BIOGRAPHICAL SKETCH

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NAME: Junhoe Kim

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Postdoctoral fellow

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Korea University, Seoul, Republic of Korea	B.S.	02/2012	Life Sciences
Korea University, Seoul, Republic of Korea	Ph.D.	02/2019	Structural biology
Korea University, Seoul, Republic of Korea	Postdoc	06/2019	Structural biology
Oregon Health and Science University, Oregon, US	Postdoc	Ongoing	Structural biology

A. Personal Statement

During undergraduate, I majored Life Sciences at Korea University and earned a B.S. degree with top graduating. I started my field career at Prof. Hyun Kyu Song's lab at the same university as an undergraduate research assistant by joining a research project for structure determination of autophagy-related protein. Then I continued pursuing a Ph.D. degree in Molecular biology in the same lab focusing on the elucidation of structures and function of core autophagy-related proteins using X-ray crystallography, small-angle X-ray scattering, biochemical and biophysical tools. Not only these fundamental skills in this field, but I also learned unique techniques such as antibody library screening with phage display and X-ray free electron laser (XFEL) to implement the projects with variable directions. These multidisciplinary approaches allowed me to experience and develop various skills. After receiving my doctoral degree, I became interested in the structure determination of membrane protein using cryo-EM. For this, I applied and joined Dr. Gouaux's lab at OHSU due to his strong record in elucidation of structures and mechanisms of neurotransmitter receptors and transporters at chemical synapses using X-ray crystallography and cryo-EM. In my postdoctoral period, I have learned about membrane protein expression, purification, and imaging, as well as functional assays to characterize the protein. Based on this, now I am making efforts to have a success on my research project.

B. Positions and Honors

Positions

07/2010-02/2012 Undergraduate research assistant in Prof. Hyun Kyu Song's lab, Korea University, Seoul, Korea
03/2012-02/2019 Ph.D. candidate in Prof. Hyun Kyu Song's lab, Korea University, Seoul, Korea
03/2012-06/2012 Teaching assistant for GENERAL CHEMISTRY LABORATORY course, Korea University, Seoul, Korea
03/2019-06/2019 Postdoctoral fellow in Prof. Hyun Kyu Song's lab, Korea University, Seoul, Korea
08/2019-present Postdoctoral fellow in Dr. Gouaux's lab, Vollum Institute, OHSU, Portland, OR

Honors

09/2005-02/2006 College specialization support project scholarship, Korea University
03/2009-08/2009 Best honors scholarship, Korea University
09/2009-08/2010 scholarship from OH HYUNHO FOUNDATION
09/2010-02/2012 scholarship from LOTTE FOUNDATION
03/2012-02/2017 Global Ph.D. Fellowship, National Research Foundation (Korea)
- Title: Structural studies of core autophagic proteins for autophagosomal formation

06/2017-05/2018 Co-PI of EAPSI program (East Asia and Pacific Summer Institutes for U.S. Graduate Students), National Science Foundation (US)
- PI-Shelby Brooks (The University of Alabama)
- Title: Crystallization of mutant N-demethylase enzymes

02/2012 Korean Society for Biochemistry and Molecular Biology award, KSBMB
03/2012 Teaching assistant scholarship, Korea University
12/2013 Poster award, Asian Crystallographic Association
01/2015 Oral presentation award, Department of Life Sciences, Korea University
02/2016 Oral presentation award, Department of Life Sciences, Korea University
02/2019 Outstanding paper award, Korea University

