KOLIS KOREAN LIFE SCIENTISTS IN THE BAY AREA

KOLIS 2020 Annual Virtual Conference

Nov 20th – 21st 2020 PST

zoom

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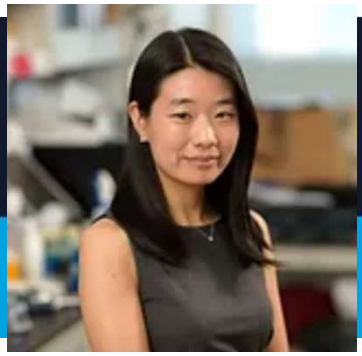

Welcome Remarks

From the KOLIS 2020 virtual conference program committee

Kihyun Lee, Ph.D.
President, KOLIS 2020

KOLIS 회원 여러분들께

2020년 올해는 다사다난한 해였습니다.
코로나 바이러스로 인하여 삶의 많은 부분이 영향을 받았고KOLIS 활동 또한 예외가 아니었습니다. 올해 초 기획하였던 여러 행사들을 진행할 수 없어 실의에 빠지기도 하였지만 온라인 활동이 활발해지는 장점을 이용하여 장소와 상관없이 생명 과학자 분들이 교류할 수 있는 자리를 만들려고 노력하였습니다. 4월부터는 학교별로 진행되던 세미나를 KOLIS 온라인 월례 세미나로 전환하여 많은 회원 분들이 교류할 수 있는 자리를 마련하였습니다.

이번 KOLIS 2020 Annual Virtual Conference에는 미국과 한국의 다양한 지역에서 활발한 연구를 하고 계신 분들을 모셨습니다. 특히나 국내외로 명망이 높으신 김빛내리 교수님을 Plenary Session Speaker 모시게 되어 영광으로 생각합니다. Neuroscience, Technology and Innovations, Machine Learning, Metabolism, Immunology 등 KOLIS 회원분들께서 관심있으실 만한 주제들로 Scientific session을 준비하였습니다. Career development session 에는 KOLIS와 인연이 있으신 교수님들을 모시고 진로 탐색의 장을 가지고자 합니다. KOLIS 2020 Annual Virtual Conference를 통하여 장소와 상관없이 다양한 지역에서 연구하시는 분들과 교류하고 새로운 학문적 자극을 즐길 수 있는 장이 되기를 바랍니다.

또한 앞으로 동부의 한인 생명 과학자 협회인 New England Bioscience Society (NEBS), New York Korean Biologists (NYKB)와 적극적인 교류를 통하여 미국 내 생명 과학자 분들의 교류를 도우려 합니다. KOLIS 2020 Annual Virtual Conference를 기획하고 진행할 수 있도록 노력과 시간을 아끼지 않으신 KOLIS 2020 회장단 여러분들과 학교 대표 분들께 특별히 감사의 인사를 전합니다. 행사에 적극적으로 참여해주시는 KOLIS회원 여러분들과 저희 후원사 분들께도 감사의 마음을 전하고 싶습니다.

KOLIS 2020 President
이 기 현

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Program

NOVEMBER 20th 2020, PST

Opening Remark & Plenary Session

17:00 - 17:20 Opening remarks: Kihyun Lee, KOLIS President (Gladstone/UCSF)

17:20 - 18:20 Plenary Lecture: V. Narry Kim (SNU)

18:20 - 18:25 Sponsor talk: Lauren Young-Mi Lee, Ph.D. (Hanmi Pharm.)

18:25 - 18:40 Break

Scientific Session 1 Neuroscience

18:40 - 19:10 Sung-Yon Kim, Ph.D. (SNU)

19:10 - 19:40 Jiook Cha, Ph.D. (SNU)

19:40 - 20:05 Jae Kyu Ryu, Ph.D. (Gladstone)

20:05 - 20:25 Taeho Han, M.D., Ph.D. (UCSF)

20:25 - 20:30 Flash talk: Hyelee Kim, M.D., M.AS. (UCSF)

20:30 - 20:35 Sponsor talk: Taejin Yoon, Ph.D. (Yuhan Cop.)

NOVEMBER 21th 2020, PST

Scientific Session 2 Technology and Innovations

10:00 - 10:20 Byungjin Hwang, Ph.D. (UCSF)

10:20 - 10:40 Kanghyun Lee, Ph.D. (UCSF)

10:40 - 10:45 Flash talk: Changman Kim, Ph.D. (LBNL)

10:45 - 10:50 Sponsor talk: Jinyong Lee, M.B.A. (Kryptos Biotechnologies)

10:50 - 11:00 Break

Career Development Session 1

11:00 - 11:15 Chang-il Hwang, Ph.D. (UC Davis)

11:15 - 11:30 Gina Lee, Ph.D. (UC Irvine)

11:30 - 11:45 Sora Shin, Ph.D. (Virginia Tech)

11:45 - 12:00 Q & A / Panel discussion

12:00 - 13:00 Lunch Break

Scientific Session 3 Machine Learning

13:00 - 13:30 Taedong Yun, Ph.D. (Google Health Research)
13:30 - 14:00 Jaewon Yang, Ph.D. (UCSF)
14:00 - 14:20 Young Suk Kim, M.S. (Stanford)
14:20 - 14:50 Ki Hwan Kim, M.D., Ph.D. (Lunit)
14:50 - 14:55 Sponsor talk: Youngkeun (Paul) Park, Ph.D. (Tomocube)
14:55 - 15:00 Break

