

## GENOME SEQUENCING

# The complete genome sequences of 14 species of demosponges (Demospongiae, Porifera)

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## Biodiversity Genomes

We present complete genome sequences of 14 species of demosponges.

## Methods

Tissues from single, wild-collected individuals were used for this study. DNA extraction was performed using the Qiagen DNEasy genomic extraction kit using the standard process. Paired-end sequencing libraries were constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger et al. 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras et al. 2021).

## Results and Data Availability

All raw data and assembled genomes are available via Genbank.

| taxname                    | specimen_voucher | accession   |
|----------------------------|------------------|-------------|
| Asbestopluma belgicae      | USNM 43495       | SRR39277383 |
| Asbestopluma ramosa        | USNM 34704       | SRR39288786 |
| Axoniderma corona          | USNM 1478697     | SRR39297573 |
| Chondrocladia clavata      | USNM 43601       | SRR39288787 |
| Chondrocladia grandis      | USNM 1558251     | SRR39277469 |
| Chondrocladia lyra         | USNM 1424173     | SRR39277382 |
| Chondrocladia verticillata | USNM 1482939     | SRR39277468 |
| Chondrocladia virgata      | USNM 1234806     | SRR39277575 |
| Cladorhiza bathyrcinoides  | USNM 1695236     | SRR39277605 |
| Guitarra abbotti           | USNM 1478705     | SRR39277576 |
| Guitarra fimbriata         | USNM 1478707     | SRR39277380 |
| Lycopodina subtile         | USNM 1424165     | SRR39277481 |
| Mycale microsigmatosa      | USNM 1660175     | SRR39268251 |
| Mycale tylota              | USNM 1478734     | SRR39277589 |

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## REFERENCES

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- Kieras, M., K. O’Neill, and S. Pirro. 2021. *Zanfona, a genome assembly finishing tool for paired-end Illumina reads*. <https://github.com/zanfona734/zanfona>.