Martina Kirchner

List of Publications by Year
in descending order

40 papers	1,573 citations	361413 20 h-index	315739 38 g-index
40 all docs	40 docs citations	40 times ranked	2523 citing authors

#	Article	IF	Citations
1	Implementing tumor mutational burden (TMB) analysis in routine diagnosticsâ€"a primer for molecular pathologists and clinicians. Translational Lung Cancer Research, 2018, 7, 703-715.	2.8	152
2	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	5.1	133
3	Size matters: Dissecting key parameters for panelâ€based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858.	5.1	131
4	Three molecular pathways model colorectal carcinogenesis in <scp>L</scp>ynch syndrome. International Journal of Cancer, 2018, 143, 139-150.	5.1	129
5	Measurement of tumor mutational burden (TMB) in routine molecular diagnostics: in silico and realâ€life analysis of three larger gene panels. International Journal of Cancer, 2019, 144, 2303-2312.	5.1	95
6	EML4â€ALK fusion variant V3 is a highâ€risk feature conferring accelerated metastatic spread, early treatment failure and worse overall survival in ALK⁺ nonâ€small cell lung cancer. International Journal of Cancer, 2018, 142, 2589-2598.	5.1	93
7	Combined targeted DNA and RNA sequencing of advanced NSCLC in routine molecular diagnostics: Analysis of the first 3,000 Heidelberg cases. International Journal of Cancer, 2019, 145, 649-661.	5.1	85
8	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	5.1	76
9	Spatial and Temporal Heterogeneity of Panel-Based Tumor Mutational Burden in Pulmonary Adenocarcinoma: Separating Biology From Technical Artifacts. Journal of Thoracic Oncology, 2019, 14, 1935-1947.	1.1	69
10	Testing NTRK testing: Wetâ€lab and in silico comparison of RNAâ€based targeted sequencing assays. Genes Chromosomes and Cancer, 2020, 59, 178-188.	2.8	52
11	A gene expression signature associated with B cells predicts benefit from immune checkpoint blockade in lung adenocarcinoma. OncoImmunology, 2021, 10, 1860586.	4.6	40
12	Detection of TP53 Mutations in Tissue or Liquid Rebiopsies at Progression Identifies ALK+ Lung Cancer Patients with Poor Survival. Cancers, 2019, 11, 124.	3.7	36
13	Defining molecular risk in ALK+ NSCLC. Oncotarget, 2019, 10, 3093-3103.	1.8	35
14	RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. Cancers, 2019, 11, 1309.	3.7	32
15	Tubular, lactating, and ductal adenomas are devoid of MED12 Exon2 mutations, and ductal adenomas show recurrent mutations in GNAS and the PI3Kâ€"AKT pathway. Genes Chromosomes and Cancer, 2017, 56, 11-17.	2.8	27
16	<scp>NTRK</scp> testing: First results of the <scp>QuiPâ€EQA</scp> scheme and a comprehensive map of <scp>NTRK</scp> fusion variants and their diagnostic coverage by targeted <scp>RNA</scp>â€based <scp>NGS</scp> assays. Genes Chromosomes and Cancer, 2020, 59, 445-453.	2.8	27
17	Novel GATA6-FOXO1 fusions in a subset of epithelioid hemangioma. Modern Pathology, 2021, 34, 934-941.	5.5	27
18	The Different Immune Profiles of Normal Colonic Mucosa in Cancer-Free Lynch Syndrome Carriers and Lynch Syndrome Colorectal Cancer Patients. Gastroenterology, 2022, 162, 907-919.e10.	1.3	27

