

## PREDAVANJE/LECTURE

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Velika predavalnica / Great Lecture Hall Kemijski inštitut / National Institute of Chemistry, Ljubljana

## Computational approaches for exploring functional relationships between 3'UTR structure and mRNA metabolism

The structure of mRNA molecules plays an important role in its interactions with RNA binding proteins (RBPs). However, current transcriptome-wide experimental methods to chart these interactions, including hiCLIP (that maps RNA duplexes bound to RBPs), are limited by their poor sensitivity.

We present Tosca, a Nextflow computational pipeline for the processing, analysis and visualisation of proximity ligation sequencing data generally. Using this pipeline, we extended hiCLIP atlas of duplexes bound by Staufen1 (STAU1) ~10-fold, through careful consideration of experimental assumptions. We discovered novel insights into the RNA selectivity of STAU1, revealing the importance of structural symmetry and duplex-span-dependent nucleotide composition. Furthermore, we identified heterogeneity in the relationship between STAU1-bound 3' UTRs and metabolism of the associated RNAs that we relate to RNA structure: transcripts with short-range proximal 3' UTR duplexes have high degradation rates, but those with long-range duplexes have low rates. Overall, our work enables the integrative analysis of proximity ligation data delivering insights into specific features and effects of RBP-RNA structure interactions.



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