# Curriculum Vitae: Bert de Groot

## Personal data


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| Full name: | Berend Lammert de Groot |
| Date of birth: | August 24 1971 |
| Place of birth: | Emmen, the Netherlands |
| Address: | Max Planck Institute for Biophysical Chemistry,<br>Computational biomolecular dynamics group,<br>Am Fassberg 11, 37077 Göttingen, Germany |
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| Nationality: | Dutch |


## Education and professional experience

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| 1989-1994 | Chemistry studies at the university of Groningen, the Netherlands. Specialisation: Biophysical chemistry. Supervisor: prof. H.J.C. Berendsen. |
| 1994-1998 | PhD student a the the university of Groningen, the Netherlands, the department of biophysical chemistry. Promotor: prof. H.J.C. Berendsen. Subject: Native state protein dynamics studied by a variety of computer simulation techniques. |
| 1998-2003 | Postdoctoral fellow in the theoretical molecular biophysics group headed by Dr. Helmut Grubmüller, at the Max-Planck Institute for Biophysical Chemistry, Göttingen, Germany. Subject: Structure and function of aquaporins, studied by Molecular Dynamics and other computational techniques. |
| 1997-2005 | Extensive research visits to Rome university, EMBL Heidelberg, the Basel Biocentre and Nijmegen university. |
| 2004- | Head of the computational biomolecular dynamics group, Max-Planck Institute for Biophysical Chemistry, Göttingen, Germany. |
| 2009- | adjunct Professor, physics faculty, university of Göttingen, Germany. |

## Teaching and advanced training

- Computational Biophysics I and II for third and fourth year physics and chemistry students, university of Göttingen, since 2006;
- Advanced simulation course (lectures+practicals) "Computersimulation biomolekularer Prozesse" for third year physics and chemistry students, university of Göttingen, 2004-2006;
- education of first and second year chemistry and physics students in practical courses university of Groningen, 1994-1998;
- participation in numerous courses/workshops/masterclasses among which C/C++ programming, protein folding, molecular modelling, advanced techniques in Molecular Dynamics.

## Research interests

Protein structure-dynamics-function relationships, studied by computational techniques. In particular:

- the use of large-scale molecular dynamics simulations and related techniques for the study of biomolecular dynamics at the atomic level tailored to unravel the functional mechanism of proteins and other biological macromolecules and complexes.
- the use of reduced dimensionality methods not only to analyse molecular dynamics simulation trajectories but also to develop novel simulation techniques tailored at enhancing simulation efficiency.
- the use of molecular dynamics simulations and related techniques in the elucidation and refinement of macromolecular structures based on experimental data (x-ray, NMR, EM).
- development and application of alternative simulation approaches, like the CONCOORD method, to address questions that because of size and/or timescale issues are not accessible by conventional molecular dynamics simulations.

## Editorial services

Editorial board member of Biophysical Journal (2011-2017) and PLOS Computational Biology (2013-).

## Reviewing

Reviewing for over 70 international journals as well as national and international funding agencies. Reviewed over 25 PhD theses.

## Grants

13 national and 6 international research grants.

## Supervised Ph.D. Theses (past and current)

Fourteen, thirteen past (with successful graduation) and one current.

## Publications

Over 190 publications in total, more than 150 of which are original research publications in international peer-reviewed journals. Hirsch index: 72.
Publication list: http://www.mpibpc.mpg.de/groups/de_groot/publications.html
Google scholar: http://scholar.google.com/citations?hl=en&user=k7hb45QAAAAJ