Harmen J G Van De Werken

List of Publications by Year
in descending order

74 papers	5,255 citations	136950 32 h-index	95266 68 g-index
91 all docs	91 docs citations	91 times ranked	10075 citing authors

#	Article	IF	Citations
1	The EGFRvIII transcriptome in glioblastoma: A meta-omics analysis. Neuro-Oncology, 2022, 24, 429-441.	1.2	7
2	The miR-200c/141-ZEB2-TGFÎ² axis is aberrant in human T-cell prolymphocytic leukemia. Haematologica, 2022, 107, 143-153.	3.5	6
3	Landscape of Driver Gene Events, Biomarkers and Druggable Targets Identified by Whole Genome Sequencing of Glioblastomas. Neuro-Oncology Advances, 2022, 4, vdab177.	0.7	3
4	Hyperresponsive cytosolic DNA-sensing pathway in monocytes from primary SjÃ¶grenâ€™s syndrome. Rheumatology, 2022, 61, 3491-3496.	1.9	11
5	Comprehensive Molecular Characterization Reveals Genomic and Transcriptomic Subtypes of Metastatic Urothelial Carcinoma. European Urology, 2022, 81, 331-336.	1.9	23
6	Identification of Early-Onset Metastasis in SF3B1 Mutated Uveal Melanoma. Cancers, 2022, 14, 846.	3.7	7
7	Stratification of hospitalized COVID-19 patients into clinical severity progression groups by immuno-phenotyping and machine learning. Nature Communications, 2022, 13, 915.	12.8	32
8	ProteoDisco: a flexible R approach to generate customized protein databases for extended search space of novel and variant proteins in proteogenomic studies. Bioinformatics, 2022, 38, 1437-1439.	4.1	1
9	Chromosome 3p25.3 Gain Is Associated With Cisplatin Resistance and Is an Independent Predictor of Poor Outcome in Male Malignant Germ Cell Tumors. Journal of Clinical Oncology, 2022, 40, 3077-3087.	1.6	13
10	Functional RECAP (REpair CAPacity) assay identifies homologous recombination deficiency undetected by DNA-based BRCAness tests. Oncogene, 2022, 41, 3498-3506.	5.9	9
11	The clonal relation of primary upper urinary tract urothelial carcinoma and paired urothelial carcinoma of the bladder. International Journal of Cancer, 2021, 148, 981-987.	5.1	12
12	Evaluation of AXIN1 and AXIN2 as targets of tankyrase inhibition in hepatocellular carcinoma cell lines. Scientific Reports, 2021, 11, 7470.	3.3	9
13	Phenotypic plasticity underlies local invasion and distant metastasis in colon cancer. ELife, 2021, 10, .	6.0	38
14	Generating human prostate cancer organoids from leukapheresis enriched circulating tumour cells. European Journal of Cancer, 2021, 150, 179-189.	2.8	47
15	The genomic landscape of 85 advanced neuroendocrine neoplasms reveals subtype-heterogeneity and potential therapeutic targets. Nature Communications, 2021, 12, 4612.	12.8	55
16	FASTAFS: file system virtualisation of random access compressed FASTA files. BMC Bioinformatics, 2021, 22, 535.	2.6	4
17	Continued androgen signalling inhibition improves cabazitaxel efficacy in prostate cancer. EBioMedicine, 2021, 73, 103681.	6.1	6
18	Fusion transcripts and their genomic breakpoints in polyadenylated and ribosomal RNAâ€“minus RNA sequencing data. GigaScience, 2021, 10, .	6.4	10

