

Guy Naamati

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2645173/publications.pdf>

Version: 2024-02-01

16
papers

2,166
citations

840776

11
h-index

940533

16
g-index

17
all docs

17
docs citations

17
times ranked

4342
citing authors

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