Military service

05/2006-08/2008 Republic of Korea Air Force, Sergeant, and Honorable discharge

C. Contributions to Science

1. Including the period of an undergraduate research assistant, my early research during Ph.D. course was focused on the structural study of core autophagic machinery proteins, such as mammalian ATG5, ATG16L1, and TECPR1 using X-ray crystallography. These proteins has been known to drive autophagosome maturation via lysosomal fusion but there was a controversy whether they make a triple complex. I discovered that they bind exclusively to ATG5 using same binding motif which sequence is highly conserved in other eukaryotes. I suggested a model of their swapping mechanism based on local pH change.
    a. **Kim, J.H.**, Hong, S.B., Lee, J.K., Han, S., Roh, K.H., Lee, K.E., Kim, Y.K., Choi, E.J. & Song, H.K. Insights into autophagosome maturation revealed by the structures of ATG5 with its interacting partners. *Autophagy* 11:1, 75-87 (2015) (*Cover illustration*)
    b. **Kim, J.H.** & Song, H.K. Swapping of interaction partners with ATG5 for autophagosome maturation. *BMB Rep.* 48(3): 129-130 (2015)

2. To broaden the comprehensive understanding of autophagy mechanism, I also collaborated on other projects in the lab by helping purify protein and conduct biochemical experiment. These works were including structural studies of Atg10 the autophagic ubiquitin E2 enzyme, xenophagy-related NDP52-galectin8 complex, Atg13-Atg101 the upstream autophagy signaling complex, and LC3B complexed Legionella effector protein RavZ.
    a. Hong, S.B., Kim, B.W., **Kim, J.H.** & Song, H.K. Structure of the autophagic E2 enzyme Atg10. *Acta Crystallog. D Biol Crystallogr.* 68, 1409-17 (2012).
    b. Kim, B.W., Hong, S.B., **Kim, J.H.**, Kwon D.H. & Song, H.K. Structural basis for recognition of autophagic receptor NDP52 by the sugar receptor galectin-8. *Nat. Commun.* 4, 1613 (2013)
    c. Kim, B.*, Jin Y.*, Kim, J.*, **Kim, J.H.***, Jung, J., Kang, S., Kim, I.Y., Kim, J., Cheong, H., & Song, H.K. The C-terminal region of ATG101 bridges ULK1 and PtdIns3K complex in autophagy initiation. *Autophagy* 14(12):2104-2116 (2018)
    *Contributed equally
    d. Kwon, D.H., Kim, L., Kim, B., **Kim, J.H.**, Roh, K.H., Choi, E.J. & Song, H.K. A novel conformation of the LC3-interacting region motif revealed by the structure of a complex between LC3B and RavZ. *Biochem Biophys Res Commun.* 26;490(3):1093-1099 (2017)
3. As a method development, I joined a project predicting the orientation of coiled-coil (CC) oligomer. The major oligomeric state of CCs is a dimer, which can be either parallel or antiparallel. Even the orientation of each α-helix in a CC domain is critical for the molecular function of CC-containing proteins, but cannot be

determined easily by sequence-based prediction. I developed a biochemical method for assessing differences between parallel and antiparallel CC homodimers which was subsequently confirmed by X-ray crystallography and small angle X-ray scattering.

a. Kim, B., Jung, Y.O., Kim, M.K., Kwon, D.H., Park, S.H., **Kim, J.H.**, Kuk Y.B., Oh, S.J., Kim, L., Kim, B.H., Yang, W.S., & Song, H.K. ACCORD: an assessment tool to determine the orientation of homodimeric coiled-coils. *Sci Rep.* 7:43318 (2017)

4. At the second half of my Ph.D. course, I studied the structures and mechanism of N-demethylases from Pseudomonas putida which enable to live them by using caffeine as a sole carbon and nitrogen source. Including their structures, I figured out the exact oligomeric states of the enzymes in solution using small-angle X-ray scattering (SAXS), and by biochemical analysis, I identified their heteromeric complexation enhances the entire caffeine degradation efficiency. By elucidating complex structures with substrates and with a component of electron transport system, I provided insights of detailed molecular mechanism of the caffeine degradation pathway by bacterial enzymes which is potentially useful for industrial application.

a. **Kim, J.H.**, Kim, B.H., Brooks, S., Kang, S.Y., Summers, R.M., & Song. H.K., Structural and Mechanistic Insights into Caffeine Degradation by the Bacterial N-Demethylase Complex. *J Mol Biol.* Sep 6;431(19):3647-3661 (2019).

