

# Haico Van Attikum

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

5,236  
citations

117625

34  
h-index

118850

62  
g-index

67  
all docs

67  
docs citations

67  
times ranked

7273  
citing authors

#	ARTICLE	IF	CITATIONS
1	Recruitment of the INO80 Complex by H2A Phosphorylation Links ATP-Dependent Chromatin Remodeling with DNA Double-Strand Break Repair. <i>Cell</i> , 2004, 119, 777-788.	28.9	538
2	Crosstalk between histone modifications during the DNA damage response. <i>Trends in Cell Biology</i> , 2009, 19, 207-217.	7.9	457
3	The shieldin complex mediates 53BP1-dependent DNA repair. <i>Nature</i> , 2018, 560, 117-121.	27.8	445
4	PARP Inhibitor Resistance: A Tug-of-War in BRCA-Mutated Cells. <i>Trends in Cell Biology</i> , 2019, 29, 820-834.	7.9	297
5	Distinct roles for SWR1 and INO80 chromatin remodeling complexes at chromosomal double-strand breaks. <i>EMBO Journal</i> , 2007, 26, 4113-4125.	7.8	292
6	Selective Loss of PARC Restores PARylation and Counteracts PARP Inhibitor-Mediated Synthetic Lethality. <i>Cancer Cell</i> , 2018, 33, 1078-1093.e12.	16.8	238
7	The yeast Fun30 and human SMARCAD1 chromatin remodellers promote DNA end resection. <i>Nature</i> , 2012, 489, 581-584.	27.8	233
8	PARP1 Links CHD2-Mediated Chromatin Expansion and H3.3 Deposition to DNA Repair by Non-homologous End-Joining. <i>Molecular Cell</i> , 2016, 61, 547-562.	9.7	214
9	The NuRD chromatin remodeling complex regulates signaling and repair of DNA damage. <i>Journal of Cell Biology</i> , 2010, 190, 741-749.	5.2	211
10	Spatiotemporal regulation of posttranslational modifications in the <scp>DNA</scp> damage response. <i>EMBO Journal</i> , 2016, 35, 6-23.	7.8	174
11	A Network of Conserved Synthetic Lethal Interactions for Exploration of Precision Cancer Therapy. <i>Molecular Cell</i> , 2016, 63, 514-525.	9.7	140
12	Poly(ADP-ribosyl)ation links the chromatin remodeler SMARCA5/SNF2H to RNF168-dependent DNA damage signaling. <i>Journal of Cell Science</i> , 2013, 126, 889-903.	2.0	113
13	Chromatin and the DNA damage response: The cancer connection. <i>Molecular Oncology</i> , 2011, 5, 349-367.	4.6	107
14	ZMYND8 Co-localizes with NuRD on Target Genes and Regulates Poly(ADP-Ribose)-Dependent Recruitment of GATAD2A/NuRD to Sites of DNA Damage. <i>Cell Reports</i> , 2016, 17, 783-798.	6.4	100
15	A new non-catalytic role for ubiquitin ligase RNF8 in unfolding higher-order chromatin structure. <i>EMBO Journal</i> , 2012, 31, 2511-2527.	7.8	94
16	Dissection of DNA Damage Responses Using Multiconditional Genetic Interaction Maps. <i>Molecular Cell</i> , 2013, 49, 346-358.	9.7	86
17	Antisense Oligonucleotide-Mediated Removal of the Polyglutamine Repeat in Spinocerebellar Ataxia Type 3 Mice. <i>Molecular Therapy - Nucleic Acids</i> , 2017, 8, 232-242.	5.1	78
18	WWP2 ubiquitylates RNA polymerase II for DNA-PK-dependent transcription arrest and repair at DNA breaks. <i>Genes and Development</i> , 2019, 33, 684-704.	5.9	71

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19	SWI/SNF complex in disorder. <i>Epigenetics</i> , 2012, 7, 1219-1224.	2.7	70
20	Gcn5 and Esa1 function as histone crotonyltransferases to regulate crotonylation-dependent transcription. <i>Journal of Biological Chemistry</i> , 2019, 294, 20122-20134.	3.4	66
21	Opposing ISWI- and CHD-class chromatin remodeling activities orchestrate heterochromatic DNA repair. <i>Journal of Cell Biology</i> , 2014, 207, 717-733.	5.2	65
22	A PALB2-interacting domain in RNF168 couples homologous recombination to DNA break-induced chromatin ubiquitylation. <i>ELife</i> , 2017, 6, .	6.0	65
23	The de-ubiquitylating enzymes USP26 and USP37 regulate homologous recombination by counteracting RAP80. <i>Nucleic Acids Research</i> , 2015, 43, 6919-6933.	14.5	64
24	Yeast PP4 Interacts with ATR Homolog Ddc2-Mec1 and Regulates Checkpoint Signaling. <i>Molecular Cell</i> , 2015, 57, 273-289.	9.7	63
25	Ataxin-3 consolidates the MDC1-dependent DNA double-strand break response by counteracting the SUMO-targeted ubiquitin ligase RNF4. <i>EMBO Journal</i> , 2017, 36, 1066-1083.	7.8	60
26	Bon voyage: A transcriptional journey around DNA breaks. <i>DNA Repair</i> , 2019, 82, 102686.	2.8	55
27	Human ISWI complexes are targeted by SMARCA5 ATPase and SLIDE domains to help resolve lesion-stalled transcription. <i>Nucleic Acids Research</i> , 2014, 42, 8473-8485.	14.5	54
28	DNA repair goes hip-hop: SMARCA and CHD chromatin remodellers join the break dance. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160285.	4.0	53
29	SUMOylation and PARylation cooperate to recruit and stabilize SLX4 at DNA damage sites. <i>EMBO Reports</i> , 2015, 16, 512-519.	4.5	51
30	Remodeling and spacing factor 1 (RSF1) deposits centromere proteins at DNA double-strand breaks to promote non-homologous end-joining. <i>Cell Cycle</i> , 2013, 12, 3070-3082.	2.6	50
31	Structural Basis of BRCC36 Function in DNA Repair and Immune Regulation. <i>Molecular Cell</i> , 2019, 75, 483-497.e9.	9.7	50
32	Meta-analysis of DNA double-strand break response kinetics. <i>Nucleic Acids Research</i> , 2017, 45, 12625-12637.	14.5	49
33	Functional analysis of genetic variants in the high-risk breast cancer susceptibility gene PALB2. <i>Nature Communications</i> , 2019, 10, 5296.	12.8	45
34	The CHD6 chromatin remodeler is an oxidative DNA damage response factor. <i>Nature Communications</i> , 2019, 10, 241.	12.8	45
35	Map of synthetic rescue interactions for the Fanconi anemia DNA repair pathway identifies USP48. <i>Nature Communications</i> , 2018, 9, 2280.	12.8	34
36	Antisense oligonucleotide-mediated exon skipping as a strategy to reduce proteolytic cleavage of ataxin-3. <i>Scientific Reports</i> , 2016, 6, 35200.	3.3	31

