

Jonas Leichsenring

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,369
citations

361413
20
h-index

345221
36
g-index

38
all docs

38
docs citations

38
times ranked

2665
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Integrating proteomics into precision oncology. <i>International Journal of Cancer</i> , 2021, 148, 1438-1451.	5.1	15
3	The Value of Prostate-specific Antigen Density for Prostate Imaging-Reporting and Data System 3 Lesions on Multiparametric Magnetic Resonance Imaging: A Strategy to Avoid Unnecessary Prostate Biopsies. <i>European Urology Focus</i> , 2021, 7, 325-331.	3.1	34
4	Targeting rare and non-canonical driver variants in NSCLC – An uncharted clinical field. <i>Lung Cancer</i> , 2021, 154, 131-141.	2.0	8
5	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
6	Patients Resistant Against PSMA-Targeting ±-Radiation Therapy Often Harbor Mutations in DNA Damage-Repair–Associated Genes. <i>Journal of Nuclear Medicine</i> , 2020, 61, 683-688.	5.0	61
7	Testing <i>NTRK</i> testing: Wet-lab and in silico comparison of RNA-based targeted sequencing assays. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 178-188.	2.8	52
8	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
9	High prevalence of DNA damage repair gene defects and TP53 alterations in men with treatment-naïve metastatic prostate cancer –Results from a prospective pilot study using a 37 gene panel. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2020, 38, 637.e17-637.e27.	1.6	12
10	Combined Immunohistochemistry after Mass Spectrometry Imaging for Superior Spatial Information. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1800035.	1.6	23
11	RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. <i>Cancers</i> , 2019, 11, 1309.	3.7	32
12	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
13	Targeted Therapy in Advanced Melanoma With Rare <i>BRAF</i> Mutations. <i>Journal of Clinical Oncology</i> , 2019, 37, 3142-3151.	1.6	83
14	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
15	Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019, 145, 2996-3010.	5.1	76
16	Comparative genetic profiling aids diagnosis and clinical decision making in challenging cases of CUP syndrome. <i>International Journal of Cancer</i> , 2019, 145, 2963-2973.	5.1	24
17	Measurement of tumor mutational burden (TMB) in routine molecular diagnostics: in silico and real-life analysis of three larger gene panels. <i>International Journal of Cancer</i> , 2019, 144, 2303-2312.	5.1	95
18	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

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19	Size matters: Dissecting key parameters for panel-based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858.	5.1	131
20	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
21	Oncogene-induced senescence: a potential breakpoint mechanism against malignant transformation in plasma cell disorders. Leukemia and Lymphoma, 2018, 59, 2660-2669.	1.3	3
22	Analysis of the proliferative activity in lung adenocarcinomas with specific driver mutations. Pathology Research and Practice, 2018, 214, 408-416.	2.3	4
23	Targeted molecular profiling reveals genetic heterogeneity of poromas and porocarcinomas. Pathology, 2018, 50, 327-332.	0.6	27
24	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
25	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DTK Molecularly Aided Stratification for Tumor Eradication Research Experience. JCO Precision Oncology, 2018, 2, 1-13.	3.0	20
26	Implementing tumor mutational burden (TMB) analysis in routine diagnostics—a primer for molecular pathologists and clinicians. Translational Lung Cancer Research, 2018, 7, 703-715.	2.8	152
27	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
28	Expression of HMB45, MelanA and SOX10 is rare in non-small cell lung cancer. Diagnostic Pathology, 2018, 13, 68.	2.0	8
29	Integrated Histogenetic Analysis Reveals BAP1 -Mutated Epithelioid Mesothelioma in a Patient With Cancer of Unknown Primary. Journal of the National Comprehensive Cancer Network: JNCCN, 2018, 16, 677-682.	4.9	6
30	Mutational profiles of Brenner tumors show distinctive features uncoupling urothelial carcinomas and ovarian carcinoma with transitional cell histology. Genes Chromosomes and Cancer, 2017, 56, 758-766.	2.8	21
31	Targeted next-generation sequencing enables reliable detection of HER2 (ERBB2) status in breast cancer and provides ancillary information of clinical relevance. Genes Chromosomes and Cancer, 2017, 56, 255-265.	2.8	21
32	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
33	Tubular, lactating, and ductal adenomas are devoid of MED12 Exon2 mutations, and ductal adenomas show recurrent mutations in GNAS and the PI3K-AKT pathway. Genes Chromosomes and Cancer, 2017, 56, 11-17.	2.8	27
34	Pan-cancer analysis of copy number changes in programmed death-ligand 1 (PD-L1, CD274) — associations with gene expression, mutational load, and survival. Genes Chromosomes and Cancer, 2016, 55, 626-639.	2.8	80
35	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
36	Taxonomic and vector-specific variation in species richness and abundance during the transport stage of biological invasions. Limnology and Oceanography, 2013, 58, 1361-1372.	3.1	44

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37	Effect of mid-oceanic ballast water exchange on virus-like particle abundance during two trans-Pacific voyages. Marine Pollution Bulletin, 2011, 62, 1103-1108.	5.0	11