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19	Cystic renalâ€epithelial derived induced pluripotent stem cells from polycystic kidney disease patients. Stem Cells Translational Medicine, 2020, 9, 478-490.	3.3	10
20	Synchronous and metachronous urothelial carcinoma of the upper urinary tract and the bladder: Are they clonally related? A systematic review. Urologic Oncology: Seminars and Original Investigations, 2020, 38, 590-598.	1.6	30
21	Blood-based kinase activity profiling: a potential predictor of response to immune checkpoint inhibition in metastatic cancer. , 2020, 8, e001607.		4
22	Multi-Modality Analysis Improves Survival Prediction in Enucleated Uveal Melanoma Patients. , 2019, 60, 3595.		12
23	PDGFRB SIGNALING IS REQUIRED TO GENERATE AORTIC HAEMATOPOIETIC CELLS IN VIVO. Experimental Hematology, 2019, 76, S84.	0.4	0
24	Identification and Characterization of a Transcribed Distal Enhancer Involved in Cardiac Kcnh2 Regulation. Cell Reports, 2019, 28, 2704-2714.e5.	6.4	15
25	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. Nature Genetics, 2019, 51, 1450-1458.	21.4	250
26	The mouse KLF1 Nan variant impairs nuclear condensation and erythroid maturation. PLoS ONE, 2019, 14, e0208659.	2.5	10
27	Molecular heterogeneity and early metastatic clone selection in testicular germ cell cancer development. British Journal of Cancer, 2019, 120, 444-452.	6.4	35
28	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells. ELife, 2019, 8, .	6.0	32
29	The genomic landscape of metastatic castration-resistant prostate cancers reveals multiple distinct genotypes with potential clinical impact. Nature Communications, 2019, 10, 5251.	12.8	130
30	Unique Case of a Rare Mesenchymal Tumor Harboring a Somatic c.119delC VHL Mutation. JCO Precision Oncology, 2019, 3, 1-8.	3.0	0
31	Oncogenic STRAP Supports Hepatocellular Carcinoma Growth by Enhancing Wnt/Î²-Catenin Signaling. Molecular Cancer Research, 2019, 17, 521-531.	3.4	8
32	Investigation of the spatial structure and interactions of the genome at sub-kilobase-pair resolution using T2C. Nature Protocols, 2018, 13, 459-477.	12.0	13
33	SNPitty. Journal of Molecular Diagnostics, 2018, 20, 166-176.	2.8	13
34	In-depth assessment of metastatic prostate cancer with high tumour mutational burden. Annals of Oncology, 2018, 29, viii274.	1.2	3
35	Paneth Cells Respond to Inflammation and Contribute to Tissue Regeneration by Acquiring Stem-like Features through SCF/c-Kit Signaling. Cell Reports, 2018, 24, 2312-2328.e7.	6.4	166
36	Fractionated Radiation of Primary Prostate Basal Cells Results in Downplay of Interferon Stem Cell and Cell Cycle Checkpoint Signatures. European Urology, 2018, 74, 847-849.	1.9	4

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37	Gene length corrected trimmed mean of M-values (GeTMM) processing of RNA-seq data performs similarly in intersample analyses while improving intrasample comparisons. BMC Bioinformatics, 2018, 19, 236.	2.6	105
38	Functional Ex Vivo Assay Reveals Homologous Recombination Deficiency in Breast Cancer Beyond BRCA Gene Defects. Clinical Cancer Research, 2018, 24, 6277-6287.	7.0	53
39	Correlation of Gene Mutation Status with Copy Number Profile in Uveal Melanoma. Ophthalmology, 2017, 124, 573-575.	5.2	26
40	Small chromosomal regions position themselves autonomously according to their chromatin class. Genome Research, 2017, 27, 922-933.	5.5	39
41	DOC1-Dependent Recruitment of NURD Reveals Antagonism with SWI/SNF during Epithelial-Mesenchymal Transition in Oral Cancer Cells. Cell Reports, 2017, 20, 61-75.	6.4	48
42	A reported 20-gene expression signature to predict lymph node-positive disease at radical cystectomy for muscle-invasive bladder cancer is clinically not applicable. PLoS ONE, 2017, 12, e0174039.	2.5	7
43	The detailed 3D multi-loop aggregate/rosette chromatin architecture and functional dynamic organization of the human and mouse genomes. Epigenetics and Chromatin, 2016, 9, 58.	3.9	25
44	Identification of a regulatory domain controlling the Nppa-Nppb gene cluster during heart development and stress. Development (Cambridge), 2016, 143, 2135-46.	2.5	40
45	An autonomous CEBPA enhancer specific for myeloid-lineage priming and neutrophilic differentiation. Blood, 2016, 127, 2991-3003.	1.4	60
46	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. Cancer Cell, 2016, 30, 806-821.	16.8	103
47	Endogenous WNT Signals Mediate BMP-Induced and Spontaneous Differentiation of Epiblast Stem Cells and Human Embryonic Stem Cells. Stem Cell Reports, 2015, 4, 114-128.	4.8	122
48	The lncRNA MIR31HG regulates p16INK4A expression to modulate senescence. Nature Communications, 2015, 6, 6967.	12.8	161
49	TAF10 Interacts with the GATA1 Transcription Factor and Controls Mouse Erythropoiesis. Molecular and Cellular Biology, 2015, 35, 2103-2118.	2.3	14
50	Sp1/Sp3 transcription factors regulate hallmarks of megakaryocyte maturation and platelet formation and function. Blood, 2015, 125, 1957-1967.	1.4	57
51	A crucial role for the ubiquitously expressed transcription factor Sp1 at early stages of hematopoietic specification. Development (Cambridge), 2014, 141, 2391-2401.	2.5	51
52	Cohesin and CTCF differentially affect chromatin architecture and gene expression in human cells. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 996-1001.	7.1	700
53	A Large Permissive Regulatory Domain Exclusively Controls Tbx3 Expression in the Cardiac Conduction System. Circulation Research, 2014, 115, 432-441.	4.5	44
54	Targeted Chromatin Capture (T2C): a novel high resolution high throughput method to detect genomic interactions and regulatory elements. Epigenetics and Chromatin, 2014, 7, 10.	3.9	74

