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List of Publications by Year
in descending order

Version: 2024-02-01

37 papers	1,369 citations	361045 20 h-index	344852 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. Genes Chromosomes and Cancer, 2022, 61, 303-313.	1.5	15
2	Integrating proteomics into precision oncology. International Journal of Cancer, 2021, 148, 1438-1451.	2.3	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. European Urology Focus, 2021, 7, 325-331.	1.6	34
4	Targeting rare and non-canonical driver variants in NSCLC â€“ An uncharted clinical field. Lung Cancer, 2021, 154, 131-141.	0.9	8
5	Conventional and semi-automatic histopathological analysis of tumor cell content for multigene sequencing of lung adenocarcinoma. Translational Lung Cancer Research, 2021, 10, 1666-1678.	1.3	6
6	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.	2.8	61
7	Testing NTRK testing: Wetâ€lab and in silico comparison of RNAâ€based targeted sequencing assays. Genes Chromosomes and Cancer, 2020, 59, 178-188.	1.5	52
8	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.	2.3	14
9	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.	0.8	12
10	Combined Immunohistochemistry after Mass Spectrometry Imaging for Superior Spatial Information. Proteomics - Clinical Applications, 2019, 13, e1800035.	0.8	23
11	RNA-Based Detection of Gene Fusions in Formalin-Fixed and Paraffin-Embedded Solid Cancer Samples. Cancers, 2019, 11, 1309.	1.7	32
12	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.	0.5	69
13	Targeted Therapy in Advanced Melanoma With Rare BRAF Mutations. Journal of Clinical Oncology, 2019, 37, 3142-3151.	0.8	83
14	Detection of TP53 Mutations in Tissue or Liquid Rebiopsies at Progression Identifies ALK+ Lung Cancer Patients with Poor Survival. Cancers, 2019, 11, 124.	1.7	36
15	Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010.	2.3	76
16	Comparative genetic profiling aids diagnosis and clinical decision making in challenging cases of CUP syndrome. International Journal of Cancer, 2019, 145, 2963-2973.	2.3	24
17	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.	2.3	95
18	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.	2.3	85

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19	Size matters: Dissecting key parameters for panelâ€based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858.	2.3	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.	1.5	14
21	Oncogene-induced senescence: a potential breakpoint mechanism against malignant transformation in plasma cell disorders. Leukemia and Lymphoma, 2018, 59, 2660-2669.	0.6	3
22	Analysis of the proliferative activity in lung adenocarcinomas with specific driver mutations. Pathology Research and Practice, 2018, 214, 408-416.	1.0	4
23	Targeted molecular profiling reveals genetic heterogeneity of poromas and porocarcinomas. Pathology, 2018, 50, 327-332.	0.3	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.	1.5	19
25	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.	1.5	20
26	Implementing tumor mutational burden (TMB) analysis in routine diagnosticsâ€”a primer for molecular pathologists and clinicians. Translational Lung Cancer Research, 2018, 7, 703-715.	1.3	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.	0.3	21
28	Expression of HMB45, MelanA and SOX10 is rare in non-small cell lung cancer. Diagnostic Pathology, 2018, 13, 68.	0.9	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.	2.3	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.	1.5	21
31	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.	1.5	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.	1.5	8
33	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.	1.5	27
34	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.	1.5	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.	0.9	8
36	Taxonâ€and vectorâ€specific variation in species richness and abundance during the transport stage of biological invasions. Limnology and Oceanography, 2013, 58, 1361-1372.	1.6	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.	2.3	11