D. Additional Information: Research Support and/or Scholastic Performance

YEAR	SCIENCE COURSE TITLE	GRADE	YEAR	SCIENCE COURSE TITLE	GRADE
Korea University – Ph.D. courses (GPA 4.5/4.5)					
2012	BIOCHEMISTRY I,II	A+	2013	MOLECULAR GENETICS I	A+
2012	STRUCTURAL BIOLOGY	A+	2013	MATRIX BIOLOGY	A+
2012	CELL DEATH AND HUMAN DISEASES	A+	2013	PLANT SIGNALING SYSTEMS BIOLOGY	A+
2012	CELL BIOLOGY II		2014	CELL SIGNALING	A+
2012	MOLECULAR IMMUNOLOGY II	A+	2014	ADVANCED MOLECULAR BIOLOGY I	A+
2013	MOLECULAR IMMUNOLOGY I	A+			
2013	CELL BIOLOGY I	A+	2014	PRINCIPLE OF REGUATION IN GENE EXPRESSION	A+
2013	MOLECULAR BIOLOGY I	A+			
Korea University – Undergraduate (GPA 4.36/4.5)					
2005	GENERAL CHEMISTRY I	A	2010	PHYSIOLOGY I	A+
2005	GENERAL PHYSICS	A	2010	BIOPROCESS UNIT OPERATION	A+
2005	GENERAL BIOLOGY II	A+			
2005	GENERAL CHEMISTRY II	A+	2010	BIOCHEMISTRY II	A+
2005	GENERAL BIOLOGY II	A+	2010	GENETICS II	A+
2009	ORGANIC CHEMISTRY I	A+	2010	PHYSIOLOGY II	A+
2009	PHYSICAL CHEMISTRY	A	2010	STRUCTURAL BIOLOGY	A+
2009	MICROBIOLOGY I	A+	2011	BIOPHYSICS	A+
2009	CELL BIOLOGY I	A	2011	IMMUNOLOGY I	A+
2009	CELL BIOLOGY II	A+	2011	NEUROBIOLOGY I	A+
2009	MICROBIOLOGY II	A+	2011	PROTEIN BIOCHEMISTRY	A+
2009	ANALYTICAL CHEMISTRY	A	2011	IMMUNOLOGY II	A+
2010	BIOCHEMISTRY I	A+	2011	SYSTEM NEUROSICENCE	A+
2010	GENETICS I	A+			

BIOGRAPHICAL SKETCH

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NAME: Gouaux, James Eric

eRA COMMONS USER NAME (credential, e.g., agency login): GOUAUX

POSITION TITLE: Senior Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Harvard College, Cambridge MA	AB	1984	Chemistry
Harvard University, Cambridge MA	PhD	1989	Physical chemistry
Harvard University, Cambridge MA	Postdoc	1989-90	Crystallography
Massachusetts Institute of Technology, Cambridge MA	Postdoc	1990-92	Membrane proteins

A. Personal Statement

My research focuses on the molecular mechanisms underpinning signal transduction at chemical synapses. To do this, I have primarily employed x-ray crystallographic methods to elucidate atomic resolution structures of crucial neurotransmitter receptors and transporters, yet I have also enthusiastically engaged and learned complimentary biochemical and biophysical methods with the ultimate aim of using all possible approaches to elaborate structure-based mechanisms. Thus, I have extensive experience in the expression, characterization and crystallization of complex neurotransmitter receptors and transporters, as well as in x-ray crystallography and electrophysiology. In addition, I have now established single particle cryo EM in my laboratory as a central method by which to elucidate neurotransmitter receptor structures. As evidence of my progress in this area, I have published multiple papers in which we have used single particle cryo-EM as the primary tool to elucidate molecular structure and, together with biochemical, electrophysiological and computational approaches have gone on to define structure-based mechanisms for important receptors and transporters. I also participate in leadership of the PNCC, an NIH-funded, national cryo-EM center.