Scientific Session 4 Metabolism

15:00 - 15:30 Cholsoon Jang, Ph.D. (UC Irvine)
15:30 - 15:50 Myungsuk Kim, M.S. (UC Davis)
15:50 - 16:20 Eun-Woo Lee, Ph.D. (KRIBB)
16:20 - 16:25 Flash talk: James Won Suk Jahng, Ph.D. (Stanford)
16:25 - 16:30 Sponsor talk: Hyunsun Jo, Ph.D. (Pin Therapeutics)
16:30 - 16:40 Break

Scientific Session 5 Immunology

16:40 - 17:10 Jie-Oh Lee, Ph.D. (POSTECH)
17:10 - 17:40 Jong-eun Park, Ph.D. (KAIST)
17:40 - 18:10 Hye Young Kim, Ph.D. (SNUCM)
18:10 - 18:15 Flash talk: Kicheol Kim, Ph.D. (Everest Detection)
18:15 - 18:20 Sponsor talk: Junghyun Hahn, Ph.D. (Dong-A ST)
18:20 - 18:30 Break

Career Development Session 2

18:30 - 18:45 Joon-Yong An, Ph.D. (Korea Univ.)
18:45 - 19:00 Jaecheol Lee, Ph.D. (Sungkyunkwan Univ.)
19:00 - 19:15 Sanghee Lee, Ph.D. (KIST)
19:15 - 19:30 Q & A / Panel discussion

Adjournment

19:30 – 20:00 Closing remarks and KOLIS exclusive meeting

Transcriptome and Proteome of SARS-CoV-2

V. Narry Kim, Ph.D.

Center for RNA Research, Institute for Basic Science
School of Biological Sciences, Seoul National University

SARS-CoV-2 is a betacoronavirus responsible for the COVID-19 pandemic. Although the SARS-CoV-2 genome was reported early this year, its transcriptomic architecture and proteomic contents were unknown. We present a high-resolution map of the SARS-CoV-2 transcriptome. We find that the viral transcriptome is highly complex owing to numerous discontinuous transcription events. Our data confirm the canonical genomic RNA and nine subgenomic RNAs while invalidating the predicted ORF10 transcript. We further find that SARS-CoV-2 produces transcripts encoding unknown ORFs with fusion, deletion, and/or frameshift. More recently, we have also performed proteomic analyses of the SARS-CoV-2 ribonucleoprotein complex. We identify many proteins that directly interact with viral RNAs and modulate viral growth. Functional investigation of the viral transcripts and host proteins discovered in this study will open new directions to our understanding of the life cycle and pathogenicity of SARS-CoV-2.

Biography

1988-1992	B.A., Microbiology, Seoul National University, Seoul, Korea
1992-1994	M.S., Microbiology, Seoul National University, Seoul, Korea
1994-1998	Ph.D., Biochemistry, Oxford University, Oxford, UK
1999-2001	Postdoc Fellow, Howard Hughes Medical Institute, University of Pennsylvania
2001-2004	Research Associate Professor, Advanced Training Program for Biological Sciences, Seoul National University
2004-2008	Assistant Professor, School of Biological Sciences, Seoul National University
2008-2013	Associate Professor, School of Biological Sciences, Seoul National University
2010-2016	SNU Distinguished Fellow, Seoul National University
2012- present	Director, Center for RNA Research, Institute for Basic Science
2013- present	Professor, School of Biological Sciences, Seoul National University
2017- present	SNU Distinguished Professor, Seoul National University

How do we stop eating when we are (mechanically) full?

Sung-Yon Kim, Ph.D.

Department of Chemistry
Institute of Molecular Biology and Genetics
Seoul National University

Mechanosensory feedback from the digestive tract to the brain is critical for limiting excessive food and water intake, but the underlying gut–brain communication pathways and mechanisms remain poorly understood. Here we show that, in mice, neurons in the parabrachial nucleus that express the prodynorphin gene (hereafter, PB^{Pdyn} neurons) monitor the intake of both fluids and solids, using mechanosensory signals that arise from the upper digestive tract. Most individual PB^{Pdyn} neurons are activated by ingestion as well as the stimulation of the mouth and stomach, which indicates the representation of integrated sensory signals across distinct parts of the digestive tract. PB^{Pdyn} neurons are anatomically connected to the digestive periphery via cranial and spinal pathways; we show that, among these pathways, the vagus nerve conveys stomach-distension signals to PB^{Pdyn} neurons. Upon receipt of these signals, these neurons produce aversive and sustained appetite-suppressing signals, which discourages the initiation of feeding and drinking (fully recapitulating the symptoms of gastric distension) in part via signaling to the paraventricular hypothalamus. By contrast, inhibiting the same population of PB^{Pdyn} neurons induces overconsumption only if a drive for ingestion exists, which confirms that these neurons mediate negative feedback signaling. Our findings reveal a neural mechanism that underlies the mechanosensory monitoring of ingestion and negative feedback control of intake behaviors upon distension of the digestive tract.

