

Eugenio LÃ³pez-Cortegano

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/916285/publications.pdf>

Version: 2024-02-01

16
papers

259
citations

933447

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996975

15
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19
all docs

19
docs citations

19
times ranked

314
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of fitness under different breeding designs in conservation programs. <i>Animal Conservation</i> , 2023, 26, 86-102.	2.9	3
2	purgeR: inbreeding and purging in pedigreed populations. <i>Bioinformatics</i> , 2022, 38, 564-565.	4.1	5
3	Inbred lab mice are not isogenic: genetic variation within inbred strains used to infer the mutation rate per nucleotide site. <i>Heredity</i> , 2021, 126, 107-116.	2.6	20
4	Conservation Priorities Analysis of Chinese Indigenous Pig Breeds in the Taihu Lake Region. <i>Frontiers in Genetics</i> , 2021, 12, 558873.	2.3	14
5	De Novo Mutation Rate Variation and Its Determinants in <i>Chlamydomonas</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 3709-3723.	8.9	19
6	Highly pleiotropic variants of human traits are enriched in genomic regions with strong background selection. <i>Human Genetics</i> , 2021, 140, 1343-1351.	3.8	3
7	Long-term exhaustion of the inbreeding load in <i>Drosophila melanogaster</i> . <i>Heredity</i> , 2021, 127, 373-383.	2.6	20
8	Genetic purging in captive endangered ungulates with extremely low effective population sizes. <i>Heredity</i> , 2021, 127, 433-442.	2.6	9
9	Mate choice based on body size similarity in sexually dimorphic populations causes strong sexual selection. <i>Animal Behaviour</i> , 2020, 160, 69-78.	1.9	10
10	GWEHS: A Genome-Wide Effect Sizes and Heritability Screener. <i>Genes</i> , 2019, 10, 558.	2.4	2
11	Optimal Management of Genetic Diversity in Subdivided Populations. <i>Frontiers in Genetics</i> , 2019, 10, 843.	2.3	24
12	Inferring the Nature of Missing Heritability in Human Traits Using Data from the GWAS Catalog. <i>Genetics</i> , 2019, 212, 891-904.	2.9	34
13	metapop2: Reimplementation of software for the analysis and management of subdivided populations using gene and allelic diversity. <i>Molecular Ecology Resources</i> , 2019, 19, 1095-1100.	4.8	35
14	Detection of genetic purging and predictive value of purging parameters estimated in pedigreed populations. <i>Heredity</i> , 2018, 121, 38-51.	2.6	12
15	Estimation of genetic purging under competitive conditions. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1856-1870.	2.3	31
16	Predictive Model and Software for Inbreeding-Purging Analysis of Pedigreed Populations. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3593-3601.	1.8	14