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GENOME SEQUENCING

# The Complete Genome Sequence of Ajuga reptans (Lamiaceae, Lamiales), Bugleweed

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Biodiversity Genomes

We present the whole genome sequence of *Ajuga reptans.* Illumina paired-end reads were assembled by a *de novo* method followed by a finishing step. The raw and assembled data are publicly available via GenBank: Sequence Read Archive (SRR24502601) and assembled genome (JAUEKW000000000).

## Methods

A single leaf from a cultivated plant was used for this study.

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. A paired-end sequencing library was constructed using the Illumina TruSeq kit, according to the manufacturer's instructions. The library was sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format. The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich, Nurk, Antipov, et al. 2012) followed by a finishing step using Zanfona v1.0 (Kieras 2021) to make additional contig joins based on conserved regions in related species.

## Data availability

Raw reads (SRR24502601) and the assembled genome (JAUEKW000000000) are available in Genbank.

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