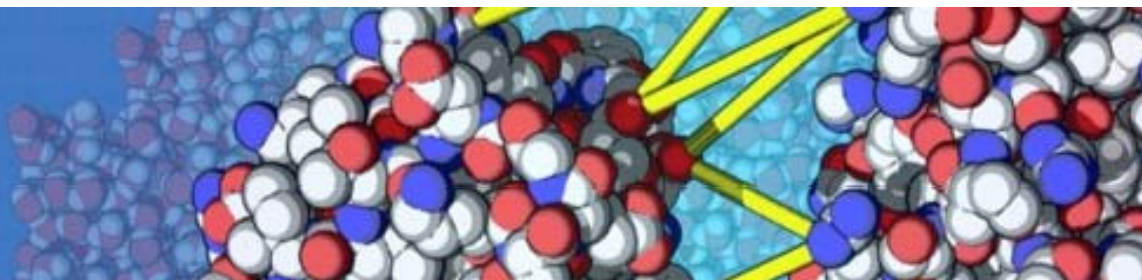


# Registration



<http://milou.science.uu.nl/cgi/services/POWERFIT/powerfit/register>

<http://milou.science.uu.nl/cgi/services/DISVIS/disvis/register>

**OR** go to <http://milou.science.uu.nl> -> POWERFIT/DISVIS -> Register

Then wait a couple of minutes for your activation (manual), in the meantime:

<http://bonvinlab.org> -> Education -> Powerfit-webserver

# Tutorial

BONVIN LAB

NEWS

EDUCATION

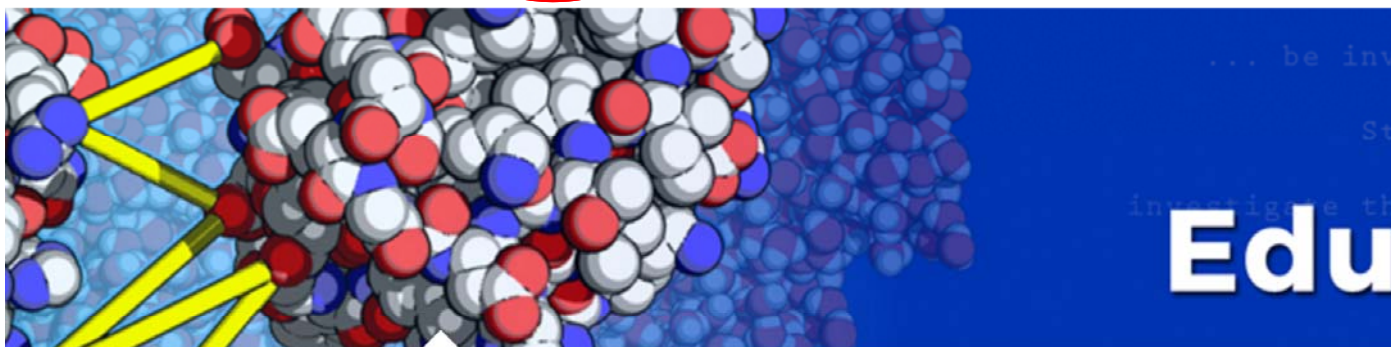
PEOPLE

PUBLICATIONS




RESEARCH

SOFTWARE

WEB PORTALS



*Computational Structural Biology group focusing on dissecting, understanding and predicting biomolecular interactions at the molecular level.*

-  Email
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-  Youtube
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## Education & Tutorials of the Bonvin Lab

In this page you can find links to our educational material, namely tutorials on the usage of our software and material for courses we teach at Utrecht University.

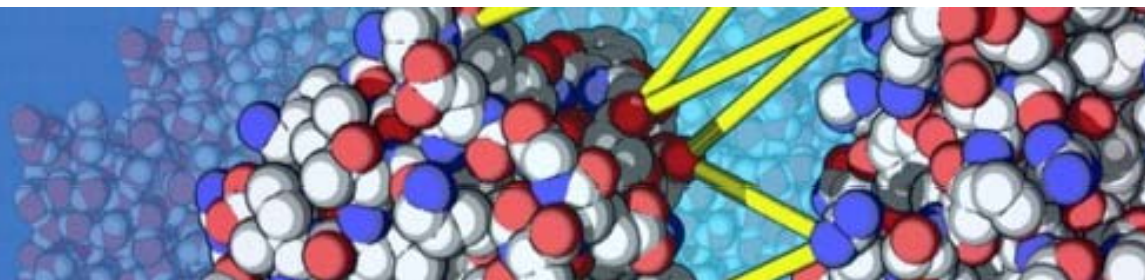
### Courses

- **[Structural Bioinformatics & Modelling](#)**: A MSc course aimed at those interested in learning homology modelling, molecular simulation, and docking of biological molecules. All the material is freely available on our Github repository and makes use of Vagrant/Virtualbox.

### Research projects



# Tutorial



- **[HADDOCK ligand binding site tutorial](#)**: A tutorial demonstrating the use of HADDOCK in ab-initio mode to screen for potential ligand binding sites. The information from the ab-initio run is then used to setup a binding pocket-targeted protein-ligand docking run. We use as example the multidrug exporter AcrB.
- **[PowerFit tutorial](#)**: A small introduction into PowerFit to automatically place a high-resolution atomic structure in a lower-resolution cryo-electron microscopy density map.
- **[PowerFit web server tutorial](#)**: A small introduction into PowerFit to automatically place a high-resolution atomic structure in a lower-resolution cryo-electron microscopy density map making use of our [web portal](#) (does not require Linux).
- **[DisVis web server tutorial](#)**: A small introduction into DisVis to analyse the interaction space between two molecules from a set of restraints. It can help to filter out putative false positive restraints and predict key residues involved in the interaction from this set of restraints. It makes use of our [web portal](#) (does not require Linux).



<http://bonvinlab.org/education/powerfit-webserver>