Einat Hazkani-Covo

List of Publications by Year
in descending order

24 papers	1,796 citations	687363 13 h-index	642732 23 g-index
26 all docs	26 docs citations	26 times ranked	2819 citing authors

#	Article	IF	Citations
1	Molecular Poltergeists: Mitochondrial DNA Copies (numts) in Sequenced Nuclear Genomes. PLoS Genetics, 2010, 6, e1000834.	3.5	522
2	Endosymbiotic origin and differential loss of eukaryotic genes. Nature, 2015, 524, 427-432.	27.8	251
3	Directed networks reveal genomic barriers and DNA repair bypasses to lateral gene transfer among prokaryotes. Genome Research, 2011, 21, 599-609.	5.5	215
4	A Comparative Analysis of numt Evolution in Human and Chimpanzee. Molecular Biology and Evolution, 2007, 24, 13-18.	8.9	113
5	Evolutionary Dynamics of Large Numts in the Human Genome: Rarity of Independent Insertions and Abundance of Post-Insertion Duplications. Journal of Molecular Evolution, 2003, 56, 169-174.	1.8	110
6	Numt-Mediated Double-Strand Break Repair Mitigates Deletions during Primate Genome Evolution. PLoS Genetics, 2008, 4, e1000237.	3.5	106
7	Endosymbiotic gene transfer from prokaryotic pangenomes: Inherited chimerism in eukaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10139-10146.	7.1	102
8	High-Resolution Genome-Wide Analysis of Irradiated (UV and Î³-Rays) Diploid Yeast Cells Reveals a High Frequency of Genomic Loss of Heterozygosity (LOH) Events. Genetics, 2012, 190, 1267-1284.	2.9	71
9	In search of the vertebrate phylotypic stage: A molecular examination of the developmental hourglass model and von Baer's third law. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2005, 304B, 150-158.	1.3	67
10	Mitochondrial Insertions into Primate Nuclear Genomes Suggest the Use of numts as a Tool for Phylogeny. Molecular Biology and Evolution, 2009, 26, 2175-2179.	8.9	48
11	LINKING BIG: THE CONTINUING PROMISE OF EVOLUTIONARY SYNTHESIS. Evolution; International Journal of Organic Evolution, 2010, 64, 871-880.	2.3	48
12	Quantifying the Number of Independent Organelle DNA Insertions in Genome Evolution and Human Health. Genome Biology and Evolution, 2017, 9, 1190-1203.	2.5	24
13	The Prevalence and Evolutionary Conservation of Inverted Repeats in Proteobacteria. Genome Biology and Evolution, 2018, 10, 918-927.	2.5	19
14	The Evolutionary History of Prosaposin: Two Successive Tandem-Duplication Events Gave Rise to the Four Saposin Domains in Vertebrates. Journal of Molecular Evolution, 2002, 54, 30-34.	1.8	16
15	Nonrandom Distribution of Interhomolog Recombination Events Induced by Breakage of a Dicentric Chromosome inSaccharomyces cerevisiae. Genetics, 2013, 194, 69-80.	2.9	16
16	Mosaic mitochondrial-plastid insertions into the nuclear genome show evidence of both non-homologous end joining and homologous recombination. BMC Evolutionary Biology, 2018, 18, 162.	3.2	15
17	Limited DNA repair gene repertoire in Ascomycete yeast revealed by comparative genomics. Genome Biology and Evolution, 2019, 11, 3409-3423.	2.5	15
18	Evolution of multicellularity in Metazoa: comparative analysis of the subcellular localization of proteins in Saccharomyces, Drosophila and Caenorhabditis. Cell Biology International, 2004, 28, 171-178.	3.0	11

#	Article	IF	Citations
19	Whole Genome Sequence Analysis of Mutations Accumulated in rad27 Î" Yeast Strains with Defects in the Processing of Okazaki Fragments Indicates Template-Switching Events. G3: Genes, Genomes, Genetics, 2017, 7, 3775-3787.	1.8	8
20	A Burst of Numt Insertion in the Dasyuridae Family During Marsupial Evolution. Frontiers in Ecology and Evolution, 2022, 10, .	2.2	6
21	Evolutionary conservation of bacterial operons: does transcriptional connectivity matter?. Genetica, 2005, 124, 145-166.	1.1	5
22	Failure to Recover Major Events of Gene Flux in Real Biological Data Due to Method Misapplication. Genome Biology and Evolution, 2018, 10, 1198-1209.	2.5	4
23	Alternative Functional rad21 Paralogs in Fusarium oxysporum. Frontiers in Microbiology, 2019, 10, 1370.	3.5	3
24	Protein innovation through template switching in the Saccharomyces cerevisiae lineage. Scientific Reports, 2021, 11, 22558.	3.3	1