

Harmen J G Van De Werken

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

5,255
citations

136885

32
h-index

95218

68
g-index

91
all docs

91
docs citations

91
times ranked

10075
citing authors

#	ARTICLE	IF	CITATIONS
1	Cohesin and CTCF differentially affect chromatin architecture and gene expression in human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 996-1001.	3.3	700
2	eRNAs Are Required for p53-Dependent Enhancer Activity and Gene Transcription. <i>Molecular Cell</i> , 2013, 49, 524-535.	4.5	484
3	Robust 4C-seq data analysis to screen for regulatory DNA interactions. <i>Nature Methods</i> , 2012, 9, 969-972.	9.0	357
4	The inactive X chromosome adopts a unique three-dimensional conformation that is dependent on Xist RNA. <i>Genes and Development</i> , 2011, 25, 1371-1383.	2.7	278
5	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. <i>Nature Genetics</i> , 2019, 51, 1450-1458.	9.4	250
6	4C Technology: Protocols and Data Analysis. <i>Methods in Enzymology</i> , 2012, 513, 89-112.	0.4	203
7	Determining long-range chromatin interactions for selected genomic sites using 4C-seq technology: From fixation to computation. <i>Methods</i> , 2012, 58, 221-230.	1.9	198
8	A common genetic variant within SCN10A modulates cardiac SCN5A expression. <i>Journal of Clinical Investigation</i> , 2014, 124, 1844-1852.	3.9	168
9	Paneth Cells Respond to Inflammation and Contribute to Tissue Regeneration by Acquiring Stem-like Features through SCF/c-Kit Signaling. <i>Cell Reports</i> , 2018, 24, 2312-2328.e7.	2.9	166
10	The lncRNA MIR31HG regulates p16INK4A expression to modulate senescence. <i>Nature Communications</i> , 2015, 6, 6967.	5.8	161
11	Hydrogenomics of the Extremely Thermophilic Bacterium <i>Caldicellulosiruptor saccharolyticus</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 6720-6729.	1.4	142
12	Variegated gene expression caused by cell-specific long-range DNA interactions. <i>Nature Cell Biology</i> , 2011, 13, 944-951.	4.6	133
13	The genomic landscape of metastatic castration-resistant prostate cancers reveals multiple distinct genotypes with potential clinical impact. <i>Nature Communications</i> , 2019, 10, 5251.	5.8	130
14	Endogenous WNT Signals Mediate BMP-Induced and Spontaneous Differentiation of Epiblast Stem Cells and Human Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2015, 4, 114-128.	2.3	122
15	DNA methylation dynamics during intestinal stem cell differentiation reveals enhancers driving gene expression in the villus. <i>Genome Biology</i> , 2013, 14, R50.	13.9	109
16	Gene length corrected trimmed mean of M-values (GeTMM) processing of RNA-seq data performs similarly in intersample analyses while improving intrasample comparisons. <i>BMC Bioinformatics</i> , 2018, 19, 236.	1.2	105
17	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. <i>Cancer Cell</i> , 2016, 30, 806-821.	7.7	103
18	Identification of the Missing Links in Prokaryotic Pentose Oxidation Pathways. <i>Journal of Biological Chemistry</i> , 2006, 281, 27378-27388.	1.6	102

