

The background of the cover features a series of blue, translucent spheres of various sizes, some of which are connected by thin, light blue lines, creating a molecular or network-like structure. The spheres have a glossy finish with highlights and shadows, giving them a three-dimensional appearance. The overall design is clean and scientific, with a color palette dominated by light blues and greens.

**LEXOGEN**

The RNA Experts

# **RiBO COP™**

Select and Deplete

rRNA Depletion Kit for Yeast

## **User Guide**

Catalog Numbers:  
190 (RiboCop rRNA Depletion Kit for Yeast)

190UG447V0100

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# 1. Overview

Lexogen's RiboCop rRNA Depletion Kit for Yeast enables removal of ribosomal RNA (rRNA) from yeast total RNA and is suited for Next Generation Sequencing (NGS) and similar applications.

RiboCop uses a set of affinity probes for specific depletion of rRNA sequences. The number and positioning of probes are designed for compatibility with intact and fragmented input RNA. RiboCop probes efficiently remove ribosomal RNA and therefore afford a comprehensive view of transcriptome composition. Samples void of 18S, 25S, 5S, 5.8S, 35S 15S, 21S, ACI60\_gr01, ACI60\_gr02 ribosomal sequences are obtained within 1.5 hours of total processing time. No enzymatic reactions or mechanical shearing steps are involved, leaving full-length transcripts intact for downstream processing.

Affinity probes are mixed with total RNA and denatured, facilitating access of probes to target sequences. Afterwards, hybridization is performed at elevated temperature. Depletion beads are washed and used to remove probes that are hybridized to ribosomal RNA from the solution. A final purification step using magnetic beads rounds off the procedure. Recovered RNA may be directly used for NGS library preparation, with sufficient volume for optional quality control. The entire protocol is automation-friendly, using magnetic beads for depletion and purification purposes.

The recommended input range for RiboCop for Yeast is 10 - 1,000 ng of total RNA. RiboCop is suitable for intact or degraded RNA (Appendix A, p.12).

The RiboCop for Yeast Probe Mix has been optimized for increased depletion efficiency even with difficult samples. Probes are designed to eliminate off-target effects. Thus, RiboCop maintains consistent transcript expression after depletion.

RiboCop is recommended for downstream NGS library preparation using the CORALL RNA-Seq V2 Library Prep Kit (Cat. No. 171 - 176). In addition, previous versions of CORALL RNA-Seq Library Prep Kits can also be used for downstream NGS library preparation. RiboCop is also compatible with library preparation kits from other vendors.

