

Jan Budczies

List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

5,856
citations

117453

34
h-index

82410

72
g-index

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. | 4.3 | 41 |
| 2 | Deciphering the immunosuppressive tumor microenvironment in ALK- and EGFR-positive lung adenocarcinoma. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 251-265. | 2.0 | 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. | 0.8 | 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. | 1.5 | 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. | 0.6 | 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. | 1.3 | 10 |
| 7 | LINC00152 Drives a Competing Endogenous RNA Network in Human Hepatocellular Carcinoma. <i>Cells</i> , 2022, 11, 1528. | 1.8 | 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. | 1.3 | 15 |
| 9 | Serum Response Factor (SRF) Drives the Transcriptional Upregulation of the MDM4 Oncogene in HCC. <i>Cancers</i> , 2021, 13, 199. | 1.7 | 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. | 2.1 | 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. | 0.6 | 9 |
| 12 | Targeting rare and non-canonical driver variants in NSCLC – An uncharted clinical field. <i>Lung Cancer</i> , 2021, 154, 131-141. | 0.9 | 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. | 1.3 | 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. | 0.6 | 109 |
| 15 | The immune microenvironment in EGFR- and ERBB2-mutated lung adenocarcinoma. <i>ESMO Open</i> , 2021, 6, 100253. | 2.0 | 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. | 4.3 | 24 |
| 17 | PARP-1 expression as a prognostic factor in Desmoid-type fibromatosis. <i>Annals of Diagnostic Pathology</i> , 2020, 44, 151442. | 0.6 | 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. | 1.2 | 4 |

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|----|---|-----|-----------|
| 19 | Tumor Mutational Burden as a Predictive Biomarker in Solid Tumors. <i>Cancer Discovery</i> , 2020, 10, 1808-1825. | 7.7 | 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. | 1.5 | 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. | 0.5 | 81 |
| 22 | Quantifying potential confounders of panel-based tumor mutational burden (TMB) measurement. <i>Lung Cancer</i> , 2020, 142, 114-119. | 0.9 | 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. | 2.3 | 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. | 3.2 | 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. | 4.4 | 45 |
| 27 | Optimizing panel-based tumor mutational burden (TMB) measurement. <i>Annals of Oncology</i> , 2019, 30, 1496-1506. | 0.6 | 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. | 2.9 | 11 |
| 29 | Morphomolecular analysis of the immune tumor microenvironment in human head and neck cancer. <i>Cancer Immunology, Immunotherapy</i> , 2019, 68, 1443-1454. | 2.0 | 13 |
| 30 | RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. <i>Cancers</i> , 2019, 11, 1309. | 1.7 | 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. | 0.5 | 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. | 1.7 | 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. | 1.1 | 10 |
| 34 | Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019, 145, 2996-3010. | 2.3 | 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. | 3.2 | 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. | 2.2 | 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. | 1.1 | 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. | 2.3 | 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. | 2.3 | 85 |
| 40 | Size matters: Dissecting key parameters for panel-based tumor mutational burden analysis. <i>International Journal of Cancer</i> , 2019, 144, 848-858. | 2.3 | 131 |
| 41 | Identification of a highly lethal V3 ⁺ TP53 ⁺ subset in ALK ⁺ lung adenocarcinoma. <i>International Journal of Cancer</i> , 2019, 144, 190-199. | 2.3 | 67 |
| 42 | Defining molecular risk in ALK+ NSCLC. <i>Oncotarget</i> , 2019, 10, 3093-3103. | 0.8 | 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. | 0.8 | 11 |
| 44 | RSPO2 gene rearrangement – a new cancer driver in the liver. <i>Zeitschrift Fur Gastroenterologie</i> , 2019, 57, . | 0.2 | 0 |
| 45 | Dynamics of the Intratumoral Immune Response during Progression of High-Grade Serous Ovarian Cancer. <i>Neoplasia</i> , 2018, 20, 280-288. | 2.3 | 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. | 1.3 | 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. | 2.9 | 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. | 5.1 | 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. | 1.5 | 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. | 1.3 | 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. | 2.1 | 60 |
| 52 | Subgroup-specific immune and stromal microenvironment in medulloblastoma. <i>Oncolmmunology</i> , 2018, 7, e1462430. | 2.1 | 77 |
| 53 | loncopy: an R Shiny app to call copy number alterations in targeted NGS data. <i>BMC Bioinformatics</i> , 2018, 19, 157. | 1.2 | 4 |
| 54 | Subtyping Of Triple Negative Breast Carcinoma On The Basis Of RTK Expression. <i>Journal of Cancer</i> , 2018, 9, 2589-2602. | 1.2 | 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. | 2.1 | 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. | 1.5 | 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. | 1.1 | 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. | 1.5 | 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. | 1.5 | 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. | 0.7 | 35 |
| 61 | DUSP4 is associated with increased resistance against anti-HER2 therapy in breast cancer. <i>Oncotarget</i> , 2017, 8, 77207-77218. | 0.8 | 30 |
| 62 | High-grade ovarian serous carcinoma patients exhibit profound alterations in lipid metabolism. <i>Oncotarget</i> , 2017, 8, 102912-102922. | 0.8 | 57 |
| 63 | Copy number variations in atypical fibroxanthomas and pleomorphic dermal sarcomas. <i>Oncotarget</i> , 2017, 8, 109457-109467. | 0.8 | 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. | 1.5 | 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. | 2.9 | 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. | 1.5 | 80 |
| 67 | Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. <i>International Journal of Cancer</i> , 2016, 138, 87-97. | 2.3 | 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. | 0.5 | 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. | 0.4 | 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. | 0.8 | 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. | 0.8 | 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. | 1.2 | 6 |
| 75 | The landscape of metastatic progression patterns across major human cancers. <i>Oncotarget</i> , 2015, 6, 570-583. | 0.8 | 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. | 1.3 | 91 |
| 77 | Strategies for developing Ki67 as a useful biomarker in breast cancer. <i>Breast</i> , 2015, 24, S67-S72. | 0.9 | 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. | 0.9 | 54 |
| 79 | Semiconductor sequencing: how many flows do you need?. <i>Bioinformatics</i> , 2015, 31, 1199-1203. | 1.8 | 5 |
| 80 | Glutamate enrichment as new diagnostic opportunity in breast cancer. <i>International Journal of Cancer</i> , 2015, 136, 1619-1628. | 2.3 | 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. | 1.0 | 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. | 2.9 | 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. | 0.8 | 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. | 1.2 | 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. | 1.2 | 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. | 1.3 | 33 |