

MICROBIAL IDENTIFICATION

Our Microbial Identification service is a great alternative to biochemical-based microbial identification, and through sequencing of the 16S gene AGRF can screen your bacterial sample to the genus / species level.



Key Highlights

All bacteria contain the 16S ribosomal RNA gene (16S), which contains conserved and variable regions. Detection of the conserved region enables all bacterial kingdoms from within a sample to be detected. Identification of the variable regions enables deeper taxonomic resolution.

AGRF can screen your bacterial sample to the genus / species level via a nucleic acid based sequencing method.

16S Sequencing

DNA sequencing of the 16S component of the bacterial genome has become the ideal tool for microbial identification. A 700bp portion of the 16S gene (found in all bacteria) is amplified and sequenced.

Data from your sample is then compared against the AGRF-curated sequence database, which contains only microbial sequences.

Key Highlights

16S Sequencing Service:

- Samples can be screened to the genus / species level
- Our 16S sequencing service is a NATA-accredited service

Data Delivery

Each batch submitted will receive a batch summary report and for each sample processed, the following files are provided:

- The raw chromatogram trace file (sample.ab1)
- A trimmed FASTA formatted text file - reads are trimmed on the basis of the quality values assigned to the basecalls (sample.fa)
- A BLAST of the trimmed FASTA file, this text file comprises the top 20 hits against our in-house 16S database (sample.bn)
- A PDF report summarising the top five hits from the BLAST file (sample.bn.pdf)

Our funding partners

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