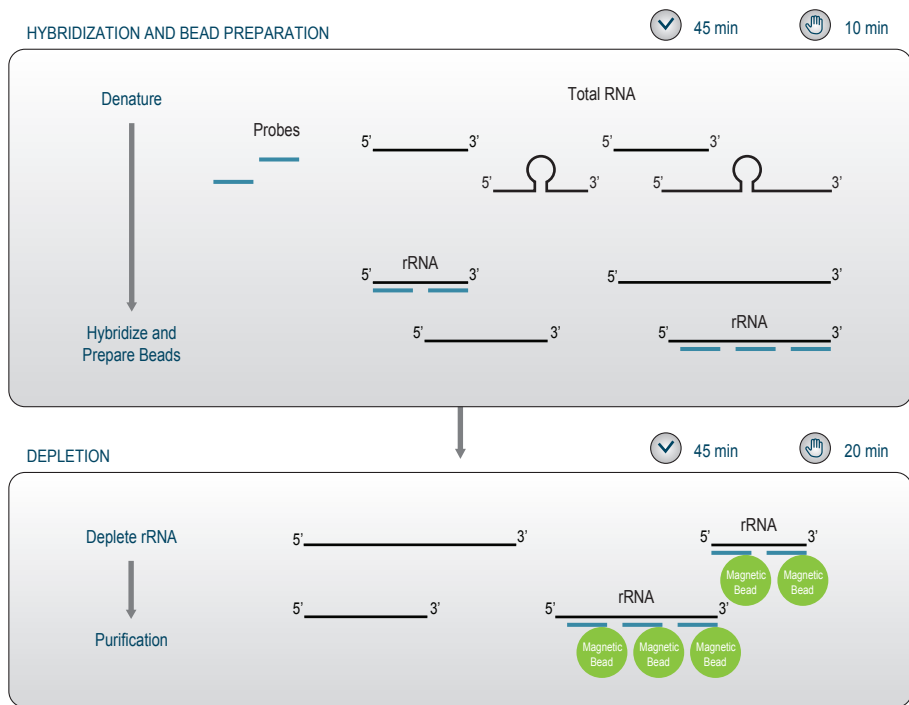


Figure 1. Schematic overview of the RiboCop workflow.

## 2. Kit Components and Storage Conditions

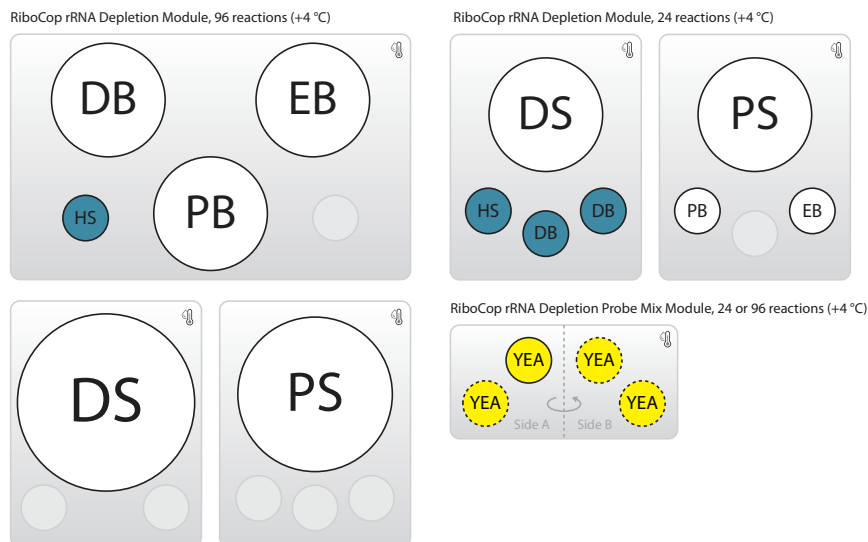


Figure 2. Location of kit components for 24 and 96 prep kits. For 96 reactions, Probe Mix Yeast is provided in 4 tubes.

Kit Component	Tube Label	Volume* for		Storage
		24 preps	96 preps	
Hybridization Solution	HS ●	106 µl	423 µl	🔒 +4 °C
Probe Mix Yeast	YEA ●	132 µl	4x 132 µl	🔒/❄️ +4 °C / -20 °C
Depletion Beads	DB ●	1,980 µl	7,920 µl	🔒 +4 °C
Depletion Solution	DS ○	4,752 µl	19,008 µl	🔒 +4 °C
Purification Beads	PB ○	634 µl	2,535 µl	🔒 +4 °C
Purification Solution	PS ○	2,852 µl	11,405 µl	🔒 +4 °C
Elution Buffer	EB ○	317 µl	1,268 µl	🔒/❄️ +4 °C / -20 °C

\*including ≥10 % surplus

Upon receiving the RiboCop kit, store all components at +4 °C. **EB** ○ and Probe Mix (**YEA**) ● can also be stored at -20 °C but avoid frequent freeze-thaw cycles. Before use, check the contents of **PS** ○ which may precipitate during shipping. If a precipitate is visible or the content appears turbid, incubate at 37 °C until solution components dissolve completely. Equilibrate to room temperature again before use.

### 3. User-Supplied Consumables and Equipment

Check to ensure that you have all of the necessary materials and equipment before beginning rRNA depletion. All reagents, equipment, and labware must be free of nucleases and nucleic acid contamination.

**ATTENTION:** Before starting this protocol, please read the [General Guidelines for Lexogen Kits](#), which is available online. This document provides a detailed overview of RNA and kit component handling, as well as general RNA input requirements.

