# MoleRNA - DISCOVERING AND DESIGNING SMALL MOLECULES TARGETING mRNA

molecure

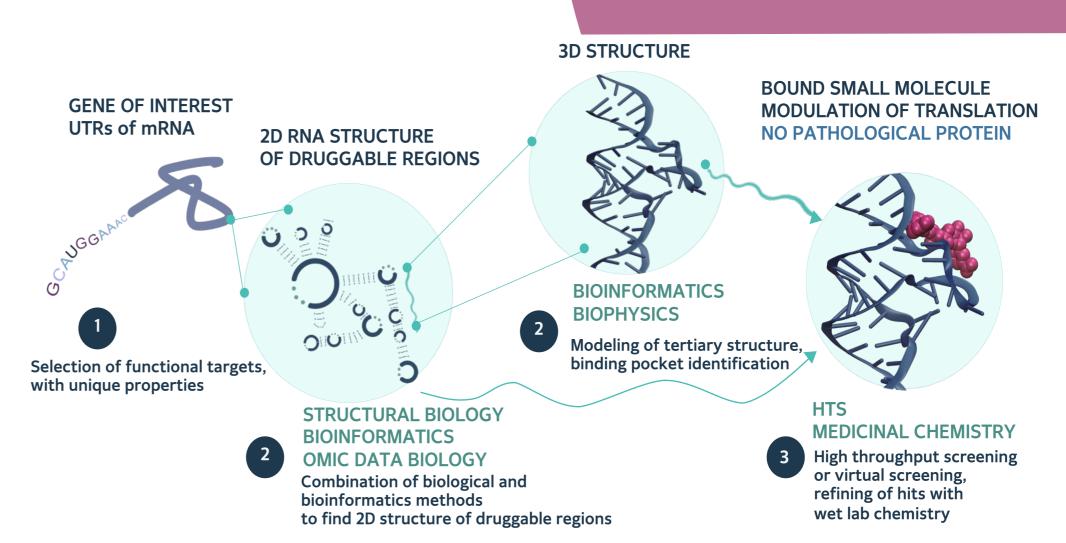
Żwirki i Wigury 101 02-089 Warsaw

RNA LEADERS **EUROPE CONGRESS** Basel, Switzerland 15-16 March 2023

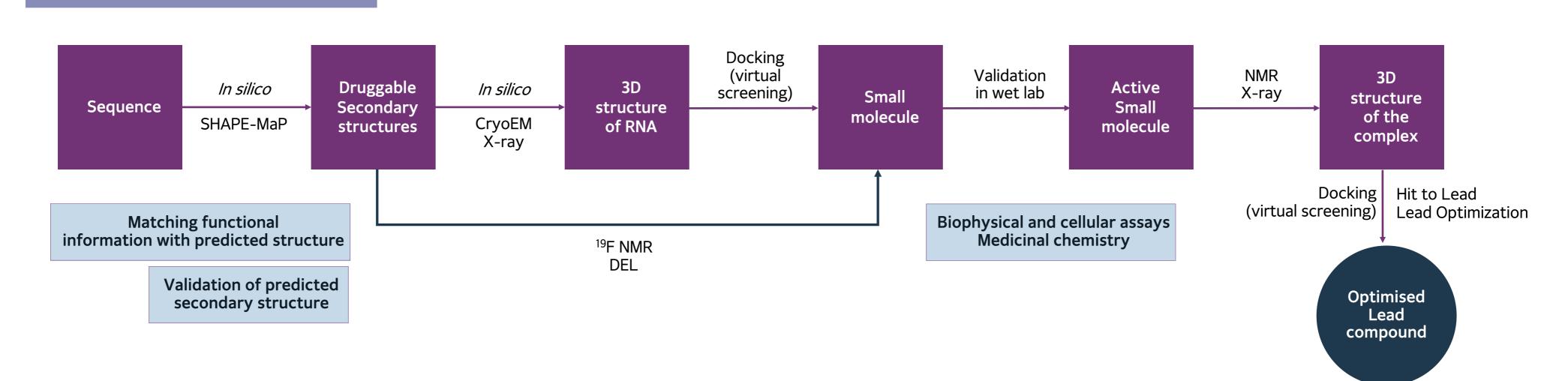
Irina Tuszyńska, Martyna Nowacka, Roman Błaszczyk, Julita Nowicka, Nithin Chandran, Dorota Niedziałek, Grzegorz Wieczorek, Sławomir Bojarowski, Anna Antosiewicz, Katarzyna Głuchowska, Katarzyna Piwowar, Katarzyna Drzewicka, Angelika Muchowicz, Aleksandra Cupriak, Jacek Olczak, Zbigniew Zasłona

# Background

Many undruggable proteins play key roles in the development and pathology of various diseases. Our strategy is to target mRNAs which encode these proteins. We utilize the fact that mRNAs adopt specific 3D structures which are integral and essential for their biological functions, specifically translation. We start with a structural biology approach and recognize defined motifs in the regulatory regions of mRNA. Subsequently, we aim at the identification of small molecules which by binding mRNA functional motifs modulate target protein levels. Our company has over 10 years of experience in the development of first-in-class drugs into clinic. For this project, within Molecure, we have created MoleRNA, a platform supported by in silico and wet lab analyses for designing small molecules targeting functional mRNA regions with defined structures. MoleRNA's objective is to develop lead compounds targeting mRNAs with optimized drug-like properties for undruggable proteins.



