

Molecular dynamics simulations of liposomes: From formation to fusion and fission

Citation for published version (APA):

Spijker, P., Markvoort, A. J., Pieterse, K., Smeijers, A. F., Santen, van, R. A., & Hilbers, P. A. J. (2007). Molecular dynamics simulations of liposomes: From formation to fusion and fission. In *Abstracts of Papers, 234th ACS National Meeting, Boston, MA, United States, August 19-23, 2007* (pp. COMP-092)

Document status and date:

Published: 01/01/2007

Document Version:

Publisher's PDF, also known as Version of Record (includes final page, issue and volume numbers)

Please check the document version of this publication:

- A submitted manuscript is the version of the article upon submission and before peer-review. There can be important differences between the submitted version and the official published version of record. People interested in the research are advised to contact the author for the final version of the publication, or visit the DOI to the publisher's website.
- The final author version and the galley proof are versions of the publication after peer review.
- The final published version features the final layout of the paper including the volume, issue and page numbers.

[Link to publication](#)

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal.

If the publication is distributed under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license above, please follow below link for the End User Agreement:

www.tue.nl/taverne

Take down policy

If you believe that this document breaches copyright please contact us at:

openaccess@tue.nl

providing details and we will investigate your claim.

COMP 91

Improved methods for predicting the structure and function of G protein-coupled receptors

Ravinder Abrol and William A Goddard III, Materials and Process Simulation Center, California Institute of Technology, MC 139-74, Beckman Institute, Pasadena, CA 91125

G protein-coupled receptors (GPCRs) are intrinsic membrane proteins with 7 transmembrane helices, and modulated by diverse bioactive molecules (biogenic amines, peptides, lipids) to regulate essential physiological processes (neurotransmission, metabolism, secretion, growth, immunity). Thus, GPCRs have been implicated in all major disease areas. Development of drugs with reduced side effects has been hampered by the availability of 3D structure for only one GPCR. Our research group has been developing computational methods based on first principles to predict the structure and function of GPCRs. The methods have been validated for many systems against experimental mutagenesis data. We will present some of the recent method developments aimed at more accurate and faster predictions of GPCR structure and function. These include the use of implicit membrane (multi-dielectric) solvation for scoring monte carlo generated helical packings, accurate placement of protein side chains, use of thermodynamic hydrophobicities, and generation of ligand rotamer libraries for flexible docking.

COMP 92

Molecular dynamics simulations of liposomes: From formation to fusion and fission

Peter Spijker¹, Albert J. Markvoort¹, Koen Pieterse¹, A. F. Smeijers¹, Rutger A. van Santen², and Peter A. J. Hilbers¹. (1) Department of Biomedical Engineering, Eindhoven University of Technology, Den Dolech 2, Eindhoven 5600MB, Netherlands, Fax: +31402472740, p.spijker@tue.nl, (2) Department of Chemical Engineering and Chemistry, Eindhoven University of Technology, Eindhoven 5600MB, Netherlands

Lipid bilayer membranes are known to form various structures, such as large sheets and vesicles. Using coarse grained molecular dynamics, we first studied the processes of spontaneous bilayer and vesicle formation, showing the bilayer-vesicle transition to be entropy-driven. Next, the same lipid model allowed us to elucidate fusion mechanisms of such vesicles in detail. Furthermore, we found that a difference in composition between the two bilayer leaflets may result in curved bilayers and a wide variety of vesicle shapes, such as ellipsoids, discoids,

pear-shaped, cup-shaped and budded vesicles. Lately, we also have been able to investigate the fission process using the same lipid model. Two distinct routes, being phase separation of lipids within the monolayers and a different composition of the monolayers, for vesicle fission are observed. The difference between the fusion and fission pathway is shown, indicating that one pathway is not simply the reverse of the other.

COMP 93

Molecular dynamics simulations of surfactant protein C mimic in phospholipid bilayers

Stephen M. Dutz¹, Zachary Ramjan¹, Patrick W. Mobley¹, Larry M. Gordon², Frans J. Walther², Brian Vovan³, Jose M. Hernandez-Juvief², Mark A. Sherman⁴, Alan J. Waring⁵, and Shantanu Sharma¹. (1) Department of Chemistry and Center for Macromolecular Modeling & Materials Design (CM3D), California State Polytechnic University, 3801 West Temple Ave, Pomona, CA 91768, Fax: 909-869-4344, smdutz@csupomona.edu, (2) L.A. Biomedical Research Institute, Harbor-UCLA Medical Center, Torrance, CA 90502, (3) Department of Pediatrics, Harbor-UCLA Medical Center, Torrance, CA 90502, (4) Department of Biomedical Informatics, Beckman Research Institute, City of Hope National Medical Center, Duarte, CA 91010, (5) Department of Medicine, UCLA School of Medicine, Los Angeles, CA 90095

Surfactant protein C (SP-C) is an extremely hydrophobic lipopeptide found in mammalian lung surfactant. Important SP-C functions include lipid bilayer interactions with the lung surface monolayer and modulation of the surfactant lipid viscosity. Previous solution NMR studies in organic solvents indicate that the secondary structure of SP-C and the (34 residue) synthetic SP-C derivative SP-Cff is largely helical in this environment and is localized to the poly-valine sequence. Our infrared measurements of SP-Cff in palmitoyl-oleoylphosphatidylcholine (POPC) bilayers confirm the helical nature of the peptide, with the helical axis oriented parallel to the long axis of the phospholipid acyl chains. Moreover, our molecular dynamics simulations of SP-Cff in hydrated POPC bilayers validate the helical structure of the poly-valine sequence, with the helical axis oriented perpendicular to the bilayer surface.

COMP 94

Molecular-scale understanding and design of low friction and biocompatible surfaces

Shaoyi Jiang, Department of Chemical Engineering, University of Washington, Benson Hall, Seattle, WA 98195, sjiang@u.washington.edu