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37	CHD7 and 53BP1 regulate distinct pathways for the re-ligation of DNA double-strand breaks. <i>Nature Communications</i> , 2020, 11, 5775.	12.8	28
38	DNA double-strand break repair: Putting zinc fingers on the sore spot. <i>Seminars in Cell and Developmental Biology</i> , 2021, 113, 65-74.	5.0	28
39	TRiC controls transcription resumption after UV damage by regulating Cockayne syndrome protein A. <i>Nature Communications</i> , 2018, 9, 1040.	12.8	27
40	Loss of ZBTB24 impairs nonhomologous end-joining and class-switch recombination in patients with ICF syndrome. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	27
41	Functional Analysis Identifies Damaging CHEK2 Missense Variants Associated with Increased Cancer Risk. <i>Cancer Research</i> , 2022, 82, 615-631.	0.9	26
42	Dot1 promotes H2B ubiquitination by a methyltransferase-independent mechanism. <i>Nucleic Acids Research</i> , 2018, 46, 11251-11261.	14.5	24
43	PHF6 promotes non-homologous end joining and G2 checkpoint recovery. <i>EMBO Reports</i> , 2020, 21, e48460.	4.5	22
44	PHF2 regulates homology-directed DNA repair by controlling the resection of DNA double strand breaks. <i>Nucleic Acids Research</i> , 2020, 48, 4915-4927.	14.5	19
45	A UV-Induced Genetic Network Links the RSC Complex to Nucleotide Excision Repair and Shows Dose-Dependent Rewiring. <i>Cell Reports</i> , 2013, 5, 1714-1724.	6.4	18
46	ERCC1 mutations impede DNA damage repair and cause liver and kidney dysfunction in patients. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	18
47	Zinc finger protein ZNF384 is an adaptor of Ku to DNA during classical non-homologous end-joining. <i>Nature Communications</i> , 2021, 12, 6560.	12.8	17
48	CHEK2 variants: linking functional impact to cancer risk. <i>Trends in Cancer</i> , 2022, 8, 759-770.	7.4	16
49	Functional Analysis of Missense Variants in the Putative Breast Cancer Susceptibility Gene XRCC2. <i>Human Mutation</i> , 2016, 37, 914-925.	2.5	12
50	Functional Characterization of PALB2 Variants of Uncertain Significance: Toward Cancer Risk and Therapy Response Prediction. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 169.	3.5	11
51	Mapping Genomic Targets of DNA Helicases by Chromatin Immunoprecipitation in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2009, 587, 113-126.	0.9	11
52	Chemogenetic profiling identifies RAD17 as synthetically lethal with checkpoint kinase inhibition. <i>Oncotarget</i> , 2015, 6, 35755-35769.	1.8	10
53	Poly(ADP-ribosyl)ation temporally confines SUMO-dependent ataxin-3 recruitment to control DNA double-strand break repair. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	8
54	Proteomic analysis identifies novel binding partners of BAP1. <i>PLoS ONE</i> , 2021, 16, e0257688.	2.5	8

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55	Genomic Reporter Constructs to Monitor Pathway-Specific Repair of DNA Double-Strand Breaks. <i>Frontiers in Genetics</i> , 2021, 12, 809832.	2.3	8
56	A BRCA1 Coiled-Coil Domain Variant Disrupting PALB2 Interaction Promotes the Development of Mammary Tumors and Confers a Targetable Defect in Homologous Recombination Repair. <i>Cancer Research</i> , 2021, 81, 6171-6182.	0.9	7
57	RNF168 E3 ligase participates in ubiquitin signaling and recruitment of SLX4 during DNA crosslink repair. <i>Cell Reports</i> , 2021, 37, 109879.	6.4	6
58	A genetic interaction map centered on cohesin reveals auxiliary factors in sister chromatid cohesion. <i>Journal of Cell Science</i> , 2020, 133, .	2.0	5
59	Characterisation of protein-truncating and missense variants in PALB2 in 15 768 women from Malaysia and Singapore. <i>Journal of Medical Genetics</i> , 2021, , jmedgenet-2020-107471.	3.2	4
60	Epigenetics Identifier screens reveal regulators of chromatin acylation and limited specificity of acylation antibodies. <i>Scientific Reports</i> , 2021, 11, 12795.	3.3	1
61	Chl1 helicase controls replication fork progression by regulating dNTP pools. <i>Life Science Alliance</i> , 2022, 5, e202101153.	2.8	1