Biography

Sung-Yon Kim obtained his B.S. degree in Chemistry and Biological Sciences from Seoul National University (*summa cum laude*) and Ph.D. in Neurosciences from Stanford University. In his doctoral thesis work, he combined cutting-edge neuroscience techniques (including optogenetics and two-photon Ca^{2+} imaging) to dissect the roles of amygdala and extended amygdala circuits in diverse features of the anxious state. This work led to two publications in *Nature*, and was internationally recognized by the *Donald B. Lindsley Prize* for the Best Thesis in Behavioral Neuroscience (awarded by Society for Neuroscience, USA). This work also raised may interesting questions about the anatomical organization of the circuits, which led him to develop novel tools for extracting structural and molecular information from intact brains as a postdoctoral fellow at MIT. Now as an independent researcher at Seoul National University, he aims to understand the neural basis of innate survival behaviors, including ingestion, thermoregulation, and aggression. He wants to find the mechanistic explanations for how it all begins, how it all ends, and everything in-between—from the sensation of relevant information from both within and outside the body to the integration of the multiple streams of information and generation of appropriate behavioral responses.

Big data science in human neuroscience

Jiook Cha, Ph.D.

Department of Psychology
Department of Brain and Cognitive Sciences
AI Institute
Seoul National University

The capability of predicting an individual's cognitive, emotional, behavioral trajectories is a barometer of our understanding of the brain. However, current human neuroscience has not yet reached that point. The majority of the models of cognition, emotion, and psychiatric disorders showing statistical significance often lacks predictability and reproducibility, thus presents suboptimal practical significance. This incapability leaves numerous urgent unmet needs in Psychology and Psychological Medicine: e.g., the ever-increasing global rates of mental disorders. Rigorous neuroimaging-based predictive models may lead to prescriptive models, which will improve our understanding of human minds and behaviors, as well as diagnostics and therapeutics of mental disorders. I suggest that neuroscience and psychology should leverage the rapidly growing biobanks hosting the large-scale, multi-modal biomedical data. These resources include structural and functional brain imaging often linked to genome and phenome data with unprecedented volumes, opening the new era of imaging-genetics in contemporary epidemiological populations. Further, the multiple biobanks allow investigation across the full spectrum of the lifespan ranging from neonatal stages to aging, as well as in those with mental disorders. The forthcoming computer-aided understanding of human minds and behaviors in normal and disease conditions will complement the mainstream reductionists approach in this field. In this talk, I will discuss the rationales, prerequisites, and applications of computational learning in big biomedical data in human neuroscience and psychology.

Biography

Jiook Cha obtained B.S. (Environmental and Ecological Engineering) at Korea University, and M.S. (Neurobiology) at The Catholic University of Korea. He completed his PhD in Neuroscience at Stony Brook University. His thesis focused on the brain circuitry underlying anxious behaviors and clinical anxiety in humans. During his postdoctoral training at Columbia University in the Department of Psychiatry, Jiook investigated multi-modal brain imaging in child and adult psychiatric disorders. With a NIMH K01 career development award in 2016, he started an assistant professorship in the same department. In 2020, he joined the Department of Psychology at Seoul National University, where he started SNU Connectome Lab. He has three kids and one wife.

Map of Toxic Immune Cells Contributing to Neurodegeneration in MS

Jae Kyu Ryu, Ph.D.

Gladstone Institute of Neurological Disease
University of California, San Francisco

A common thread in many inflammatory and neurodegenerative diseases, including multiple sclerosis (MS), is damage caused by oxidative stress. Oxidative stress occurs when cells produce toxic substances known as reactive oxygen species, which are damaging to neurons and other cells in the body. In patients with progressive MS, brain immune cells called microglia are now recognized to be early contributors to oxidative stress and the ensuing damage to the brain. In addition, oxidative stress is a key contributor to autoimmune and infectious diseases. Yet, how immune cells regulate and turn on their production of reactive oxygen species remains unknown. To address this question, we recently combined single-cell RNA-sequencing technology with selective labeling of cells that produce oxidative stress to generate a comprehensive molecular profile of the toxic immune cells that damage the brain. Using high throughput screening and animal models of neuroinflammation, we demonstrated the value of this atlas by using it to identify a potential new drug target for MS and, possibly, many other diseases.

Biography

Dr. Jae Kyu Ryu was trained in pharmacology, and has specific expertise in glial-vascular interactions and chronic inflammation in neurodegenerative diseases. His research is focused on the cellular and molecular pathways responsible for the effects of redox dysregulation in neurologic diseases, as an essential step toward developing therapeutic strategies for MS and other conditions that involve neuroinflammation. He is currently an assistant adjunct professor at UCSF, and staff research scientist at Gladstone Institutes.

Interleukin 33 promotes activity-dependent microglial synapse engulfment and restricts seizure susceptibility

Taeho Han, M.D., Ph.D.

University of California, San Francisco

Microglia play a critical role in central nervous system (CNS) development, acting in part by remodeling neuronal synapses. Recent findings have highlighted the importance of microglia in regulating synaptic refinement and identified diverse transcriptomic states in physiology and disease. However, defining how these transcriptomic states correlate to microglial phagocytic function has remained challenging.

