

Pan-Prokaryote riboPOOL

Universal, Affordable Ribosomal RNA Depletion For Microbes (Bacteria/Archaea)

- ✓ Broad microbial coverage, suited for Metagenomic/Microbiome analysis
- ✓ Highly efficient rRNA depletion
- ✓ Targets 5S, 16S and 23S rRNA
- ✓ Affordable, versatile solution

The high abundance of ribosomal RNA (rRNA) in prokaryotes (> 85% of total RNA) limits detection efficiency of relevant RNAs by Next-Generation RNA Sequencing (RNA-Seq) or other analysis. The **Pan-Prokaryote riboPOOL** offers a universal and affordable solution to deplete rRNAs from a wide spectrum of bacteria and archaeobacteria.

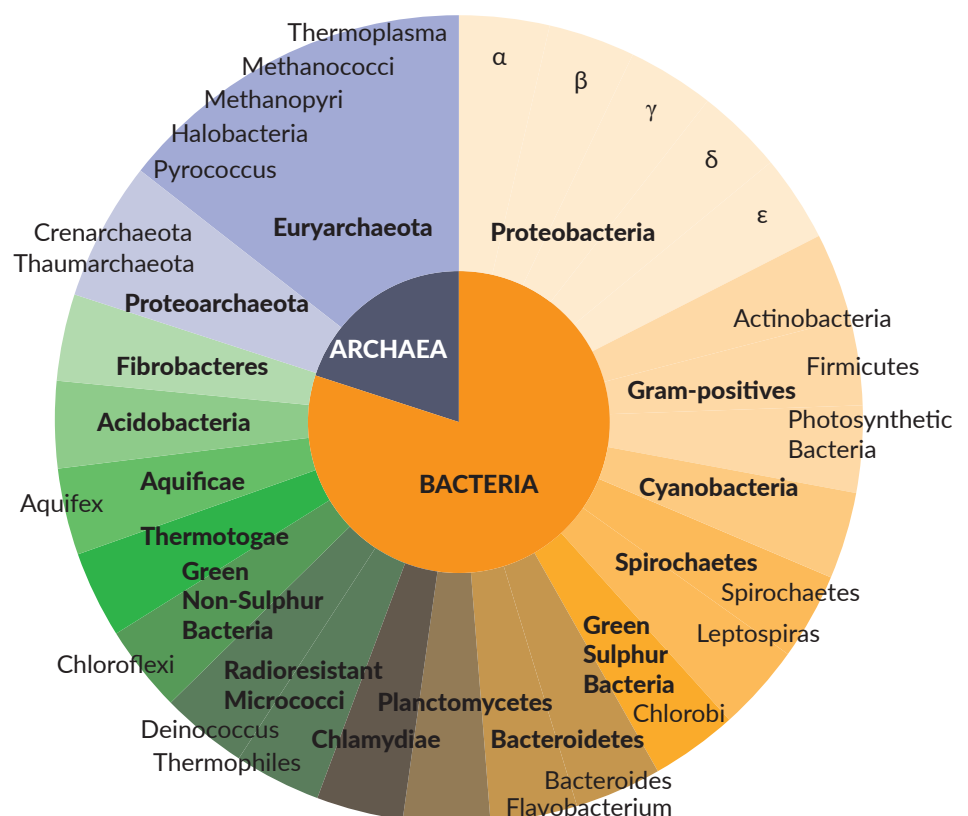
Consisting of a highly complex mixture of biotinylated oligos, optimally designed for maximal coverage of major phyla, the Pan-Prokaryote riboPOOL can be applied to culture preparations, metagenomic or microbiome samples. The Pan-Prokaryote riboPOOL targets 5S, 16S and 23S rRNA, and is used together with streptavidin-coated magnetic beads to remove rRNAs efficiently.

The Pan-Prokaryote riboPOOL is an affordable and versatile solution for the microbiology community and has been RNA-Seq validated for a growing list of species (next page).

Wide-Spectrum Microbial Coverage with Pan-Prokaryote riboPOOL

Designed based on rRNAs from 76 representative species, the Pan-Prokaryote riboPOOL is suited for bacteria and archaeobacteria from these common phyla (inner circle, bold) and sub-phyla (outer circle).

If your species is not within these phyla, please enquire about our **custom riboPOOLS.*



Species Tested	rRNA Depletion Reported
Escherichia coli	✓
Salmonella typhimurium	✓
Vibrio cholerae	✓
Staphylococcus aureus	✓
Thermoanaerobacter kivui	✓
Acinetobacter baumannii	✓
Pseudomonas putida	✓
Moorella thermoacetica	✓
Janthinobacterium sp.	✓
Fusobacterium nucleatum	✓
Helicobacter pylori	✓
Campylobacter jejuni	✓
Clostridioides difficile	✓

Species RNA-Seq Validated with the Pan-Prokaryote riboPOOL

Test results came from various labs with rRNA depletion efficiencies ranging from ~50-98% with majority of species showing > 70% rRNA depletion. Efficiencies may vary across sample types and experimental conditions (last update: 10-May-2019).

Further information:

- Works best for high quality RNA samples
- Suitable for RNA input amounts from 100 ng - 10 µg
- Compatible with various clean-up methods including ethanol precipitation, column-purification and bead-based RNA purification
- Suitable for use in downstream analysis such as RNA-Seq, microarray analysis and quantitative real-time PCR
- Available in 2, 5 and 10 nmol scales for 20, 50 and 100 reactions

Please contact us or our [Distributors](#) for questions and orders.



+49 (0)5152 9020 - support@biozym.com - www.biozym.com

Contact Us

info@sitools.de | +49 (0) 89 12501 4800 | www.sitoolsbiotech.com |  [siTOOLSbiotech](#)