# Barbara Hutter

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6718441/publications.pdf

Version: 2024-02-01

| 40 | 14,104 | 236612 | 301761 |
|---|---|---|---|
| papers | citations | 25 h-index | 39 g-index |

| 44 | 44 | 44 | 26944 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421. | 13.7 | 8,060 |
| 2 | The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327. | 13.7 | 1,068 |
| 3 | The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317. | 13.7 | 787 |
| 4 | Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105. | 13.7 | 765 |
| 5 | Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. Nature Genetics, 2013, 45, 927-932. | 9.4 | 674 |
| 6 | Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341. | 9.4 | 431 |
| 7 | A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001. | 5.8 | 266 |
| 8 | Next-generation personalised medicine for high-risk paediatric cancer patients â€“ The INFORM pilot study. European Journal of Cancer, 2016, 65, 91-101. | 1.3 | 262 |
| 9 | Accurate and efficient detection of gene fusions from RNA sequencing data. Genome Research, 2021, 31, 448-460. | 2.4 | 215 |
| 10 | Integrative genomic and transcriptomic analysis of leiomyosarcoma. Nature Communications, 2018, 9, 144. | 5.8 | 197 |
| 11 | NRG1 Fusions in KRAS Wild-Type Pancreatic Cancer. Cancer Discovery, 2018, 8, 1087-1095. | 7.7 | 189 |
| 12 | Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886. | 2.3 | 133 |
| 13 | Comprehensive Genomic and Transcriptomic Analysis for Guiding Therapeutic Decisions in Patients with Rare Cancers. Cancer Discovery, 2021, 11, 2780-2795. | 7.7 | 125 |
| 14 | Whole genome sequencing puts forward hypotheses on metastasis evolution and therapy in colorectal cancer. Nature Communications, 2018, 9, 4782. | 5.8 | 103 |
| 15 | Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733. | 5.8 | 87 |
| 16 | Variant classification in precision oncology. International Journal of Cancer, 2019, 145, 2996-3010. | 2.3 | 76 |
| 17 | The landscape of chromothripsis across adult cancer types. Nature Communications, 2020, 11, 2320. | 5.8 | 75 |
| 18 | Coverage Bias and Sensitivity of Variant Calling for Four Whole-genome Sequencing Technologies. PLoS ONE, 2013, 8, e66621. | 1.1 | 74 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Defective homologous recombination DNA repair as therapeutic target in advanced chordoma. Nature Communications, 2019, 10, 1635. | 5.8 | 64 |
| 20 | 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 |
| 21 | BRAF inhibitorâ€“associated ERK activation drives development of chronic lymphocytic leukemia. Journal of Clinical Investigation, 2014, 124, 5074-5084. | 3.9 | 56 |
| 22 | TelomereHunter â€“ in silico estimation of telomere content and composition from cancer genomes. BMC Bioinformatics, 2019, 20, 272. | 1.2 | 56 |
| 23 | Cooperation of BRAFF595L and mutant HRAS in histiocytic sarcoma provides new insights into oncogenic BRAF signaling. Leukemia, 2016, 30, 937-946. | 3.3 | 52 |
| 24 | Mutant KIT as imatinib-sensitive target in metastatic sinonasal carcinoma. Annals of Oncology, 2017, 28, 142-148. | 0.6 | 30 |
| 25 | Targeting Fibroblast Growth Factor Receptor 1 for Treatment of Soft-Tissue Sarcoma. Clinical Cancer Research, 2017, 23, 962-973. | 3.2 | 29 |
| 26 | Targetable ERBB2 mutations identified in neurofibroma/schwannoma hybrid nerve sheath tumors. Journal of Clinical Investigation, 2020, 130, 2488-2495. | 3.9 | 23 |
| 27 | 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. | 1.5 | 20 |
| 28 | CATCH: A Prospective Precision Oncology Trial in Metastatic Breast Cancer. JCO Precision Oncology, 2021, 5, 676-686. | 1.5 | 20 |
| 29 | Identification and characterization of a BRAF fusion oncoprotein with retained autoinhibitory domains. Oncogene, 2020, 39, 814-832. | 2.6 | 19 |
| 30 | Successful BRAF/MEK inhibition in a patient with BRAF<sup>V600E</sup>-mutated extrapancreatic acinar cell carcinoma. Journal of Physical Education and Sports Management, 2020, 6, a005553. | 0.5 | 13 |
| 31 | Metastatic adult pancreatoblastoma: Multimodal treatment and molecular characterization of a very rare disease. Pancreatology, 2020, 20, 425-432. | 0.5 | 11 |
| 32 | Whole-exome sequencing in eccrine porocarcinoma indicates promising therapeutic strategies. Cancer Gene Therapy, 2022, 29, 697-708. | 2.2 | 10 |
| 33 | High tumour mutational burden and EGFR/MAPK pathway activation are therapeutic targets in metastatic porocarcinoma. British Journal of Dermatology, 2021, , . | 1.4 | 6 |
| 34 | Rationale and design of the CRAFT (Continuous ReAssessment with Flexible ExTension in Rare) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 | 2.0 | 6 |
| 35 | Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040. | 5.8 | 5 |
| 36 | Germline SDHB â€inactivating mutation in gastric spindle cell sarcoma. Genes Chromosomes and Cancer, 2020, 59, 601-608. | 1.5 | 4 |

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|---|---|---|---|
| 37 | Comprehensive genomic characterization of gene therapy-induced T-cell acute lymphoblastic leukemia. Leukemia, 2020, 34, 2785-2789. | 3.3 | 4 |
| 38 | Ruxolitinib is effective in the treatment of a patient with refractory Tâ€ALL. EJHaem, 2021, 2, 139-142. | 0.4 | 4 |
| 39 | Response to Cabozantinib Following Acquired Entrectinib Resistance in a Patient WithETV6-NTRK3Fusion-Positive Carcinoma Harboring theNTRK3<sup>G623R</sup>Solvent-Front Mutation. JCO Precision Oncology, 2021, 5, 687-694. | 1.5 | 3 |
| 40 | TBIO-04. Comprehensive analysis of mutational signatures in pediatric cancers. Neuro-Oncology, 2022, 24, i183-i183. | 0.6 | 0 |