Here we identify mechanisms through which the IL-1 family cytokine Interleukin-33 (IL-33) regulates microglial phagocytic capacity in the developing brain. We find that IL-33 induces a transcriptional program associated with phagocytosis and identify the scavenger receptor MARCO and toll-like receptor 2 as a downstream mediator of IL-33 induced synaptic engulfment. We also find that IL-33 leads to a pronounced shift in the microglial epigenomic landscape towards stimulus-responsive transcription factors such as NF-kB and ATF/AP1. We show that IL-33 is required for microglia to engulf synaptic proteins in a neuronal activity-dependent manner. Finally, we find that conditional deletion of IL-33 in the CNS (*hGFAPcre:Il33*$^{fl/fl}$) leads to excess excitatory synapses and elicits absence seizure-like behaviors by early adulthood. These findings define novel mechanisms through which IL-33 coordinates synaptic refinement and excitatory/inhibitory balance in the developing brain.

Biography

Taeho Han obtained M.D. and Ph.D. from Korea University in Medicine and Neuroscience, respectively. During his PhD study at Korea University, he investigated the circuit plasticity in a mouse model of chronic pain and depression using electrophysiology and molecular biology. Currently, Dr. Han is a postdoctoral fellow in the laboratory of Dr. Anna Molofsky at University of California, San Francisco since 2018.

Development and validation of the prediction model for the autism spectrum disorder diagnosis in a Korean general population

Hyelee Kim, M.D., M.AS.

UCSF Center for ASD & NDDs
Harvard T.H. Chan School of Public Health

This study aims to develop and validate the autism spectrum disorder (ASD) diagnosis prediction models among screen-positives using parental questionnaires. Children from regular elementary schools in a Korean community were screened with ASSQ during 2005-2013. Screen-positives were invited to the comprehensive diagnostic process with ADOS, ADI-R, cognitive tests, BASC-2, and/or SRS. Best estimate clinical diagnoses for ASD were made based on the DSM-5. Among 394 1st-2nd graders, a random sample (n=166) of children who completed all questionnaires (n=332) were designated as a testing set. The remaining (n=228) became a training set. Responses for questionnaire items were transformed into 0, 1, and 9 (missing). Lasso logistic regression with cross-validation was performed in the training set (outcome: ASD, predictors: questionnaire items, sex, age, and performance IQ), resulting in the single (ASSQ, BASC, and SRS) and the combined (ASSQ+BASC, ASSQ+SRS, and BASC+SRS) prediction models. In the testing set, the discrimination ability was estimated by the area under the receiver operating curve (AUC) and calibration by the Hosmer-Lemeshow goodness-of-fit test and the calibration plot. We also estimated the Brier score, ranging from 0, total accuracy, to 1, total inaccuracy. Children with a median age of 8.0 years (IQR 7.4-8.9), 68% male, 46% ASD, and median performance IQ of 97 (IQR 83-108) participated in this study. Among single prediction models, the BASC prediction model performed best in the testing set (AUC 0.77 (95% CI: 0.70, 0.84) and Brier score 0.20). Combined prediction models showed slightly better discrimination ability than single models, and the ASSQ+BASC model performed the best (AUC 0.78 (95% CI: 0.71, 0.85) and Brier score 0.20). The combined models demonstrated the better agreement between the predicted probability of ASD and the actual diagnosis of ASD than the single models in the calibration plots. At a cut-off of 0.53, the ASSQ+BASC model showed 70% sensitivity and 75% specificity. In all prediction models, the Hosmer-Lemeshow test showed p-values greater than .05, suggesting satisfactory goodness-of-fit of the models. Our results suggest the ASD prediction model might help primary physicians in the resource-poor communities to address the significant gap in access to clinical care.

Biography

Hyelee Kim, a board-certified psychiatrist from Korea, obtained MD from the Seoul National University and MAS in clinical research from the University of California San Francisco. Dr. Kim is studying the neuropsychiatric epidemiology under the supervision of Dr. Deborah Blacker at the Harvard T.H. Chan School of Public Health, Boston.

Ultrahigh-throughput single cell analysis of proteins

Byungjin Hwang, Ph.D.

Institute for Human Genetics
University of California, San Francisco

The development of DNA-barcoded antibodies to tag cell-surface molecules has enabled the use of droplet-based single cell sequencing (dsc-seq) to profile the surface proteomes of cells. Compared to flow and mass cytometry, the major limitation of current dsc-seq-based workflows is the high cost associated with profiling each cell, thus precluding its use in applications where millions of cells are required. Here, we introduce single cell combinatorial indexed cytometry by sequencing (SCITO-seq), a new workflow that combines combinatorial indexing and commercially available dsc-seq to enable cost-effective cell surface proteomic sequencing of greater than 10^5 cells per microfluidic reaction. We demonstrate SCITO-seq's feasibility and scalability by profiling mixed species cell lines and mixed human T and B lymphocytes. To further demonstrate its applicability, we show comparable cellular composition estimates in peripheral blood mononuclear cells obtained with SCITO-seq and mass cytometry. SCITO-seq can be extended to include simultaneous profiling of additional modalities such as transcripts and accessible chromatin or tracking of experimental perturbations such as genome edits or extracellular stimuli.

