

# Insuk Lee

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## EDUCATION

- **Ph.D.**, University of Texas at Austin, TX (09/1996 – 12/2002)  
Major: Molecular genetics & Microbiology  
Advisor: Prof. Rasika M. Harshey  
Dissertation: Importance of the Conserved TG/CA Dinucleotide Termini in Phage Mu Transposition: Similarities to Transposable Elements in the Human Genome
- Texas State University at San Marcos, TX (06/2000 – 12/2002)  
Complete 37 (31 undergraduate, 6 graduate) credit hours in Computer Science
- **M.S.**, Western Illinois University, Macomb, IL (09/1993 – 05/1996)  
Major: Biology  
Advisor: Prof. Thomas Alton  
Thesis: Genetic analysis of *Agrobacterium vir* region by generating gene fusion using bacterial transposon
- **B.S.**, Hanyang University, Seoul, Korea (03/1986 – 02/1993, military service: 02/1988 – 05/1990)  
Major: Biology

## AFFILIATIONS AND HONORS

- Member of International Society for Computational Biology (ISCB)
- Intelligent Systems for Molecular Biology (ISMB) Travel Fellowship Award, 2006
- National Institute of General Medicine Science (NIGMS) Scholarship for Keystone Symposia of Systems Biology, 2006
- Intelligent Systems for Molecular Biology (ISMB) Travel Fellowship Award, 2005
- The L. Joe Berry Memorial Scholarship, University of Texas at Austin, 2001
- David Bruton, Jr. Fellowship, University of Texas at Austin, 2000
- Korean Honor Scholarship from Embassy of the Republic of Korea in the U.S., 1999
- The Hal H. Ramsey, III Memorial Scholarship, University of Texas at Austin, 1999
- Academic Achievement Scholarship, Hanyang University, 1986, 1991, 1992

## PROFESSIONAL SERVICE AND EXPERIENCE

- Journal Reviewing: *Ad hoc* reviewer for Genome Research and BioTechniques.
- Long-term sponsored participant, Institute of Pure and Applied Mathematics (IPAM) Special Semester on “Proteomics: Sequence, Structure, Function”, University of California at Los Angeles, Spring 2004
- Sponsored participant, Institute of Pure and Applied Mathematics (IPAM) short program “Sequence Analysis Toward System Biology”, University of California at Los Angeles, Jan 2006
- Sponsored participant, Institute of Pure and Applied Mathematics (IPAM) short program “System Biology and Molecular Modeling”, University of California at Los Angeles, May 2006

## RESEARCH EXPERIENCE AND ACCOMPLISHMENTS

- Center for Systems and Synthetic Biology, University of Texas at Austin, Research Associate (09/2006 – Present), Post-doctoral fellow (01/2003 – 08/2006), biological data mining from various genomics and proteomics data, integration biological data into gene/protein network models, cellular system analysis by network topology, comparative network analysis (biological, social, internet), prediction of gene functions, phenotypic change prediction, probabilistic gene network modeling for various organisms (yeast, *C. elegans*, Arabidopsis, human, and Rice)
- Department of Microbiology, University of Texas at Austin, Graduate research assistant (09/1996 – 12/2002), developed sensitive, plasmid-based assay system to monitor Mu transposition in vivo, biochemical/genetic study of functional roles of highly conserved terminal dinucleotides of Mu, computational analysis of conserved terminal sequences of transposable-like elements in human genome
- Department of Biology, Western Illinois University, Macomb, IL, Graduate student (09/1993 – 05/1996), transposon mutagenesis and Expression analysis in the virulent gene *virD* region of *Agrobacterium Tumefaciens*.
- Department of Chemistry, Western Illinois University, Macomb, IL, Research assistant (01/1994 – 08/1995), analysis of the inhibitory specificity and function of *Cucurbita maxima* trypsin inhibitor (CMTI)-V by site-directed mutagenesis, Cloning/expression/purification of CMTI-III and blood coagulation factor XIIIa.

## TEACHING EXPERIENCE

- Department of Microbiology, University of Texas at Austin, Graduate teaching assistant (1997, 2000), instructor in undergraduate Microbiology Laboratory Course (MIC129K: Spring 1997, Spring 2000) and Public Health Bacteriology Laboratory (MIC361K: Fall 1997).

## INVITED BOOK CHAPTER

1. **Insuk Lee** and Edward Marcotte. Effects of functional bias on supervised learning of a gene network model. In Computational Systems Biology (ed. J. McDermott, R. Samudrala, R. Bumgarner). Totowa, THE HUMANA. In press.
2. **Insuk Lee** and Edward Marcotte. Integrating Functional Genomics Data. In Bioinformatics (ed. Jonathan Keith). Totowa, THE HUMANA. In press
3. **Insuk Lee**, Rammohan Narayanaswamy, Edward Marcotte. Bioinformatic prediction of yeast gene function. In METHOD IN MICROBIOLOGY Vol. 36, Yeast Gene Analysis (ed. M. Tuite and A. Brown), Elsevier. p597-628, (2007)