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19	Transcriptome Analysis of Infection of the Archaeon <i>Sulfolobus solfataricus</i> with <i>Sulfolobus</i> Turreted Icosahedral Virus. <i>Journal of Virology</i> , 2008, 82, 4874-4883.	1.5	84
20	A Global Transcriptional Regulator in <i>Thermococcus kodakaraensis</i> Controls the Expression Levels of Both Glycolytic and Gluconeogenic Enzyme-encoding Genes. <i>Journal of Biological Chemistry</i> , 2007, 282, 33659-33670.	1.6	79
21	Targeted Chromatin Capture (T2C): a novel high resolution high throughput method to detect genomic interactions and regulatory elements. <i>Epigenetics and Chromatin</i> , 2014, 7, 10.	1.8	74
22	An autonomous CEBPA enhancer specific for myeloid-lineage priming and neutrophilic differentiation. <i>Blood</i> , 2016, 127, 2991-3003.	0.6	60
23	Sp1/Sp3 transcription factors regulate hallmarks of megakaryocyte maturation and platelet formation and function. <i>Blood</i> , 2015, 125, 1957-1967.	0.6	57
24	The genomic landscape of 85 advanced neuroendocrine neoplasms reveals subtype-heterogeneity and potential therapeutic targets. <i>Nature Communications</i> , 2021, 12, 4612.	5.8	55
25	Functional <i>Ex Vivo</i> Assay Reveals Homologous Recombination Deficiency in Breast Cancer Beyond BRCA Gene Defects. <i>Clinical Cancer Research</i> , 2018, 24, 6277-6287.	3.2	53
26	Reconstruction of central carbon metabolism in <i>Sulfolobus solfataricus</i> using a two-dimensional gel electrophoresis map, stable isotope labelling and DNA microarray analysis. <i>Proteomics</i> , 2006, 6, 1518-1529.	1.3	52
27	A crucial role for the ubiquitously expressed transcription factor Sp1 at early stages of hematopoietic specification. <i>Development (Cambridge)</i> , 2014, 141, 2391-2401.	1.2	51
28	DOC1-Dependent Recruitment of NURD Reveals Antagonism with SWI/SNF during Epithelial-Mesenchymal Transition in Oral Cancer Cells. <i>Cell Reports</i> , 2017, 20, 61-75.	2.9	48
29	Generating human prostate cancer organoids from leukapheresis enriched circulating tumour cells. <i>European Journal of Cancer</i> , 2021, 150, 179-189.	1.3	47
30	A Large Permissive Regulatory Domain Exclusively Controls Tbx3 Expression in the Cardiac Conduction System. <i>Circulation Research</i> , 2014, 115, 432-441.	2.0	44
31	Identification of a regulatory domain controlling the Nppa-Nppb gene cluster during heart development and stress. <i>Development (Cambridge)</i> , 2016, 143, 2135-46.	1.2	40
32	Identification of a glycolytic regulon in the archaea <i>Pyrococcus</i> and <i>Thermococcus</i> . <i>FEMS Microbiology Letters</i> , 2006, 260, 69-76.	0.7	39
33	Small chromosomal regions position themselves autonomously according to their chromatin class. <i>Genome Research</i> , 2017, 27, 922-933.	2.4	39
34	Phenotypic plasticity underlies local invasion and distant metastasis in colon cancer. <i>ELife</i> , 2021, 10, .	2.8	38
35	Molecular heterogeneity and early metastatic clone selection in testicular germ cell cancer development. <i>British Journal of Cancer</i> , 2019, 120, 444-452.	2.9	35
36	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells. <i>ELife</i> , 2019, 8, .	2.8	32

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37	Stratification of hospitalized COVID-19 patients into clinical severity progression groups by immuno-phenotyping and machine learning. <i>Nature Communications</i> , 2022, 13, 915.	5.8	32
38	Synchronous and metachronous urothelial carcinoma of the upper urinary tract and the bladder: Are they clonally related? A systematic review. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2020, 38, 590-598.	0.8	30
39	Two novel conjugative plasmids from a single strain of <i>Sulfolobus</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 1951-1968.	0.7	26
40	Allelic exclusion of the immunoglobulin heavy chain locus is independent of its nuclear localization in mature B cells. <i>Nucleic Acids Research</i> , 2013, 41, 6905-6916.	6.5	26
41	Correlation of Gene Mutation Status with Copy Number Profile in Uveal Melanoma. <i>Ophthalmology</i> , 2017, 124, 573-575.	2.5	26
42	The detailed 3D multi-loop aggregate/rosette chromatin architecture and functional dynamic organization of the human and mouse genomes. <i>Epigenetics and Chromatin</i> , 2016, 9, 58.	1.8	25
43	Comprehensive Molecular Characterization Reveals Genomic and Transcriptomic Subtypes of Metastatic Urothelial Carcinoma. <i>European Urology</i> , 2022, 81, 331-336.	0.9	23
44	Identification and Characterization of a Transcribed Distal Enhancer Involved in Cardiac <i>Kcnh2</i> Regulation. <i>Cell Reports</i> , 2019, 28, 2704-2714.e5.	2.9	15
45	TAF10 Interacts with the GATA1 Transcription Factor and Controls Mouse Erythropoiesis. <i>Molecular and Cellular Biology</i> , 2015, 35, 2103-2118.	1.1	14
46	Investigation of the spatial structure and interactions of the genome at sub-kilobase-pair resolution using T2C. <i>Nature Protocols</i> , 2018, 13, 459-477.	5.5	13
47	SNPitty. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 166-176.	1.2	13
48	Chromosome 3p25.3 Gain Is Associated With Cisplatin Resistance and Is an Independent Predictor of Poor Outcome in Male Malignant Germ Cell Tumors. <i>Journal of Clinical Oncology</i> , 2022, 40, 3077-3087.	0.8	13
49	Multi-Modality Analysis Improves Survival Prediction in Enucleated Uveal Melanoma Patients. , 2019, 60, 3595.		12
50	The clonal relation of primary upper urinary tract urothelial carcinoma and paired urothelial carcinoma of the bladder. <i>International Journal of Cancer</i> , 2021, 148, 981-987.	2.3	12
51	Hyperresponsive cytosolic DNA-sensing pathway in monocytes from primary Sjögren's syndrome. <i>Rheumatology</i> , 2022, 61, 3491-3496.	0.9	11
52	The mouse <i>KLF1</i> Nan variant impairs nuclear condensation and erythroid maturation. <i>PLoS ONE</i> , 2019, 14, e0208659.	1.1	10
53	Cystic renal epithelial derived induced pluripotent stem cells from polycystic kidney disease patients. <i>Stem Cells Translational Medicine</i> , 2020, 9, 478-490.	1.6	10
54	Fusion transcripts and their genomic breakpoints in polyadenylated and ribosomal RNA minus RNA sequencing data. <i>GigaScience</i> , 2021, 10, .	3.3	10