It is also strongly recommended to carefully read the input guidelines and notes listed on p.12.

#### Reagents

- 80 % fresh ethanol (washing of Purification Beads, **PB** ○).

#### Equipment

- Magnetic rack or plate e.g., for 1.5 ml tubes: BcMag Magnetic separator-24, article# MS-03 from Bioclone; for 96-well plates: 96S Super Magnet Plate, article# A001322 from Alpaqua, or Dynamag-96 Side/Side Skirted. Magnets, article # 12331D/12027 from Thermo Fisher.
- Benchtop centrifuge for spinning down liquids.
- Vortex mixer.
- Calibrated single-channel pipettes for handling 1 µl to 1,000 µl volumes.
- Thermomixer.
- UV-spectrophotometer to quantify RNA.

#### Labware

- Suitable low-binding pipette tips (pipette tips with aerosol barriers recommended).
- 1.5 ml tubes, low binding, certified ribonuclease-free.
- 200 µl PCR tubes or 96-well plates and caps or sealing foil.
- Benchtop cooler or ice pellets in ice box (for short-term storage of RNA).

#### Optional Equipment and Solutions

- Automated microfluidic electrophoresis station (Agilent Technologies 2100 Bioanalyzer).
- Benchtop fluorometer and appropriate assays (for RNA quality control and quantification).
- Agarose gels, dyes, and electrophoresis rig (for RNA quality control).
- RNaseZap.
- RNase inhibitor.

The complete set of materials, reagents, and labware for quality control is not listed. Consult Appendix A (p.12) for more information.

# 4. Detailed Protocol RiboCop for Yeast

## Preparation

Hybridization	Bead Preparation and Depletion	Purification
HS ● YEA ● } equilibrated } at RT	DB ● } equilibrated DS ○ } at RT	PB ○ – stored at +4 °C PS ○ – stored at +4 °C 80 % EtOH – provided by user, <b>prepare fresh!</b> EB ○ – thawed at RT or stored at +4 °C
Thermomixer set to 75 °C / 1,250 rpm	Thermomixer set to 60 °C / 1,250 rpm	Equilibrate all reagents to room temperature for 30 minutes prior to use

## Hybridization

The depletion Probe Mix for Yeast (YEA ●) and total RNA are mixed, denatured, and hybridized.

**ATTENTION:** Important notes for RiboCop hybridization steps:

- RiboCop for Yeast recommend input amounts are 10 - 1000 ng total RNA.
- If a thermomixer is not available, input amounts ≤500 ng of total RNA can be processed in PCR tubes or plates and incubated in a thermocycler, without shaking.
- Bead Washing (p.9) can be performed during the incubation at step 5.
- Place the Purification Beads (PB ○) and Purification Solution (PS ○) for step 16 at room temperature prior to starting the protocol, to ensure these have at least 30 minutes to equilibrate.

1 Prepare 10 - 1,000 ng of total RNA in a total volume of 26 µl. Dilute using RNase-free water if required.

2 Add 4 µl Hybridization Solution (HS ●).

3 Add 5 µl Probe Mix Yeast (YEA ●) and mix thoroughly until homogeneous.

4 Denature samples using a thermomixer at 75 °C for 5 minutes with agitation at 1,250 rpm.

5 Decrease the temperature of the thermomixer to 60 °C and incubate the samples for 30 minutes with agitation at 1,250 rpm. **OPTIONAL:** Transfer the samples from step 4 to a second thermomixer set to 60 °C.



## Bead Washing

Depletion Beads (DB ●) must be washed before use. These steps may be performed as a batch for up to 6 samples.

**ATTENTION:** Mix Depletion Beads (DB ●) fully before use.

- 6 Transfer 75 µl Depletion Beads (DB ●) per reaction to a fresh tube.
- 7 Place the tube onto the magnet and let the beads collect for 2 - 5 minutes or until the supernatant is completely clear. Remove and discard the supernatant with a pipette while the tube remains in contact with the magnet.
- 8 Add 75 µl Depletion Solution (DS ○) per reaction to the beads. Remove the tube from the magnet and resuspend the beads.
- 9 Place the tube back onto the magnet and let the beads collect for 2 - 5 minutes or until the supernatant is completely clear. Remove and discard the supernatant.
- 10 Repeat this washing step once (for a total of two washes).
- 11 Resuspend the beads in 30 µl Depletion Solution (DS ○) per reaction.

