Fernando Cruz

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9143566/publications.pdf

Version: 2024-02-01

22	1,034	759190 12	677123 22
papers	citations	h-index	g-index

27	27	27	2130
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome sequence of the olive tree, Olea europaea. GigaScience, 2016, 5, 29.	6.4	201
2	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131
3	The Legacy of Domestication: Accumulation of Deleterious Mutations in the Dog Genome. Molecular Biology and Evolution, 2008, 25, 2331-2336.	8.9	129
4	Massive gene presence-absence variation shapes an open pan-genome in the Mediterranean mussel. Genome Biology, 2020, 21, 275.	8.8	105
5	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472.	5.7	94
6	Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. Nature Communications, 2020, 11, 2631.	12.8	57
7	A Reference Genome Sequence for the European Silver Fir (Abies albaMill.): A Community-Generated Genomic Resource. G3: Genes, Genomes, Genetics, 2019, 9, 2039-2049.	1.8	53
8	Distribution and abundance of microsatellites in the genome of bivalves. Gene, 2005, 346, 241-247.	2.2	42
9	Genomic evidence for recurrent genetic admixture during the domestication of Mediterranean olive trees (Olea europaea L.). BMC Biology, 2020, 18, 148.	3.8	39
10	Novel efficient genome-wide SNP panels for the conservation of the highly endangered Iberian lynx. BMC Genomics, 2017, 18, 556.	2.8	31
11	Phylogenomics Identifies an Ancestral Burst of Gene Duplications Predating the Diversification of Aphidomorpha. Molecular Biology and Evolution, 2020, 37, 730-756.	8.9	29
12	The evolutionary forces maintaining a wild polymorphism of Littorina saxatilis: model selection by computer simulations. Journal of Evolutionary Biology, 2005, 18, 191-202.	1.7	22
13	The High-Quality Genome Sequence of the Oceanic Island Endemic Species Drosophila guanche Reveals Signals of Adaptive Evolution in Genes Related to Flight and Genome Stability. Genome Biology and Evolution, 2018, 10, 1956-1969.	2.5	14
14	The Genome Sequence of the Eastern Woodchuck (Marmota monax) â€“ A Preclinical Animal Model for Chronic Hepatitis B. G3: Genes, Genomes, Genetics, 2019, 9, 3943-3952.	1.8	13
15	Emergence of 16S rRNA methyltransferases among carbapenemase-producing Enterobacterales in Spain studied by whole-genome sequencing. International Journal of Antimicrobial Agents, 2022, 59, 106456.	2.5	11
16	Development of whole-genome multiplex assays and construction of an integrated genetic map using SSR markers in Senegalese sole. Scientific Reports, 2020, 10, 21905.	3.3	9
17	Distribution Properties of Polymononucleotide Repeats in Molluscan Genomes. Journal of Heredity, 2005, 96, 40-51.	2.4	7
18	The expansion of amino-acid repeats is not associated to adaptive evolution in mammalian genes. BMC Genomics, 2009, 10, 619.	2.8	6

#	Article	IF	Citations
19	Genetics and genomics in wildlife studies: Implications for ecology, evolution, and conservation biology. BioEssays, 2012, 34, 245-246.	2.5	6
20	The Genome Sequence of the Octocoral Paramuricea clavata â€“ A Key Resource To Study the Impact of Climate Change in the Mediterranean. G3: Genes, Genomes, Genetics, 2020, 10, 2941-2952.	1.8	6
21	Evidence of positive selection on the Atlantic salmon CD3Î³Î´ gene. Immunogenetics, 2007, 59, 225-232.	2.4	4
22	Combining Nanopore and Illumina Sequencing Permits Detailed Analysis of Insertion Mutations and Structural Variations Produced by PEG-Mediated Transformation in Ostreococcus tauri. Cells, 2021, 10, 664.	4.1	3