Jonas Leichsenring

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11739998/publications.pdf

Version: 2024-02-01

37	1,369	361413	345221
papers	citations	20 h-index	36 g-index

38	38	38	2665
all docs	docs citations	times ranked	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	Size matters: Dissecting key parameters for panelâ€based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858.	5.1	131
3	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
4	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
5	Targeted Therapy in Advanced Melanoma With Rare BRAF Mutations. Journal of Clinical Oncology, 2019, 37, 3142-3151.	1.6	83
6	Panâ€cancer analysis of copy number changes in programmed deathâ€ligand 1 (PDâ€L1, CD274) â€" associations with gene expression, mutational load, and survival. Genes Chromosomes and Cancer, 2016, 55, 626-639.	2.8	80
7	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	5.1	76
8	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
9	Patients Resistant Against PSMA-Targeting Î±-Radiation Therapy Often Harbor Mutations in DNA Damage-Repairâ€"Associated Genes. Journal of Nuclear Medicine, 2020, 61, 683-688.	5.0	61
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	Taxonâ€and vectorâ€specific variation in species richness and abundance during the transport stage of biological invasions. Limnology and Oceanography, 2013, 58, 1361-1372.	3.1	44
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	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. European Urology Focus, 2021, 7, 325-331.	3.1	34
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	Targeted molecular profiling reveals genetic heterogeneity of poromas and porocarcinomas. Pathology, 2018, 50, 327-332.	0.6	27
17	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
18	Combined Immunohistochemistry after Mass Spectrometry Imaging for Superior Spatial Information. Proteomics - Clinical Applications, 2019, 13, e1800035.	1.6	23

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19	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
20	Targeted nextâ€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
21	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
22	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
23	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
24	Integrating proteomics into precision oncology. International Journal of Cancer, 2021, 148, 1438-1451.	5.1	15
25	Assigning evidence to actionability: An introduction to variant interpretation in precision cancer medicine. Genes Chromosomes and Cancer, 2022, 61, 303-313.	2.8	15
26	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
27	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
28	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
29	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
30	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
31	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
32	Expression of HMB45, MelanA and SOX10 is rare in non-small cell lung cancer. Diagnostic Pathology, 2018, 13, 68.	2.0	8
33	Targeting rare and non-canonical driver variants in NSCLC â€“ An uncharted clinical field. Lung Cancer, 2021, 154, 131-141.	2.0	8
34	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
35	Conventional and semi-automatic histopathological analysis of tumor cell content for multigene sequencing of lung adenocarcinoma. Translational Lung Cancer Research, 2021, 10, 1666-1678.	2.8	6
36	Analysis of the proliferative activity in lung adenocarcinomas with specific driver mutations. Pathology Research and Practice, 2018, 214, 408-416.	2.3	4

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37	Oncogene-induced senescence: a potential breakpoint mechanism against malignant transformation in plasma cell disorders. Leukemia and Lymphoma, 2018, 59, 2660-2669.	1.3	3