

# Resource Summary Report

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## 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 TT-seq 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:** access service resource, service resource, core facility

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

**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:** 20260806T054824+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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [dkNET](#) .

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