

# Joachim Weischenfeldt

## List of Publications by Citations

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**Version:** 2024-04-27

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55  
papers

7,095  
citations

30  
h-index

63  
g-index

63  
ext. papers

9,796  
ext. citations

17.6  
avg, IF

7.14  
L-index

#	Paper	IF	Citations
55	Pan-cancer analysis of whole genomes. <i>Nature</i> , <b>2020</b> , 578, 82-93	50.4	840
54	Dissecting the genomic complexity underlying medulloblastoma. <i>Nature</i> , <b>2012</b> , 488, 100-5	50.4	623
53	The landscape of genomic alterations across childhood cancers. <i>Nature</i> , <b>2018</b> , 555, 321-327	50.4	603
52	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. <i>Cell</i> , <b>2012</b> , 148, 59-71	56.2	600
51	Bone Marrow-Derived Macrophages (BMM): Isolation and Applications. <i>Cold Spring Harbor Protocols</i> , <b>2008</b> , 2008, pdb.prot5080	1.2	495
50	The whole-genome landscape of medulloblastoma subtypes. <i>Nature</i> , <b>2017</b> , 547, 311-317	50.4	472
49	Phenotypic impact of genomic structural variation: insights from and for human disease. <i>Nature Reviews Genetics</i> , <b>2013</b> , 14, 125-38	30.1	340
48	Integrative genomic analyses reveal an androgen-driven somatic alteration landscape in early-onset prostate cancer. <i>Cancer Cell</i> , <b>2013</b> , 23, 159-70	24.3	259
47	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , <b>2020</b> , 578, 112-121	50.4	232
46	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , <b>2020</b> , 578, 102-111	50.4	220
45	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. <i>Nature Genetics</i> , <b>2017</b> , 49, 65-74	36.3	220
44	NMD is essential for hematopoietic stem and progenitor cells and for eliminating by-products of programmed DNA rearrangements. <i>Genes and Development</i> , <b>2008</b> , 22, 1381-96	12.6	196
43	Intratumor DNA methylation heterogeneity reflects clonal evolution in aggressive prostate cancer. <i>Cell Reports</i> , <b>2014</b> , 8, 798-806	10.6	177
42	Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. <i>Nature Communications</i> , <b>2015</b> , 6, 8940	17.4	175
41	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , <b>2020</b> , 52, 331-341	36.3	168
40	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. <i>Lancet Oncology, The</i> , <b>2018</b> , 19, 785-798	21.7	159
39	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , <b>2018</b> , 28, 581-591	9.7	149

38	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , <b>2020</b> , 52, 306-319	36.3	122
37	Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. <i>Genome Biology</i> , <b>2012</b> , 13, R35	18.3	90
36	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , <b>2018</b> , 34, 996-1011.e8	24.3	89
35	A cell-based model system links chromothripsis with hyperploidy. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 828	12.2	88
34	Clinical significance of different types of p53 gene alteration in surgically treated prostate cancer. <i>International Journal of Cancer</i> , <b>2014</b> , 135, 1369-80	7.5	85
33	Messenger RNA surveillance: neutralizing natural nonsense. <i>Current Biology</i> , <b>2005</b> , 15, R559-62	6.3	71
32	Mitochondrial mutations drive prostate cancer aggression. <i>Nature Communications</i> , <b>2017</b> , 8, 656	17.4	66
31	Comparative analysis of different vaccine constructs expressing defined antigens from <i>Mycobacterium tuberculosis</i> . <i>Journal of Infectious Diseases</i> , <b>2004</b> , 190, 2146-53	7	54
30	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. <i>Haematologica</i> , <b>2015</b> , 100, 1442-50	6.6	50
29	TMPRSS2-ERG fusions are strongly linked to young patient age in low-grade prostate cancer. <i>European Urology</i> , <b>2014</b> , 66, 978-81	10.2	48
28	UPF2 is a critical regulator of liver development, function and regeneration. <i>PLoS ONE</i> , <b>2010</b> , 5, e11650	3.7	47
27	The whole-genome panorama of cancer drivers		38
26	A Novel Gene Signature-Based Model Predicts Biochemical Recurrence-Free Survival in Prostate Cancer Patients after Radical Prostatectomy. <i>Cancers</i> , <b>2019</b> , 12,	6.6	30
25	Patterns of structural variation in human cancer		26
24	Clonal hematopoiesis in elderly twins: concordance, discordance, and mortality. <i>Blood</i> , <b>2020</b> , 135, 261-268	6.8	25
23	Response to olaparib in a germline mutated prostate cancer and genetic events associated with resistance. <i>Journal of Physical Education and Sports Management</i> , <b>2019</b> , 5,	2.8	21
22	Deletion lengthening at chromosomes 6q and 16q targets multiple tumor suppressor genes and is associated with an increasingly poor prognosis in prostate cancer. <i>Oncotarget</i> , <b>2017</b> , 8, 108923-108935	3.3	21
21	Selective and mechanistic sources of recurrent rearrangements across the cancer genome		20

