

# Birte MÃ¶hlendick

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

597  
citations

566801

15  
h-index

610482

24  
g-index

27  
all docs

27  
docs citations

27  
times ranked

968  
citing authors

#	ARTICLE	IF	CITATIONS
1	Patients with Liver Cirrhosis Show High Immunogenicity upon COVID-19 Vaccination but Develop Premature Deterioration of Antibody Titers. <i>Vaccines</i> , 2022, 10, 377.	2.1	30
2	NAT2 polymorphisms as a cause of metamizole-induced agranulocytosis. <i>Pharmacogenetics and Genomics</i> , 2021, Publish Ahead of Print, 140-143.	0.7	2
3	Transmembrane serine protease 2 Polymorphisms and Susceptibility to Severe Acute Respiratory Syndrome Coronavirus Type 2 Infection: A German Case-Control Study. <i>Frontiers in Genetics</i> , 2021, 12, 667231.	1.1	43
4	ACE2 polymorphism and susceptibility for SARS-CoV-2 infection and severity of COVID-19. <i>Pharmacogenetics and Genomics</i> , 2021, 31, 165-171.	0.7	73
5	The influence of IFITM3 polymorphisms on susceptibility to SARS-CoV-2 infection and severity of COVID-19. <i>Cytokine</i> , 2021, 142, 155492.	1.4	37
6	Development Of De Novo Donor-Specific HLA Antibodies and ABMR in Renal Transplant Patients Depends on CYP3A5 Genotype. <i>Transplantation</i> , 2021, Publish Ahead of Print, .	0.5	3
7	BRAF <sup>V600E</sup> mutation: A promising target in colorectal neuroendocrine carcinoma. <i>International Journal of Cancer</i> , 2019, 144, 1379-1390.	2.3	33
8	The <i>GNAS</i> SNP c.393C>T (rs7121) as a marker for disease progression and survival in cancer. <i>Pharmacogenomics</i> , 2019, 20, 553-562.	0.6	11
9	Diagnostic pathology of early systemic cancer: <i>ERBB2</i> gene amplification in single disseminated cancer cells determines patient survival in operable esophageal cancer. <i>International Journal of Cancer</i> , 2018, 142, 833-843.	2.3	15
10	Establishment and Characterization of a Novel Cell Line Derived from a Small Cell Neuroendocrine Carcinoma of the Anal Canal. <i>Neuroendocrinology</i> , 2018, 107, 246-256.	1.2	4
11	A streamlined workflow for single-cells genome-wide copy-number profiling by low-pass sequencing of LM-PCR whole-genome amplification products. <i>PLoS ONE</i> , 2018, 13, e0193689.	1.1	20
12	Disseminated tumour cells with highly aberrant genomes are linked to poor prognosis in operable oesophageal adenocarcinoma. <i>British Journal of Cancer</i> , 2017, 117, 725-733.	2.9	17
13	Preclinical assesement of survivin and XIAP as prognostic biomarkers and therapeutic targets in gastroenteropancreatic neuroendocrine neoplasia. <i>Oncotarget</i> , 2017, 8, 8369-8382.	0.8	17
14	Isolation of circulating tumor cells from pancreatic cancer by automated filtration. <i>Oncotarget</i> , 2017, 8, 86143-86156.	0.8	24
15	Peritoneal sarcomatosis: site of origin for the establishment of an in vitro and in vivo cell line model to study therapeutic resistance in dedifferentiated liposarcoma. <i>Tumor Biology</i> , 2016, 37, 2341-2351.	0.8	4
16	Unscrambling the genomic chaos of osteosarcoma reveals extensive transcript fusion, recurrent rearrangements and frequent novel TP53 aberrations. <i>Oncotarget</i> , 2016, 7, 5273-5288.	0.8	60
17	Abstract 2394: Scalable, rapid and affordable low-pass whole genome sequencing method for single-cell copy-number profiling on LM-PCR based WGA products. , 2016, , .		0
18	Serum microRNA profiles as prognostic or predictive markers in the multimodality treatment of patients with gastric cancer. <i>Oncology Letters</i> , 2015, 10, 869-874.	0.8	8

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19	Serum microRNA profiles as prognostic/predictive markers in the multimodality therapy of locally advanced adenocarcinomas of the gastroesophageal junction. <i>International Journal of Cancer</i> , 2015, 137, 230-237.	2.3	24
20	New Model for Gastroenteropancreatic Large-Cell Neuroendocrine Carcinoma: Establishment of Two Clinically Relevant Cell Lines. <i>PLoS ONE</i> , 2014, 9, e88713.	1.1	28
21	A New Workflow for Whole-Genome Sequencing of Single Human Cells. <i>Human Mutation</i> , 2014, 35, 1260-1270.	1.1	19
22	Analysis of Copy Number Alterations in Single Cells Using Microarray-Based Comparative Genomic Hybridization (aCGH). <i>Current Protocols in Cell Biology</i> , 2014, 65, 22.19.1-23.	2.3	10
23	Genomic High-Resolution Profiling of Single CKpos/CD45neg Flow-Sorting Purified Circulating Tumor Cells from Patients with Metastatic Breast Cancer. <i>Clinical Chemistry</i> , 2014, 60, 1290-1297.	1.5	74
24	A Robust Method to Analyze Copy Number Alterations of Less than 100 kb in Single Cells Using Oligonucleotide Array CGH. <i>PLoS ONE</i> , 2013, 8, e67031.	1.1	40
25	From primary to secondary cancer formation – models for disseminating cancer cells. <i>Drug Discovery Today: Disease Models</i> , 2011, 8, 75-79.	1.2	1