

# Irwin Jungreis

## List of Publications by Year in descending order

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35  
papers

9,028  
citations

236925

25  
h-index

345221

36  
g-index

46  
all docs

46  
docs citations

46  
times ranked

19079  
citing authors

#	ARTICLE	IF	CITATIONS
1	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2022, 40, 209-217.	17.5	127
2	Evolution of enhanced innate immune evasion by SARS-CoV-2. <i>Nature</i> , 2022, 602, 487-495.	27.8	237
3	Standardized annotation of translated open reading frames. <i>Nature Biotechnology</i> , 2022, 40, 994-999.	17.5	86
4	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	14.5	633
5	Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. <i>Molecular Biology and Evolution</i> , 2021, 38, 486-501.	8.9	58
6	SARS-CoV-2 gene content and COVID-19 mutation impact by comparing 44 Sarbecovirus genomes. <i>Nature Communications</i> , 2021, 12, 2642.	12.8	136
7	Calcifediol Treatment and Hospital Mortality Due to COVID-19: A Cohort Study. <i>Nutrients</i> , 2021, 13, 1760.	4.1	71
8	Conflicting and ambiguous names of overlapping ORFs in the SARS-CoV-2 genome: A homology-based resolution. <i>Virology</i> , 2021, 558, 145-151.	2.4	40
9	Evidence for secondary-variant genetic burden and non-random distribution across biological modules in a recessive ciliopathy. <i>Nature Genetics</i> , 2020, 52, 1145-1150.	21.4	22
10	Translation Initiation Site Profiling Reveals Widespread Synthesis of Non-AUG-Initiated Protein Isoforms in Yeast. <i>Cell Systems</i> , 2020, 11, 145-160.e5.	6.2	41
11	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020, 80, 1078-1091.e6.	9.7	255
12	Few SINEs of life: Alu elements have little evidence for biological relevance despite elevated translation. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz023.	3.2	12
13	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. <i>BMC Genetics</i> , 2020, 21, 25.	2.7	30
14	Elucidation of Codon Usage Signatures across the Domains of Life. <i>Molecular Biology and Evolution</i> , 2019, 36, 2328-2339.	8.9	54
15	A gene expression atlas of embryonic neurogenesis in <i>Drosophila</i> reveals complex spatiotemporal regulation of lncRNAs. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	21
16	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , 2019, 29, 2073-2087.	5.5	52
17	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	14.5	2,350
18	Stop codon readthrough generates a C-terminally extended variant of the human vitamin D receptor with reduced calcitriol response. <i>Journal of Biological Chemistry</i> , 2018, 293, 4434-4444.	3.4	59

#	ARTICLE	IF	CITATIONS
19	Loose ends: almost one in five human genes still have unresolved coding status. <i>Nucleic Acids Research</i> , 2018, 46, 7070-7084.	14.5	62
20	Evolutionary Dynamics of Abundant Stop Codon Readthrough. <i>Molecular Biology and Evolution</i> , 2016, 33, 3108-3132.	8.9	53
21	Improved Identification and Analysis of Small Open Reading Frame Encoded Polypeptides. <i>Analytical Chemistry</i> , 2016, 88, 3967-3975.	6.5	119
22	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	28.9	275
23	FRESCO: finding regions of excess synonymous constraint in diverse viruses. <i>Genome Biology</i> , 2015, 16, 38.	8.8	35
24	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258-1262.	12.6	492
25	The Discovery of Human sORF-Encoded Polypeptides (SEPs) in Cell Lines and Tissue. <i>FASEB Journal</i> , 2015, 29, 567-21.	0.5	0
26	Evidence of efficient stop codon readthrough in four mammalian genes. <i>Nucleic Acids Research</i> , 2014, 42, 8928-8938.	14.5	184
27	Discovery of Human sORF-Encoded Polypeptides (SEPs) in Cell Lines and Tissue. <i>Journal of Proteome Research</i> , 2014, 13, 1757-1765.	3.7	149
28	Heterologous Stop Codon Readthrough of Metazoan Readthrough Candidates in Yeast. <i>PLoS ONE</i> , 2013, 8, e59450.	2.5	8
29	PhyloCSF: a comparative genomics method to distinguish protein coding and non-coding regions. <i>Bioinformatics</i> , 2011, 27, i275-i282.	4.1	864
30	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	27.8	1,016
31	Evidence of abundant stop codon readthrough in <i>Drosophila</i> and other metazoa. <i>Genome Research</i> , 2011, 21, 2096-2113.	5.5	196
32	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
33	A method for proving that monotone twist maps have no invariant circles. <i>Ergodic Theory and Dynamical Systems</i> , 1991, 11, 79-84.	0.6	19
34	Some results on the ÅarkovskiĀ-partial ordering of permutations. <i>Transactions of the American Mathematical Society</i> , 1991, 325, 319-344.	0.9	6
35	The uniformization of the complement of the Mandelbrot set. <i>Duke Mathematical Journal</i> , 1985, 52, 935.	1.5	11