Ivo Buchhalter

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7546728/publications.pdf

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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	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	27.8	1,068
2	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
3	New Brain Tumor Entities Emerge from Molecular Classification of CNS-PNETs. Cell, 2016, 164, 1060-1072.	28.9	702
4	Enhancer hijacking activates GFI1 family oncogenes in medulloblastoma. Nature, 2014, 511, 428-434.	27.8	520
5	Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. Cancer Cell, 2016, 29, 379-393.	16.8	438
6	Active medulloblastoma enhancers reveal subgroup-specific cellular origins. Nature, 2016, 530, 57-62.	27.8	318
7	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. Lancet Oncology, The, 2018, 19, 785-798.	10.7	268
8	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	12.8	266
9	Next-generation sequencing in routine brain tumor diagnostics enables an integrated diagnosis and identifies actionable targets. Acta Neuropathologica, 2016, 131, 903-910.	7.7	203
10	Risk-adapted therapy for young children with medulloblastoma (SJYC07): therapeutic and molecular outcomes from a multicentre, phase 2 trial. Lancet Oncology, The, 2018, 19, 768-784.	10.7	151
11	Size matters: Dissecting key parameters for panelâ€based tumor mutational burden analysis. International Journal of Cancer, 2019, 144, 848-858.	5.1	131
12	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. Cancer Discovery, 2021, 11, 2780-2795.	9.4	125
13	Outcomes by Clinical and Molecular Features in Children With Medulloblastoma Treated With Risk-Adapted Therapy: Results of an International Phase III Trial (SJMB03). Journal of Clinical Oncology, 2021, 39, 822-835.	1.6	106
14	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
15	The molecular landscape of ETMR at diagnosis and relapse. Nature, 2019, 576, 274-280.	27.8	94
16	Germline Elongator mutations in Sonic Hedgehog medulloblastoma. Nature, 2020, 580, 396-401.	27.8	94
17	EML4â€ALK fusion variant V3 is a highâ€risk feature conferring accelerated metastatic spread, early treatment failure and worse overall survival in ALK⁺ nonâ€small cell lung cancer. International Journal of Cancer, 2018, 142, 2589-2598.	5.1	93
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.	5.1	85

#	Article	IF	Citations
19	Genomic Characterization of Cholangiocarcinoma in Primary Sclerosing Cholangitis Reveals Therapeutic Opportunities. Hepatology, 2020, 72, 1253-1266.	7.3	42
20	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	8.5	30
21	Targeted molecular profiling reveals genetic heterogeneity of poromas and porocarcinomas. Pathology, 2018, 50, 327-332.	0.6	27
22	Meningiomas induced by low-dose radiation carry structural variants of NF2 and a distinct mutational signature. Acta Neuropathologica, 2017, 134, 155-158.	7.7	26
23	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
24	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
25	Deep sequencing of WNT-activated medulloblastomas reveals secondary SHH pathway activation. Acta Neuropathologica, 2018, 135, 635-638.	7.7	17
26	Identification of immunotherapeutic targets by genomic profiling of rectal NET metastases. OncoImmunology, 2016, 5, e1213931.	4.6	14
27	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	17.5	11
28	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	12.8	5