

# Jessica Alfoldi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2257173/publications.pdf>

Version: 2024-02-01

21  
papers

11,844  
citations

331538

21  
h-index

580701

25  
g-index

33  
all docs

33  
docs citations

33  
times ranked

26470  
citing authors

#	ARTICLE	IF	CITATIONS
1	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	13.7	6,140
2	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
3	A structural variation reference for medical and population genetics. <i>Nature</i> , 2020, 581, 444-451.	13.7	614
4	The African coelacanth genome provides insights into tetrapod evolution. <i>Nature</i> , 2013, 496, 311-316.	13.7	612
5	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	13.7	575
6	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. <i>Nature Genetics</i> , 2016, 48, 427-437.	9.4	545
7	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 2015, 47, 272-275.	9.4	392
8	An Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts. <i>PLoS ONE</i> , 2014, 9, e91172.	1.1	206
9	Transcript expression-aware annotation improves rare variant interpretation. <i>Nature</i> , 2020, 581, 452-458.	13.7	142
10	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020, 581, 459-464.	13.7	115
11	The draft genome sequence of the ferret ( <i>Mustela putorius furo</i> ) facilitates study of human respiratory disease. <i>Nature Biotechnology</i> , 2014, 32, 1250-1255.	9.4	110
12	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. <i>American Journal of Human Genetics</i> , 2018, 102, 1204-1211.	2.6	102
13	Characterising the loss-of-function impact of 5' UTR untranslated region variants in 15,708 individuals. <i>Nature Communications</i> , 2020, 11, 2523.	5.8	99
14	Landscape of multi-nucleotide variants in 125,748 human exomes and 15,708 genomes. <i>Nature Communications</i> , 2020, 11, 2539.	5.8	98
15	Human genetic variation alters CRISPR-Cas9 on- and off-targeting specificity at therapeutically implicated loci. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E11257-E11266.	3.3	96
16	The effect of LRRK2 loss-of-function variants in humans. <i>Nature Medicine</i> , 2020, 26, 869-877.	15.2	79
17	The Naked Mole Rat Genome Resource: facilitating analyses of cancer and longevity-related adaptations. <i>Bioinformatics</i> , 2014, 30, 3558-3560.	1.8	71
18	Genome reannotation of the lizard <i>Anolis carolinensis</i> based on 14 adult and embryonic deep transcriptomes. <i>BMC Genomics</i> , 2013, 14, 49.	1.2	55

#	ARTICLE	IF	CITATIONS
19	Acf7 (MACF) is an actin and microtubule linker protein whose expression predominates in neural, muscle, and lung development. <i>Developmental Dynamics</i> , 2000, 219, 216-225.	0.8	52
20	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2021, 597, E3-E4.	13.7	45
21	The Antarctic Weddell seal genome reveals evidence of selection on cardiovascular phenotype and lipid handling. <i>Communications Biology</i> , 2022, 5, 140.	2.0	5