Daniel Huebschmann

List of Publications by Year
in descending order

49 papers	4,381 citations	257101 24 h-index	205818 48 g-index
63 all docs	63 docs citations	63 times ranked	8474 citing authors

#	Article	IF	Citations
1	Focal structural variants revealed by whole genome sequencing disrupt the histone demethylase KDM4C in B-cell lymphomas. Haematologica, 2023, 108, 543-554.	1.7	2
2	*spiralize*: an R package for visualizing data on spirals. Bioinformatics, 2022, 38, 1434-1436.	1.8	6
3	Comprehensive genomic analysis of refractory multiple myeloma reveals a complex mutational landscape associated with drug resistance and novel therapeutic vulnerabilities. Haematologica, 2022, 107, 1891-1901.	1.7	15
4	The proteogenomic subtypes of acute myeloid leukemia. Cancer Cell, 2022, 40, 301-317.e12.	7.7	43
5	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	5.8	52
6	Human activation-induced deaminase lacks strong replicative strand bias or preference for cytosines in hairpin loops. Nucleic Acids Research, 2022, 50, 5145-5157.	6.5	8
7	Antigen presentation safeguards the integrity of the hematopoietic stem cell pool. Cell Stem Cell, 2022, 29, 760-775.e10.	5.2	29
8	<scp>MGMT</scp> inactivation as a new biomarker in patients with advanced biliary tract cancers. Molecular Oncology, 2022, 16, 2733-2746.	2.1	2
9	TBIO-04. Comprehensive analysis of mutational signatures in pediatric cancers. Neuro-Oncology, 2022, 24, i183-i183.	0.6	0
10	*Pkgndep*: a tool for analyzing dependency heaviness of R packages. Bioinformatics, 2022, 38, 4248-4251.	1.8	2
11	Gene expression-based prediction of pazopanib efficacy in sarcoma. European Journal of Cancer, 2022, 172, 107-118.	1.3	0
12	Analysis of mutational signatures with yet another package for signature analysis. Genes Chromosomes and Cancer, 2021, 60, 314-331.	1.5	40
13	*cola*: an R/Bioconductor package for consensus partitioning through a general framework. Nucleic Acids Research, 2021, 49, e15-e15.	6.5	32
14	Poly(<scp>ADP</scp>â€¬ibose) polymerase inhibition in pancreatic cancer. Genes Chromosomes and Cancer, 2021, 60, 373-384.	1.5	11
15	Case Report: Abdominal Lymph Node Metastases of Parathyroid Carcinoma: Diagnostic Workup, Molecular Diagnosis, and Clinical Management. Frontiers in Endocrinology, 2021, 12, 643328.	1.5	12
16	Swarm Learning for decentralized and confidential clinical machine learning. Nature, 2021, 594, 265-270.	13.7	375
17	Carbon ion radiotherapy eradicates medulloblastomas with chromothripsis in an orthotopic Li-Fraumeni patient-derived mouse model. Neuro-Oncology, 2021, 23, 2028-2041.	0.6	7
18	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	3.3	34

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19	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. Cancer Discovery, 2021, 11, 2780-2795.	7.7	125
20	RSPO2 inhibits BMP signaling to promote self-renewal in acute myeloid leukemia. Cell Reports, 2021, 36, 109559.	2.9	10
21	Single-cell proteo-genomic reference maps of the hematopoietic system enable the purification and massive profiling of precisely defined cell states. Nature Immunology, 2021, 22, 1577-1589.	7.0	76
22	Genetic Interactions and Tissue Specificity Modulate the Association of Mutations with Drug Response. Molecular Cancer Therapeutics, 2020, 19, 927-936.	1.9	5
23	Detection of Structural Variants in Circulating Cell-Free DNA from Sarcoma Patients Using Next Generation Sequencing. Cancers, 2020, 12, 3627.	1.7	7
24	The landscape of chromothripsis across adult cancer types. Nature Communications, 2020, 11, 2320.	5.8	75
25	Germline <i>SDHB</i>â€‘inactivating mutation in gastric spindle cell sarcoma. Genes Chromosomes and Cancer, 2020, 59, 601-608.	1.5	4
26	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	9.4	11
27	Comprehensive Comparison of Early Relapse and End-Stage Relapsed Refractory Multiple Myeloma. Blood, 2020, 136, 1-1.	0.6	4
28	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. Biology Methods and Protocols, 2020, 5, bpaa022.	1.0	11
29	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. Acta Neuropathologica, 2019, 138, 295-308.	3.9	74
30	Response to olaparib in a <i>PALB2</i> germline mutated prostate cancer and genetic events associated with resistance. Journal of Physical Education and Sports Management, 2019, 5, a003657.	0.5	36
31	Evolutionary Trajectories of IDHWT Glioblastomas Reveal a Common Path of Early Tumorigenesis Instigated Years ahead of Initial Diagnosis. Cancer Cell, 2019, 35, 692-704.e12.	7.7	172
32	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. Nature Communications, 2019, 10, 1635.	5.8	64
33	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	5.8	99
34	Evaluation of Whole Genome Sequencing Data. Methods in Molecular Biology, 2019, 1956, 321-336.	0.4	6
35	Community-driven development of a modified progression-free survival ratio for precision oncology. ESMO Open, 2019, 4, e000583.	2.0	22
36	The mutational landscape of Burkitt-like lymphoma with 11q aberration is distinct from that of Burkitt lymphoma. Blood, 2019, 133, 962-966.	0.6	69

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37	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	13.7	1,068
38	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	5.8	197
39	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. Nature Communications, 2018, 9, 4782.	5.8	103
40	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	7.7	190
41	IG-MYC+ neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. Blood, 2018, 132, 2280-2285.	0.6	50
42	Genomic features of renal cell carcinoma with venous tumor thrombus. Scientific Reports, 2018, 8, 7477.	1.6	19
43	Meningiomas induced by low-dose radiation carry structural variants of NF2 and a distinct mutational signature. Acta Neuropathologica, 2017, 134, 155-158.	3.9	26
44	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	2.3	133
45	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	4.2	30
46	Newborn screening for severe combined immunodeficiency using a novel and simplified method to measure T-cell excision circles (TREC). Clinical Immunology, 2017, 175, 51-55.	1.4	20
47	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	13.7	787
48	Integration of genomics and histology revises diagnosis and enables effective therapy of refractory cancer of unknown primary with *PDL1* amplification. Journal of Physical Education and Sports Management, 2016, 2, a001180.	0.5	57
49	Spatial niche formation but not malignant progression is a driving force for intratumoural heterogeneity. Nature Communications, 2016, 7, ncomms11845.	5.8	44