Joachim Weischenfeldt

List of Publications by Year in Descending Order

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	Level of unique T cell clonotypes is associated with clonal hematopoiesis and survival in patients with lymphoma undergoing ASCT.. *Bone Marrow Transplantation*, **2022**,	4.4	0
54	Somatic structural variant formation is guided by and influences genome architecture.. *Genome Research*, **2022**,	9.7	1
53	TET2 mutations are associated with hypermethylation at key regulatory enhancers in normal and malignant hematopoiesis. *Nature Communications*, **2021**, 12, 6061	17.4	7
52	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	
51	Clonal hematopoiesis evolves from pretreatment clones and stabilizes after end of chemotherapy in patients with MCL. *Blood*, **2020**, 135, 2000-2004	2.2	11
50	Clinical impact of clonal hematopoiesis in patients with lymphoma undergoing ASCT: a national population-based cohort study. *Leukemia*, **2020**, 34, 3256-3268	10.7	17
49	Patterns of somatic structural variation in human cancer genomes. *Nature*, **2020**, 578, 112-121	50.4	232
48	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
47	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
46	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
45	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
44	Butler enables rapid cloud-based analysis of thousands of human genomes. *Nature Biotechnology*, **2020**, 38, 288-292	44.5	9
43	Identification of unique and shared mitochondrial DNA mutations in neurodegeneration and cancer by single-cell mitochondrial DNA structural variation sequencing (MitoSV-seq). *EBioMedicine*, **2020**, 57, 102868	8.8	2
42	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
41	Clonal hematopoiesis in elderly twins: concordance, discordance, and mortality. *Blood*, **2020**, 135, 261-268	22	25
40	Response to olaparib in a germline mutated prostate cancer and genetic events associated with resistance. *Journal of Physical Education and Sports Management*, **2019**, 5,	2.8	21
39	Regulation of ETAA1-mediated ATR activation couples DNA replication fidelity and genome stability. *Journal of Cell Biology*, **2019**, 218, 3943-3953	7.3	9

38	A Novel Gene Signature-Based Model Predicts Biochemical Recurrence-Free Survival in Prostate Cancer Patients after Radical Prostatectomy. *Cancers*, **2019**, 12,	6.6	30
37	The landscape of genomic alterations across childhood cancers. *Nature*, **2018**, 555, 321-327	50.4	603
36	SvABA: genome-wide detection of structural variants and indels by local assembly. *Genome Research*, **2018**, 28, 581-591	9.7	149
35	Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort. *Lancet Oncology, The*, **2018**, 19, 785-798	21.7	159
34	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. *Cancer Cell*, **2018**, 34, 996-1011.e8	24.3	89
33	Mitochondrial mutations drive prostate cancer aggression. *Nature Communications*, **2017**, 8, 656	17.4	66
32	The whole-genome landscape of medulloblastoma subtypes. *Nature*, **2017**, 547, 311-317	50.4	472
31	Genomes of early onset prostate cancer. *Current Opinion in Urology*, **2017**, 27, 481-487	2.8	7
30	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. *Nature Genetics*, **2017**, 49, 65-74	36.3	220
29	Deletion lengthening at chromosomes 6q and 16q targets multiple tumor suppressor genes and is associated with an increasingly poor prognosis in prostate cancer. *Oncotarget*, **2017**, 8, 108923-108935	3.3	21
28	Heterogeneity of ERG expression in prostate cancer: a large section mapping study of entire prostatectomy specimens from 125 patients. *BMC Cancer*, **2016**, 16, 641	4.8	19
27	Immortalization capacity of HPV types is inversely related to chromosomal instability. *Oncotarget*, **2016**, 7, 37608-37621	3.3	17
26	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. *Haematologica*, **2015**, 100, 1442-50	6.6	50
25	A cell-based model system links chromothripsis with hyperploidy. *Molecular Systems Biology*, **2015**, 11, 828	12.2	88
24	Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. *Nature Communications*, **2015**, 6, 8940	17.4	175
23	Prevalence of chromosomal rearrangements involving non-ETS genes in prostate cancer. *International Journal of Oncology*, **2015**, 46, 1637-42	4.4	9
22	TMPRSS2-ERG fusions are strongly linked to young patient age in low-grade prostate cancer. *European Urology*, **2014**, 66, 978-81	10.2	48
21	Intratumor DNA methylation heterogeneity reflects clonal evolution in aggressive prostate cancer. *Cell Reports*, **2014**, 8, 798-806	10.6	177

20	Clinical significance of different types of p53 gene alteration in surgically treated prostate cancer. *International Journal of Cancer*, **2014**, 135, 1369-80	7.5	85
19	Phenotypic impact of genomic structural variation: insights from and for human disease. *Nature Reviews Genetics*, **2013**, 14, 125-38	30.1	340
18	Integrative genomic analyses reveal an androgen-driven somatic alteration landscape in early-onset prostate cancer. *Cancer Cell*, **2013**, 23, 159-70	24.3	259
17	Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. *Genome Biology*, **2012**, 13, R35	18.3	90
16	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. *Cell*, **2012**, 148, 59-71	56.2	600
15	Dissecting the genomic complexity underlying medulloblastoma. *Nature*, **2012**, 488, 100-5	50.4	623
14	UPF2 is a critical regulator of liver development, function and regeneration. *PLoS ONE*, **2010**, 5, e11650	3.7	47
13	Bone Marrow-Derived Macrophages (BMM): Isolation and Applications. *Cold Spring Harbor Protocols* , **2008**, 2008, pdb.prot5080	1.2	495
12	NMD is essential for hematopoietic stem and progenitor cells and for eliminating by-products of programmed DNA rearrangements. *Genes and Development*, **2008**, 22, 1381-96	12.6	196
11	Nonsense-Mediated mRNA Decay Is Essential for the Hematopietic Compartement.. *Blood*, **2007**, 110, 506-506	2.2	
10	Messenger RNA surveillance: neutralizing natural nonsense. *Current Biology*, **2005**, 15, R559-62	6.3	71
9	Comparative analysis of different vaccine constructs expressing defined antigens from Mycobacterium tuberculosis. *Journal of Infectious Diseases*, **2004**, 190, 2146-53	7	54
8	SvABA: Genome-wide detection of structural variants and indels by local assembly		5
7	Large-Scale Uniform Analysis of Cancer Whole Genomes in Multiple Computing Environments		14
6	Pan-cancer analysis of whole genomes reveals driver rearrangements promoted by LINE-1 retrotransposition in human tumours		10
5	Patterns of structural variation in human cancer		26
4	Selective and mechanistic sources of recurrent rearrangements across the cancer genome		20
3	The whole-genome panorama of cancer drivers		38

List of Publications

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1	Somatic structural variant formation is guided by and influences genome architecture	1