

An alternative to biochemical based microbial identification.



What is Microbial Identification?

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.



Our funding partners

AGRF is a not-for-profit organisation supported by the Commonwealth Government infrastructure schemes administered through Bioplatforms Australia.

These schemes include NCRIS, EIF, Super Science Initiative CRIS and NCRIS 2



BIOPLATFOMRS
AUSTRALIA

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)

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