Biography

Byungjin Hwang obtained B.S. and Ph.D. from Yonsei University in Chemistry. During his PhD study at Yonsei University, he developed various tools encompassing genome engineering to cancer genomics. Among many others he developed a novel protein engineering tool using codon-barcoded de novo assembly, lineage tracing method using CRISPR genome editing technology, and molecular barcoding tool to efficiently analyze cfDNA. Currently, Dr. Hwang is a postdoctoral fellow in the laboratory of Dr. Jimmie Ye at Institute of Human Genetics and the University of California, San Francisco since 2019.

Introduction of Advanced Biofuels and bioproducts Process Development Unit (ABPDU)

Changman Kim, Ph.D.

Advanced Biofuels and bioproducts Process Development Unit
Lawrence Berkeley National Laboratory

As greater demands place elevating the pressure on bioproduction, bench-to-lab-to-pilot scale process development is essential. Advanced Biofuels and bioproducts Process Development Unit (ABPDU) in Lawrence Berkeley National Laboratory was established to address this by Department of Energy's (DOE) Bioenergy Technologies Office in 2009. The mission of ABPDU is to hasten the industrialization of bio-based production through not only scaling up but also designing entire process. ABPDU has the biorefinery approach by integrating the conventional/cutting-edge technologies from deconstruction of biomass and lab-scale fermentation to pilot-scale fermentation, recovery process, and techno-economic analysis. This presentation will present the entire bioproduction process with ABPDU's researches.

Biography

Changman Kim obtained B.S. and M.S. from Pusan National University (Microbiology) and POSTECH (Ocean science), respectively. During his PhD in Department of Chemical Engineering in Pusan National University, he demonstrated various bioelectrochemical system applications including bioelectricity generation, metal recovery, electro-fermentation and electro-synthesis. Currently, Dr. Kim is a postdoctoral researcher in Advanced Biofuels and bioproducts Process Development Unit (ABPDU) in Lawrence Berkeley National Laboratory since 2019.

Structural basis for recognition of the Hsp90 closed, ATP state by the TPR-containing co-chaperone FKBP51

Kanghyun Lee, Ph.D.

Institute for Neurodegenerative Diseases
University of California, San Francisco

Molecular chaperones Hsp90 and Hsp70 are critical in protein homeostasis (proteostasis), interacting directly with many "client" proteins to promote ATP-driven remodeling and activation. Co-chaperones bind Hsp90 and Hsp70 forming dynamic chaperone complexes which specify the client folding pathway. Many interact via their tetratricopeptide repeat (TPR) domain, which binds the EEVD motif at the flexible carboxyl-terminus of Hsp90 and Hsp70. However, for many TPR cochaperones, the protein:protein interactions and mechanisms which enable Hsp70/Hsp90 specificity and regulation in the folding pathway remain unclear. The peptidyl-prolyl isomerase FK506-binding protein 51 (FKBP51) interacts specifically with Hsp90 (and not Hsp70) to promote the folding of key client proteins including kinases, steroid hormone receptors, and Tau. Here we have determined a cryo-EM structure of the human Hsp90:FKBP51:p23 complex to 3.3 Å resolution, revealing a distinct TPR interaction mechanism which enables recognition of the Hsp90 closed, ATP state via binding to the C-terminal Hsp90 dimer. Moreover, this interaction positions the FK1 domain of FKBP51 close to the middle domain of Hsp90 revealing a potential mechanism for isomerase activity targeted to distinct sites of Hsp90-bound clients. Together with biochemical analysis to probe interactions, these results reveal how the immunophilin class of TPR co-chaperones may act on specific client regulation and folding steps of the Hsp90-driven chaperone pathway.

Biography

Kanghyun Lee obtained B.S. and M.S. from Seoul National University in Chemical and Biological Engineering. Kanghyun Lee received his Ph.D. in Biochemistry from the University of Wisconsin-Madison under the guidance of Dr. Elizabeth Craig. Dr. Lee's graduate research was focused on understanding the Hsp70-based molecular chaperone system assisting folding of nascent chains translated by the ribosome. Dr. Lee joined the Southworth lab in the Institute for Neurodegenerative Diseases as a postdoctoral scholar in December 2018. He is interested in understanding the interaction between Hsp90/Hsp70 and their cochaperones that are involved in maintaining Tau homeostasis using biochemical tools such as cryo-EM.

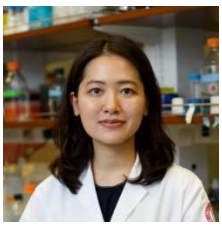
How to land your first faculty job in the US

How I prepared for a tenure-track faculty position in the US

Chang-il Hwang, Ph.D.
Assistant Professor
Department of Microbiology and Molecular Genetics, College of Biological Sciences
University of California, Davis

I will be sharing my experience on how I found a faculty position in US. Three practical advices include: (1) prepare in advance, (2) seek help and advices from colleagues, junior faculty members and mentors, and (3) be confident.