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55	Evaluation of AXIN1 and AXIN2 as targets of tankyrase inhibition in hepatocellular carcinoma cell lines. <i>Scientific Reports</i> , 2021, 11, 7470.	1.6	9
56	Functional RECAP (REpair CAPacity) assay identifies homologous recombination deficiency undetected by DNA-based BRCAness tests. <i>Oncogene</i> , 2022, 41, 3498-3506.	2.6	9
57	Oncogenic STRAP Supports Hepatocellular Carcinoma Growth by Enhancing Wnt/ β^2 -Catenin Signaling. <i>Molecular Cancer Research</i> , 2019, 17, 521-531.	1.5	8
58	The <i>EGFRvIII</i> transcriptome in glioblastoma: A meta-omics analysis. <i>Neuro-Oncology</i> , 2022, 24, 429-441.	0.6	7
59	A reported 20-gene expression signature to predict lymph node-positive disease at radical cystectomy for muscle-invasive bladder cancer is clinically not applicable. <i>PLoS ONE</i> , 2017, 12, e0174039.	1.1	7
60	Identification of Early-Onset Metastasis in SF3B1 Mutated Uveal Melanoma. <i>Cancers</i> , 2022, 14, 846.	1.7	7
61	The miR-200c/141-ZEB2-TGF β^2 axis is aberrant in human T-cell prolymphocytic leukemia. <i>Haematologica</i> , 2022, 107, 143-153.	1.7	6
62	Continued androgen signalling inhibition improves cabazitaxel efficacy in prostate cancer. <i>EBioMedicine</i> , 2021, 73, 103681.	2.7	6
63	Fractionated Radiation of Primary Prostate Basal Cells Results in Downplay of Interferon Stem Cell and Cell Cycle Checkpoint Signatures. <i>European Urology</i> , 2018, 74, 847-849.	0.9	4
64	Blood-based kinase activity profiling: a potential predictor of response to immune checkpoint inhibition in metastatic cancer. , 2020, 8, e001607.		4
65	FASTAFS: file system virtualisation of random access compressed FASTA files. <i>BMC Bioinformatics</i> , 2021, 22, 535.	1.2	4
66	In-depth assessment of metastatic prostate cancer with high tumour mutational burden. <i>Annals of Oncology</i> , 2018, 29, viii274.	0.6	3
67	Landscape of Driver Gene Events, Biomarkers and Druggable Targets Identified by Whole Genome Sequencing of Glioblastomas. <i>Neuro-Oncology Advances</i> , 2022, 4, vdab177.	0.4	3
68	Molecular Characterization Reveals Genomic and Transcriptomic Subtypes of Metastatic Urothelial Carcinoma. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
69	A Myeloid-Specific Gene-Dosage Regulator for CEBPA Expression in Myeloid Cells Is Commonly Targeted By Onco-Proteins in AML. <i>Blood</i> , 2014, 124, 2205-2205.	0.6	1
70	ProteoDisco: a flexible R approach to generate customized protein databases for extended search space of novel and variant proteins in proteogenomic studies. <i>Bioinformatics</i> , 2022, 38, 1437-1439.	1.8	1
71	9 Functional Genomics of the Thermo-Acidophilic Archaeon <i>Sulfolobus solfataricus</i> . <i>Methods in Microbiology</i> , 2006, 35, 201-231.	0.4	0
72	PDGFRB SIGNALING IS REQUIRED TO GENERATE AORTIC HAEMATOPOIETIC CELLS IN VIVO. <i>Experimental Hematology</i> , 2019, 76, S84.	0.2	0

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73	Unique Case of a Rare Mesenchymal Tumor Harboring a Somatic c.119delC VHL Mutation. JCO Precision Oncology, 2019, 3, 1-8.	1.5	0
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