



riboPOOL

Efficient Ribosomal RNA Depletion For Any Species



mRNA and other ncRNA

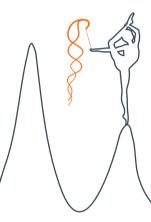


Ribosomal RNAs occupy up to 90% of RNA-Seq reads.

RIbosomal RNAs (rRNA) are highly abundant and limit detection of relevant coding and non-coding RNAs by Next Generation RNA Sequencing (RNA-Seq), microarray and other analysis. Their removal greatly improves and economizes RNA-Seq experiments.

riboPOOL[™] for efficient and flexible ribosomal RNA depletion

riboPOOL uses siTOOLs' technology of high complexity pooling of optimally designed biotinylated oligos to deplete rRNAs with high efficiency and specificity. Available for any species or any RNA sequence, riboPOOLs provide a superbly flexible solution for scientists with demanding sequencing applications.



Great for metatranscriptomics and microbial sequencing

For microbial sequencing, the Pan-Prokaryote riboPOOL can be broadly applied across many microbial species. Combination riboPOOLs containing up to four existing riboPOOLs enable rRNA depletion from samples containing multiple species such as pathogen infected tissue or metagenomic samples (e.g. soil, sludge).



riboPOOL Key Benefits

Any Species

Affordable

Deplete rRNAs from any species. Diverse species in-stock with Custom riboPOOLs on-demand. riboPOOLs are priced competitively and suitable for high-throughput sequencing.

Highly Efficient and Specific

Human and mouse riboPOOLs depleted > 95% cytoplasmic and mitochondrial rRNAs.

HPLC Purified

Low risk of contaminants.

Applicable for Nonpolyadenylated RNA

Detects non-polyadenylated RNA (e.g. snoRNA, IncRNA, histones) with uniform transcript coverage.



Suitable for Metatranscriptomics

Pan-prokaryote and Combination riboPOOLs available for samples containing multiple species.

Deplete Custom RNA

Deplete any abundant RNA of choice. E.g. globin from whole blood samples

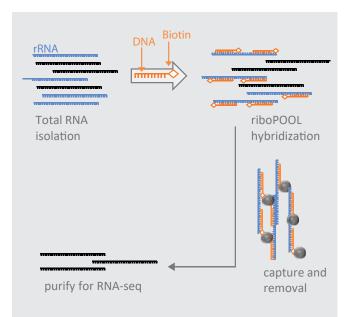
Fast Workflow

Workflow completed in ~70 min with column-based purification.

Broad Input Range

Efficient rRNA depletion between 100 ng and 5 µg input RNA.

riboPOOL Workflow





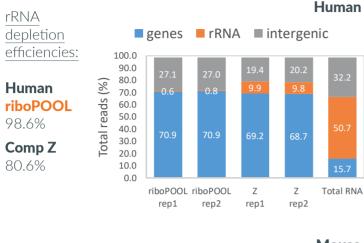
Remaining relevant RNAs are purified by ethanol, silica column or SPRI beads prior to downstream analysis.

*Time required dependant on clean-up method



Data with riboPOOL

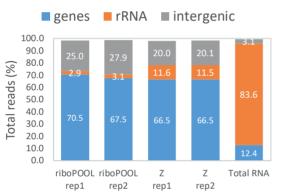
10% greater rRNA depletion efficiency with riboPOOL



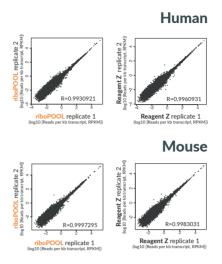
Mouse

Mouse riboPOOL 96.4%

Comp Z 86.1%



High reproducibility with both reagents



Study performed by Core Unit Systems Medicine (University of Würzburg) and IMGM Laboratories GmbH with protocol developed by Kim et al. (University of Bayreuth)₁. RNA (1 µg, RIN \geq 7.5) from HeLa cells or mouse embryonic fibroblasts subject to rRNA depletion with human or mouse riboPOOLs vs. human/mouse/rat rRNA depletion kit from Competitor Z and sequenced with Illumina TruSeq® Stranded Total RNA technology.

1 Kim, I et. al (2019) Efficient depletion of ribosomal RNA for RNA sequencing in planarians. bioRxiv (**Preprint with riboPOOL**)

List of Ready-Made riboPOOLs

riboPOOLs for Eukaryotes

- Homo sapien (human)
- Mus musculus/Rattus norvegicus (mouse/rat)
- Drosophila melanogaster (fruitfly)
- Arabidopsis thaliana
- Danio rerio (zebrafish)

Sacchromyces cerevisiae (yeast)

- Pichia pastoris (yeast)
- Bombyx morii (silkworm)
- Ustilago maydis
- Amphimedon queenslandica (sponge)
- Schmidtea mediterranea (planaria)
- Platia stali (brown winged green bug)

Chinchilla Laginera

Last Update: 14-Oct-2019



riboPOOLs for Prokaryotes

- Pan-Prokaryote (Universal Microbe)
- Escherichia coli
- Pseudomonas aeruginosa
- Staphylococcus aureus
- Bacillus subtilis
- Salmonella enterica
- Stenotrophomonas sp.
- Caulobacter crescentus
- Haloferax volcanii
- **Clostridium perfringens**

riboPOOLs for Abundant RNAs

Human Globin (mRNA)

Special Applications with riboPOOL

Metatranscriptomics with Pan-Prokaryote riboPOOL

The Pan-Prokaryote riboPOOL, designed for universal microbial rRNA depletion, has been applied for metagenomic samples. Depletion efficiency however may vary between species and sample quality.

Depletion of abundant RNAs

Aside from rRNA, depletion of abundant tissue-specific mRNAs (e.g. globin) or other abundant RNAs found in sequencing data can be performed with riboPOOLs.

Ribosome profiling

riboPOOLs have been applied for ribosome profiling samples with depletion efficiencies of ~50-80%. Please contact us for more information.

Depletion of rRNAs from multiple species with Combination riboPOOLs

Combination riboPOOLs are mixtures of up to four riboPOOLs combined in custom ratios for use in samples containing multiple species. Please refer to **riboPOOL Application Note** on website for data on the Human/Mouse/Pan-Prokaryote Combination riboPOOL.

Product Properties

- 3'-biotinylated, single-stranded DNA
- HPLC-purified
- Provided as probes alone with nuclease-free water **OR** in kits that include buffers, streptavidin-magnetic beads and ethanol precipitation reagents. A protocol is provided for either format.
- Delivered as freeze-dried powder at room-temperature.
- Upon resuspension, riboPOOLs are stable up to 6 months when stored at or below -20°C. Store in aliquots to avoid multiple freeze-thaw cycles.

Ordering Information

| Products available | Scales available |
|--|--|
| riboPOOL probes | 20, 50 or 100 reactions |
| Combination riboPOOL probes | 20, 50 or 100 reactions |
| Human/Mouse riboPOOL kit | 6 (trial), 12, 24 or 96 reactions |
| Pan-Prokaryote/Globin/Other Species riboPOOL kit | 6 (trial), 12, 24 or 96 reactions |
| Combination riboPOOL kit | 12, 24 or 96 reactions |
| Custom riboPOOL set up service | (one-time purchase required for new species) |



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