

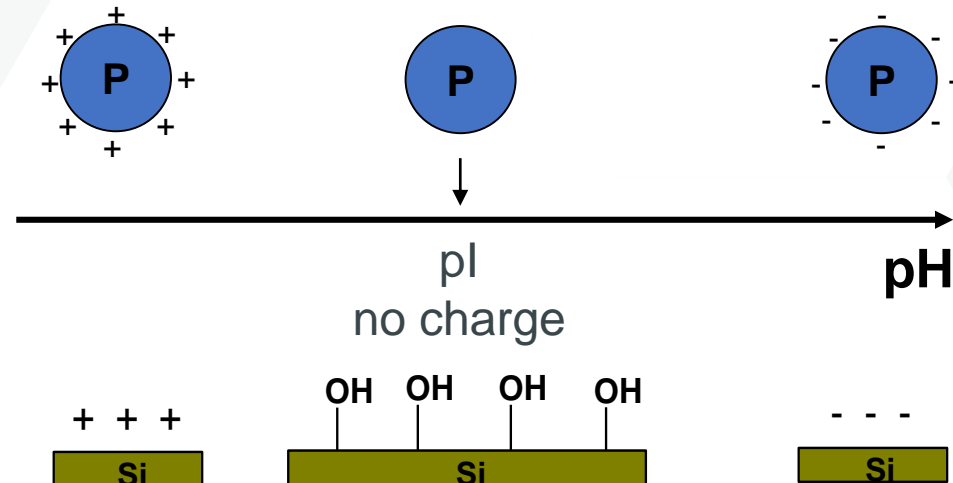


# My experience with Atomic Force Microscopy

**Andrea Tripepi**  
**Peter Lukavsky Research group**

# Fixation of proteins on mica

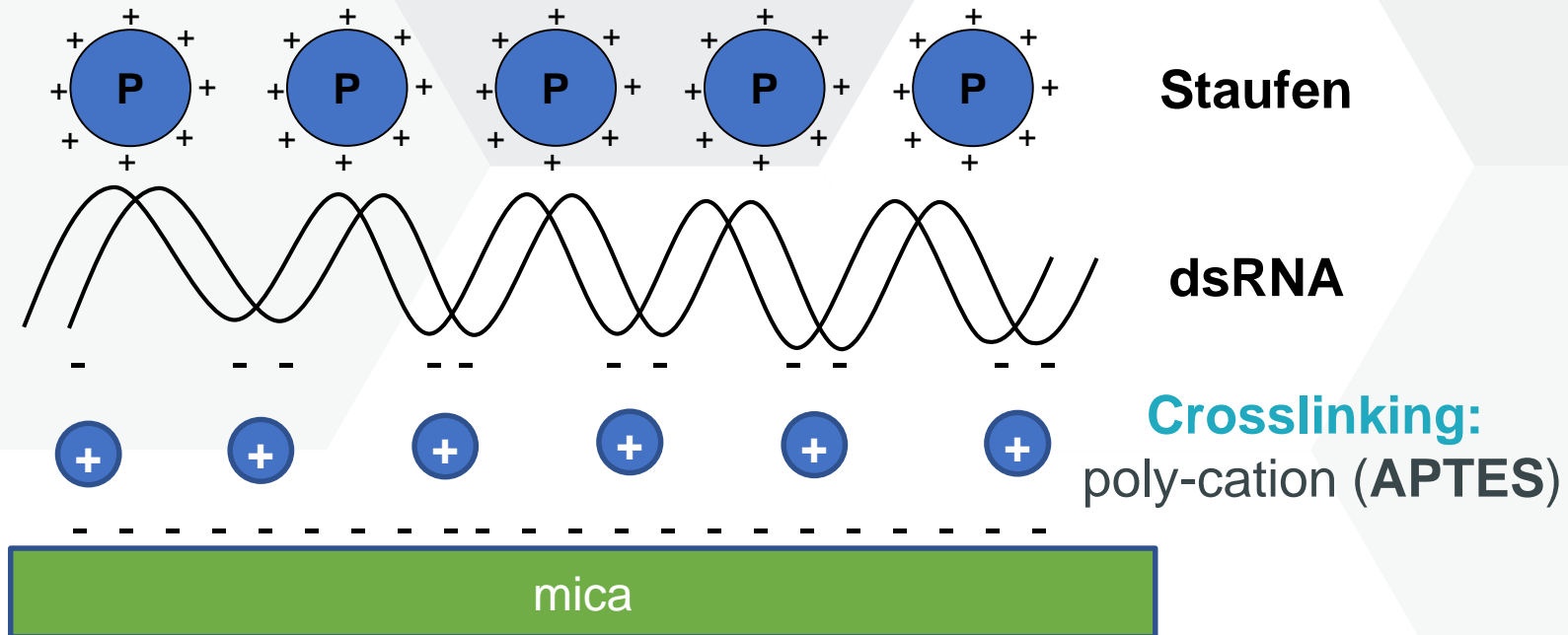
- **Protein:** charge is given by its isoelectric point (pI, pKa) + pH
- Immobilization on mica: **pKa (mica) < pH < pI (mica - pKa = 3.0)**
- Our proteins have pIs ranging from 8.8 till 9.5.
- This means that at pH 8.0, our proteins are positively charged and MICA is negatively charged



