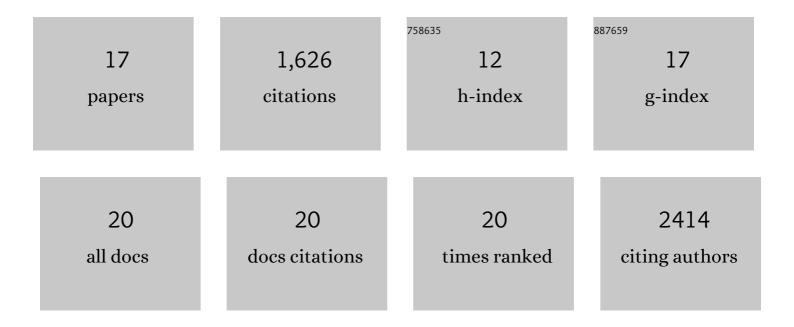
## René Wardenaar

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2342403/publications.pdf Version: 2024-02-01



RENÃO WARDENAAR

#	Article	IF	CITATIONS
1	Genetic instability from a single S phase after whole-genome duplication. Nature, 2022, 604, 146-151.	13.7	54
2	Diesel exhaust particles distort lung epithelial progenitors and their fibroblast niche. Environmental Pollution, 2022, 305, 119292.	3.7	8
3	Gut microbiota transplantation drives the adoptive transfer of colonic genotype-phenotype characteristics between mice lacking catestatin and their wild type counterparts. Gut Microbes, 2022, 14, .	4.3	2
4	cGAS–STING drives the IL-6-dependent survival of chromosomally instable cancers. Nature, 2022, 607, 366-373.	13.7	132
5	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. Nature, 2021, 590, 486-491.	13.7	135
6	Transient genomic instability drives tumorigenesis through accelerated clonal evolution. Genes and Development, 2021, 35, 1093-1108.	2.7	48
7	Gene copy-number changes and chromosomal instability induced by aneuploidy confer resistance to chemotherapy. Developmental Cell, 2021, 56, 2440-2454.e6.	3.1	87
8	<i>TP53</i> loss initiates chromosomal instability in fallopian tube epithelial cells. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	17
9	Replication catastrophe is responsible for intrinsic PAR glycohydrolase inhibitor-sensitivity in patient-derived ovarian cancer models. Journal of Experimental and Clinical Cancer Research, 2021, 40, 323.	3.5	12
10	The H3.3K27M oncohistone affects replication stress outcome and provokes genomic instability in pediatric glioma. PLoS Genetics, 2021, 17, e1009868.	1.5	14
11	A living biobank of ovarian cancer ex vivo models reveals profound mitotic heterogeneity. Nature Communications, 2020, 11, 822.	5.8	62
12	E2F-Family Members Engage the PIDDosome to Limit Hepatocyte Ploidy in Liver Development and Regeneration. Developmental Cell, 2020, 52, 335-349.e7.	3.1	40
13	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	5.8	99
14	Methylome evolution in plants. Genome Biology, 2016, 17, 264.	3.8	114
15	Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6676-6681.	3.3	251
16	Mapping the Epigenetic Basis of Complex Traits. Science, 2014, 343, 1145-1148.	6.0	403
17	Features of the <i>Arabidopsis</i> recombination landscape resulting from the combined loss of sequence variation and DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16240-16245.	3.3	145