prioritization of metabolic genes as novel therapeutic targets in estrogen-receptor negative breast tumors using multi-omics data and text mining. <i>Oncotarget</i> , 2019, 10, 3894-3909.	1.8	11
44	RSPO2 gene rearrangement – a new cancer driver in the liver. <i>Zeitschrift Fur Gastroenterologie</i> , 2019, 57, .	0.5	0
45	Dynamics of the Intratumoral Immune Response during Progression of High-Grade Serous Ovarian Cancer. <i>Neoplasia</i> , 2018, 20, 280-288.	5.3	23
46	A multi-omics analysis reveals metabolic reprogramming in THP-1 cells upon treatment with the contact allergen DNCB. <i>Toxicology and Applied Pharmacology</i> , 2018, 340, 21-29.	2.8	9
47	An integrative bioinformatics approach reveals coding and non-coding gene variants associated with gene expression profiles and outcome in breast cancer molecular subtypes. <i>British Journal of Cancer</i> , 2018, 118, 1107-1114.	6.4	26
48	Tumour-infiltrating lymphocytes and prognosis in different subtypes of breast cancer: a pooled analysis of 3771 patients treated with neoadjuvant therapy. <i>Lancet Oncology</i> , The, 2018, 19, 40-50.	10.7	1,327
49	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DKTK Molecularly Aided Stratification for Tumor Eradication Research Experience. <i>JCO Precision Oncology</i> , 2018, 2, 1-13.	3.0	20
50	Implementing tumor mutational burden (TMB) analysis in routine diagnostics – a primer for molecular pathologists and clinicians. <i>Translational Lung Cancer Research</i> , 2018, 7, 703-715.	2.8	152
51	Integrated analysis of the immunological and genetic status in and across cancer types: impact of mutational signatures beyond tumor mutational burden. <i>Oncolmmunology</i> , 2018, 7, e1526613.	4.6	60
52	Subgroup-specific immune and stromal microenvironment in medulloblastoma. <i>Oncolmmunology</i> , 2018, 7, e1462430.	4.6	77
53	loncopy: an R Shiny app to call copy number alterations in targeted NGS data. <i>BMC Bioinformatics</i> , 2018, 19, 157.	2.6	4
54	Subtyping Of Triple Negative Breast Carcinoma On The Basis Of RTK Expression. <i>Journal of Cancer</i> , 2018, 9, 2589-2602.	2.5	3

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55	PD-L1 (CD274) copy number gain, expression, and immune cell infiltration as candidate predictors for response to immune checkpoint inhibitors in soft-tissue sarcoma. <i>Oncolmunology</i> , 2017, 6, e1279777.	4.6	50
56	Mutation patterns in genes encoding interferon signaling and antigen presentation: A pan-cancer survey with implications for the use of immune checkpoint inhibitors. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 651-659.	2.8	35
57	Cytokeratin 5/6 expression, prognosis, and association with estrogen receptor \pm in high-grade serous ovarian carcinoma. <i>Human Pathology</i> , 2017, 67, 30-36.	2.0	11
58	Targeted next-generation sequencing enables reliable detection of HER2 (ERBB2) status in breast cancer and provides ancillary information of clinical relevance. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 255-265.	2.8	21
59	Tubular, lactating, and ductal adenomas are devoid of MED12 Exon2 mutations, and ductal adenomas show recurrent mutations in GNAS and the PI3K-AKT pathway. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 11-17.	2.8	27
60	Chromosome 9p copy number gains involving PD-L1 are associated with a specific proliferation and immune-modulating gene expression program active across major cancer types. <i>BMC Medical Genomics</i> , 2017, 10, 74.	1.5	35
61	DUSP4 is associated with increased resistance against anti-HER2 therapy in breast cancer. <i>Oncotarget</i> , 2017, 8, 77207-77218.	1.8	30
62	High-grade ovarian serous carcinoma patients exhibit profound alterations in lipid metabolism. <i>Oncotarget</i> , 2017, 8, 102912-102922.	1.8	57
63	Copy number variations in atypical fibroxanthomas and pleomorphic dermal sarcomas. <i>Oncotarget</i> , 2017, 8, 109457-109467.	1.8	32
64	Mutations in genes encoding PI3K-AKT and MAPK signaling define anogenital papillary hidradenoma. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 113-119.	2.8	29
