

Ivo Buchhalter

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

5,780
citations

304743

22
h-index

501196

28
g-index

30
all docs

30
docs citations

30
times ranked

10560
citing authors

#	ARTICLE	IF	CITATIONS
1	Outcomes by Clinical and Molecular Features in Children With Medulloblastoma Treated With Risk-Adapted Therapy: Results of an International Phase III Trial (SJMB03). <i>Journal of Clinical Oncology</i> , 2021, 39, 822-835.	1.6	106
2	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. <i>Cancer Discovery</i> , 2021, 11, 2780-2795.	9.4	125
3	Genomic Characterization of Cholangiocarcinoma in Primary Sclerosing Cholangitis Reveals Therapeutic Opportunities. <i>Hepatology</i> , 2020, 72, 1253-1266.	7.3	42
4	Framework for quality assessment of whole genome cancer sequences. <i>Nature Communications</i> , 2020, 11, 5040.	12.8	5
5	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. <i>Nature</i> , 2020, 580, 396-401.	27.8	94
6	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020, 38, 288-292.	17.5	11
7	The molecular landscape of ETMR at diagnosis and relapse. <i>Nature</i> , 2019, 576, 274-280.	27.8	94
8	Measurement of tumor mutational burden (TMB) in routine molecular diagnostics: <i>in silico</i> and real-life analysis of three larger gene panels. <i>International Journal of Cancer</i> , 2019, 144, 2303-2312.	5.1	95
9	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
10	Size matters: Dissecting key parameters for panel-based tumor mutational burden analysis. <i>International Journal of Cancer</i> , 2019, 144, 848-858.	5.1	131
11	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018, 555, 321-327.	27.8	1,068
12	Deep sequencing of WNT-activated medulloblastomas reveals secondary SHH pathway activation. <i>Acta Neuropathologica</i> , 2018, 135, 635-638.	7.7	17
13	<i>EML4-ALK</i> fusion variant V3 is a high-risk feature conferring accelerated metastatic spread, early treatment failure and worse overall survival in <i>ALK</i> non-small cell lung cancer. <i>International Journal of Cancer</i> , 2018, 142, 2589-2598.	5.1	93
14	Targeted molecular profiling reveals genetic heterogeneity of poromas and porocarcinomas. <i>Pathology</i> , 2018, 50, 327-332.	0.6	27
15	Validating Comprehensive Next-Generation Sequencing Results for Precision Oncology: The NCT/DTK Molecularly Aided Stratification for Tumor Eradication Research Experience. <i>JCO Precision Oncology</i> , 2018, 2, 1-13.	3.0	20
16	Genetic profiling of melanoma in routine diagnostics: assay performance and molecular characteristics in a consecutive series of 274 cases. <i>Pathology</i> , 2018, 50, 703-710.	0.6	21
17	Risk-adapted therapy for young children with medulloblastoma (SJYC07): therapeutic and molecular outcomes from a multicentre, phase 2 trial. <i>Lancet Oncology</i> , The, 2018, 19, 768-784.	10.7	151
18	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology</i> , The, 2018, 19, 785-798.	10.7	268

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19	Meningiomas induced by low-dose radiation carry structural variants of NF2 and a distinct mutational signature. <i>Acta Neuropathologica</i> , 2017, 134, 155-158.	7.7	26
20	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. <i>Journal of Experimental Medicine</i> , 2017, 214, 2073-2088.	8.5	30
21	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	27.8	787
22	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. <i>OncImmunology</i> , 2016, 5, e1213931.	4.6	14
23	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. <i>Nature</i> , 2016, 530, 57-62.	27.8	318
24	Next-generation sequencing in routine brain tumor diagnostics enables an integrated diagnosis and identifies actionable targets. <i>Acta Neuropathologica</i> , 2016, 131, 903-910.	7.7	203
25	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. <i>Cancer Cell</i> , 2016, 29, 379-393.	16.8	438
26	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. <i>Cell</i> , 2016, 164, 1060-1072.	28.9	702
27	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	12.8	266
28	Enhancer hijacking activates GF11 family oncogenes in medulloblastoma. <i>Nature</i> , 2014, 511, 428-434.	27.8	520