

Publication

An Optimized Protocol for the Mapping of Cell Type-Specific Ribosome-Associated Transcript Isoforms from Small Mouse Brain Regions

Book Item (Buchkapitel, Lexikonartikel, jur. Kommentierung, Beiträge in Sammelbänden)**ID** 4661884**Author(s)** Di Bartolomei, Giulia; Scheiffele, Peter**Author(s) at UniBasel** [Scheiffele, Peter](#) ; [Di Bartolomei, Giulia](#) ;**Year** 2022**Title** An Optimized Protocol for the Mapping of Cell Type-Specific Ribosome-Associated Transcript Isoforms from Small Mouse Brain Regions**Editor(s)** Scheiffele, Peter; Mauger, Oriane**Book title** Alternative Splicing: Methods and Protocols**Volume** 2537**Publisher** Springer**Place of publication** New York, NY**Pages** 37-49**ISSN/ISBN** 1064-3745 ; 1940-6029 ; 978-1-0716-2520-0 ; 978-1-0716-2521-7**Series title** Methods in Molecular Biology**Mesh terms** Animals; Brain, metabolism; Mice; Protein Biosynthesis; Protein Isoforms, metabolism; RNA, Messenger, metabolism; Ribosomes, metabolism; Transcriptome

Over the past years, technological advances in transcriptomics provided deep insights into gene expression programs and their role in tissue organization and cellular functions. The isolation of ribosome-associated transcripts is a powerful approach for deep profiling of cell type-specific transcripts, and particularly well-suited for quantitative analysis of transcript isoforms. This method employs conditional ribosome epitope-tagging in genetically defined cell types, followed by affinity-isolation of ribosome-associated mRNAs. Advantages of this approach are twofold: first, the method enables rapid retrieval of mRNAs without tissue dissociation and cell sorting steps. Second, capturing of ribosome-associated mRNAs, enriches for transcripts recruited for active translation, therefore providing an approximation to the cellular translome. Here, we describe one application of this method for the identification of the transcriptome of excitatory neuronal cells (mitral and tufted cells) of the mouse olfactory bulb, through RiboTag isolation from the vGlut2-IRES-cre mouse line as genetic driver of endogenously tagged ribosome expression.

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