## Depletion


Depletion Beads (DB ●) are used to remove the probe-hybridized ribosomal RNA.

**ATTENTION:** Avoid the formation of air bubbles while mixing.

- 12 Spin down the hybridized sample from step 5 and add 30 µl of freshly prepared beads from step 11. Mix by pipetting up and down at least 8 times, or until homogeneous.
- 13 Put the sample back to the thermomixer and incubate at 60 °C for 15 minutes with agitation at 1,250 rpm.
- 14 Spin down briefly then place the sample on the magnet and let the beads collect for 5 minutes.
- 15 Recover and transfer 60 µl of the supernatant containing the rRNA depleted RNA to a fresh tube. Avoid disturbing the collected beads to prevent rRNA contamination.  
**ATTENTION:** Do not throw away the supernatant.

## Purification

The depleted RNA is purified using magnetic beads. The purification reagents (**PB** ○, **PS** ○, and **EB** ○) should equilibrate for 30 minutes at room temperature before use. The Purification Beads (**PB** ○) must be fully resuspended before use. Thorough mixing by pipetting or vortexing is recommended.

- 16 Add 24  $\mu$ l Purification Beads (**PB** ○) and 108  $\mu$ l Purification Solution (**PS** ○) to the supernatant. Mix well by pipetting. Incubate for 5 minutes at room temperature.
- 17 Place the sample onto a magnet and let the beads collect for 5 - 10 minutes or until the supernatant is completely clear. **NOTE:** The speed of bead collection depends on the strength of the magnet.
- 18 Remove and discard the clear supernatant without removing the sample from the magnet. Make sure that accumulated beads are not disturbed.
- 19 Add 120  $\mu$ l of 80 % EtOH and incubate the beads for 30 seconds. Leave the sample on the magnet as beads should not be resuspended during this washing step. Remove and discard the supernatant. **ATTENTION:** When using 1.5 ml tubes use 150  $\mu$ l of 80 % EtOH to ensure beads are fully covered by EtOH.
- 20 Repeat this washing step once for a total of two washes. Make sure the supernatant is removed completely.
- 21 Leave the sample in contact with the magnet and let the beads dry for 5 -10 minutes or until all ethanol has evaporated. **ATTENTION:** Dry the beads at room temperature only and do not let the beads dry too long (visible cracks appear). This will negatively influence the elution and the resulting RNA recovery.
- 22 Add 12  $\mu$ l of Elution Buffer (**EB** ○), remove the sample from the magnet, and resuspend the beads properly in **EB** ○. Incubate for 2 minutes at room temperature.
- 23 Place the sample onto the magnet and let the beads collect for 2 - 5 minutes or until the supernatant is completely clear.
- 24 Transfer 10  $\mu$ l of the supernatant into a fresh tube. Depleted RNA is now ready for quality control and downstream use (e.g., for NGS library preparation).  Safe stop-point. RNA can be stored at  $\leq -20$  °C at this point.

## 5. Short Procedure RiboCop for Yeast

**ATTENTION:** Spin down solutions before opening tubes or plates!

45 min

Hybridization and Bead Washing

### Hybridization

- ☐ Prepare 10 - 1,000 ng total RNA in 26 µl.
- ☐ Add 4 µl **HS** ●.
- ☐ Add 5 µl **YEA** ● and mix until homogeneous.
- ☐ Denature for 5 min at 75 °C / 1,250 rpm.
- ☐ Incubate for 30 min at 60 °C / 1,250 rpm.

### Bead Washing

- ☐ Resuspend **DB** ●, transfer 75 µl to a fresh tube.
- ☐ Place on magnet for 2 - 5 min, discard supernatant.
- ☐ Resuspend beads in 75 µl **DS** ○, incubate 2 min on magnet, discard supernatant. Repeat once.
- ☐ Resuspend beads in 30 µl **DS** ○.

