

{rokbox title=|The main plot is divided into 1,000 size-ordered bins around the circumference, with each bin representing 0.1% of the 3,249,387,216 bp assembly including the mitochondrial genome :: Image: Authors|
thumb=|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-erga-bge-genome-bernal-2025-thumb-et-al.jpg|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-erga-bge-genome-bernal-2025-et-al.jpg{/rokbox}

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[**ERGA-BGE genome of *Stigmatoteuthis arcturi* Robson, 1948: the jewelled squid**](#)

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Abstract: The *Stigmatoteuthis arcturi* reference genome offers a valuable resource for understanding the evolutionary patterns of oceanic squids, who perform important ecological roles as both predators and prey in mesopelagic and deep-sea environments, while their genomes remain understudied. The entirety of the genome sequence was assembled into 46 contiguous chromosomal pseudomolecules. This chromosome-level assembly encompasses 3.25 Gb, composed of 1,268 contigs and 497 scaffolds, with contig and scaffold N50 values of 11.0 Mb and 74.6 Mb, respectively.

Keywords: *Stigmatoteuthis arcturi*, Genome assembly, European Reference Genome Atlas, Biodiversity Genomics Europe, Earth Biogenome Project, Jewelled squid.