Daniel Huebschmann

List of Publications by Year
in descending order

49 papers	4,381 citations	257357 24 h-index	206029 48 g-index
63 all docs	63 docs citations	63 times ranked	8474 citing authors

#	Article	IF	Citations
1	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	13.7	1,068
2	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	13.7	787
3	Swarm Learning for decentralized and confidential clinical machine learning. Nature, 2021, 594, 265-270.	13.7	375
4	Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144.	5.8	197
5	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	7.7	190
6	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
7	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	2.3	133
8	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. Cancer Discovery, 2021, 11, 2780-2795.	7.7	125
9	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. Nature Communications, 2018, 9, 4782.	5.8	103
10	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	5.8	99
11	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
12	The landscape of chromothripsis across adult cancer types. Nature Communications, 2020, 11, 2320.	5.8	75
13	Mutational patterns and regulatory networks in epigenetic subgroups of meningioma. Acta Neuropathologica, 2019, 138, 295-308.	3.9	74
14	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
15	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. Nature Communications, 2019, 10, 1635.	5.8	64
16	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
17	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	5.8	52
18	IG-MYC+ neoplasms with precursor B-cell phenotype are molecularly distinct from Burkitt lymphomas. Blood, 2018, 132, 2280-2285.	0.6	50

#	ARTICLE	IF	CITATIONS
19	Spatial niche formation but not malignant progression is a driving force for intratumoural heterogeneity. Nature Communications, 2016, 7, ncomms11845.	5.8	44
20	The proteogenomic subtypes of acute myeloid leukemia. Cancer Cell, 2022, 40, 301-317.e12.	7.7	43
21	Analysis of mutational signatures with yet another package for signature analysis. Genes Chromosomes and Cancer, 2021, 60, 314-331.	1.5	40
22	Response to olaparib in a *PALB2* germline mutated prostate cancer and genetic events associated with resistance. Journal of Physical Education and Sports Management, 2019, 5, a003657.	0.5	36
23	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	3.3	34
24	*cola*: an R/Bioconductor package for consensus partitioning through a general framework. Nucleic Acids Research, 2021, 49, e15-e15.	6.5	32
25	Genetic subclone architecture of tumor clone-initiating cells in colorectal cancer. Journal of Experimental Medicine, 2017, 214, 2073-2088.	4.2	30
26	Antigen presentation safeguards the integrity of the hematopoietic stem cell pool. Cell Stem Cell, 2022, 29, 760-775.e10.	5.2	29
27	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
28	Community-driven development of a modified progression-free survival ratio for precision oncology. ESMO Open, 2019, 4, e000583.	2.0	22
29	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
30	Genomic features of renal cell carcinoma with venous tumor thrombus. Scientific Reports, 2018, 8, 7477.	1.6	19
31	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
32	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
33	Poly(ADP‑ribose) polymerase inhibition in pancreatic cancer. Genes Chromosomes and Cancer, 2021, 60, 373-384.	1.5	11
34	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	9.4	11
35	ShinyButchR: Interactive NMF-based decomposition workflow of genome-scale datasets. Biology Methods and Protocols, 2020, 5, bpaa022.	1.0	11
36	RSPO2 inhibits BMP signaling to promote self-renewal in acute myeloid leukemia. Cell Reports, 2021, 36, 109559.	2.9	10

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37	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
38	Detection of Structural Variants in Circulating Cell-Free DNA from Sarcoma Patients Using Next Generation Sequencing. Cancers, 2020, 12, 3627.	1.7	7
39	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
40	Evaluation of Whole Genome Sequencing Data. Methods in Molecular Biology, 2019, 1956, 321-336.	0.4	6
41	<i>spiralize</i>: an R package for visualizing data on spirals. Bioinformatics, 2022, 38, 1434-1436.	1.8	6
42	Genetic Interactions and Tissue Specificity Modulate the Association of Mutations with Drug Response. Molecular Cancer Therapeutics, 2020, 19, 927-936.	1.9	5
43	Germline <i>SDHB</i> â€‘inactivating mutation in gastric spindle cell sarcoma. Genes Chromosomes and Cancer, 2020, 59, 601-608.	1.5	4
44	Comprehensive Comparison of Early Relapse and End-Stage Relapsed Refractory Multiple Myeloma. Blood, 2020, 136, 1-1.	0.6	4
45	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
46	<scp>MGMT</scp> inactivation as a new biomarker in patients with advanced biliary tract cancers. Molecular Oncology, 2022, 16, 2733-2746.	2.1	2
47	<i>Pkgndep</i>: a tool for analyzing dependency heaviness of R packages. Bioinformatics, 2022, 38, 4248-4251.	1.8	2
48	TBIO-04. Comprehensive analysis of mutational signatures in pediatric cancers. Neuro-Oncology, 2022, 24, i183-i183.	0.6	0
49	Gene expression-based prediction of pazopanib efficacy in sarcoma. European Journal of Cancer, 2022, 172, 107-118.	1.3	0