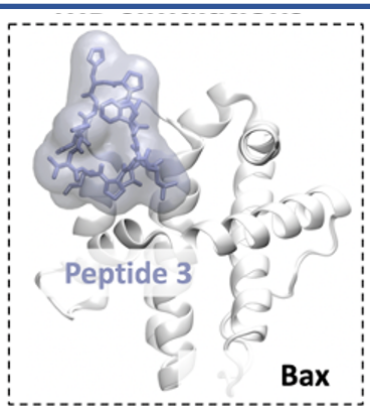
Computational peptide design against neurodegenerative diseases



Contact: Dr. Ioana M. ILIE
Van 't Hoff Institute for Molecular Sciences
University of Amsterdam
Email: i.m.ilie@uva.nl
Website: biosim-lab.com

Background: Neurodegenerative diseases, such as Parkinson's and Alzheimer's (PD and AD), affect millions of people world-wide. To date no preventive therapies against these diseases exist. The lack of preventive therapies is hampered by the limited understanding of the underlying protein folding and accumulation mechanisms.

Rationale: Understanding the structural and dynamic folding mechanisms of proteins associated with neurodegeneration (e.g. α-synuclein in PD, amyloid-β in AD) will enable the development of novel agents to modulate potential toxic effects.

Goal:

- Understand the interaction mechanisms between proteins associated with neurodegeneration
- Develop a modulating agent (e.g. peptide, small molecule) to inhibit toxic effects

Research questions

1. How do different proteins interact?
2. How to design an effective inhibitor?
3. What are the effects of inhibitors?

Research approaches

1. Molecular dynamics simulations (enhanced sampling)
2. Molecular design
3. AI

Bibliography

1. D. de Raffele and **I.M. Ilie***, Unlocking novel therapies: cyclic peptide design for amyloidogenic targets through synergies of experiments, simulations, and machine learning, Chem. Commun., 60, 632 - 645 (2024)
2. T. Vlaar, B. Mayer, L. van der Heide and **I.M. Ilie***, Computational design of Bax-inhibiting peptides, bioRxiv (2024)