I am interested in pancreatic cancer pathogenesis. Currently, my group is studying how genetic and epigenetic alterations contribute to pancreatic cancer progression using 3D pancreatic organoid and genetically engineered mouse models. I believe that better understanding of the disease ultimately will lead to the improvement of diagnostics and therapeutics for pancreatic cancer. (https://cihwang.wordpress.com/)



Timelines for faculty job application

Gina Lee, Ph.D.
Assistant Professor
Department of Microbiology and Molecular Genetics, School of Medicine
University of California, Irvine

학위와 포닥 과정 중에도 마찬가지이지만, 교수 임용 지원과 인터뷰 기간에는 특히 정신력과 체력이 잘 뒷받침되는 것이 좋습니다. COVID-19 로 인해 어려운 상황이지만, 규칙적인 생활과 운동으로 몸과 마음을 항상 건강하게 관리하라는 당부를 드리고 싶습니다. 온라인으로도 동료, 친구들과 꾸준히 만나고 학회와 세미나에도 활발히 참여하시길 바랍니다.

저희 연구실은 암과 같은 질병에서 신호 전달 및 대사 조절 체계가 m6A RNA methylation 을 포함한 RNA epigenetic modification 을 어떻게 조절하는지에 대한 연구를 합니다. 박사 후 연구원을 모집 중이고, 특히 관심있는 전공 분야는 다음과 같습니다: Molecular Biology and Biochemistry; RNA Biology and Bioinformatics; Cancer Metabolism and Signaling 날씨와 연구 환경이 좋은 Southern California 에서 RNA 신호 전달 연구에 대한 열정을 공유하실 분들의 적극적인 관심과 지원 부탁드립니다.
(https://sites.uci.edu/ginalee/).

My first job interview

Sora Shin, Ph.D.
Assistant Professor
Fralin Biomedical Research Institute
Virginia Tech

I'd like to share my first job interview experience: how I prepared for it, what I was struggling with, and how it went.

The Shin Lab (https://fbri.vtc.vt.edu/research/labs/shin.html) aims to understand the role of brain circuit-specific mechanisms using translationally relevant animal models of stress-induced psychiatric diseases. We seek to answer such questions as: How does the harsh early environment affect mental health in adulthood? How are unfulfilled needs in early life stored and transduced into behavioral dysfunctions after a long time? What processes are set into motion that link stress experiences to symptoms of eating disorders or major depression in later life?

Accurate, scalable cohort variant calls using DeepVariant and GLnexus

Taedong Yun, Ph.D.

Google Health Research

Population-scale sequenced cohorts are foundational resources for genetic analyses, but processing raw reads into analysis-ready variants remains challenging. Here we introduce an open-source cohort variant-calling method using the highly-accurate caller DeepVariant and scalable merging tool GLnexus. We optimized callset quality based on benchmark samples and Mendelian consistency across many sample sizes and sequencing specifications, resulting in substantial quality improvements and cost savings over existing best practices. We further evaluated our pipeline in the 1000 Genomes Project (1KGP) samples, showing superior quality metrics and imputation performance. We publicly release the 1KGP callset to foster development of broad studies of genetic variation.

In this talk I will give a brief overview of the variant calling process in genomics using next-generation sequencing (NGS) data, will introduce DeepVariant, an accurate variant caller using a deep convolutaional neural network, and will talk about how we developed the “best practices” workflow for using DeepVariant to generate large-scale cohort callsets.

Biography

Taedong Yun is a researcher and software engineer in the genomics team at Google Health Research, and his recent work focuses on genomic analysis of cohorts and its application to genomic medicine. Before joining Google, he worked on research and development of data visualization cloud applications at Oracle. He studied algebraic combinatorics at Massachusetts Institute of Technology (MIT) for his Ph.D. in mathematics supervised by Richard P. Stanley, and has B.S. in mathematics from Korea Advanced Institute of Science and Technology (KAIST) in South Korea.

Direct Image-based deep learning solution for quantitative PET and SPECT imaging

Jaewon Yang, Ph.D.

Department of Radiology and Biomedical Imaging
University of California, San Francisco

Latest advances in radionuclide imaging technology include the development of organ-specific small transaxial field-of-view (FOV) imaging systems such as dedicated cardiac SPECT (e.g., Discovery NM 530c, GE Healthcare), extremely long axial FOV total-body PET (e.g., uEXPLORER, UC Davis) as well as combined PET/MRI. In these emerging scanners, quantitative imaging is still challenging since there is no robust and efficient method to correct physical errors like attenuation and scatters. Most of organ-specific scanners typically do not allow room for transmission imaging like CT for attenuation and scatter correction, both of which are crucial for quantitative accuracy as well as image quality. Even in conventional systems, the majority (around 80%) of commercial SPECT scanners are not combined with CT. In the uEXPLORER, the external radiation dose of CT for generating attenuation maps can mitigate the merit of ultralow-dose scan that is the major advantage of using total-body PET especially for pediatric patients. In PET/MRI, MR-based attenuation correction (MRAC) approaches suffer from artifacts in μ-maps derived from MR images.

Innovatively, we consider attenuation and scatter correction as a computer vision task since a deep convolutional neural network (DCNN) can derive important patterns from how attenuation and scatter corrections simultaneously change uncorrected image patterns to corrected image patterns. A direct image-to-image deep learning (DL) solution is an accelerated one-step process to generate corrected images directly from uncorrected images in image space, distinct from conventional methods. The goal of this project is to address the unmet need of quantitative imaging solutions for both conventional and emerging radionuclide imaging systems by further improving the novel DL approach developed by our research group.

