Peter Ulz

List of Publications by Year in Descending Order

41 papers	3,335 citations	24 h-index	45 g-index
45 ext. papers	3,901 ext. citations	9.2 avg, IF	4.99 L-index

#	Paper	IF	Citations
41	catenin regulates FOXP2 transcriptional activity via multiple binding sites. *FEBS Journal*, **2021**, 288, 3261-3284	5.7	3
40	Evaluation of a sensitive blood test for the detection of colorectal advanced adenomas in a prospective cohort using a multiomics approach.. *Journal of Clinical Oncology*, **2021**, 39, 43-43	2.2	0
39	Cell-free DNA analysis reveals POLR1D-mediated resistance to bevacizumab in colorectal cancer. *Genome Medicine*, **2020**, 12, 20	14.4	16
38	Untargeted Assessment of Tumor Fractions in Plasma for Monitoring and Prognostication from Metastatic Breast Cancer Patients Undergoing Systemic Treatment. *Cancers*, **2019**, 11,	6.6	11
37	Inference of transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection. *Nature Communications*, **2019**, 10, 4666	17.4	54
36	Genome-Wide Analysis of the Nucleosome Landscape in Individuals with Coffin-Siris Syndrome. *Cytogenetic and Genome Research*, **2019**, 159, 1-11	1.9	3
35	Genomic alterations in plasma DNA from patients with metastasized prostate cancer receiving abiraterone or enzalutamide. *International Journal of Cancer*, **2018**, 143, 1236-1248	7.5	33
34	Somatic mutations characterize preleukemic stem cells in acute myeloid leukemia. *Blood*, **2017**, 129, 2587-2591	2.2	27
33	Patient monitoring through liquid biopsies using circulating tumor DNA. *International Journal of Cancer*, **2017**, 141, 887-896	7.5	35
32	Autosomal Recessive Keratoderma-Ichthyosis-Deafness (ARKID) Syndrome Is Caused by VPS33B Mutations Affecting Rab Protein Interaction and Collagen Modification. *Journal of Investigative Dermatology*, **2017**, 137, 845-854	4.3	24
31	Single-Stranded DNA Library Preparation Does Not Preferentially Enrich Circulating Tumor DNA. *Clinical Chemistry*, **2017**, 63, 1656-1659	5.5	11
30	Expanded molecular profiling of myxofibrosarcoma reveals potentially actionable targets. *Modern Pathology*, **2017**, 30, 1698-1709	9.8	14
29	Inferring expressed genes by whole-genome sequencing of plasma DNA. *Nature Genetics*, **2016**, 48, 1273-8	36.3	171
28	Whole-genome plasma sequencing reveals focal amplifications as a driving force in metastatic prostate cancer. *Nature Communications*, **2016**, 7, 12008	17.4	98
27	Neueste technologische Entwicklungen f die Analyse von zirkulierender Tumor-DNA. *Medizinische Genetik*, **2016**, 28, 234-244	0.5	
26	mFast-SeqS as a Monitoring and Pre-screening Tool for Tumor-Specific Aneuploidy in Plasma DNA. *Advances in Experimental Medicine and Biology*, **2016**, 924, 147-155	3.6	13
25	Co-occurrence of MYC amplification and TP53 mutations in human cancer. *Nature Genetics*, **2016**, 48, 104-6	36.3	33

24	Non-invasive detection of genome-wide somatic copy number alterations by liquid biopsies. *Molecular Oncology*, **2016**, 10, 494-502	7.9	54
23	Detection of Circulating Tumor DNA in the Blood of Cancer Patients: An Important Tool in Cancer Chemoprevention. *Methods in Molecular Biology*, **2016**, 1379, 45-68	1.4	15
22	Exploring chromosomal abnormalities and genetic changes in uterine smooth muscle tumors. *Modern Pathology*, **2016**, 29, 1262-77	9.8	20
21	D2HGDH regulates alpha-ketoglutarate levels and dioxygenase function by modulating IDH2. *Nature Communications*, **2015**, 6, 7768	17.4	47
20	Rapid Identification of Plasma DNA Samples with Increased ctDNA Levels by a Modified FAST-SeqS Approach. *Clinical Chemistry*, **2015**, 61, 838-49	5.5	76
19	Circulating tumor DNA as a liquid biopsy for cancer. *Clinical Chemistry*, **2015**, 61, 112-23	5.5	531
18	The dynamic range of circulating tumor DNA in metastatic breast cancer. *Breast Cancer Research*, **2014**, 16, 421	8.3	93
17	Germline variants in the SEMA4A gene predispose to familial colorectal cancer type X. *Nature Communications*, **2014**, 5, 5191	17.4	47
16	Changes in colorectal carcinoma genomes under anti-EGFR therapy identified by whole-genome plasma DNA sequencing. *PLoS Genetics*, **2014**, 10, e1004271	6	132
15	Tumor-associated copy number changes in the circulation of patients with prostate cancer identified through whole-genome sequencing. *Genome Medicine*, **2013**, 5, 30	14.4	246
14	Circulating tumor cells and DNA as liquid biopsies. *Genome Medicine*, **2013**, 5, 73	14.4	99
13	Establishment of tumor-specific copy number alterations from plasma DNA of patients with cancer. *International Journal of Cancer*, **2013**, 133, 346-56	7.5	135
12	Complex tumor genomes inferred from single circulating tumor cells by array-CGH and next-generation sequencing. *Cancer Research*, **2013**, 73, 2965-75	10.1	442
11	Multiplex genetic cancer testing identifies pathogenic mutations in TP53 and CDH1 in a patient with bilateral breast and endometrial adenocarcinoma. *BMC Medical Genetics*, **2013**, 14, 129	2.1	14
10	Germline mutations in the DNA damage response genes BRCA1, BRCA2, BARD1 and TP53 in patients with therapy related myeloid neoplasms. *Journal of Medical Genetics*, **2012**, 49, 422-8	5.8	72
9	High-resolution analysis of alterations in medullary thyroid carcinoma genomes. *International Journal of Cancer*, **2012**, 131, E66-73	7.5	19
8	Toward an improved definition of the tumor spectrum associated with BAP1 germline mutations. *Journal of Clinical Oncology*, **2012**, 30, e337-40	2.2	86
7	Germline mutations in BAP1 predispose to melanocytic tumors. *Nature Genetics*, **2011**, 43, 1018-21	36.3	562

6	Evolution of genomic instability in diethylnitrosamine-induced hepatocarcinogenesis in mice. *Hepatology*, **2011**, 53, 895-904	11.2	41
5	Extra phenotypic features in a girl with Miller syndrome. *Clinical Dysmorphology*, **2011**, 20, 66-72	0.9	5
4	Combined molecular genetic and cytogenetic analysis from single cells after isothermal whole-genome amplification. *Clinical Chemistry*, **2011**, 57, 1032-41	5.5	31
3	Mapping of balanced chromosome translocation breakpoints to the basepair level from microdissected chromosomes. *Journal of Cellular and Molecular Medicine*, **2010**, 14, 2078-84	5.6	5
2	Inferring expressed genes by whole-genome sequencing of plasma DNA		3
1	Inference of tumor cell-specific transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection of cancer		3