

Resource Summary Report

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In situ sequencing for RNA analysis in tissue sections

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Type: Protocol

Proper Citation

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Protocol Information

URL: <https://dx.doi.org/10.17504/protocols.io.bb2giqbw>

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Group: Molecular Diagnostics - Mats Nilsson Group

Summary: In situ sequencing method for parallel targeted analysis of short RNA fragments in morphologically preserved tissue. This protocol can be used to detect RNA molecules at the single cell level to aid in the identification of cell types according to their gene expression. The technique uses padlock probes to target desired genes of interest and rolling circle amplification to amplify signal for a high throughput methodology of spatial transcriptomics. With the use of barcode sequencing, identification of numerous genes is possible through multiplexing. Version 2 Update: Only minor mistakes were corrected for version 2 of this protocol, no major changes to protocol were done. Some references were also updated.

Associated Publications: Gyllborg D, Langseth CM, Qian X, Choi E, Salas SM, Hilscher MM, Lein ES, Nilsson M, Hybridization-based sequencing (HybISS) for spatially resolved transcriptomics in human and mouse brain tissue. Nucleic Acids Research 48(19). doi: [10.1093/nar/gkaa792](https://doi.org/10.1093/nar/gkaa792)

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