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19	Comparative genetic profiling aids diagnosis and clinical decision making in challenging cases of CUP syndrome. International Journal of Cancer, 2019, 145, 2963-2973.	5.1	24
20	Real-world implementation of sequential targeted therapies for EGFR-mutated lung cancer. Therapeutic Advances in Medical Oncology, 2021, 13, 175883592199650.	3.2	24
21	Targetable ERBB2 mutations identified in neurofibroma/schwannoma hybrid nerve sheath tumors. Journal of Clinical Investigation, 2020, 130, 2488-2495.	8.2	23
22	Deciphering the immunosuppressive tumor microenvironment in ALK- and EGFR-positive lung adenocarcinoma. Cancer Immunology, Immunotherapy, 2022, 71, 251-265.	4.2	22
23	Genetic profiling of melanoma in routine diagnostics: assay performance and molecular characteristics in a consecutive series of 274 cases. Pathology, 2018, 50, 703-710.	0.6	21
24	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DKTK Molecularly Aided Stratification for Tumor Eradication Research Experience. JCO Precision Oncology, 2018, 2, 1-13.	3.0	20
25	Targeted deep sequencing of effusion cytology samples is feasible, informs spatiotemporal tumor evolution, and has clinical and diagnostic utility. Genes Chromosomes and Cancer, 2018, 57, 70-79.	2.8	19
26	<scp>miRNA</scp> profiling of biliary intraepithelial neoplasia reveals stepwise tumorigenesis in distal cholangiocarcinoma via the <scp>miR</scp>â€451a/<scp>ATF2</scp> axis. Journal of Pathology, 2020, 252, 239-251.	4.5	18
27	Assigning evidence to actionability: An introduction to variant interpretation in precision cancer medicine. Genes Chromosomes and Cancer, 2022, 61, 303-313.	2.8	15
28	The impact of TP53 co-mutations and immunologic microenvironment on outcome of lung cancer with EGFR exon 20 insertions. European Journal of Cancer, 2022, 170, 106-118.	2.8	15
29	Next generation sequencing of the cellular and liquid fraction of pancreatic cyst fluid supports discrimination of IPMN from pseudocysts and reveals cases with multiple mutated driver clones: First findings from the prospective ZYSTEUS biomarker study. Genes Chromosomes and Cancer, 2019, 58, 3-11.	2.8	14
30	Integrated clinicomolecular characterization identifies RAS activation and CDKN2A deletion as independent adverse prognostic factors in cancer of unknown primary. International Journal of Cancer, 2020, 146, 3053-3064.	5.1	14
31	High prevalence of DNA damage repair gene defects and TP53 alterations in men with treatment-naÃ¯ve metastatic prostate cancer â€“Results from a prospective pilot study using a 37 gene panel. Urologic Oncology: Seminars and Original Investigations, 2020, 38, 637.e17-637.e27.	1.6	12
32	Immunoâ€oncology gene expression profiling of formalinâ€fixed and paraffinâ€embedded clear cell renal cell carcinoma: Performance comparison of the <scp>NanoString nCounter</scp> technology with targeted <scp>RNA</scp> sequencing. Genes Chromosomes and Cancer, 2020, 59, 406-416.	2.8	10
33	Next-generation sequencing facilitates detection of the classic E13-A20 EML4-ALK fusion in an ALK-FISH/IHC inconclusive biopsy of a stage IV lung cancer patient: a case report. Diagnostic Pathology, 2016, 11, 133.	2.0	8
34	Synonymous EGFR variant p.Q787Q is neither prognostic nor predictive in patients with lung adenocarcinoma. Genes Chromosomes and Cancer, 2017, 56, 214-220.	2.8	8
35	Combination of Crizotinib and Osimertinib in T790M+ EGFR-Mutant Non-Small Cell Lung Cancer with Emerging MET Amplification Post-Osimertinib Progression in a 10-Year Survivor: A Case Report. Case Reports in Oncology, 2021, 14, 477-482.	0.7	8
36	Targeting rare and non-canonical driver variants in NSCLC â€“ An uncharted clinical field. Lung Cancer, 2021, 154, 131-141.	2.0	8

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37	Mutations in TP53 or DNA damage repair genes define poor prognostic subgroups in primary prostate cancer. Urologic Oncology: Seminars and Original Investigations, 2022, 40, 8.e11-8.e18.	1.6	8
38	Frequent Molecular Subtype Switching and Gene Expression Alterations in Lung and Pleural Metastasis From Luminal Aâ€“Type Breast Cancer. JCO Precision Oncology, 2020, 4, 848-859.	3.0	7
39	Histological and Molecular Plasticity of ALK-positive Non-Small-Cell Lung Cancer under Targeted Therapy - a Case Report. Journal of Physical Education and Sports Management, 2022, , mcs.a006156.	1.2	5
40	De Novo Versus Secondary Metastatic EGFR-Mutated Non-Small-Cell Lung Cancer. Frontiers in Oncology, 2021, 11, 640048.	2.8	4