

## Accelerating Insights from Bacteria

Mining meta-transcriptomes for functional activities, characterizing production strains, and more...

## Streamlined Bacterial Transcriptomics with RiboCop and CORALL

**Sequence what matters most!** RNA-Seq of ribo-depleted bacterial RNA affords an unbiased view of the transcriptome and allows analysis of mRNA, non-coding RNAs and insights to host-microbe responses.

Bacterial total RNA is comprised of large amounts of **undesired ribosomal RNA (rRNA) accounting for up to ~99 % of all transcripts**. Lexogen's RiboCop rRNA Depletion Kits for Bacteria **remove undesired 5S, 16S and 23S rRNA** from intact as well as degraded input RNA. Ribodepletion thus affords an unbiased view of the transcriptome, including non-coding and regulatory transcripts.

### Preserve RNA Integrity with Fragmentation-free rRNA Removal and Library Preparation

RiboCop uses a set of affinity probes designed for specific and efficient depletion of rRNA sequences from intact as well as degraded input RNA. Lexogen's sophisticated probe design minimizes off-target effects that can distort NGS data.

Input amounts as low as 1 ng and up to 1 µg total RNA are applicable. No enzymatic reactions or mechanical shearing steps are involved, **preserving full-length transcripts intact for downstream processing**. RiboCop for Bacteria is ideally suited for Next Generation Sequencing (NGS) approaches and seamlessly integrates into fragmentation-free CORALL RNA-Seq library preparation with UMIs (Fig. 1). In addition, RiboCop is compatible with all common RNA-Seq library preps.

### Broad Species Compatibility and Efficient Depletion

RiboCop enriches RNAs of interest across a **wide range of species and inputs** by removing all subclasses of undesired rRNA. Thereby, RiboCop enriches RNAs of interest and affords a comprehensive insight into bacterial transcriptomes (Fig. 2).

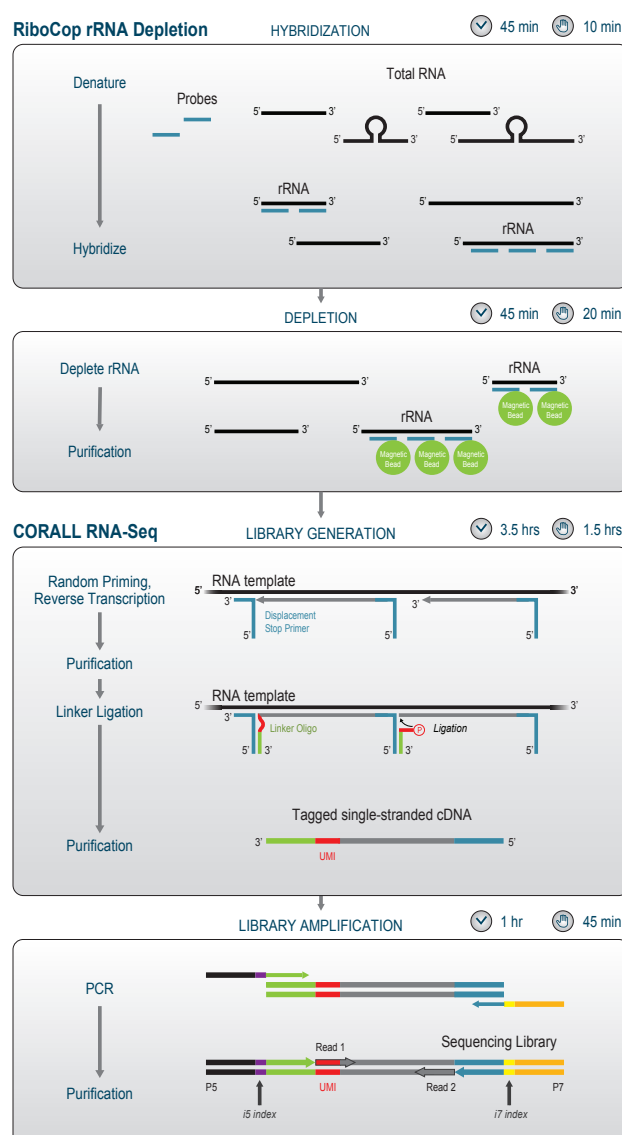


Figure 1 | RiboCop rRNA Depletion and CORALL RNA-Seq Workflow.

