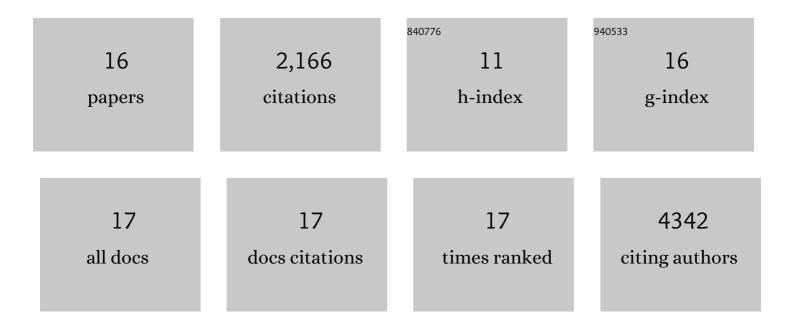
Guy Naamati

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2645173/publications.pdf Version: 2024-02-01



<u>CUV Νλαματι</u>

#	Article	IF	CITATIONS
1	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. Nucleic Acids Research, 2018, 46, D802-D808.	14.5	489
2	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. Genome Research, 2017, 27, 885-896.	5.5	464
3	Ensembl Genomes 2020—enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	14.5	416
4	Gene expression variability across cells and species shapes innate immunity. Nature, 2018, 563, 197-202.	27.8	165
5	Gramene 2018: unifying comparative genomics and pathway resources for plant research. Nucleic Acids Research, 2018, 46, D1181-D1189.	14.5	147
6	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	14.5	141
7	Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. Nucleic Acids Research, 2021, 49, D1452-D1463.	14.5	83
8	ClanTox: a classifier of short animal toxins. Nucleic Acids Research, 2009, 37, W363-W368.	14.5	78
9	A roadmap for gene functional characterisation in crops with large genomes: Lessons from polyploid wheat. ELife, 2020, 9, .	6.0	78
10	MiRror: a combinatorial analysis web tool for ensembles of microRNAs and their targets. Bioinformatics, 2010, 26, 1920-1921.	4.1	53
11	Genetic Diversity, Population Structure and Linkage Disequilibrium Assessment among International Sunflower Breeding Collections. Genes, 2020, 11, 283.	2.4	17
12	Susceptibility of the human pathways graphs to fragmentation by small sets of microRNAs. Bioinformatics, 2012, 28, 983-990.	4.1	9
13	A predictor for toxin-like proteins exposes cell modulator candidates within viral genomes. Bioinformatics, 2010, 26, i482-i488.	4.1	8
14	Expansion of tandem repeats in sea anemone Nematostella vectensis proteome: A source for gene novelty?. BMC Genomics, 2009, 10, 593.	2.8	7
15	Scripting Analyses of Genomes in Ensembl Plants. Methods in Molecular Biology, 2022, 2443, 27-55.	0.9	6
16	Kâ€mer counting and curated libraries drive efficient annotation of repeats in plant genomes. Plant Genome, 2021, 14, e20143.	2.8	5