18S RRNA SEQUENCING
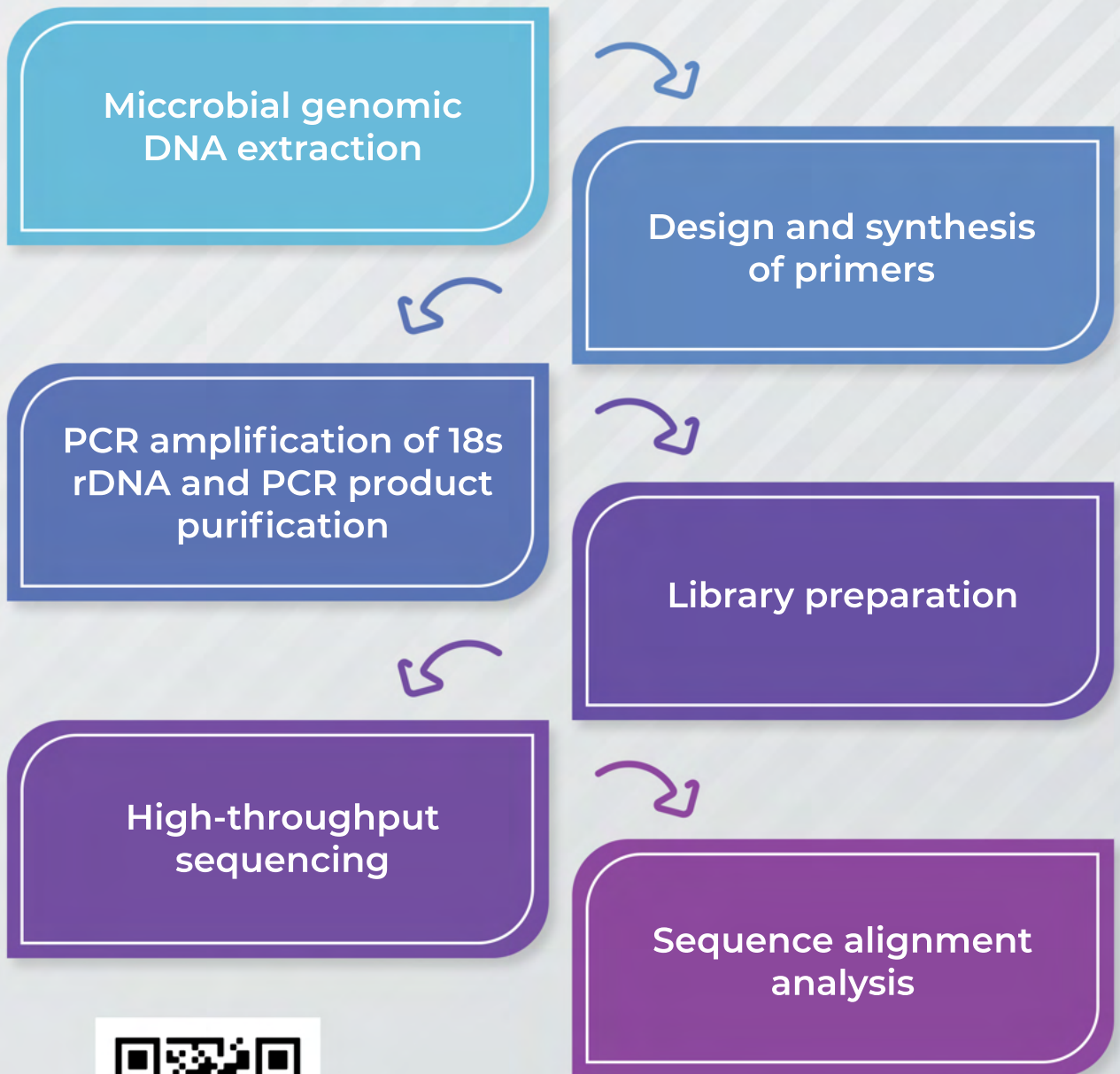
18S RRNA SEQUENCING

To identify, categorize, and quantify microorganisms in complex biological mixes, such as samples taken from the environment and the gut, 18S rRNA gene sequencing is frequently used. Different eukaryotic 18S rRNA gene sequences can be used to build a phylogenetic tree, which can be used to examine the genetic diversity and historical ties of eukaryotes. Due to the significant roles that eukaryotic microorganisms play as producers, parasites, predators, and scavengers in most ecological situations, 18S rRNA sequencing is a powerful technique for analyzing the taxonomy, evolution, ecology, and diversity of eukaryotic microbes. It is also possible to find eukaryotes linked to human and animal sickness using 18S rRNA sequencing.

In recent years, partial 18S rRNA sequences have been used as molecular DNA markers in high-throughput DNA sequencing techniques. The advantage of using 18S rRNA is the abundance of sequencing information available in open databases like GenBank. In addition, there are both conserved sections and variable regions in the eight regions of the 18S rRNA found in eukaryotes (V1-V9; no V6 region). The variable sections, which are appropriate for classification standards at the species level and above, reflect the differences between species whereas the conserved portions reflect the genetic relationships between biological species. The greatest option for 18S rRNA gene analysis and annotation among them is the V4 region since it has the most comprehensive database information and the best classification impact.

The identification and molecular systematics study of eukaryotic microorganisms, such as microalgae and protozoa, is currently largely conducted using the 18S rRNA gene.

OUR SERVICE PROCESS

Miccrobial genomic DNA extraction

Design and synthesis of primers

PCR amplification of 18s rDNA and PCR product purification

Library preparation

High-throughput sequencing

Sequence alignment analysis

MAKING THE UNKNOWN KNOWN...