45 min

Depletion and Purification

### Depletion

- ☐ Spin down hybridized sample. Add 30 µl of prepared beads. Mix by pipetting 8x, or until homogeneous.
- ☐ Incubate for 15 min at 60 °C / 1,250 rpm. Spin down.
- ☐ Place on magnet for 5 min.
- ☐ Transfer 60 µl supernatant to a fresh tube. **ATTENTION:** The supernatant contains the rRNA depleted RNA.

### Purification

- ☐ Add 24 µl **PB** ○ and 108 µl **PS** ○, mix well, incubate for 5 min at RT.
- ☐ Place on magnet for 5 - 10 min, discard supernatant.
- ☐ Wash the beads twice with 120 - 150 µl 80 % EtOH for 30 sec. **ATTENTION:** Use 150 µl for 1.5 ml tubes.
- ☐ Air dry beads for 5 - 10 min. **ATTENTION:** Do not over dry the beads!
- ☐ Add 12 µl **EB** ○, remove from magnet, mix well, incubate 2 min at RT.
- ☐ Place on magnet for 2 - 5 min, transfer 10 µl of the supernatant to a fresh tube. 📌 Safe stopping point.

## 6. Appendix A: RNA Requirements and Results

### Potential Contaminants

RNA samples should be free of salts, metal ions, and organic solvents, which can be carried over from RNA extraction. Several sources of contamination (e.g., proteins, chaotropic salts, and phenol) can be detected with a UV-Vis spectrophotometer. An acceptably pure RNA sample should have an A260/A280 ratio between 1.8 and 2.1. The A260/A230 ratio should also be greater than 1.8. Contaminants may have a negative impact on the efficiency of the protocol.

### RNA Input Amount and Quality

The recommended input range for RiboCop for Yeast is 10 - 1,000 ng of total RNA. RiboCop is suitable for intact or degraded RNA, including formalin fixed, paraffin-embedded (FFPE) samples. FFPE RNA should best be treated with DNase prior to ribo-depletion with RiboCop. Recommended input for DNase treatment is  $\geq 50$  ng of FFPE total RNA. Spike-in controls, including Lexogen's Spike-In RNA Variant Controls (SIRVs, Cat. No. 025, 050, 051, and 141), should be added to the RNA sample before RiboCop (or prior to DNase treatment). The spike-in amount must be calculated relative to the target RNA fraction (e.g., ribo-depleted RNA). We recommend targeting 1 % of the non-rRNA content of a samples. For assistance with SIRV spike-in calculation, please contact [support@lexogen.com](mailto:support@lexogen.com).

## 7. Appendix B: Downstream Processing

This protocol was tested extensively with intact and degraded total RNA obtained from *S. cerevisiae*. Depleted RNA samples are ideally suited for downstream NGS library preparation using Lexogen's CORALL RNA-Seq V2 Library Prep Kits (Cat. No. 171 - 176). In addition, previous versions of CORALL RNA-Seq Library kits can also be used for downstream NGS library preparation. Up to 10 µl of the eluted rRNA depleted RNA may be used as input for CORALL library preparation.

# 8. Appendix C: Revision History

Publication No. / Revision Date	Change	Page
190UG447V0100 Aug. 25, 2022	Initial Release.	

# 9. Appendix D: Notes

Associated Products:

022 (Purification Module with Magnetic Beads)  
025, 050, 051, 141 (SIRVs Spike-in RNA Variant Control Mixes)  
125-127 (RiboCop rRNA Depletion Kits for Bacteria)  
144-145 (RiboCop rRNA Depletion Kits for Human/Mouse/Rat)  
171-176 (CORALL RNA-Seq V2 Library Prep Kits)  
183-184 (CORALL RNA-Seq V2 Library Prep Kit with RiboCop (HMR))  
185-186 (CORALL RNA-Seq V2 Library Prep Kit with RiboCop (HMR+Globin))

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