



Call for Abstracts

The NSBM cordially invites you to visit its fall meeting 2012. During the meeting, the floor will be given to PhD students and postdocs who study protein structure and/or structural bioinformatics or related topics (see a list below).

The main topic for this year's meeting will be: ***"Dissecting and designing interactions"***

As guest speaker, **Dr. Carlos Camacho** of Pittsburgh University, USA, will give a lecture on an "Interactive and efficient discovery tool of small molecule protein-protein interaction antagonists".

Abstract Format

Abstracts should be limited to a maximum of 10 lines, with 12-pt font and single-spaced text, giving a short description of the research done.

Please include a title in bold. The name(s) and affiliation(s) of the author(s) should follow the title. The opportunity will be given to present a poster, though this is not mandatory. If you wish to present a poster, please indicate so.

Abstract Submission

All abstracts, should be submitted electronically in MSWord via e-mail attachment to science.secr.nmr@uu.nl with as subject line "NSBM meeting 2012".

The deadline for receipt of all abstracts is November 5th 2012. Selected candidates will be notified no later than November 13th 2012.

Presentations will be 20 min, including a 5 min discussion. Starting PhD students are particularly encouraged to present their research.

For questions regarding the abstract or meeting please contact Gerry Nicolaes, +31-(0)43 3881688, g.nicolaes@maastrichtuniversity.nl

Registration

Registration can be made free of charge via e-mail to science.secr.nmr@uu.nl with as subject line "NSBM meeting 2012". A lunch and coffee/tea breaks will be provided for.

Should a lack of funding be a hurdle for visiting the NSBM Spring Meeting, please contact prof. Gert Vriend at vriend@cmbi.ru.nl so that an arrangement can be made.

Topics for presentations may include, but are not limited to:

- Computational Biology and Bioinformatics
- Computer-aided drug design
- Drug design and drug discovery
- Grid computing
- Homology modelling
- Molecular and supramolecular dynamics
- Molecular modeling and simulation
- Mutational analysis
- Protein crystallography
- Protein NMR
- Protein structure analysis
- Protein structure prediction
- Protein-protein interactions
- Protein-small molecules interaction
- Protein software design
- Proteomics
- Structural bioinformatics
- Structure-function analysis
- Text mining & information extraction
- Virtual screening

Conference Chairs: **Prof. Dr. Alexandre Bonvin**, professor of Computational Structural Biology and **Dr. Gerry Nicolaes**, Cardiovascular Research Institute Maastricht