## JOURNAL PUBLICATIONS

1. **Insuk Lee**, Ben Lehner, Catriona Crombie, Wendy Wong, Andrew G. Fraser, Edward M. Marcotte. A single network comprising the majority of genes accurately predicts the phenotypic effects of gene perturbation in *C. elegans*. Accepted for *Nature Genetics*
2. Kris McGary, **Insuk Lee**, Edward M. Marcotte. Broad network-based predictability of *S. cerevisiae* gene loss-of-function phenotypes. Accepted for *Genome Biology*
3. **Insuk Lee**, Zhihua Li, and Edward M. Marcotte. An improved bias-reduced probabilistic functional gene network of baker's yeast *Saccharomyces cerevisiae*. *PLOS One* 2:e988 (2007)
4. G. Traver Hart, **Insuk Lee**, Edward Marcotte. A high-accuracy consensus map of yeast protein complexes reveals modular nature of gene essentiality. *BMC Bioinformatic* 8:236 (2007)
5. **Insuk Lee**, Shailesh V. Date, Alex T. Adai, Edward Marcotte. A Probabilistic functional network of yeast genes. *Science* 306:1555-1558, (2004)
6. Bork, P., Jensen, L.J., Von Mering, C., Ramani, A.K., **Lee I**, Marcotte, E.M. Protein interaction networks from yeast to human. *Curr. Opin. Struct. Biol.* 14:292-9, (2004)
7. **Insuk Lee** and Rasika Harshey. Patterns of Sequence conservation at termini of LTR retrotransposons and DNA transposons in the human genome: Lessons from phage Mu. *Nucleic Acids Res.* 31:4531-4540, (2003)
8. **Insuk Lee** and Rasika Harshey. The conserved CA/TG motif at Mu termini: T specifies stable transpososome assembly. *J. Mol. Biol.* 330:261-275, (2003)
9. **Insuk Lee** and Rasika Harshey. Importance of the conserved CA dinucleotide at Mu termini. *J. Mol. Biol.* 314:433-444, (2001)
10. Xue, Y., Bai, X., **Lee, I.**, Kallstrom, G., Ho, J., Brown, J., Stevens, A., and Johnson, A. W. *Saccharomyces cerevisiae* RAI1 (YGL246c) is homologous to human DOM3Z and encodes a protein that binds the nuclear exoribonuclease Rat1p. *Mol. Cell. Biol.* 20:4006-4015, (2000)
11. Liu, J., Gong, Y., Prakash, O., Wen, L., **Lee, I.**, Huang J.-K., and Krishnamoorthi, R. NMR studies of internal dynamics of serine proteinase protein inhibitors: Binding region mobilities of intact and reactive-site hydrolyzed CMTI-III of the squash family and comparison with those of counterparts of CMTI-V of the potato I family. *Protein Science* 7:132-141, (1998)

12. Wen, L., **Lee, I.**, Chen, G., Huang, J.,-K., Gong, Y., and Krishnamoorthi, R. Changing the inhibitory specificity and function of CMTI-V by site-directed mutagenesis. *Biochem. Biophys. Res. Commun.* 207:897-902, (1995)

## TALKS

1. Yonsei University, Korea (**Nov, 2007**)
2. Cold Spring Harbor Laboratory/Wellcome Trust Conference-Functional Genomics & Systems Biology, Hinxton, UK (**Oct, 2007**)
3. Pochon Cha University College of medicine, Korea (**Sept, 2007**)
4. Myongji University, Korea (**Sept, 2007**)
5. Yeungnam University, Korea (**Sept, 2007**)
6. Pohang University of Science and Technology (POSTECH), Korea (**Sept, 2007**)
7. Seoul National University, Korea (**Sept, 2007**)
8. Hanyang University, Korea (**Sept, 2007**)
9. Sungshin Women's University, Korea (**Sept, 2007**)
10. Solanaceae Genomics meeting, Jeju, Korea (**Sept, 2007**)
11. Intelligent Systems for Molecular Biology Conference, Fortaleza, Brazil (**Aug, 2006**)
12. Indiana University School of Medicine, Indianapolis, IN, USA (**April, 2006**)
13. Pohang University of Science and Technology (POSTECH), Korea (**Mar, 2006**)
14. Keystone Symposia, Systems Biology meeting, Taos, NM, USA (**Mar, 2006**)
15. University of North Carolina at Charlotte, NC, USA (**Feb, 2006**)
16. Institute of Pure and Applied Mathematics (IPAM), Proteomics Reunion Conference, Los Angeles, CA, USA (**Dec, 2005**)
17. Monsanto company, St. Louis, MO, USA (**Aug, 2005**)
18. Intelligent Systems for Molecular Biology Conference, Detroit, MI, USA (**June, 2005**)
19. Rosetta Inpharmatics Inc. Seattle, WA, USA (**May, 2005**)

## REFERENCES

**Dr. Edward M. Marcotte (Post-doc mentor)**

William and Gwyn Shive Professorship in Metabolism and Bioinformatics  
Director, Center for Systems and Synthetic Biology  
Department of Chemistry and Biochemistry  
Institute for Cellular and Molecular Biology  
University of Texas at Austin

**Dr. Andrew Fraser (Collaborator)**

Investigator  
The Wellcome Trust Sanger Institute

**Dr. Ben Lehner (Collaborator)**

Group leader  
EMBL-CRG Systems Biology Program  
Center for Genomic Regulation

**Dr. Seung Yon (Sue) Rhee (Collaborator)**

Staff Member, Department of Plant Biology  
Carnegie Institution of Washington  
Stanford University

**Dr. Pamela C. Ronald (Collaborator)**

Faculty Assistant to the Provost  
Chair, Plant Genomics Program  
Professor, Department of Plant Pathology  
University of California, Davis

\*Contact information will be given upon request.