In this talk, I will demonstrate the feasibility of our direct DL approach for PET and SPECT myocardial perfusion imaging (MPI), illustrating clinical cases for presenting potential benefits and pitfalls of the proposed technique. This new technique can potentially overcome the current limitations of conventional CT-based approaches, benefiting patients sensitive to radiation from CT.

Biography

Dr. Jaewon Yang obtained B.S. from Yonsei University in Electrical Engineering and M.S./PhD in Electrical Engineering at Stanford University. During his PhD, he investigated the feasibility of PET-guided external beam radiation therapy, funded by Kwanjeong Educational Foundation (KEF) and Reflexion Medical. Currently, Dr. Yang is an associate specialist in the Physics Research Laboratory at UCSF since 2014.

Machine Learning-Based Natural Language Processing for Automated Extraction and Standardized Annotation of IHC Results from Free Text Pathology Reports

Young Suk Kim, M.S.

Stanford University

Natural language processing (NLP) is a subfield of computer science that combines Artificial Intelligence (AI) and other Machine Learning (ML) disciplines. Here, we extend our previously validated NLP work to automatically extract meaningful information from real-world unstructured and narrative pathology reports. We extract key standardized information about tumors as measured by immunohistochemistry (IHC), specials stains, or molecular tests such as FISH.

We used various NLP methods such as multiple cTAKES (clinical Text Analysis and Knowledge Extraction System; Mayo) components, word2vec (Google), as well as our large cancer center in-house Application Programming Interfaces (API). To get optimal ground truth data, we manually encoded free-text reported IHC results, special stains, and FISH results in a standardized manner (comprising >130 individual test types). We pre-processed raw free-text datasets to make our input more uniform and to improve performance with unknown tokens such as abbreviation, acronyms, or ambiguous words. Pre-processed datasets enhance the classifier outcomes when using ML and NLP analysis tools including CoreNLP (Stanford), NLTK, scikit-learn, and other text analysis tools. We compared several standard supervised classifiers using k-fold cross validation.

We processed surgical pathology reports (36,431) from a two-year period and added additional data (8,174) from another year to assess whether our model works well with unseen data. We evaluated different supervised classifiers including SVM (Support Vector Machine), Linear Discriminant Analysis (LDA), Logistic Regression (LR), and K-Nearest Neighbors (KNN) to compare ML accuracy. We observed that a SVM has the highest accuracy score for most stains. We show that our NLP approach is able to automatically transform virtually any free-text resulted stain into structured quantitative data (e.g., overall positive/negative, intensity (weak/moderate/strong), % staining, heterogeneity (uniform, focal, scattered), cellular localization (membranous, nuclear, cytoplasmic), and tissue compartment (tumor, inflammatory, stromal, etc.)).

We developed a set of NLP tools for automated stain result annotation from narrative free-text pathology reports. Our NLP software can find large-scale IHC protein expression patterns in tumors, drive global biomarker discovery, and guide practicing pathologists in optimal diagnostic test ordering.

Biography

Young Suk Kim obtained B.S. from Seoul Women's University in Computer Science. She started her career as a software engineer and a database engineer. Then, she obtained M.S. from Carnegie Mellon University studying Bioinformatics. She worked at Memorial Sloan Kettering Cancer Center in New York as a data scientist to find hidden patterns from pathology-related data using AI methods. Currently, she works at Stanford University to research multi-omics data sets using AI.

Development and Validation of Artificial Intelligence for Breast Cancer Detection in Mammography

Ki Hwan Kim, M.D., Ph.D.

Lunit Inc

Mammography is the current standard for breast cancer screening. Multiple randomized controlled studies have shown that mammography screening significantly reduces breast cancer mortality. Despite such benefits, unfortunately, 10–30% of breast cancers are still missed, which is commonly attributed to dense parenchyma obscuring lesions, poor positioning, perception error, and interpretation error, among other reasons. This study aimed to develop an artificial intelligence (AI) algorithm for diagnosis of breast cancer in mammography, and explore whether it could benefit radiologists by improving accuracy of diagnosis. An AI algorithm was developed and validated with 170 230 mammography examinations collected from five institutions in South Korea, the USA, and the UK, including 36,468 cancer positive confirmed by biopsy, 59,544 benign, and 74,218 normal. And most of cancer cases were annotated by radiologists. With the aid of the large-scale mammography data, the AI algorithm showed improved diagnostic performance compared with radiologists, especially in early-stage invasive breast cancers. For better understanding of AI behavior, mammographic features of cancers detected by the AI algorithm were analyzed through the comparison study with radiologists.

This study showed that AI has the potential to improve early-stage breast cancer detection in mammography. Especially in dense breast areas on a mammogram which pose one of the major difficulties in screening, the performance of radiologists was significantly improved when aided with AI. Such improvements could result in an increase in screen-detected cancers and decrease in interval cancers, which would improve the efficacy of mammography screening.

Biography

Ki Hwan Kim obtained M.D. from Korea University College of Medicine. During his PhD study at Korea Advanced Institute of Science and Technology, he developed novel MRI pulse sequences and MR image processing technology using Artificial Intelligence. Currently, Dr. Kim is a Chief Medical Officer at Lunit, Seoul-based Medical AI company focusing on chest and breast imaging since 2018.

