Name	:	Wonpil Im	Date of Birth	: March 10, 1970
Sex	:	Male	Nationality	: Korean
Address	:	Department of Molecular Biology (TPC6) The Scripps Research Institute 10550 North Torrey Pines Rd La Jolla, CA 92037	Email Mobile Phone Office Phone Fax Number	: wonpil@scripps.edu : (858) 405-3595 : (858) 784-8214 : (858) 784-8688

Curriculum Vitae

I. EDUCATION

06/2002 -	- Present	NSF CTBP (Center for Theoretical Biological Physics) Fellow
		Postdoctral Associate in the group of Prof. Charles Brooks,
		The Scripps Research Institute, La Jolla
02/1997 -	- 05/2002	Ph. D. in Biochemistry
		Weill Medical College of Cornell University, New York
		Thesis Supervisor: Prof. Benoit Roux
(02/1997 -	- 05/2000	in Chemistry, University of Montreal, Montreal)
03/1994 -	- 02/1996	M. Sc. in Chemistry, Hanyang University, Seoul
		Thesis Supervisor: Prof. Youngdo Won
03/1990 -	- 02/1994	B. Sc. in Chemistry, Hanyang University, Seoul

II. EXPERIENCE

1. Postdoctoral Research Experience

Development of Generalized Born Model (GBSW module in CHARMM).Folding, assembly, and modeling of membrane peptides/proteins.Membrane insertion and interfacial folding of synthetic peptides (WALP and TMX).Structure refinement of proteins with implicit solvent models.Molecular dynamics simulations with implicit solvent models for proteins and DNA.

2. Doctoral Research Experience

Molecular dynamics simulations of aqueous salt solutions. Molecular dynamics simulations of the membrane-protein system (OmpF porin). Grand Canonical Monte Carlo - Brownian Dynamics (GCMC/BD) simulations of ion permeations through the porin (OmpF, PhoE, OmpK36, and mutants of OmpF). PNP (Poisson-Nernst-Planck) solver and its applications to porins. Generalized Solvation Boundary Potentials (GSBP). Electrostatic solvation forces based on the Poisson-Boltzmann equation. Development of CHARMM source code (PBEQ/GSBP module). 3. Pre-doctoral Research Experience

Molecular dynamics simulations of liquid systems (normal alkanes and acetonitrile). Parameterization of acetonitrile.

Potential of mean force (PMF) calculations for the anion pair formation of acetonitrile. Development of CHARMM source code (CRYSTAL module).

4. Teaching experience

Aug. 9 2004 Jan. 2002	_	Aug. 20 2004 April 2002
March 1995	_	Feb. 1996

2004 CTBP Summer Workshop, UCSD Teaching Assistant in Department of Biochemistry Weill Medical College of Cornell University Teaching Assistant in Department of Chemistry Hanyang University

5. Honors

2002 Graduate School Scholarship Award of Excellence (May, 2002)

III. REFEREES

- Professor Charles L. Brooks, III Department of Molecular Biology (TPC6), The Scripps Research Institute 10550 North Torrey Pines Rd, La Jolla, CA 92037 Tel.~: (858) 784-8035 Email: brooks@scripps.edu
- Professor Benoit Roux Department of Biochemistry, Weill Medical College of Cornell University 1300 York Avenue, New York, NY 10021 Tel.~: (212) 746-6018 Email: benoit.roux@med.cornell.edu
- Professor David A. Case Department of Molecular Biology (TPC15), The Scripps Research Institute 10550 North Torrey Pines Rd, La Jolla, CA 92037 Tel.~: (858) 784-9768 Email: case@scripps.edu
- Professor Shin-Ho Chung Biophysics Group, Department of Physics, The Australian National University Canberra ACT 0200, Australia Tel.~: +61-2-6-125-2024 Email: Shin-Ho.Chung@anu.edu.au
- Professor Olaf Sparre Andersen Department of Physiology and Biophysics, Weill Medical College of Cornell University 1300 York Avenue, New York, NY 10021 Tel.~: (212) 774-2289 Email: sparre@med.cornell.edu

IV. INVITED TALKS

- 1. Insertion and Folding Mechanism of Membrane Peptides and Proteins Studied by Molecular Simulation, The Protein Society's 18th Annual Symposium, San Diego, USA (2004)
- 2. Atoms in Motion, 3rd Symposium of Korean-American Scientists and Engineers Association at San Diego Chapter (KSEA-SD), San Diego, USA (2004)
- 3. De Novo Folding of Membrane Proteins, Theory and Applications of Computational Chemistry, Gyeongju, KOREA (2004)
- An Implicit Membrane Generalized Born Theory for the Study of Structure, Stability, and Interactions of Membrane Proteins. 5th Canadian Computational Chemistry Conference, Toronto, CANADA (2003)
- 5. The Role of Electrostatics in Ion Permeation and Selectivity of Biological Membrane Channels. Department of Chemistry, Hanyang University, Seoul, KOREA (2002)
- Ion Permeation and Selectivity of OmpF Porin from Eschericha coli: Theoretical Studies using Molecular Dynamics, Brownian Dynamics, and the Electrodiffusion Theory. 46th Annual Biophysical Society Meeting, San Francisco, USA (2002)
- 7. Ion Permeation and Selectivity of OmpF Porin from Eschericha coli: Theoretical Studies using Molecular Dynamics, Brownian Dynamics, and the Electrodiffusion Theory. Laboratory of Chemical Physics, NIDDK, National Institutes of Health, USA (2001)