# How do I immobilize proteins on mica surface?

- Heating 1 nM proteins at 94 °C for 3 minutes
- Cooling in ice
- Loading the samples on mica coated grids
- Washing the grids with buffer in order to remove improperly fixed particles

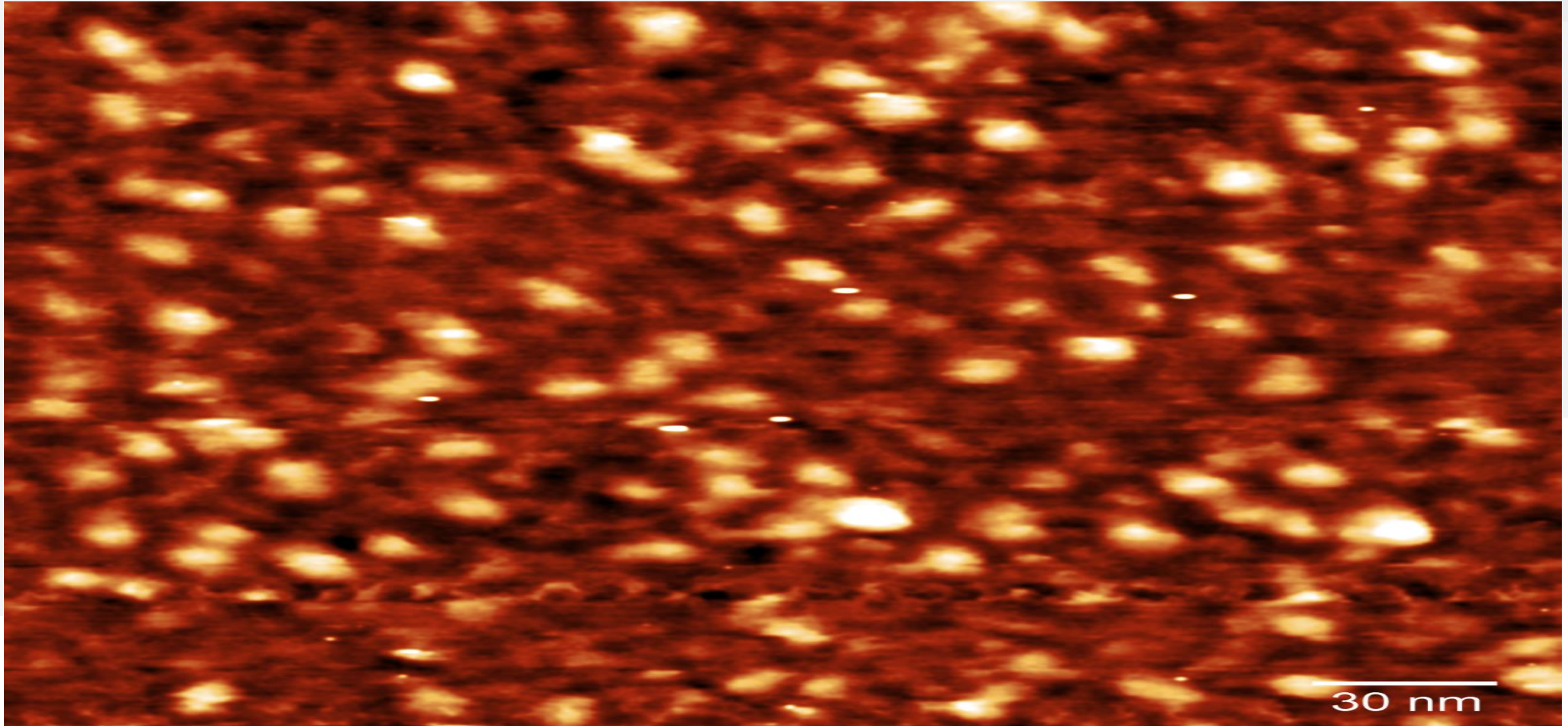
# RNA-protein complexes on APTES grid



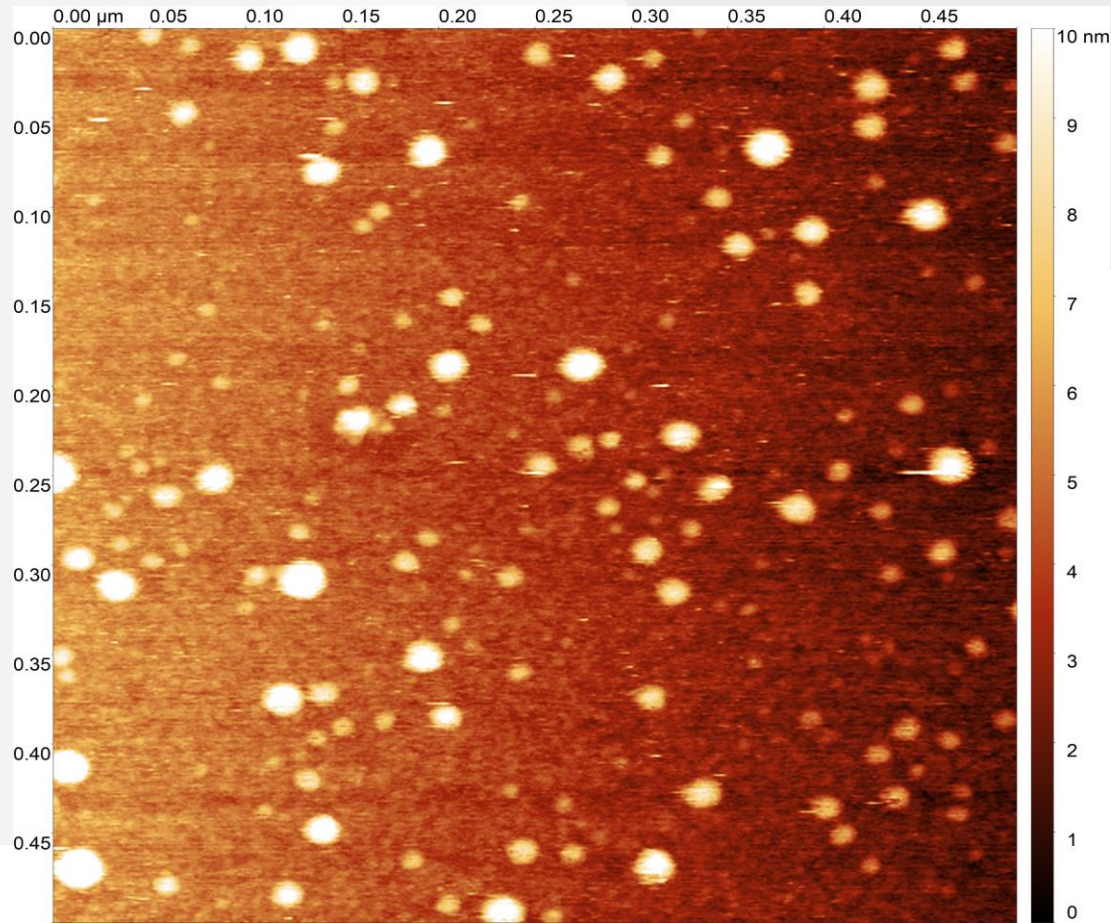
# How do we immobilize proteins on aptes surface?

- Heating 1 nM proteins at 94 °C and 2 nM RNAs at 72 °C for 3 minutes
- Cooling in ice
- Loading RNA samples on APTES coated grids for 2 minutes
- Washing the grid with the buffer
- Loading protein samples on the grid
- Washing the grid with the buffer
- Observing the samples at AFM

