Joachim Weischenfeldt

List of Publications by Year
in descending order

53	11,913	126858	182361
papers	citations	33 h-index	51 g-index

63	63	63	20749
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
2	The landscape of genomic alterations across childhood cancers. Nature, 2018, 555, 321-327.	13.7	1,068
3	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	13.7	787
4	Dissecting the genomic complexity underlying medulloblastoma. Nature, 2012, 488, 100-105.	13.7	765
5	Genome Sequencing of Pediatric Medulloblastoma Links Catastrophic DNA Rearrangements with TP53 Mutations. Cell, 2012, 148, 59-71.	13.5	743
6	Bone Marrow-Derived Macrophages (BMM): Isolation and Applications. Cold Spring Harbor Protocols, 2008, 2008, pdb.prot5080.	0.2	677
7	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
8	Phenotypic impact of genomic structural variation: insights from and for human disease. Nature Reviews Genetics, 2013, 14, 125-138.	7.7	502
9	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
10	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
11	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. Nature Genetics, 2017, 49, 65-74.	9.4	326
12	A Novel Gene Signature-Based Model Predicts Biochemical Recurrence-Free Survival in Prostate Cancer Patients after Radical Prostatectomy. Cancers, 2020, 12, 1.	1.7	300
13	Integrative Genomic Analyses Reveal an Androgen-Driven Somatic Alteration Landscape in Early-Onset Prostate Cancer. Cancer Cell, 2013, 23, 159-170.	7.7	292
14	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	2.4	288
15	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
16	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.	5.1	268
17	Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. Nature Communications, 2015, 6, 8940.	5.8	242
18	NMD is essential for hematopoietic stem and progenitor cells and for eliminating by-products of programmed DNA rearrangements. Genes and Development, 2008, 22, 1381-1396.	2.7	231

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19	Intratumor DNA Methylation Heterogeneity Reflects Clonal Evolution in Aggressive Prostate Cancer. Cell Reports, 2014, 8, 798-806.	2.9	219
20	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. Cancer Cell, 2018, 34, 996-1011.e8.	7.7	190
21	A cellâ€based model system links chromothripsis with hyperploidy. Molecular Systems Biology, 2015, 11, 828.	3.2	118
22	Mammalian tissues defective in nonsense-mediated mRNA decay display highly aberrant splicing patterns. Genome Biology, 2012, 13, R35.	13.9	113
23	Mitochondrial mutations drive prostate cancer aggression. Nature Communications, 2017, 8, 656.	5.8	100
24	Clinical significance of different types ofp53gene alteration in surgically treated prostate cancer. International Journal of Cancer, 2014, 135, 1369-1380.	2.3	95
25	UPF2 Is a Critical Regulator of Liver Development, Function and Regeneration. PLoS ONE, 2010, 5, e11650.	1.1	80
26	Messenger RNA Surveillance: Neutralizing Natural Nonsense. Current Biology, 2005, 15, R559-R562.	1.8	79
27	Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. Haematologica, 2015, 100, 1442-1450.	1.7	65
28	Comparative Analysis of Different Vaccine Constructs Expressing Defined Antigens fromMycobacterium tuberculosis. Journal of Infectious Diseases, 2004, 190, 2146-2153.	1.9	57
29	TMPRSS2-ERG Fusions Are Strongly Linked to Young Patient Age in Low-grade Prostate Cancer. European Urology, 2014, 66, 978-981.	0.9	54
30	Clonal hematopoiesis in elderly twins: concordance, discordance, and mortality. Blood, 2020, 135, 261-268.	0.6	47
31	TET2 mutations are associated with hypermethylation at key regulatory enhancers in normal and malignant hematopoiesis. Nature Communications, 2021, 12, 6061.	5.8	47
32	Clinical impact of clonal hematopoiesis in patients with lymphoma undergoing ASCT: a national population-based cohort study. Leukemia, 2020, 34, 3256-3268.	3.3	46
33	Response to olaparib in a PALB2 germline mutated prostate cancer and genetic events associated with resistance. Journal of Physical Education and Sports Management, 2019, 5, a003657.	0.5	36
34	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
35	Structural variations in cancer and the 3D genome. Nature Reviews Cancer, 2022, 22, 533-546.	12.8	27
36	Clonal hematopoiesis evolves from pretreatment clones and stabilizes after end of chemotherapy in patients with MCL. Blood, 2020, 135, 2000-2004.	0.6	26

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37	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.	0.8	26
38	Immortalization capacity of HPV types is inversely related to chromosomal instability. Oncotarget, 2016, 7, 37608-37621.	0.8	25
39	Heterogeneity of ERG expression in prostate cancer: a large section mapping study of entire prostatectomy specimens from 125 patients. BMC Cancer, 2016, 16, 641.	1.1	24
40	Prevalence of chromosomal rearrangements involving non-ETS genes in prostate cancer. International Journal of Oncology, 2015, 46, 1637-1642.	1.4	13
41	Regulation of ETAA1-mediated ATR activation couples DNA replication fidelity and genome stability. Journal of Cell Biology, 2019, 218, 3943-3953.	2.3	13
42	Somatic structural variant formation is guided by and influences genome architecture. Genome Research, 2022, 32, 643-655.	2.4	12
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.	2.7	11
44	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	9.4	11
45	Genomes of early onset prostate cancer. Current Opinion in Urology, 2017, 27, 481-487.	0.9	9
46	The Aging Prostate Is Never â€œNormalâ€• Implications from the Genomic Characterization of Multifocal Prostate Cancers. European Urology, 2015, 68, 348-350.	0.9	5
47	Rare Germline Variants Are Associated with Rapid Biochemical Recurrence After Radical Prostate Cancer Treatment: A Pan Prostate Cancer Group Study. European Urology, 2022, 82, 201-211.	0.9	2
48	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.	0.6	1
49	Abstract 4872: ICGC PedBrain Tumor - Next-generation sequencing identifies novel subgroup-specific mutations and copy number aberrations in medulloblastoma. Cancer Research, 2012, 72, 4872-4872.	0.4	1
50	Nonsense-Mediated mRNA Decay Is Essential for the Hematopietic Compartement.. Blood, 2007, 110, 506-506.	0.6	1
51	Level of unique T cell clonotypes is associated with clonal hematopoiesis and survival in patients with lymphoma undergoing ASCT. Bone Marrow Transplantation, 2022, , .	1.3	1
52	Abstract 1272: MALDI imaging and next generation sequencing for dissecting prostate cancer heterogeneity. , 2012, , .		0
53	Abstract 2893: IGF2 is essential for tumor initiating cell activity in human colorectal cancer. , 2017, , .		0