B. Positions and Honors

1993-1996 Assistant professor, Dept. Biochem. Mol. Biol., Univ. Chicago, Chicago IL
1996-2000 Assistant professor, Dept. Biochem. Mol. Biophys., Columbia Univ., New York NY
2000-2001 Associate professor, Dept. Biochem. Mol. Biophys., Columbia Univ., New York, NY
2000- Present Investigator, Howard Hughes Medical Institute
2001-2005 Professor, Dept. Biochem. Mol. Biophys., Columbia Univ., New York NY
2005-Present Senior scientist, Vollum Institute, Oregon Health and Science Univ., Portland OR
2015-Present Jennifer and Bernard Lacroute Term Chair in Neuroscience Research, Portland OR

1994 Searle Scholar
1995 National Science Foundation Young Investigator
1997 Alfred P. Sloan Research Fellow
1998 Klingenstein Research Fellow
2000 P&S Doctor Harold & Golden Lamport Award for Excellence in Basic Science Research, Columbia University

2003 P&S Dean's Distinguished Award in the Basic Sciences, Columbia University
2007 American Association for the Advancement of Science Fellow
2008 NINDS Javits Investigator Award
2009 NIHMH MERIT Award
2009 Medical Research Foundation Discovery Award, Oregon Health & Science University
2010 National Academy of Sciences Member
2010 Distinguished Faculty Awards Winner for Outstanding Research
2013 Physiological Society Annual Review Prize Lecture
2014 Alexander M. Cruickshank Lecture, Gordon Research Conferences
2014 W. Alden Spencer Award, Columbia University
2014 Honorary Doctorate, University of Copenhagen
2016 Anatrace Membrane Protein Award, Biophysical Society

C. Contributions to Science

My major contributions have been to provide a molecular basis for understanding the function of neurotransmitter receptor and transporters, fundamental molecular machines that mediate signal transduction at the chemical synapses of the central nervous system. We have focused on ionotropic glutamate receptors, acid sensing ion channels, ATP-gated P2X receptors and pentameric Cys-loop receptors, as well as on the transporters for glutamate and the biogenic amines. My work has not only provided insights into the three-dimensional structures of these crucial receptors and transporters, but because all of our results are deposited in the publically accessible protein data bank, the results of my work are available to everyone throughout the world. Thus, our studies will not only inform society on the fundamental building blocks of the brain, but they will also provide a foundation for those who are devoted to developing new therapeutic agents.

1. Our studies on the ionotropic glutamate receptors have provided deep insight into their mechanism of action, showing how antagonists, agonists and allosteric modulators act on these fundamental receptors.

a. Zhao Y, Chen S, Swensen AC, Qian WJ, Gouaux E. Architecture and subunit arrangement of native AMPA receptors illuminated by cryo-EM. Science 364, 355-362 (2019). PMCID: PMC6701862
b. Zhu S. Stein RA, Yoshioka C, Lee CH, Goehring A, Mchaourab HS, Gouaux E. Mechanism of NMDA receptor inhibition and activation. Cell 165: 704-14 (2016). PMCID: PMC4914038
c. Chen S, Zhao Y, Wang Y, Shekhar M, Tajkhorshid E, Gouaux E. Activation and desensitization mechanism of AMPA receptor-TARP complex by cryo-EM. Cell 170:1234-1246 (2017). NIHMSID: NIHMS 900397

2. We have also elaborated the molecular structure of the two major classes of neurotransmitter transporters, showing how these remarkably machines carry neurotransmitter from one side of the membrane to the other.

