

Barbara Hutter

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

14,104
citations

236612

25
h-index

301761

39
g-index

44
all docs

44
docs citations

44
times ranked

26944
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-exome sequencing in eccrine porocarcinoma indicates promising therapeutic strategies. <i>Cancer Gene Therapy</i> , 2022, 29, 697-708.	2.2	10
2	TBIO-04. Comprehensive analysis of mutational signatures in pediatric cancers. <i>Neuro-Oncology</i> , 2022, 24, i183-i183.	0.6	0
3	Ruxolitinib is effective in the treatment of a patient with refractory Tâ€ALL. <i>EJHaem</i> , 2021, 2, 139-142.	0.4	4
4	Accurate and efficient detection of gene fusions from RNA sequencing data. <i>Genome Research</i> , 2021, 31, 448-460.	2.4	215
5	Response to Cabozantinib Following Acquired Entrectinib Resistance in a Patient With <i>ETV6-NTRK3</i> Fusion-Positive Carcinoma Harboring the <i>NTRK3</i> ^{G623R} Solvent-Front Mutation. <i>JCO Precision Oncology</i> , 2021, 5, 687-694.	1.5	3
6	CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. <i>JCO Precision Oncology</i> , 2021, 5, 676-686.	1.5	20
7	Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. <i>Cancer Discovery</i> , 2021, 11, 2780-2795.	7.7	125
8	High tumour mutational burden and EGFR/MAPK pathway activation are therapeutic targets in metastatic porocarcinoma. <i>British Journal of Dermatology</i> , 2021, , .	1.4	6
9	Rationale and design of the CRAFT (Continuous ReAssessment with Flexible ExTension in Rare) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.0	6
10	Identification and characterization of a BRAF fusion oncoprotein with retained autoinhibitory domains. <i>Oncogene</i> , 2020, 39, 814-832.	2.6	19
11	Framework for quality assessment of whole genome cancer sequences. <i>Nature Communications</i> , 2020, 11, 5040.	5.8	5
12	Successful BRAF/MEK inhibition in a patient with <i>BRAF</i> ^{V600E} -mutated extrapancreatic acinar cell carcinoma. <i>Journal of Physical Education and Sports Management</i> , 2020, 6, a005553.	0.5	13
13	The landscape of chromothripsis across adult cancer types. <i>Nature Communications</i> , 2020, 11, 2320.	5.8	75
14	Germline <i>SDHB</i> inactivating mutation in gastric spindle cell sarcoma. <i>Genes Chromosomes and Cancer</i> , 2020, 59, 601-608.	1.5	4
15	Comprehensive genomic characterization of gene therapy-induced T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2020, 34, 2785-2789.	3.3	4
16	Metastatic adult pancreatoblastoma: Multimodal treatment and molecular characterization of a very rare disease. <i>Pancreatology</i> , 2020, 20, 425-432.	0.5	11
17	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020, 11, 733.	5.8	87
18	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	9.4	431

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19	Targetable ERBB2 mutations identified in neurofibroma/schwannoma hybrid nerve sheath tumors. <i>Journal of Clinical Investigation</i> , 2020, 130, 2488-2495.	3.9	23
20	TelomereHunter “ in silico estimation of telomere content and composition from cancer genomes. <i>BMC Bioinformatics</i> , 2019, 20, 272.	1.2	56
21	Variant classification in precision oncology. <i>International Journal of Cancer</i> , 2019, 145, 2996-3010.	2.3	76
22	Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. <i>Nature Communications</i> , 2019, 10, 1635.	5.8	64
23	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , 2018, 555, 321-327.	13.7	1,068
24	Integrative genomic and transcriptomic analysis of leiomyosarcoma. <i>Nature Communications</i> , 2018, 9, 144.	5.8	197
25	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.	1.5	20
26	Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. <i>Nature Communications</i> , 2018, 9, 4782.	5.8	103
27	<i>NRG1</i> Fusions in <i>KRAS</i> Wild-Type Pancreatic Cancer. <i>Cancer Discovery</i> , 2018, 8, 1087-1095.	7.7	189
28	Precision oncology based on omics data: The NCT Heidelberg experience. <i>International Journal of Cancer</i> , 2017, 141, 877-886.	2.3	133
29	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , 2017, 547, 311-317.	13.7	787
30	Targeting Fibroblast Growth Factor Receptor 1 for Treatment of Soft-Tissue Sarcoma. <i>Clinical Cancer Research</i> , 2017, 23, 962-973.	3.2	29
31	Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. <i>Annals of Oncology</i> , 2017, 28, 142-148.	0.6	30
32	Next-generation personalised medicine for high-risk paediatric cancer patients “ The INFORM pilot study. <i>European Journal of Cancer</i> , 2016, 65, 91-101.	1.3	262
33	Integration of genomics and histology revises diagnosis and enables effective therapy of refractory cancer of unknown primary with <i>PDL1</i> amplification. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a001180.	0.5	57
34	Cooperation of BRAFF595L and mutant HRAS in histiocytic sarcoma provides new insights into oncogenic BRAF signaling. <i>Leukemia</i> , 2016, 30, 937-946.	3.3	52
35	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	5.8	266
36	BRAF inhibitor“ associated ERK activation drives development of chronic lymphocytic leukemia. <i>Journal of Clinical Investigation</i> , 2014, 124, 5074-5084.	3.9	56

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37	Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932.	9.4	674
38	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
39	Coverage Bias and Sensitivity of Variant Calling for Four Whole-genome Sequencing Technologies. PLoS ONE, 2013, 8, e66621.	1.1	74
40	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	13.7	765