V. REFEREED JOURNALS

- 1. **W. Im**, J. Chen, and C.L. Brooks III Performance of a Generalized Born / Nonpolar Solvation Model with a Simple Switching Function. in preparation (2004).
- W. Im and C.L. Brooks III Interfacial Folding and Membrane Insertion: A Molecular Dynamics Study with Synthetic Peptides. submitted (2004).
- 3. J. Chen, H. Won, **W. Im**, H.J. Dyson and C.L. Brooks III Generation of Native-like Models from limited NMR data. *J. Biomolec. NMR* in press (2004).
- J. Chen, W. Im, and C.L. Brooks III Refinement of NMR Structure Using Implicit Solvent and Advanced Sampling Techniques. J. Am. Chem. Soc. in press (2004).
- S.Y. Noskov, W. Im, and B. Roux Ion Permeation through the α-Hemolysin Channel: Theoretical Studies based on Brownian Dynamics and Poisson-Nernst-Plank Electrodiffusion Theory. *Biophys. J.* 87:2299-2309 (2004).
- 6. B. Roux, T. Allen, S. Berneche, and **W. Im** Theoretical and Computational Models of Ion Channels. *Q. Rev. Biophys.* 37:15-103 (2004).
- W. Im and C.L. Brooks III De Novo Folding of Membrane Proteins: An Exploration of the Structure and NMR Properties of the fd Coat Protein. *J. Mol. Biol.* 337:513-519 (2004).

- M. Feig, W. Im, and C.L. Brooks, III Implicit Solvation Based on Generalized Born Theory in Different Dielectric Environment. J. Chem. Phys. 120:903-911 (2004).
- M. Feig, A. Onufriev1, M.S. Lee, W. Im, D.A. Case, and C.L. Brooks, III Performance Comparison of Generalized Born and Poisson Methods in the Calculation of Electrostatic Solvation Energies for Protein Structures. J. Comput. Chem. 25:265-284 (2004).
- W. Im, M. Feig, and C.L. Brooks III An Implicit Membrane Generalized Born Theory for the Study of Structure, Stability, and Interactions of Membrane Proteins. *Biophys. J.* 85:2900-2918 (2003).
- W. Im, M.S. Lee, and C.L. Brooks III Generalized Born Model with a Simple Smoothing Function. J. Comput. Chem. 24:1691-1702 (2003).
- N.K. Banavali, W. Im, and B. Roux Electrostatic Free Energy Calculations using the Generalized Solvent Boundary Potential Method. J. Chem. Phys. 117:7381-7388 (2002).
- 13. W. Im and B. Roux

Ion Permeation and Selectivity of OmpF Porin: A Theoretical Study Based on Molecular Dynamics, Brownian Dynamics, and Continuum Electrodiffusion Theory. J. Mol. Biol. 322:851-869 (2002).

- W. Im and B. Roux Ions and Counterions in a Biological Channel: A Molecular Dynamics Simulation of OmpF Porin from Escherichia coli in an Explicit Membrane with 1 M KCl Aqueous Salt Solution. J. Mol. Biol. 319:1177-1197 (2002).
- A. Philippsen, W. Im, A. Engel, T. Schirmer, B. Roux, and D.J. Muller Imaging the Electrostatic Potential of Transmembrane Channels: Atomic Probe Microscopy of OmpF Porin. *Biophys. J.* 82:1667-1676 (2002).
- W. Im and B. Roux Brownian Dynamics Simulations of Ions Channels: A General Treatment of the Electrostatic Reaction Field for Molecular Pores of Arbitrary Geometry. J. Chem. Phys. 115:4850-4861 (2001)
- W. Im, S. Berneche, and B. Roux Generalized Solvent Boundary Potentials for Computer Simulations. J. Chem. Phys. 114:2924-2937 (2001).
- B. Roux, S. Berneche and W. Im Ion Channels, Permeation, and Electrostatics: Insight into the Function of KcsA. *Biochemistry* 39:13295-13306 (2000).
- W. Im, S. Seefeld and B. Roux Grand Canonical Monte Carlo - Brownian Dynamics Algorithm for Simulating Ion Channels. *Biophys. J.* 79:788-801 (2000).
- M. Nina, W. Im, and B. Roux Optimized Atomic Radii for Protein Continuum Electrostatics Solvation Forces. Biophys. Chem. 78:89-96 (1999).

21. W. Im, D. Beglov, and B. Roux

Continuum Solvation Model: Computation of Electrostatic Forces from Numerical Solutions to the Poisson-Boltzmann Equation. *Comput. Phys. Comm.* 111:59-75 (1998).

22. W. Im and Y. Won

Molecular Dynamics Simulation on Thermodynamic and Structural Properties of Liquid Hydrocarbons : Normal Alkanes. *bull. Korean Chem. Soc.* 15:852-856 (1994).

VI. BOOK CHAPTERS & THESIS

1. W. Im and C.L. Brooks III

Structure prediction of membrane proteins. *In* Computational Methods for Protein Structure Prediction and Modeling, Springer-Verlag Press, Ying Xu, Dong Xu, and Jie Liang Eds. in preparation (2005)

2. B. Roux, D. Beglov, and W. Im

Generalized Solvent Boundary Potentials for Computer Simulations. *In* Treatments of electrostatics interactions in computer simulations of condensed media, Santa Fe Workshop, L.R. Pratt and G. Hummer Eds. 492:473-491 (1999).

3. **W. Im**

The Role of Electrostatics in Ion Permeation and Selectivity of Biological Membrane Channels. Ph.D. Thesis. Cornell University. (2002)

4. **W. Im**

Molecular Dynamics Simulation on Thermodynamic, Structural, and Dynamic Properties of Liquid Alkanes and Liquid Acetonitrile. M. Sc. Thesis}. Hanyang University. (1996)