Profiling Translation Rate With Ribo-Eclip

Tech ID: 32086 / UC Case 2020-239-0

BACKGROUND

The eukaryotic ribosome is composed of 79 ribosomal protein – large (RPL) and ribosomal protein – small (RPS) subunit proteins that interweave with 4 highly structured RNAs (5S, 5.8S, 18S, and 28S rRNAs) to form the final translation-capable ribonucleoprotein. Thus, quantification of ribosome-associated RNA is highly similar to profiling of RNAs associated with other RNA binding proteins. We recently described the development of enhanced crosslinking and immunoprecipitation (eCLIP), a method to profile RNAs bound by an RNA binding protein of interest that showed thousand-fold improved recovery of protein-bound RNA [Van Nostrand et al 2016].

Van Nostrand EL, Pratt GA, Shishkin AA, Gelboin-Burkhart C, Fang MY, Sundararaman B, Blue SM, Nguyen TB, Surka C, Elkins K, et al: Robust transcriptome-wide discovery of RNA-binding protein binding sites with enhanced CLIP (eCLIP). Nat Methods 2016, 13:508-514.

https://pubmed.ncbi.nlm.nih.gov/27018577/

TECHNOLOGY DESCRIPTION

Researchers from UC San Diego have developed a new method to quantify translation rate of individual genes. This technology enables more accurate quantification of ribosome occupancy.

INTELLECTUAL PROPERTY INFO

UC San Diego is seeking companies interested in developing new services/products utilizing this technology.

RELATED MATERIALS

- no publication, technology is not published.

PATENT STATUS

Patent Pending

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OTHER INFORMATION

CATEGORIZED AS

- **Biotechnology**
  - Genomics
- **Research Tools**
  - Screening Assays

RELATED CASES

2020-239-0