Peter Ulz

List of Publications by Year in descending order

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all docs

41 4,253 25 41 papers citations h-index g-index

45

docs citations

45 7172 times ranked citing authors

#	Article	IF	CITATIONS
1	Germline mutations in BAP1 predispose to melanocytic tumors. Nature Genetics, 2011, 43, 1018-1021.	9.4	662
2	Circulating Tumor DNA as a Liquid Biopsy for Cancer. Clinical Chemistry, 2015, 61, 112-123.	1.5	654
3	Complex Tumor Genomes Inferred from Single Circulating Tumor Cells by Array-CGH and Next-Generation Sequencing. Cancer Research, 2013, 73, 2965-2975.	0.4	497
4	Tumor-associated copy number changes in the circulation of patients with prostate cancer identified through whole-genome sequencing. Genome Medicine, 2013, 5, 30.	3.6	306
5	Inferring expressed genes by whole-genome sequencing of plasma DNA. Nature Genetics, 2016, 48, 1273-1278.	9.4	295
6	Changes in Colorectal Carcinoma Genomes under Anti-EGFR Therapy Identified by Whole-Genome Plasma DNA Sequencing. PLoS Genetics, 2014, 10, e1004271.	1.5	157
7	Establishment of tumorâ€specific copy number alterations from plasma DNA of patients with cancer. International Journal of Cancer, 2013, 133, 346-356.	2.3	155
8	Inference of transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection. Nature Communications, 2019, 10, 4666.	5.8	146
9	Whole-genome plasma sequencing reveals focal amplifications as a driving force in metastatic prostate cancer. Nature Communications, 2016, 7, 12008.	5.8	134
10	Circulating tumor cells and DNA as liquid biopsies. Genome Medicine, 2013, 5, 73.	3.6	116
11	The dynamic range of circulating tumor DNA in metastatic breast cancer. Breast Cancer Research, 2014, 16, 421.	2.2	113
12	Toward an Improved Definition of the Tumor Spectrum Associated With <i>BAP1</i> Germline Mutations. Journal of Clinical Oncology, 2012, 30, e337-e340.	0.8	99
13	Rapid Identification of Plasma DNA Samples with Increased ctDNA Levels by a Modified FAST-SeqS Approach. Clinical Chemistry, 2015, 61, 838-849.	1.5	94
14	Germline mutations in the DNA damage response genes <i>BRCA1</i> , <i>BRCA2</i> , <i>BARD1</i> ,and <i>TP53</i> in patients with therapy related myeloid neoplasms. Journal of Medical Genetics, 2012, 49, 422-428.	1.5	87
15	D2HGDH regulates alpha-ketoglutarate levels and dioxygenase function by modulating IDH2. Nature Communications, 2015, 6, 7768.	5.8	64
16	Nonâ€invasive detection of genomeâ€wide somatic copy number alterations by liquid biopsies. Molecular Oncology, 2016, 10, 494-502.	2.1	63
17	Germline variants in the SEMA4A gene predispose to familial colorectal cancer type X. Nature Communications, 2014, 5, 5191.	5.8	51
18	Evolution of genomic instability in diethylnitrosamine-induced hepatocarcinogenesis in mice. Hepatology, 2011, 53, 895-904.	3.6	47

#	Article	lF	Citations
19	Patient monitoring through liquid biopsies using circulating tumor DNA. International Journal of Cancer, 2017, 141, 887-896.	2.3	46
20	Somatic TP53 mutations characterize preleukemic stem cells in acute myeloid leukemia. Blood, 2017, 129, 2587-2591.	0.6	44
21	Co-occurrence of MYC amplification and TP53 mutations in human cancer. Nature Genetics, 2016, 48, 104-106.	9.4	42
22	Exploring chromosomal abnormalities and genetic changes in uterine smooth muscle tumors. Modern Pathology, 2016, 29, 1262-1277.	2.9	39
23	Autosomal Recessive Keratoderma-Ichthyosis-Deafness (ARKID) Syndrome IsÂCaused by VPS33B Mutations AffectingÂRab Protein Interaction andÂCollagen Modification. Journal of Investigative Dermatology, 2017, 137, 845-854.	0.3	37
24	Genomic alterations in plasma DNA from patients with metastasized prostate cancer receiving abiraterone or enzalutamide. International Journal of Cancer, 2018, 143, 1236-1248.	2.3	37
25	Combined Molecular Genetic and Cytogenetic Analysis from Single Cells after Isothermal Whole-Genome Amplification. Clinical Chemistry, 2011, 57, 1032-1041.	1.5	36
26	Expanded molecular profiling of myxofibrosarcoma reveals potentially actionable targets. Modern Pathology, 2017, 30, 1698-1709.	2.9	27
27	Cell-free DNA analysis reveals POLR1D-mediated resistance to bevacizumab in colorectal cancer. Genome Medicine, 2020, 12, 20.	3.6	25
28	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.	0.8	23
29	Untargeted Assessment of Tumor Fractions in Plasma for Monitoring and Prognostication from Metastatic Breast Cancer Patients Undergoing Systemic Treatment. Cancers, 2019, 11, 1171.	1.7	21
30	Highâ€resolution analysis of alterations in medullary thyroid carcinoma genomes. International Journal of Cancer, 2012, 131, E66-73.	2.3	19
31	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.	0.4	19
32	Multiplex genetic cancer testing identifies pathogenic mutations in TP53 and CDH1in a patient with bilateral breast and endometrial adenocarcinoma. BMC Medical Genetics, 2013, 14, 129.	2.1	17
33	Extra phenotypic features in a girl with Miller syndrome. Clinical Dysmorphology, 2011, 20, 66-72.	0.1	15
34	Single-Stranded DNA Library Preparation Does Not Preferentially Enrich Circulating Tumor DNA. Clinical Chemistry, 2017, 63, 1656-1659.	1.5	15
35	Single circulating tumor cell sequencing for monitoring. Oncotarget, 2013, 4, 812-813.	0.8	13
36	βâ€catenin regulates FOXP2 transcriptional activity via multiple binding sites. FEBS Journal, 2021, 288, 3261-3284.	2.2	11

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37	Mapping of balanced chromosome translocation breakpoints to the basepair level from microdissected chromosomes. Journal of Cellular and Molecular Medicine, 2010, 14, 2078-2084.	1.6	8
38	Genome-Wide Analysis of the Nucleosome Landscape in Individuals with Coffin-Siris Syndrome. Cytogenetic and Genome Research, 2019, 159, 1-11.	0.6	5
39	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.	0.8	4
40	Potentials, challenges and limitations of a molecular characterization of circulating tumor DNA for the management of cancer patients. Laboratoriums Medizin, 2016, 40, 323-334.	0.1	1
41	Reconstruction of Mitochondrial Genotypes from Diverse next Generation Sequencing Datasets. , 2017, , .		0