Ribosome fingerprinting with a solid-state nanopore

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KEYWORDS: nanopore, nanopipette, ribosome, single molecule, polysome, translation.

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# Equal contribution

**Dataset – Ribosome analysis**

The main folder “Ribosome analysis” consists of two sub folders namely,

1. Ion current data – data in abf files, can be opened with software including MATLAB, Origin, and Clampfit.
2. Polysome data – data in csv and bmp files.

**Ion current data:**

This folder contains the raw ion current data files obtained for nanopipette translocation experiments in abf file format for the different ribosome samples, in the folder “raw data”. They are further divided into 3 subfolders as follows,

1. D.melanogaster ovaries sample – contains two sample sets of 80S and polysome samples in separate folders named O2 and O3.
2. D.melanogaster S2 cells sample – contains 40S, 80S and polysome samples.
3. Human neuronal cell samples – contains the respective 80S and polysome samples.

This folder also contains the datasets used in the paper in excel file format.

**Polysome data:**

Contains the various data collected for the sucrose gradient experiments in csv and bmp files.