## **Resource Summary Report**

Generated by RRID on May 15, 2025

# Harvard Medical School Nascent Transcriptomics Core Facility

RRID:SCR\_025844 Type: Tool

**Proper Citation** 

Harvard Medical School Nascent Transcriptomics Core Facility (RRID:SCR\_025844)

## **Resource Information**

URL: https://ntc.hms.harvard.edu/

**Proper Citation:** Harvard Medical School Nascent Transcriptomics Core Facility (RRID:SCR\_025844)

**Description:** Core specializes in analysis of nascent transcriptome using PRO-seq and TTseq NGS methods. Provides services allowing users to submit prepared cells and receive analyzed data. Offers free consultations to help with experimental design, answer questions, and discuss data analysis.

**Synonyms:** Nascent Transcriptomics Core, Harvard Medical School Nascent Transcriptomics Core

Resource Type: service resource, core facility, access service resource

Keywords: analysis of nascent transcriptome, PRO-seq, TT-seq, NGS methods,

**Funding:** 

Resource Name: Harvard Medical School Nascent Transcriptomics Core Facility

Resource ID: SCR\_025844

Alternate IDs: ABRF\_2940

Alternate URLs: https://coremarketplace.org/?FacilityID=2940&citation=1

#### Record Creation Time: 20241004T053248+0000

Record Last Update: 20250514T062045+0000

## **Ratings and Alerts**

No rating or validation information has been found for Harvard Medical School Nascent Transcriptomics Core Facility.

No alerts have been found for Harvard Medical School Nascent Transcriptomics Core Facility.

## Data and Source Information

Source: <u>SciCrunch Registry</u>

## **Usage and Citation Metrics**

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>RRID</u>.

Martin-Rufino JD, et al. (2024) Transcription factor networks disproportionately enrich for heritability of blood cell phenotypes. bioRxiv : the preprint server for biology.