20	Heterogeneity of ERG expression in prostate cancer: a large section mapping study of entire prostatectomy specimens from 125 patients. <i>BMC Cancer</i> , <b>2016</b> , 16, 641	4.8	19
19	Clinical impact of clonal hematopoiesis in patients with lymphoma undergoing ASCT: a national population-based cohort study. <i>Leukemia</i> , <b>2020</b> , 34, 3256-3268	10.7	17
18	Immortalization capacity of HPV types is inversely related to chromosomal instability. <i>Oncotarget</i> , <b>2016</b> , 7, 37608-37621	3.3	17
17	Large-Scale Uniform Analysis of Cancer Whole Genomes in Multiple Computing Environments		14
16	Germline determinants of the somatic mutation landscape in 2,642 cancer genomes		13
15	Clonal hematopoiesis evolves from pretreatment clones and stabilizes after end of chemotherapy in patients with MCL. <i>Blood</i> , <b>2020</b> , 135, 2000-2004	2.2	11
14	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
13	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , <b>2020</b> , 11, 4748	17.4	10
12	Regulation of ETAA1-mediated ATR activation couples DNA replication fidelity and genome stability. <i>Journal of Cell Biology</i> , <b>2019</b> , 218, 3943-3953	7.3	9
11	Prevalence of chromosomal rearrangements involving non-ETS genes in prostate cancer. <i>International Journal of Oncology</i> , <b>2015</b> , 46, 1637-42	4.4	9
10	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 288-292	44.5	9
9	Genomes of early onset prostate cancer. <i>Current Opinion in Urology</i> , <b>2017</b> , 27, 481-487	2.8	7
8	TET2 mutations are associated with hypermethylation at key regulatory enhancers in normal and malignant hematopoiesis. <i>Nature Communications</i> , <b>2021</b> , 12, 6061	17.4	7
7	SvABA: Genome-wide detection of structural variants and indels by local assembly		5
6	Identification of unique and shared mitochondrial DNA mutations in neurodegeneration and cancer by single-cell mitochondrial DNA structural variation sequencing (MitoSV-seq). <i>EBioMedicine</i> , <b>2020</b> , 57, 102868	8.8	2
5	Somatic structural variant formation is guided by and influences genome architecture		1
4	Somatic structural variant formation is guided by and influences genome architecture.. <i>Genome Research</i> , <b>2022</b> ,	9.7	1
3	Level of unique T cell clonotypes is associated with clonal hematopoiesis and survival in patients with lymphoma undergoing ASCT.. <i>Bone Marrow Transplantation</i> , <b>2022</b> ,	4.4	0

- 2 Nonsense-Mediated mRNA Decay Is Essential for the Hematopoietic Compartement.. *Blood*, **2007**, 110, 506-506 2.2
- 1 Mutations known from B-cell lymphoid malignancies are not found in CD34 stem cells from patients with lymphoma. *Leukemia and Lymphoma*, **2021**, 62, 2808-2811 1.9