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## 🌐 Protocols for the assembly and annotation of snake genomes V.2

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### ABSTRACT

**Background:** Snakes are one of the most important wildlife resources and are widely distributed. *Bungarus multicinctus* is a highly venomous snake and is distributed in central and southern China. In recent years, venomous snake bites have gradually increased. Genomic resources are significant for understanding the evolution of a specie and the molecular mechanisms of toxin production.

**Find:** Here we present a highly- continuous genome assembly of *B. multicinctus*. The genome size of *B. multicinctus* is 1.51Gb. The maximal length of scaffold is 39.68M and the N50 length is 6.55M. The *B. multicinctus* has a GC content of 37.8%.

**Keywords:** Bungarus  
multicinctus, genome  
assembly, protocols' collection

## FILES

### Protocol



NAME

DNA extraction protocol for snake genomic sequencing by using AxyPrep™ Multisource Genomic DNA Miniprep Kit

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### Protocol



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RNA extraction protocol for snake genomes using TRIZOL reagent (Invitrogen)

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⌘ BGISEQ-500 WGS library construction

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STLFR library construction for snake genomes

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The annotation pipeline for the genome of a snake

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