

# Jochen B Geigl

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1993048/publications.pdf>

Version: 2024-02-01

27  
papers

3,645  
citations

304743

22  
h-index

501196

28  
g-index

30  
all docs

30  
docs citations

30  
times ranked

6442  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of three commercial decision support platforms for matching of next-generation sequencing results with therapies in patients with cancer. <i>ESMO Open</i> , 2020, 5, e000872.	4.5	26
2	On-treatment measurements of circulating tumor DNA during FOLFOX therapy in patients with colorectal cancer. <i>Npj Precision Oncology</i> , 2020, 4, 30.	5.4	13
3	Cell-free DNA analysis reveals POLR1D-mediated resistance to bevacizumab in colorectal cancer. <i>Genome Medicine</i> , 2020, 12, 20.	8.2	25
4	Inference of transcription factor binding from cell-free DNA enables tumor subtype prediction and early detection. <i>Nature Communications</i> , 2019, 10, 4666.	12.8	146
5	Genomic alterations in plasma DNA from patients with metastasized prostate cancer receiving abiraterone or enzalutamide. <i>International Journal of Cancer</i> , 2018, 143, 1236-1248.	5.1	37
6	Patient monitoring through liquid biopsies using circulating tumor DNA. <i>International Journal of Cancer</i> , 2017, 141, 887-896.	5.1	46
7	A novel mutation in <i>ATRX</i> associated with intellectual disability, syndromic features, and osteosarcoma. <i>Pediatric Blood and Cancer</i> , 2017, 64, e26522.	1.5	18
8	The potential of liquid biopsies for the early detection of cancer. <i>Npj Precision Oncology</i> , 2017, 1, 36.	5.4	126
9	Inferring expressed genes by whole-genome sequencing of plasma DNA. <i>Nature Genetics</i> , 2016, 48, 1273-1278.	21.4	295
10	Whole-genome plasma sequencing reveals focal amplifications as a driving force in metastatic prostate cancer. <i>Nature Communications</i> , 2016, 7, 12008.	12.8	134
11	mFast-SeqS as a Monitoring and Pre-screening Tool for Tumor-Specific Aneuploidy in Plasma DNA. <i>Advances in Experimental Medicine and Biology</i> , 2016, 924, 147-155.	1.6	23
12	Acute myeloid leukemia with TP53 germ line mutations. <i>Blood</i> , 2016, 128, 2270-2272.	1.4	39
13	Noninvasive detection of genome-wide somatic copy number alterations by liquid biopsies. <i>Molecular Oncology</i> , 2016, 10, 494-502.	4.6	63
14	Exploring chromosomal abnormalities and genetic changes in uterine smooth muscle tumors. <i>Modern Pathology</i> , 2016, 29, 1262-1277.	5.5	39
15	Circulating Tumor DNA as a Liquid Biopsy for Cancer. <i>Clinical Chemistry</i> , 2015, 61, 112-123.	3.2	654
16	Germline variants in the SEMA4A gene predispose to familial colorectal cancer type X. <i>Nature Communications</i> , 2014, 5, 5191.	12.8	51
17	Changes in Colorectal Carcinoma Genomes under Anti-EGFR Therapy Identified by Whole-Genome Plasma DNA Sequencing. <i>PLoS Genetics</i> , 2014, 10, e1004271.	3.5	157
18	Hematogenous dissemination of glioblastoma multiforme. <i>Science Translational Medicine</i> , 2014, 6, 247ra101.	12.4	264

#	ARTICLE	IF	CITATIONS
19	The dynamic range of circulating tumor DNA in metastatic breast cancer. <i>Breast Cancer Research</i> , 2014, 16, 421.	5.0	113
20	Tumor-associated copy number changes in the circulation of patients with prostate cancer identified through whole-genome sequencing. <i>Genome Medicine</i> , 2013, 5, 30.	8.2	306
21	Circulating tumor cells and DNA as liquid biopsies. <i>Genome Medicine</i> , 2013, 5, 73.	8.2	116
22	Complex Tumor Genomes Inferred from Single Circulating Tumor Cells by Array-CGH and Next-Generation Sequencing. <i>Cancer Research</i> , 2013, 73, 2965-2975.	0.9	497
23	Multiplex genetic cancer testing identifies pathogenic mutations in TP53 and CDH1 in a patient with bilateral breast and endometrial adenocarcinoma. <i>BMC Medical Genetics</i> , 2013, 14, 129.	2.1	17
24	Identification of small gains and losses in single cells after whole genome amplification on tiling oligo arrays. <i>Nucleic Acids Research</i> , 2009, 37, e105-e105.	14.5	65
25	Defining "chromosomal instability". <i>Trends in Genetics</i> , 2008, 24, 64-69.	6.7	268
26	Single-cell isolation from cell suspensions and whole genome amplification from single cells to provide templates for CGH analysis. <i>Nature Protocols</i> , 2007, 2, 3173-3184.	12.0	60
27	Multiplex-fluorescence in situ hybridization for chromosome karyotyping. <i>Nature Protocols</i> , 2006, 1, 1172-1184.	12.0	42