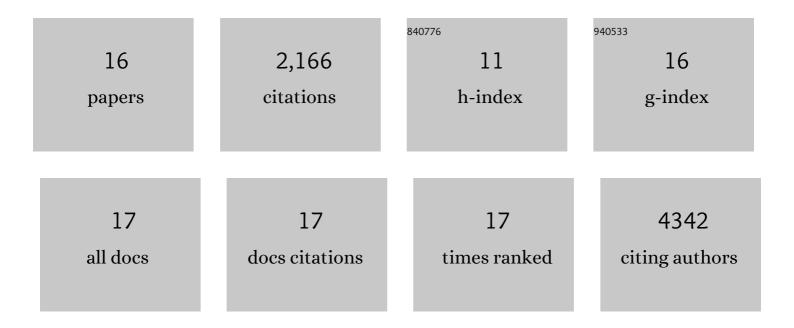
Guy Naamati

List of Publications by Year in descending order

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Ουν Νλαματι

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