

Jan 10, 2024

Version 2



C DAT-TRAP Protocol V.2



In 2 collections

DOI

dx.doi.org/10.17504/protocols.io.6qpvr4eo2gmk/v2

Peter Kilfeather¹

¹University of Oxford



Peter Kilfeather

Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

Create free account





DOI: https://dx.doi.org/10.17504/protocols.io.6qpvr4eo2gmk/v2

Protocol Citation: Peter Kilfeather 2024. DAT-TRAP Protocol. protocols.io

https://dx.doi.org/10.17504/protocols.io.6qpvr4eo2gmk/v2Version created by Peter Kilfeather

License: This is an open access protocol distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working

We use this protocol and it's working



Created: January 10, 2024

Last Modified: January 10, 2024

Protocol Integer ID: 93238

Keywords: mrna from dat, mrna, capture of egfp, cells in mouse, ventral midbrain, egfp, expressing cell, cell

Abstract

This protocol describes the capture of eGFP-L10a-tagged ribosomes and mRNA from DAT-expressing cells in mouse ventral midbrain.

Guidelines

Prepare all reagents under RNAse-free conditions, preferably with the use of a PCR hood.



Materials

- Tissue-lysis buffer, Low-salt buffer and High-salt buffer made according to the Reagent Setup section of Heiman et al., 2014:
- Tissue-lysis buffer: Mix 20 mM HEPES KOH (pH 7.4), 150 mM KCl and 10 mM MgCl₂in RNase-free water. Store it at 4 °C for several months. Add EDTA-free protease inhibitors, 0.5 mM DTT, 100 µg/ml cycloheximide and 10 µl/ml rRNasin and Superasin to an aliquot immediately before use.
- Low-salt buffer: Mix 20 mM HEPES KOH (pH 7.3), 150 mM KCl, 10 mM MgCl₂and 1% (vol/vol) NP-40 in RNasefree water. Store the buffer at 4 °C for up to several months. Add EDTA-free protease inhibitors (one mini tablet per 10 ml), 0.5 mM DTT, 100 μg/ml cycloheximide and 10 μl/ml rRNasin and Superasin to an aliquot immediately before use.
- High-salt buffer: Mix 20 mM HEPES KOH (pH 7.3), 350 mM KCl, 10 mM MgCl₂and 1% (vol/vol) NP-40 in RNase-free water. Store it at 4 °C for up to several months. To an aliquot, add DTT to a final concentration of 0.5 mM and cycloheximide to a final concentration of 100 μg/ml immediately before use.

Reagent list

А	В	С	D
Item	Specific name	Vendor	Code
anti-eGFP antibody (clone 19C8)	anti-eGFP antibody (clone 19C8)	Memorial Sloan Kettering	Heintz Lab TRAP anti- GFP 19C8
anti-eGFP antibody (clone 19F7)	anti-eGFP antibody (clone 19F7)	Memorial Sloan Kettering	Heintz Lab TRAP anti- GFP 19F7
RNaseZap	RNaseZap RNase Decontamin ation Wipes-100 sheets	Life Technologie s	AM9786
HEPES	HEPES, 1 M, 100 mL, pH 7.3, RNase- free	Fisher	10041703
KCI	KCI, 2M, 100 mL, RNase-free	Life Technologie s	AM9640G



Α	В	С	D
MgCl2	MgCl2, 1M, 100 mL, RNase-free	Life Technologie s	AM9530G
RNase-free water			
EDTA-free Protease Inhibitors	cOmplete, Mini, EDTA- free Protease I	Sigma	11836170001
DTT	DL-DTT	Sigma	D9779-1G
Cycloheximi de	Cycloheximi de from Steptomyce s griseus, 1g	Sigma	D769801G
rRNasin	Recombinan t RNasin Ribonucleas e Inhibitor, 10,000u	Promega	N2515
Superasin	SUPERase In RNase Inhibitor (20 U/uL)-10,00 0 units	Life Technologie s	AM2696
HBSS	HBSS (10X), calcium, magnesium, no phenol red-500	Life Technologie s	14065056
Glucose	D-(+)- GLUCOSE BIOXTRA	Sigma	G7528- 250G
NaHCO3	SODIUM BICARBONA TE BIOXTRA		S6297- 250G
NP-40			
Streptavidin Dynabeads	Dynabeads MyOne Streptavidin T1-2 mL	Life Technologie s	65601
Streptavidin Dynabeads	Dynabeads MyOne Streptavidin T1-10 mL	Life Technologie s	65602