# MoleRNA platform discovery workflow

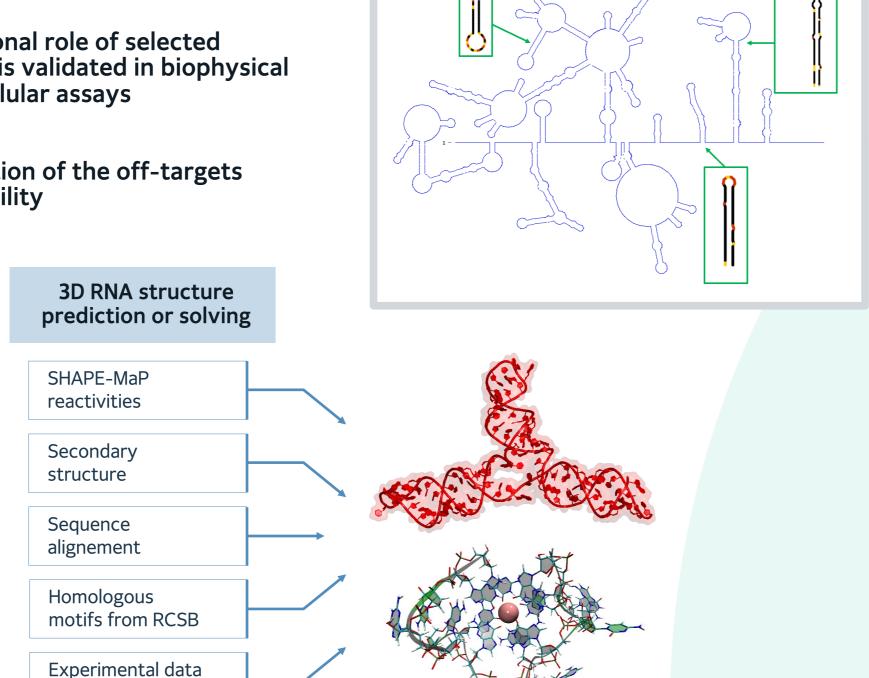


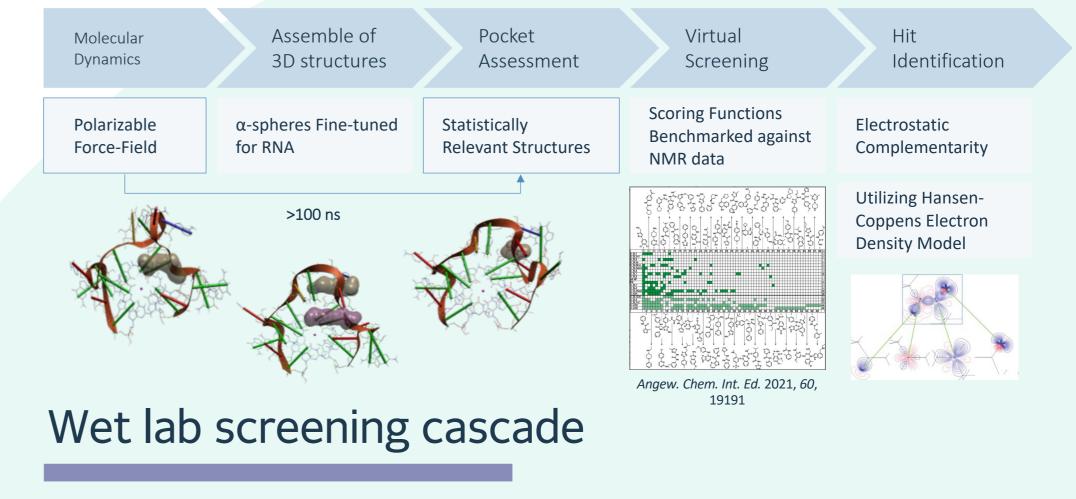
### Druggable regions selection

**Predicted secondary structures** are validated by SHAPE-MaP (in vitro, in cellulo) and structure conservation

Functional role of selected region is validated in biophysical and cellular assays

Prediction of the off-targets probability





### specificity) Short RNA motifs (< tRNA size) + SM DEL, NMR MST, SPR, ITC (binding affinities) + protein → AlphaScreen SHAPE-MaP (determine the occupancy of potential binding sites) ► RT-qPCR Long RNA motifs (> tRNA size) + SM →phenotypic assay synthesis of

High-throughput assays

(rapid evaluation of large

number of chemicals)

Lead compounds with optimized drug-like properties

Virtual screening pipeline

### Medicinal chemistry Hit and Lead Property Series Analysis

establishment

Low-throughput assays

(high-quality data, affinity,

kinetics, concentration,

### Conclusions

(distance restrains)

To develop and test the MoleRNA pipeline, six structural motifs from different mRNAs were selected by in silico methods and validated in the wet lab, three of them entered virtual screening and high-throughput screening cascade. The identified hits will be checked in binding and cellular assays, and then to obtain a lead they will go through the optimization procedure.