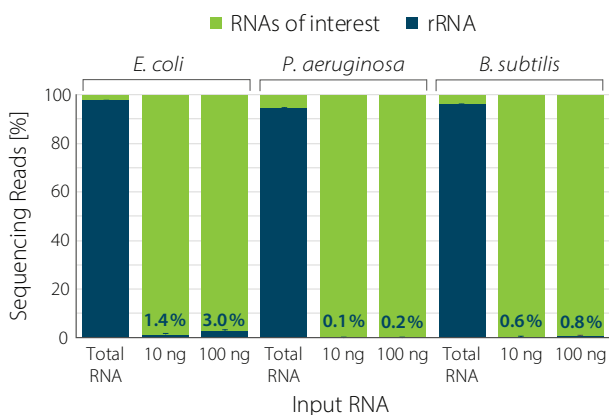


Figure 2 | RiboCop rRNA Depletion for Mixed Bacterial Samples (META) efficiently removes rRNA from various bacterial species as shown for *E. coli* MG1655, *P. aeruginosa* PAO1, and *B. subtilis* 168. The percentage of reads mapping to rRNA is plotted in blue.

## RiboCop and CORALL for Metatranscriptomics

**RiboCop for Mixed Bacterial Samples (META)** is designed for depletion of **complex mixed bacterial populations** and is therefore ideal to study microbiomes from various sources. Table 1 shows depletion rates for human stool samples of various input RNA amounts.

Table 1 | Depletion rates for metatranscriptome analysis.

Sample	% rRNA reads
stool microbiome 10 ng	14.75 (± 1.4)
stool microbiome 100 ng	15.32 (± 1.4)
stool microbiome 1 µg	23.37 (± 1.6)

Stool microbiome analysis using RiboCop META (Cat. No. 125) together with CORALL RNA-Seq for excellent depletion rates.

## Key Benefits for Bacterial RNA-Seq with RiboCop



Unlock the full potential of low input and lowly concentrated samples - RiboCop supports a wide input range from **1 ng - 1 µg** total RNA.



**Enzyme-free rRNA depletion preserves full-length RNA** and is ideally suited for processing even degraded samples.



**Simultaneous one-step depletion of host and pathogen** with convenient combinations of RiboCop for Human/Mouse/Rat and Bacteria kits.

## In Need for Data Analysis?



**Get your results faster!** Lexogen's CORALL RNA-Seq library preparation kits include codes for data analysis on our plug-and-play platform Kangooroo.

## Full NGS Services Available!



Lexogen NGS Services offers a variety of workflow options for bacterial transcriptomics, including expression profiling, non-coding RNA analysis, regulatory small RNA transcriptomics, and DNA sequencing. Simply send your samples and let our experts extract the best data possible for you! Contact us today at [services@lexogen.com](mailto:services@lexogen.com).

## End-to-end Workflow Solutions for RNA-Seq with Bacterial Samples

	RNA Extraction	RNA Preparation	NGS Library Prep	NGS Data Analysis
<b>Whole Transcriptome and Expression Profiling</b>	RNA Extraction	RiboCop for Bacteria	CORALL RNA-Seq	Kangooroo Data Analysis
<b>Host / Pathogen</b>	RNA Extraction	RiboCop HMR / RiboCop META	CORALL RNA-Seq	Custom Bioinformatics
<b>Bacterial Small RNA-Seq</b>	RNA Extraction	RiboCop for Bacteria	Small RNA-Seq	Custom Bioinformatics
<b>Plant-Microbe Interaction</b>	RNA Extraction	RiboCop for Plants / RiboCop META	CORALL RNA-Seq	Custom Bioinformatics
<b>RNA- and DNA-Seq</b>	Lexogen NGS Services			

## Ordering Information

Cat. №	Product Name
125, 126, 127	RiboCop rRNA Depletion for Mixed Bacterial Samples (META), Gram-Negative (G-), or Gram-Positive Bacteria (G+)
144 - 145	RiboCop rRNA Depletion for Human/Mouse/Rat (HMR) or Human/Mouse/Rat Plus Globin (HMR+Globin)
237	RiboCop rRNA Depletion for Plants
171, 175	CORALL RNA-Seq Library Prep Kit with UDI 12 nt Set A1 (171) or Set B1 (175) - further UDI Sets are also available!
183 - 184	same as 171 and 175, including RiboCop rRNA Depletion HMR, UDI Set A1 (183) and Set B1 (184)
185 - 186	same as 171 and 175, including RiboCop rRNA Depletion HMR+Globin, UDI Set A1 (185) and Set B1 (186)

For more information and additional resources, please visit our [website](https://www.lexogen.com).