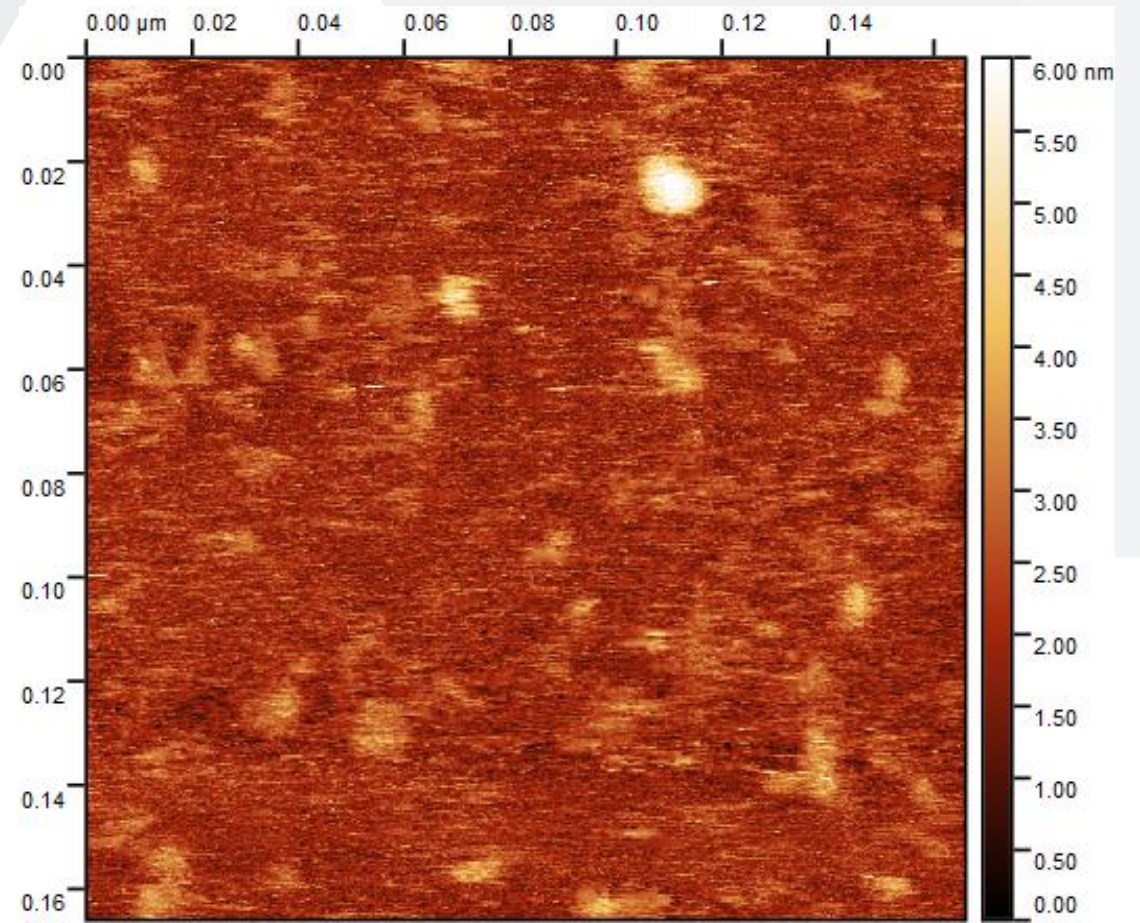
# What I saw at the beginning...



# How did I improve?



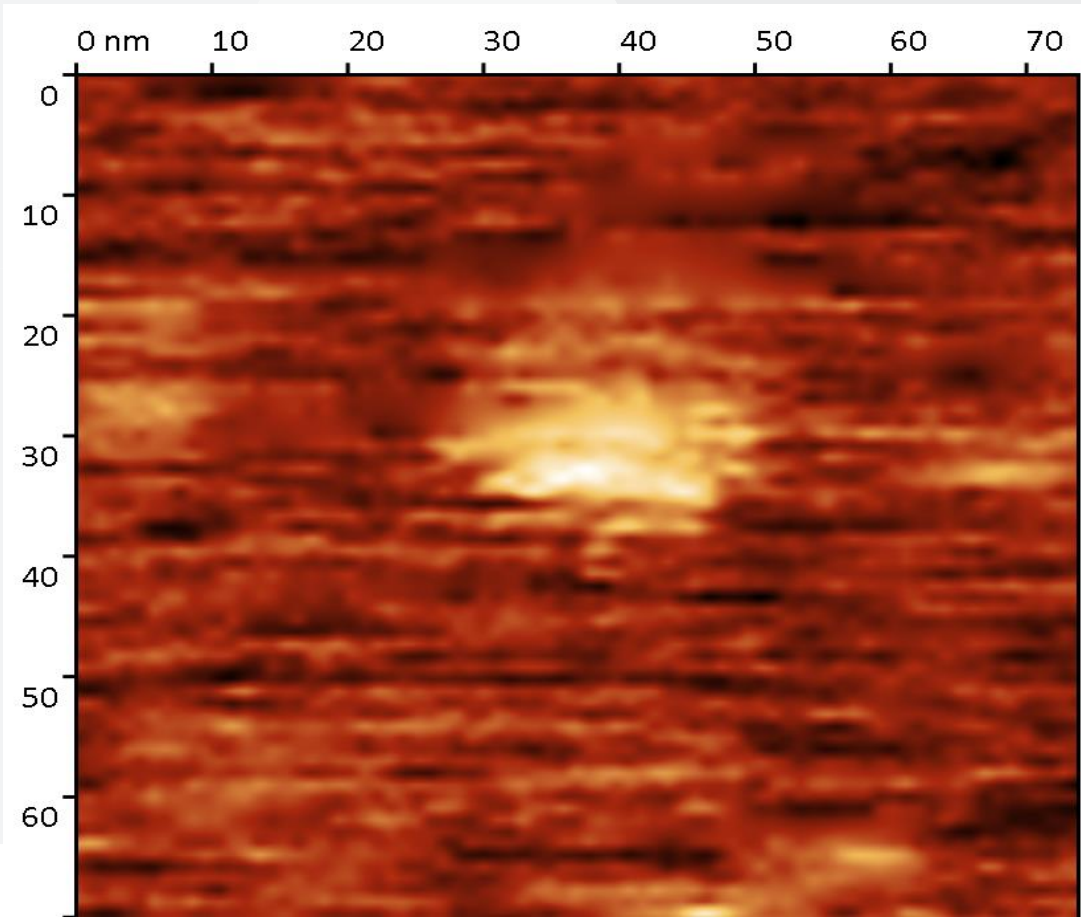
1 nM Staufen1 without pre-heating and observed at 22 °C



