

# Arian F A Smit

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8180720/publications.pdf>

Version: 2024-02-01

18  
papers

26,470  
citations

623734

14  
h-index

839539

18  
g-index

21  
all docs

21  
docs citations

21  
times ranked

29497  
citing authors

#	ARTICLE	IF	CITATIONS
1	From telomere to telomere: The transcriptional and epigenetic state of human repeat elements. <i>Science</i> , 2022, 376, eabk3112.	12.6	146
2	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
3	Methodologies for the De novo Discovery of Transposable Element Families. <i>Genes</i> , 2022, 13, 709.	2.4	10
4	Accuracy of multiple sequence alignment methods in the reconstruction of transposable element families. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac040.	3.2	6
5	Curation Guidelines for <i>de novo</i> Generated Transposable Element Families. <i>Current Protocols</i> , 2021, 1, e154.	2.9	25
6	The Dfam community resource of transposable element families, sequence models, and genome annotations. <i>Mobile DNA</i> , 2021, 12, 2.	3.6	279
7	The transposable element-rich genome of the cereal pest <i>Sitophilus oryzae</i> . <i>BMC Biology</i> , 2021, 19, 241.	3.8	40
8	RepeatModeler2 for automated genomic discovery of transposable element families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9451-9457.	7.1	1,480
9	The Dfam database of repetitive DNA families. <i>Nucleic Acids Research</i> , 2016, 44, D81-D89.	14.5	543
10	Discovery of a new repeat family in the <i>Callithrix jacchus</i> genome. <i>Genome Research</i> , 2016, 26, 649-659.	5.5	11
11	Multiple Lineages of Ancient CR1 Retroposons Shaped the Early Genome Evolution of Amniotes. <i>Genome Biology and Evolution</i> , 2015, 7, 205-217.	2.5	62
12	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	14.5	891
13	Evolution and gene capture in ancient endogenous retroviruses - insights from the crocodilian genomes. <i>Retrovirology</i> , 2014, 11, 71.	2.0	27
14	Realistic artificial DNA sequences as negative controls for computational genomics. <i>Nucleic Acids Research</i> , 2014, 42, e99-e99.	14.5	26
15	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	12.6	300
16	Multiscale representation of genomic signals. <i>Nature Methods</i> , 2014, 11, 689-694.	19.0	31
17	Dfam: a database of repetitive DNA based on profile hidden Markov models. <i>Nucleic Acids Research</i> , 2012, 41, D70-D82.	14.5	243
18	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074