a. Coleman JA, Yang, D, Zhao, Z, Wen, PC, Yoshioka, C, Tajkhorshid, E, Gouaux, E. Serotonin transporter ibogaine complexes illuminate mechanisms of inhibition and transport. Nature 569, 141-145 (2019). PMCID: PMC6750207
b. Coleman JA, Green EM, Gouaux E. X-ray structures and mechanism of the human serotonin transporter. Nature 532: 334-39 (2016). PMCID: PMC4898786
c. Wang KH, Penmatsa A, Gouaux E. Neurotransmitter and psychostimulant recognition by the dopamine transporter. Nature 521:322-27 (2015). PMCID: PMC4469479

3. In addition, we have elaborated the structures of other neurotransmitter receptors and ligand gated ion channels of the brain, from acid sensing ion channels and ATP-gated P2X receptors to pentameric Cys-loop receptors, thus providing the neuroscience field with molecular blueprints upon which to ground studies of mechanism and drug development.

a. Du J, Lü W, Wu S, Cheng Y, Gouaux E. Glycine receptor mechanism illuminated by electron cryo-microscopy. Nature 526:224-29 (2015). PMCID: PMC4659708
b. Baconguis I, Bohlen, CJ, Goehring A, Julius D, Gouaux E. X-ray structure of acid-sensing ion channel 1–snake toxin complex reveals open state of a sodium-selective channel. Cell 156:717-29 (2014). PMCID: PMC4190031

c. Mansoor SE, Lü W, Oosterheert W, Shekhar M, Tajkhorshid E, Gouaux E. X-ray structures define human P2X3 receptor gating cycle and antagonist action. Nature 538: 66-71 (2016). PMCID: PMC5161641.

Complete List of Published Work in MyBibliography:
http://www.ncbi.nlm.nih.gov/sites/myncbi/james.gouaux.1/bibliography/40629156/public/?sort=date&direction=ascending

D. Additional Information: Research Support and/or Scholastic Performance

NIH 2 R01 NS038631-23 Gouaux, James Eric (PI) 03/19/1999-02/28/2025
3D Structure and Function of Ligand-Gated Ion Channels
The focus of this work is on determining the atomic structure of ligand-gated ion channels activated glutamate (AMPA receptors) or protons (ASICs) using x-ray diffraction techniques, on developing mechanisms for the activity of these channels, and on testing the mechanisms by a variety of techniques that include electrophysiology and other biochemical and biophysical methods. I am involved in all aspects of these studies, from experimental design to manuscript preparation.
Role: PI

NIH 5 R01 MH070039-18 Gouaux, James Eric (PI) 07/01/2004-02/29/2024
Structure and Function of Neurotransmitter Transporters
The research supported by this grant is concentrated on determining structures of bacterial homologs of human neurotransmitter transporters by x-ray crystallography and on studying the mechanism of these bacterial proteins using a combination of site-directed mutagenesis, flux assays and other biochemical and biophysical studies, with the aim being to understand the architecture of this important family of proteins and how that architecture relates the function of both prokaryotic and eukaryotic transporters. I am involved in all aspects of these studies, from experimental design to manuscript preparation.
Role: PI

NIH 5 R01 GM100400-08 Gouaux, James Eric (PI) 06/01/2012-03/31/2021
NIH/NIGMS
Structural biology of neurotransmitter ion channels
The aim of this work is to solve high resolution x-ray crystal structures of P2X and Cys-loop receptors bound to their cognate neurotransmitter and to competitive antagonists, to test the veracity of the mapped sites by site-directed mutagenesis and ligand-binding assays, and to develop molecular mechanisms for the action of agonists and antagonists in these receptors. I am involved in all aspects of these studies, from experimental design to manuscript preparation.
Role: PI

HHMI (no number) Gouaux, James Eric (PI) 09/01/2010-08/31/2027
Molecular Studies of Synapses
The research supported by these funds is focused on developing new methods for the isolation of crucial signaling complexes from the hair cells of the inner ear using novel fluorescently labeled affinity tags, in the development of new methods for EM grid preparation and in the isolation and structural study of complexes involved in mechanotransduction. I am involved in all aspects of these studies, from experimental design to manuscript preparation.
Role: PI