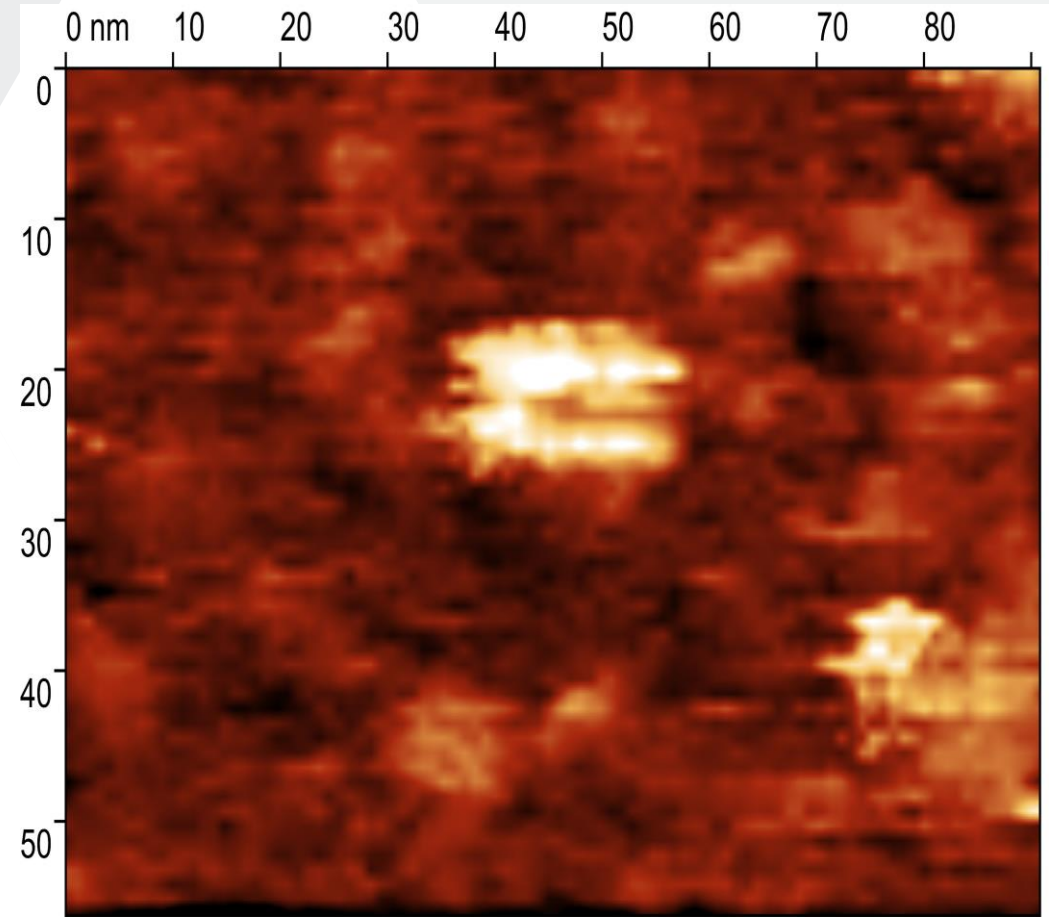
Preheated 1 nM Staufen1 and observed at 37 °C

# Examples of pictures we made by AFM

Peak force amplitude	6 nm
Peak force frequency	2 kHz
Peak force	30 pN
Lift height	12 nm
Tip radius	5 nm
Spring constant	0.084 N/m