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55	A common genetic variant within SCN10A modulates cardiac SCN5A expression. Journal of Clinical Investigation, 2014, 124, 1844-1852.	8.2	168
56	A Myeloid-Specific Gene-Dosage Regulator for CEBPA Expression in Myeloid Cells Is Commonly Targeted By Onco-Proteins in AML. Blood, 2014, 124, 2205-2205.	1.4	1
57	DNA methylation dynamics during intestinal stem cell differentiation reveals enhancers driving gene expression in the villus. Genome Biology, 2013, 14, R50.	9.6	109
58	eRNAs Are Required for p53-Dependent Enhancer Activity and Gene Transcription. Molecular Cell, 2013, 49, 524-535.	9.7	484
59	Allelic exclusion of the immunoglobulin heavy chain locus is independent of its nuclear localization in mature B cells. Nucleic Acids Research, 2013, 41, 6905-6916.	14.5	26
60	Determining long-range chromatin interactions for selected genomic sites using 4C-seq technology: From fixation to computation. Methods, 2012, 58, 221-230.	3.8	198
61	Robust 4C-seq data analysis to screen for regulatory DNA interactions. Nature Methods, 2012, 9, 969-972.	19.0	357
62	4C Technology: Protocols and Data Analysis. Methods in Enzymology, 2012, 513, 89-112.	1.0	203
63	Variegated gene expression caused by cell-specific long-range DNA interactions. Nature Cell Biology, 2011, 13, 944-951.	10.3	133
64	The inactive X chromosome adopts a unique three-dimensional conformation that is dependent on Xist RNA. Genes and Development, 2011, 25, 1371-1383.	5.9	278
65	Hydrogenomics of the Extremely Thermophilic Bacterium Caldicellulosiruptor saccharolyticus. Applied and Environmental Microbiology, 2008, 74, 6720-6729.	3.1	142
66	Transcriptome Analysis of Infection of the Archaeon Sulfolobus solfataricus with Sulfolobus Turreted Icosahedral Virus. Journal of Virology, 2008, 82, 4874-4883.	3.4	84
67	A Global Transcriptional Regulator in Thermococcus kodakaraensis Controls the Expression Levels of Both Glycolytic and Gluconeogenic Enzyme-encoding Genes. Journal of Biological Chemistry, 2007, 282, 33659-33670.	3.4	79
68	Identification of the Missing Links in Prokaryotic Pentose Oxidation Pathways. Journal of Biological Chemistry, 2006, 281, 27378-27388.	3.4	102
69	9 Functional Genomics of the Thermo-Acidophilic Archaeon Sulfolobus solfataricus. Methods in Microbiology, 2006, 35, 201-231.	0.8	0
70	Reconstruction of central carbon metabolism inSulfolobus solfataricus using a two-dimensional gel electrophoresis map, stable isotope labelling and DNA microarray analysis. Proteomics, 2006, 6, 1518-1529.	2.2	52
71	Identification of a glycolytic regulon in the archaeaPyrococcusandThermococcus. FEMS Microbiology Letters, 2006, 260, 69-76.	1.8	39
72	Two novel conjugative plasmids from a single strain of Sulfolobus. Microbiology (United Kingdom), 2006, 152, 1951-1968.	1.8	26

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73	Molecular Characterization Reveals Genomic and Transcriptomic Subtypes of Metastatic Urothelial Carcinoma. SSRN Electronic Journal, 0, , .	0.4	1
74	Clinical Implementation of Single-Cell RNA Sequencing Using Liver Fine Needle Aspirate Tissuesampling and Centralized Processing Captures Compartment Specific Immuno-Diversity. SSRN Electronic Journal, 0, , .	0.4	0