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## OVERVIEW

The **RNA Informatics, Technologies & Therapies Core (RITTC)** at the University of Colorado Anschutz Medical Campus is now open for business. RITTC is a centralized, expert-operated, shared resource for RNA technologies, informatics, and emerging therapeutics, built as an extension of the RNA Bioscience Initiative (RBI).

To jumpstart the application of ribosome profiling to cancer research, the **University of Colorado Cancer Center (UCCC)** has committed funds to subsidize these experiments for its members. This program directly supports the mission of the **Molecular & Cellular Oncology (MCO)** program, whose members study gene-expression regulation and its deregulation in cancer, which are questions that ribosome profiling is uniquely positioned to address.

Our goals for this program are to help investigators **generate strong preliminary data for grant submissions** and to **build a network of collaborators** who contribute to the core's long-term success.

Questions should be directed to Neel Mukherjee, PhD, at [rirttc-core@cuanschutz.edu](mailto:rirttc-core@cuanschutz.edu).

## THE AWARD

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RITTC will provide a **50% discount on the cost of a standard ribosome profiling experiment to three (3) UCCC investigators**.

- The internal price of a standard experiment (3 replicates each of treatment and control, **6 samples total**) is **\$11,800** — already a substantial reduction relative to commercial providers. Cancer Center funds cover 50% of this cost, so a selected investigator's lab contributes **\$5,900** per experiment.
- RITTC provides **end-to-end support**, including both the molecular-biology workup (cell lysis, ribosome-footprint isolation, rRNA depletion, library preparation, sequencing, and matched input RNA-seq) and the **informatics analysis** (alignment, QC, P-site assignment, codon-level occupancy, and differential-translation analysis).

## WHAT IS RIBOSOME PROFILING?

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Whereas RNA-seq captures only a static picture of mRNA abundance, ribosome profiling ("Ribo-seq") measures the precise position of ribosomes on mRNAs in cells to give a dynamic, genome-wide readout of ongoing translation. It reveals translational efficiency per transcript and uncovers fundamental aspects of translational regulation [1]. Ribo-seq is also a powerful approach for discovering non-canonical (unannotated) peptides and antigens that are potential targets for cancer immunotherapy [2].

Investigators across the CU Anschutz campus have already applied ribosome profiling in collaborative cancer studies, from translational control of the hypoxia response in breast cancer [3] to drug-resistance mechanisms in multiple myeloma [4].

A typical experiment involves cell culture and flash-freezing of samples (performed by the investigator), followed by cell lysis, isolation of ribosome-protected footprints, library preparation, sequencing, and informatics analysis (performed by RITTC). Experiments should be planned in advance with RITTC consultation.

## SAMPLE REQUIREMENTS

Cell pellets

**~8 million cells per sample**

Flash-frozen tissue

**20–50 mg tissue**

## ELIGIBILITY

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- Applicants must be **members of the UCCC**, and members of the **Molecular & Cellular Oncology (MCO)** program are especially encouraged to apply.

- Principal Investigators must hold a faculty appointment at the University of Colorado Anschutz Medical Campus (Assistant, Associate, or Full Professor; Research Professor; or Instructor). Postdoctoral trainees may apply with a faculty sponsor's Letter of Support.
- The proposal may not describe the same specific research already funded by other sources during the award period.

## KEY DATES

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Application due	<b>August 7, 2026, 5:00 PM MT</b>
Decisions communicated	<b>August 21, 2026</b>
Experiments begin	<b>Immediately upon award (rolling scheduling with RITTC)</b>

## APPLICATION GUIDELINES

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There is **no Letter of Intent**. Submit a single PDF (filename: PName.ProposalTitle.RITTC-RiboPilot.pdf) by **5:00 PM MT on August 7, 2026** via the [RITTC Ribo-Pilot application form](#), containing:

- **a.** A brief cover letter from the PI with the proposal title, a statement of the project's value, and confirmation that all listed collaborators agree with the proposal.
- **b.** A proposal of **no more than one page** in standard NIH format. Suggested (not required) organization: specific aims, background and significance, and research plan — including the biological question, the treatment/control conditions, and how the resulting data will support a future grant application.
- **c.** An NIH-format Biosketch (old or new format) for the PI.

Eligibility and appropriate project scope will be determined by RITTC leadership (**Jay Hesselberth, PhD, Director; Neel Mukherjee, PhD, Co-Director**) in consultation with UCCC. These awards subsidize RITTC services; they **do not provide a monetary budget** to the investigator.

## AWARD RECIPIENT REQUIREMENTS

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Recipients are expected to become active members of the CU RNA and cancer research communities. Both PIs and personnel working on funded projects agree to:

- **Acknowledge UCCC and RITTC support** in all publications and presentations resulting from the award.
- **Include RITTC informatics staff as co-authors** on publications for which they provided substantial analytical contributions.
- Use the awarded subsidy solely to support the ribosome profiling experiment described in the proposal.
- Provide a **brief progress report** within 30 days of experiment completion.
- Present research accomplishments at a future RITTC/RBI or UCCC symposium.

## REVIEW CRITERIA

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Applications will be evaluated competitively by a panel with relevant expertise. Primary factors are the **scientific merit** of the proposed research, the **likelihood of seeding extramural (R-series or equivalent) funding**, the **fit of ribosome profiling** to the biological question, and the **relevance to cancer research**. No written critiques will be provided; applicants will be informed with a response of "Funded," "Not funded," or "Not eligible."

## CONTACT

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[RITTC Core website](#)

## REFERENCES

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1. Ingolia NT, Hussmann JA, Weissman JS. Ribosome Profiling: Global Views of Translation. PMID: [30037969](#); PMCID: [PMC6496350](#)
2. Ouspenskaia T, Law T, Clauser KR, et al. Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. PMID: [34663921](#); PMCID: [PMC10198624](#)
3. Purdy SC, Matlin K, Alderman C, et al. eIF3d and eIF3e mediate selective translational control of hypoxia that can be inhibited by small molecules. PMID: [41364558](#); PMCID: [PMC12822916](#)
4. Walker ZJ, Vaeth KF, Baldwin A, et al. Ribosome Profiling Reveals Translational Reprogramming via mTOR Activation in Omacetaxine-Resistant Multiple Myeloma. PMID: [40047825](#); PMCID: [PMC12221815](#)