

## BASICS OF MOLECULAR DYNAMIC SIMULATIONS

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## WHO IS THIS COURSE FOR?

This course is for those interested in learning the basics of molecular dynamics simulations and a hands-on approach to the capabilities of GROMACS and free energy calculations. No previous experience in the field of structural bioinformatics is required, but a basic knowledge of protein structure is an advantage. Experience with a UNIX-like command-line environment is not required, but it helps to type the commands into the modeling concepts and biology.

- **Basics of MD simulations**
- 2 Key concepts of molecular interactions
- 3 Binding free energy calculations
- 4 Hands-on training

09:30 AM Basics of MD simulations

10:00 AM - 11.00 AM Key concepts of molecular interactions

11:30 AM - 12.30 PM Binding free energy calculations

12:30 PM - 1.30 PM Hands-on training