65	Standardized evaluation of tumor-infiltrating lymphocytes in breast cancer: results of the ring studies of the international immuno-oncology biomarker working group. <i>Modern Pathology</i> , 2016, 29, 1155-1164.	5.5	230
66	Pan-cancer analysis of copy number changes in programmed death-ligand 1 (PD-L1, CD274) associations with gene expression, mutational load, and survival. <i>Genes Chromosomes and Cancer</i> , 2016, 55, 626-639.	2.8	80
67	Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. <i>International Journal of Cancer</i> , 2016, 138, 87-97.	5.1	136
68	Tissue-Based Metabolomics to Analyze the Breast Cancer Metabolome. <i>Recent Results in Cancer Research</i> , 2016, 207, 157-175.	1.8	25
69	Integration of genomics and histology revises diagnosis and enables effective therapy of refractory cancer of unknown primary with PDL1 amplification. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001180.	1.2	57
70	Accumulated Metabolites of Hydroxybutyric Acid Serve as Diagnostic and Prognostic Biomarkers of Ovarian High-Grade Serous Carcinomas. <i>Cancer Research</i> , 2016, 76, 796-804.	0.9	74
71	Prognostic impact of programmed cell death-1 (PD-1) and PD-ligand 1 (PD-L1) expression in cancer cells and tumor-infiltrating lymphocytes in ovarian high grade serous carcinoma. <i>Oncotarget</i> , 2016, 7, 1486-1499.	1.8	212
72	loncopy: a novel method for calling copy number alterations in amplicon sequencing data including significance assessment. <i>Oncotarget</i> , 2016, 7, 13236-13247.	1.8	23

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73	Comparison of targeted next-generation sequencing and Sanger sequencing for the detection of PIK3CA mutations in breast cancer. <i>BMC Clinical Pathology</i> , 2015, 15, 20.	1.8	61
74	Microfluidic sampling system for tissue analytics. <i>Biomicrofluidics</i> , 2015, 9, 054109.	2.4	6
75	The landscape of metastatic progression patterns across major human cancers. <i>Oncotarget</i> , 2015, 6, 570-583.	1.8	208
76	Classical pathology and mutational load of breast cancer – integration of two worlds. <i>Journal of Pathology: Clinical Research</i> , 2015, 1, 225-238.	3.0	91
77	Strategies for developing Ki67 as a useful biomarker in breast cancer. <i>Breast</i> , 2015, 24, S67-S72.	2.2	130
78	Parallel screening for ALK, MET and ROS1 alterations in non-small cell lung cancer with implications for daily routine testing. <i>Lung Cancer</i> , 2015, 87, 122-129.	2.0	54
79	Semiconductor sequencing: how many flows do you need?. <i>Bioinformatics</i> , 2015, 31, 1199-1203.	4.1	5
80	Glutamate enrichment as new diagnostic opportunity in breast cancer. <i>International Journal of Cancer</i> , 2015, 136, 1619-1628.	5.1	103
81	Comprehensive analysis of clinico-pathological data reveals heterogeneous relations between atherosclerosis and cancer. <i>Journal of Clinical Pathology</i> , 2014, 67, 482-490.	2.0	13
82	Tumour cell proliferation (Ki-67) in non-small cell lung cancer: a critical reappraisal of its prognostic role. <i>British Journal of Cancer</i> , 2014, 111, 1222-1229.	6.4	114
83	Mutational profiles in triple-negative breast cancer defined by ultradeep multigene sequencing show high rates of PI3K pathway alterations and clinically relevant entity subgroup specific differences. <i>Oncotarget</i> , 2014, 5, 9952-9965.	1.8	58
84	Comparative metabolomics of estrogen receptor positive and estrogen receptor negative breast cancer: alterations in glutamine and beta-alanine metabolism. <i>Journal of Proteomics</i> , 2013, 94, 279-288.	2.4	144
85	Remodeling of central metabolism in invasive breast cancer compared to normal breast tissue – a GC-TOFMS based metabolomics study. <i>BMC Genomics</i> , 2012, 13, 334.	2.8	123
86	Genome-wide Gene Expression Profiling of Formalin-fixed Paraffin-Embedded Breast Cancer Core Biopsies Using Microarrays. <i>Journal of Histochemistry and Cytochemistry</i> , 2011, 59, 146-157.	2.5	33