Α	В	С	D
NaOH			
NaCl			
BSA IgG- free, RNase-free	Bovine Serum Albumin (IgG-Free, Protease- Free)	Stratech Scientific	001-000- 162-JIR-50g
Proclin 300	PROCLIN 300, 50ML	Sigma	48912-U
DEPC water		Autoclave	
Graeff forceps	Size 5 Graeff Forceps		
Cutting Blades			
Dounce homogenise rs	DOUNCE TISSUE GRINDER, ALL-GLASS, 2 ML	Sigma	D8938- 1SET
1.5 mL DNA- LoBind Eppendorf Tubes	Eppendorf® DNA LoBind tubes	Sigma	EP0030108 051-250EA
Cervical dislocation tool			
Surgical scissors			
Fine scissors for skull			
Spatula for brain			
PBS			
Wide orifice P200 tips			
DHPC	1,2- Diheptanoyl -sn- Glycero-3- Phosphocho	Generon (Non- catalogue)	D607- 250MG



Α	В	С	D	
	line (DHPC) - Purity: ≥ 99% (by HPLC analysis)			
B- Mercaptoet hanol				
70% Ethanol				
80% Ethanol				
RNeasy Micro Columns	RNeasy Plus Micro Kit (50)	Qiagen	74034	
DNA Eliminator Columns				
Buffer RLT+				
Buffer RW1				
Buffer RPE				
Elution water				
Ribogreen Kit	Quant-iT RiboGreen RNA Assay Kit-1 kit	Life Technologie s	R11490	
Magnetic rack	DynaMag-2	ThermoFish er	12321D	
PCR Hood HEPA Filter	HEPA Filter for 32 Laminar Flow PCR Cabinet	Starlab	N3942- 7000	
PCR Hood HEPA Pre- Filter	Pre-Filters for 32 Laminar Flow PCR Cabinet	Starlab	N3942- 7500	

Troubleshooting



Safety warnings



1 Toxicity: Contact your departmental safety office for specific advice about handling and safe disposal of cycloheximide.

Ethics statement

This protocol needs prior approval by the users' Institutional Animal Care and Use Committee (IACUC)



Matrix preparation

Prepare anti-GFP-coated paramagnetic bead matrix according to Box 1 of *Heiman et al.*, 2014.

Citation

Heiman M, Kulicke R, Fenster RJ, Greengard P, Heintz N (2014)

. Cell type-specific mRNA purification by translating ribosome affinity purification (TRAP)..

Nature protocols.

https://doi.org/10.1038/nprot.2014.085

LINK

The quantity of beads/antibody must be titrated according to the eGFP-content of the sample of interest. See the Supplementary text of *Dougherty et al., 2010* further information.

Citation

Dougherty JD, Schmidt EF, Nakajima M, Heintz N (2010)

. Analytical approaches to RNA profiling data for the identification of genes enriched in specific cells..

Nucleic acids research.

https://doi.org/10.1093/nar/gkq130

LINK

Tissue Collection

- Prepare all dissection instruments and collection tubes on ice. Set a refrigerated centrifuge to 4 °C. Be prepared to work swiftly, to minimise changes in translation occurring after death. Collection materials should be prepared in an RNase-free manner, to minimise the risk of sample degradation.
- 3 Cull the mouse by cervical dislocation. Extract the brain and perform rapid chilling by submersion in **Dissection Buffer**. Place the brain into a matrix or onto a flat surface for



sectioning.