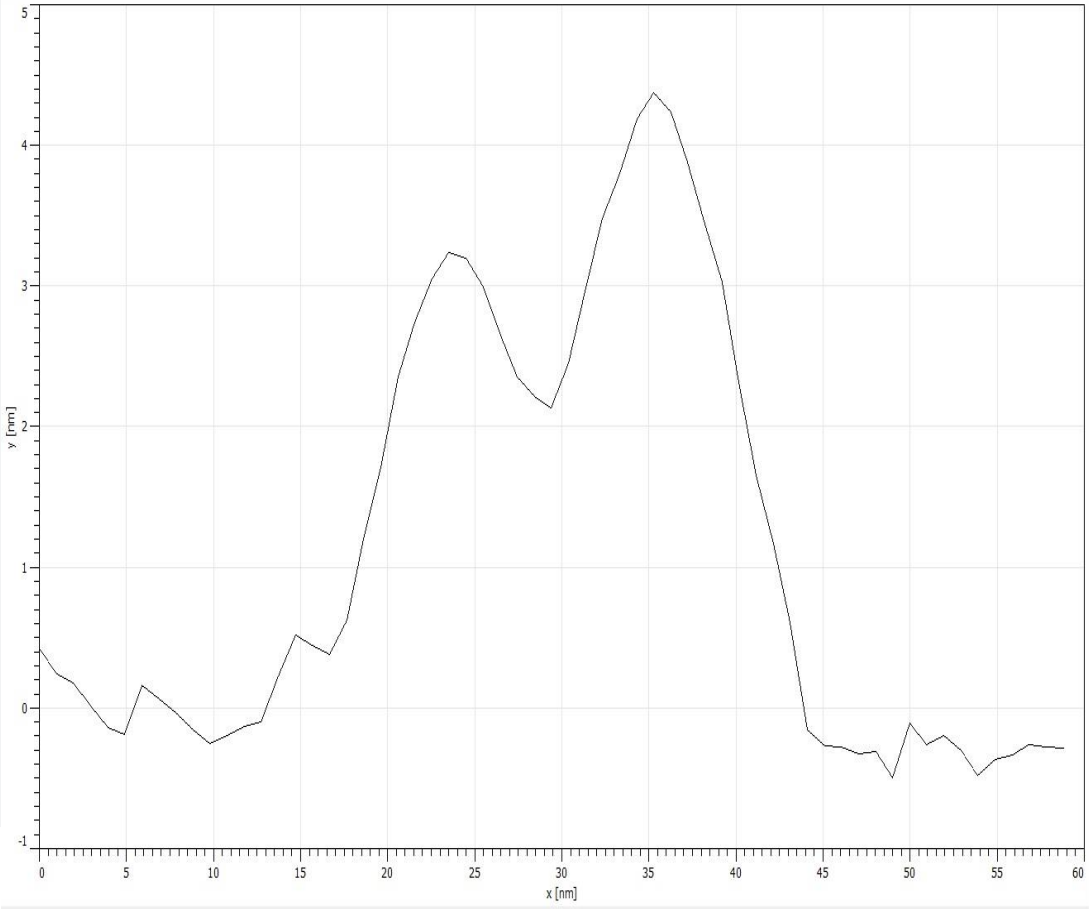
RBD3-End dimer



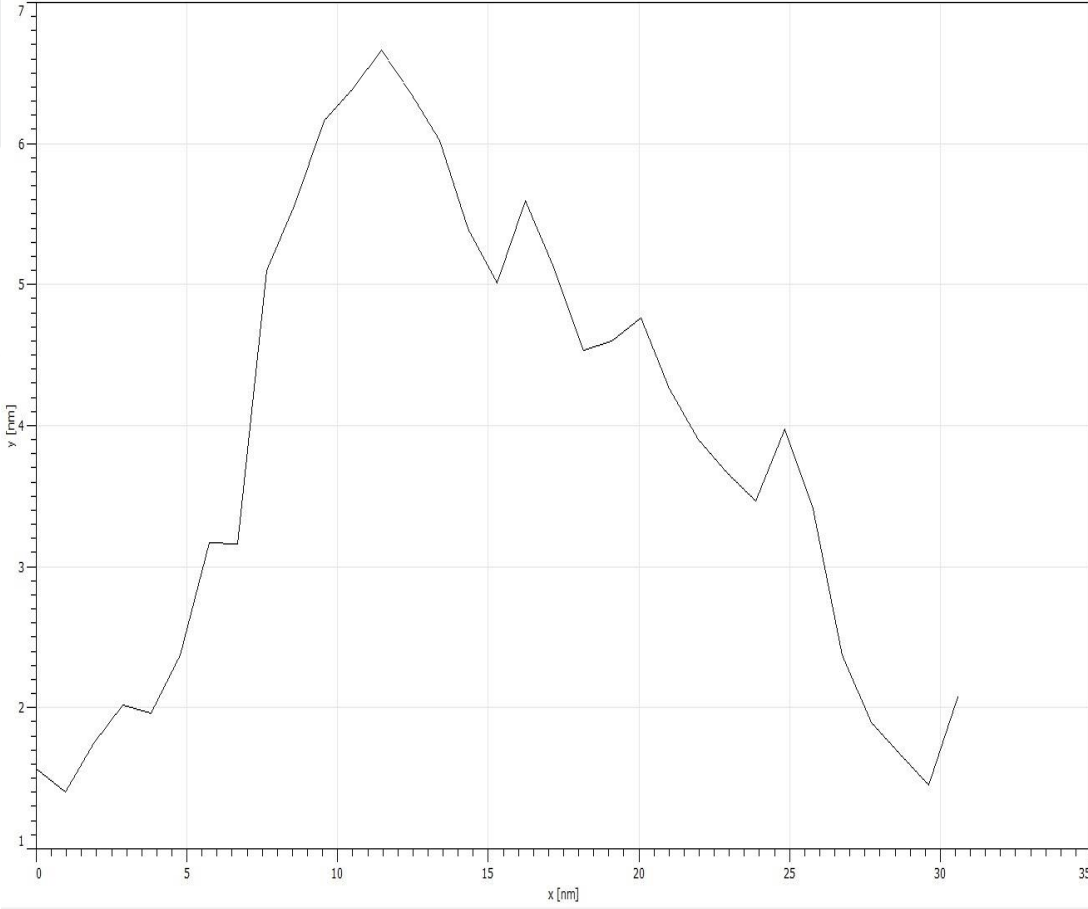
RBD3-end/19bp RNA complex. Stoichiometry 2:1



