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- 546 De novo Assembly and Comparative Analyses of Mitochondrial Genomes in Piperales. **2023**, 15, o
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- 422 Genome-wide phylogeography reveals cryptic speciation in the circumglobal planktonic calcifier *Limacina bulimoides*. ○
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- 404 A view of the pan-genome of domesticated Cowpea (*Vigna unguiculata* [L.] Walp.). o
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- 397 Recovery of metagenomic data from the *Aedes aegypti* microbiome using a reproducible snakemake pipeline: MINUUR. 8, 131 o
- 396 Identification of a suppressor for the wheat stripe rust resistance gene Yr81 in Chinese wheat landrace Dahongpao. **2023**, 136, o
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- 387 Multiple gene co-options underlie the rapid evolution of sexually deceptive flowers in *Gorteria diffusa*. **2023**, o
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- 385 Cost-effective genotyping for classical congenital adrenal hyperplasia (CAH) due to 21-hydroxylase deficiency (21-OHD) in resource-poor settings: multiplex ligation probe amplification (MLPA) with/without sequential next-generation sequencing (NGS). o
- 384 Metagenomic analysis of coastal Kenya female *Aedes aegypti* mosquito RNA metaviromes reveal presence of diverse insect specific viruses. 8, 136 o
- 383 Rapid systemic responses of *Arabidopsis* to waterlogging stress. o
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- 381 Coordination of Alternative Splicing and Alternative Polyadenylation revealed by Targeted Long-Read Sequencing. o
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- 350 Fine mapping and candidate gene analysis of CaFCD1 affecting cuticle biosynthesis in *Capsicum annuum* L.. **2023**, 136, ○
- 349 Evidence for ancient selective sweeps followed by differentiation among three species of *Sphyrapicus* sapsuckers. ○
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- 345 Characterization of stilbene synthase genes by comparative genome sequencing of *Vitis flexuosa* with high contents of stilbene compounds to *Vitis vinifera* genome. ○
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- 339 The genomic epidemiology of *Escherichia albertii* infecting humans and birds in Great Britain. **2023**, 14, ○
- 338 Characterization of centromeric DNA of *Gossypium anomalum* reveals sequence-independent enrichment dynamics of centromeric repeats. **2023**, 31, ○
- 337 Discovery of SNP Molecular Markers and Candidate Genes Associated with Sacbrood Virus Resistance in *Apis cerana cerana* Larvae by Whole-Genome Resequencing. **2023**, 24, 6238 ○

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- 332 Histone deacetylase 1 maintains lineage integrity through histone acetylome refinement during early embryogenesis. 12, ○
- 331 Genome-wide identification and annotation of SNPs and their mapping in candidate genes related to milk production and fertility traits in Badri cattle. **2023**, 55, ○
- 330 Introgression of morphological, phenological and productivity traits along with disease resistance from *Cicer pinnatifidum* into cultivated chickpea: a success story. **2023**, 219, ○
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- 324 Population transcriptomics uncover the relative roles of positive selection and differential expression in *Batrachium bungei* adaptation to the Qinghai-Tibetan plateau. ○
- 323 Preadapted to adapt: underpinnings of adaptive plasticity revealed by the downy brome genome. **2023**, 6, ○
- 322 Patterns of within-host spread of *Chlamydia trachomatis* between vagina, endocervix and rectum revealed by comparative genomic analysis. 14, ○
- 321 RNA-seq analysis of tomato genotypes resistant to bacterial spot (*Xanthomonas perforans*) race T4. **2023**, 147-154 ○
- 320 Diversity of RNA editing in chloroplast transcripts across three main plant clades. **2023**, 309, ○
- 319 Identification of CaPs locus involving in purple stripe formation on unripe fruit, reveals allelic variation and alternative splicing of R2R3-MYB transcription factor in pepper (*Capsicum annuum* L.). 14, ○

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- 317 Nascent evolution of recombination rate differences as a consequence of chromosomal rearrangements. ○
- 316 Arabidopsis TRB proteins function in H3K4me3 demethylation by recruiting JMJ14. **2023**, 14, ○
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- 314 The genome of *Lactuca saligna*, a wild relative of lettuce, provides insight into non-host resistance to the downy mildew *Bremia lactucae*. ○
- 313 Insights into the genetic determination of tuber shape and eye depth in potato natural population based on autotetraploid potato genome. 14, ○
- 312 Comprehensive proteogenomic characterization of early duodenal cancer reveals the carcinogenesis tracks of different subtypes. **2023**, 14, ○
- 311 ULK4 and Fused/STK36 interact to mediate assembly of a motile flagellum. ○
- 310 STING inhibits the reactivation of dormant metastasis in lung adenocarcinoma. 1
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- 308 Integrative multi-omic sequencing reveals the MMTV-Myc mouse model mimics human breast cancer heterogeneity. ○
- 307 A reference assembly for the legume cover crop, hairy vetch (*Vicia villosa*). ○
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