Olaf Neumann

List of Publications by Year
in descending order

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26	1,388	516710 16	552781 26
papers	citations	h-index	g-index

26	26	26	2496
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrative analysis reveals early and distinct genetic and epigenetic changes in intraductal papillary and tubulopapillary cholangiocarcinogenesis. Gut, 2022, 71, 391-401.	12.1	21
2	Assigning evidence to actionability: An introduction to variant interpretation in precision cancer medicine. Genes Chromosomes and Cancer, 2022, 61, 303-313.	2.8	15
3	Prognostic impact of copy number alterations and tumor mutational burden in carcinoma of unknown primary. Genes Chromosomes and Cancer, 2022, 61, 551-560.	2.8	4
4	Pan-cancer analysis of genomic scar patterns caused by homologous repair deficiency (HRD). Npj Precision Oncology, 2022, 6, .	5.4	23
5	Accurate and efficient detection of gene fusions from RNA sequencing data. Genome Research, 2021, 31, 448-460.	5.5	215
6	Targeting rare and non-canonical driver variants in NSCLC â€“ An uncharted clinical field. Lung Cancer, 2021, 154, 131-141.	2.0	8
7	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. Cancer Discovery, 2021, 11, 2780-2795.	9.4	125
8	Local ablative treatment with surgery and/or radiotherapy in single-site and oligometastatic carcinoma of unknown primary. European Journal of Cancer, 2021, 157, 179-189.	2.8	13
9	Identification and characterization of a BRAF fusion oncoprotein with retained autoinhibitory domains. Oncogene, 2020, 39, 814-832.	5.9	19
10	Primary pulmonary myxoid sarcoma with an unusual gene fusion between exon 7 of EWSR1 and exon 5 of CREB1. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2020, 476, 787-791.	2.8	7
11	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
12	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
13	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
14	RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. Cancers, 2019, 11, 1309.	3.7	32
15	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
16	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
17	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	5.1	76
18	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

#	Article	IF	Citations
19	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
20	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
21	Size matters: Dissecting key parameters for panelâ€based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858.	5.1	131
22	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
23	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
24	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
25	Protumorigenic role of Timeless in hepatocellular carcinoma. International Journal of Oncology, 2015, 46, 597-606.	3.3	32
26	Methylome analysis and integrative profiling of human HCCs identify novel protumorigenic factors. Hepatology, 2012, 56, 1817-1827.	7.3	136