# Section surface profile: a useful way to get data

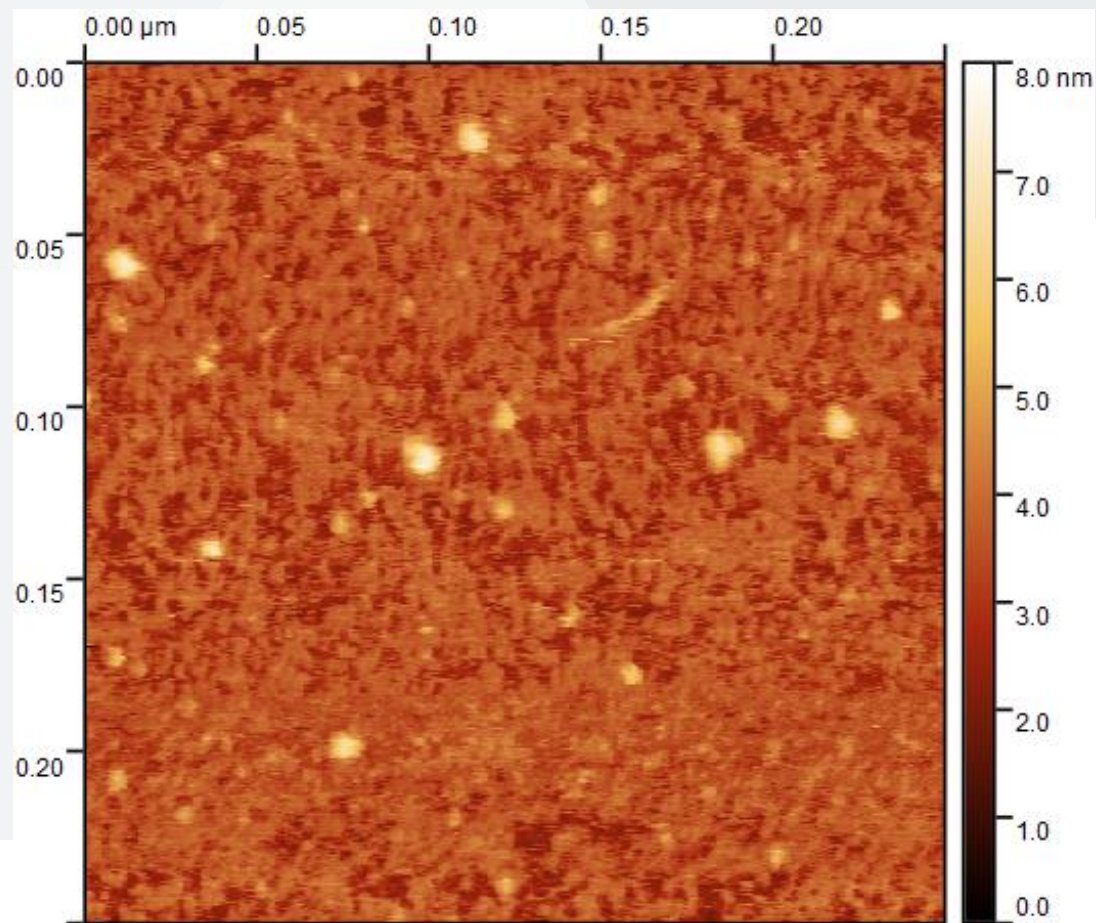


RBD3-End

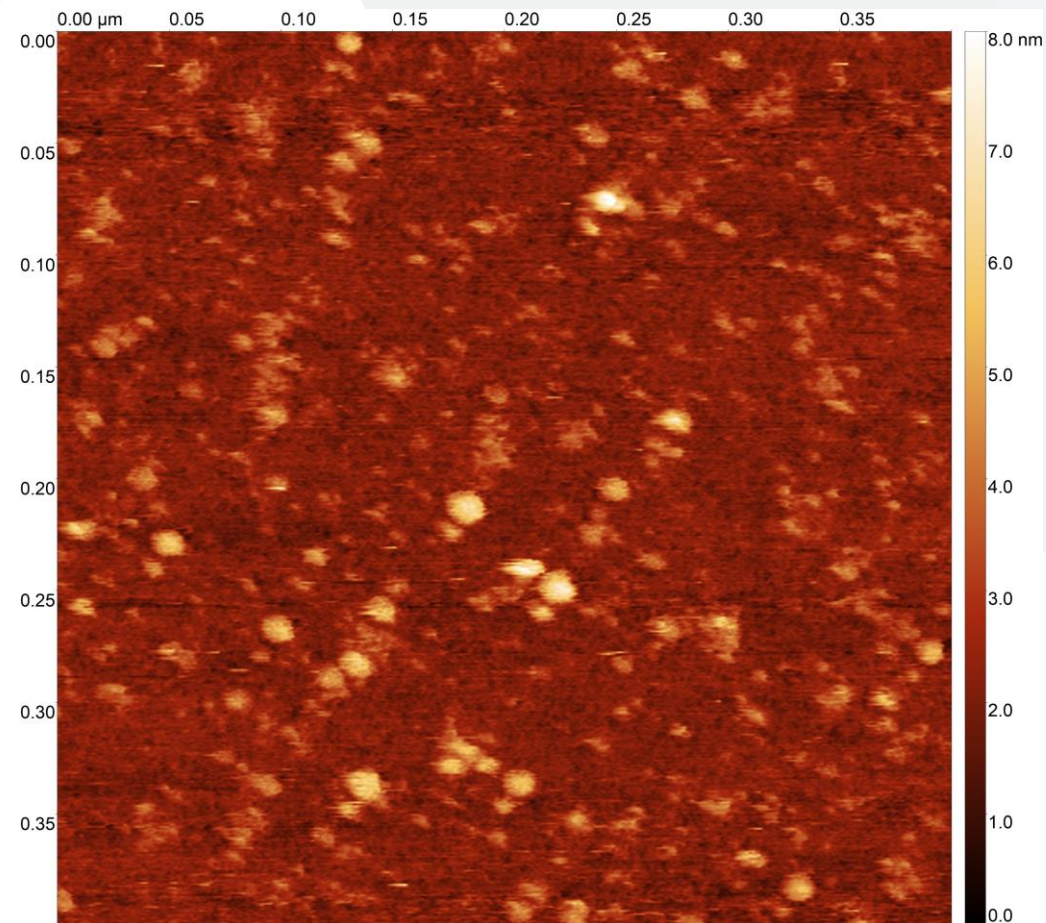


RBD3-End $\Delta$ SSM

# RNA-small molecule interaction



RNA control



RNA treated with small molecule

# What will we do?

- Continue examining our samples by AFM
- Find new settings of parameters and probes for better resolution
- Create model of our biomolecules
- Improve our data by processing multiple images
- Interacting with AFM experts

# In conclusion

- AFM represents a fast and reliable method to analyze the samples, but it requires an optimization work that depends on many factors
- It is a technique that observe biomolecules in quasi-natural conditions
- Along with other techniques (EFM, SAXS, X-Ray crystallography, Sec-Mals, AUC, MS etc.), AFM is a valid tool to study biomolecules

# Acknowledgements

- Our supervisor Dr. Peter Lukavsky
- All my team members
- Jan Příbyl, Radka Obořilová and the other team members
- Nanobiotechnology Core Facility

**Thank You**