From each section, dissect the target brain region. Immediately homogenise dissected tissue in **Tissue Lysis Buffer** using a dounce homogeniser. The volume of tissue lysis buffer used should be decided in optimisation experiments and should scale with the total mass of tissue dissected. *For information on choosing an appropriate volume, see Dougherty et al., 2010.*

Citation

Dougherty JD, Schmidt EF, Nakajima M, Heintz N (2010)

. Analytical approaches to RNA profiling data for the identification of genes enriched in specific cells..

Nucleic acids research.

https://doi.org/10.1093/nar/gkq130

LINK

To ensure consistent and thorough disruption, use a fixed number of strokes for every sample (e.g 20, 30) and select a pestle that provides minimal clearance. Avoid foaming by keeping the pestle below the surface of the buffer at all times.

Note: Tissue can be snap-frozen immediately after dissection, to facilitate collection of large numbers of samples. Alternatively, homogenized contents can be stored on ice while additional samples are collected. **Tissue Lysis Buffer** contains cycloheximide to stall translation.

Immunoprecipitation

- Transfer each lysate into ice-cold Eppendorf tubes and centrifuge at 2,000 x g at 4 °C for 10 minutes. Carefully transfer the supernatant to a new tube.
- To the supernatant, add $1/8^{th}$ volume of **300 mM DHPC** and $1/8^{th}$ volume of **10 % NP-40**. Mix the solutions by inversion. Hold the mixtures on ice for 5 minutes before centrifugation at 20,000 x g at 4 °C for 10 minutes. Carefully transfer the supernatant to a new tube.
- 7 Transfer 50 ul of lysate into a separate tube to be used as a paired 'Input' sample. To ensure the same conditions are kept, hold this sample at 4 °C until the 'IP' sample is processed for RNA extraction the following day.
- Add titrated volume of anti-eGFP-coated paramagnetic bead matrix to the 'IP' sample. Rotate overnight at 4°C.



Washing and extraction

- 9 On day 2, proceed to washing the bead matrix: Place each IP sample on a magnetic rack to pellet beads on the sidewall. Aspirate and discard all supernatant. Resuspend the bead matrix in 1 mL of ice-cold High Salt buffer and dispense into a fresh tube.
- 10 Incubate for 5 minutes on ice, repeat pelleting, resuspension and transfer to a fresh tube. Perform this washing step 6 times in total.
- 11 After the final wash, pellet the bead matrix using a magnet rack, remove the supernatant, warm the tube to room temperature and resuspend in 100 µL of room temperature Buffer RLT-Plus with 1 % β-mercaptoethanol. Vortex vigorously and incubate for 10 minutes.
- 12 Pellet the bead matrix using a magnetic rack and transfer the supernatant to a Qiagen RNEasy Micro collection column (Qiagen, #74034). Follow manufacturer's instructions for RNA extraction. Use 14 µL of nuclease-free water for RNA elution and divide the elute into 2 μL and 10 μL (allowing for 2 μL loss) volumes. Store the 10 μL volume immediately at -80 °C.
- 13 Hold the 2 μL volume at 4 °C and proceed to RNA yield quantification using the Quant-it™ RiboGreen RNA Assay Kit (ThermoFisher #R11490). Measure RNA integrity using the Agilent 2100 RNA Pico BioAnalyzer.

Citations

Step 1

Heiman M, Kulicke R, Fenster RJ, Greengard P, Heintz N. Cell type-specific mRNA purification by translating ribosome affinity purification (TRAP).

https://doi.org/10.1038/nprot.2014.085

Step 1

Dougherty JD, Schmidt EF, Nakajima M, Heintz N. Analytical approaches to RNA profiling data for the identification of genes enriched in specific cells.

https://doi.org/10.1093/nar/gkq130

Step 4

Dougherty JD, Schmidt EF, Nakajima M, Heintz N. Analytical approaches to RNA profiling data for the identification of genes enriched in specific cells.

https://doi.org/10.1093/nar/gkq130