Comprehensive quantification of fuel use by the failing and non-failing human heart

Cholsoon Jang, Ph.D.

Department of Biological Chemistry
University of California, Irvine

The heart consumes circulating nutrients to fuel lifelong contraction. Despite the importance of cardiac metabolism in health and disease, a comprehensive mapping of human cardiac fuel use is lacking. Using metabolomics on simultaneously sampled blood from radial artery, coronary sinus, and femoral vein in a total of 110 patients with or without heart failure, we systematically quantified the uptake and release of 277 metabolites by the human heart and leg. We calculated the contribution of all major circulating nutrients, including glucose, lactate, ketones, individual fatty acids and amino acids, and acetate, to cardiac oxygen consumption and ATP production. The heart primarily consumes fatty acids and, surprisingly, negligibly consumes circulating glucose, in contrast to strong glucose consumption by the leg. Moreover, the heart secretes, rather than consumes, glutamine and other nitrogen-rich amino acids, indicating active protein breakdown, at a rate ~10 times that of the leg. The heart also releases TCA intermediates, possibly to balance the influx of anaplerotic carbons from amino acid breakdown. Both the heart and leg consume ketones, glutamate, and acetate in direct proportionality to circulating levels, indicating control of clearance by mass action rather than more complex regulation. Compared to the nonfailing heart, the failing heart consumes significantly more ketones and lactate, and releases more nitrogen reflecting higher rates of proteolysis. These data provide a comprehensive and quantitative picture of human cardiac fuel use, providing a foundation for understanding aberrant cardiac metabolism in disease.

Biography

Cholsoon Jang obtained B.S. and M.S. from KAIST in Biological Sciences. During his PhD with Dr. Zolt Arany at Harvard University and postdoc with Dr. Joshua Rabinowitz at Princeton University, he studied the whole-body metabolic flux of various dietary nutrients in the context of diabetes and fatty liver disease. Currently, he is an Assistant Professor in the Department of Biological Chemistry at the University of California, Irvine since May 2020.

An Integrative Systems Genetic Analysis of Atherosclerosis and Gut Microbiota

Myungsuk Kim, M.S.

USDA-ARS-Western Human Nutrition Research Center

Atherosclerosis is a precipitating event in the development of cardiovascular disease. Recent studies report that gut microbiota contributes to the pathogenesis of cardiovascular disease, including metabolic syndrome. While host genetic variants are known factors that affect atherosclerosis development and gut microbiota composition, the mechanisms underlying genetic variations are not yet clear. Here, we interrogated atherosclerosis regulatory networks in hyperlipidemic Diversity Outbred mice to reveal key insights into control of atherosclerosis using system genetic approaches of cardio-metabolic traits, microbiome and liver transcriptome. We collected offspring (238 female and 234 male mice) from a cross between transgenic male C57BL/6J mice, which were made susceptible to atherosclerosis by microinjection of human apolipoprotein E-Leiden and cholesterol ester transfer protein genes, and ~200 female DO mice, a population derived from 8 inbred strains. We fed the offspring a high fat/cholesterol diet for 12 weeks. Out results include identifying abundance of fecal microbial taxa associated with atherosclerotic traits, defining the functionality of genes associated with the atherosclerotic traits and gut microbiota, and identifying signatures of functional gene variants predicted to modulate those traits. Trans-omic analysis facilitated identification of Ptprk as a previously unknown regulatory gene for atherosclerotic traits and Lactococcus abundance. Collectively, this study provides a rich resource for investigating the pathogenesis of atherosclerosis and suggests an opportunity to discover therapeutics and biomarkers in the setting of hyperlipidemia.

Biography

Myungsuk Kim obtained B.S., B.B.A, and M.S. from Yonsei University in Biotechnology and Business administration. He worked for the Korea Institute of Science and Technology as a research scientist for 4 years. During his PhD study at University of California, Davis, he investigated the effect of genetic, microbial, and dietary factors on atherosclerosis using Diversity Outbred mice and multi-omics approaches including RNA-sequencing and metagenomics analysis.

The polyunsaturated fatty acid (PUFA) biosynthesis pathway and ferroptosis in gastric cancer

Eun-Woo Lee, Ph.D.

Metabolic Regulation Research Center
Korea Research Institute of Bioscience & Biotechnology (KRIBB)

Ferroptosis is an iron-dependent regulated necrosis mediated by lipid peroxidation. Cancer cells survive under metabolic stress conditions by altering lipid metabolism, which may alter their sensitivity to ferroptosis. However, the association between lipid metabolism and ferroptosis is not completely understood. In this study, we found that the expression of elongation of very long-chain fatty acid protein 5 (ELOVL5) and fatty acid desaturase 1 (FADS1) is upregulated in mesenchymal-type gastric cancer cells (GCs), leading to ferroptosis sensitization. In contrast, these enzymes are silenced by DNA methylation in intestinal-type GCs, rendering cells resistant to ferroptosis. Lipid profiling and isotope tracing analyses revealed that intestinal-type GCs are unable to generate arachidonic acid (AA) and adrenic acid (AdA) from linoleic acid. AA supplementation of intestinal-type GCs restores their sensitivity to ferroptosis. Based on these data, the polyunsaturated fatty acid (PUFA) biosynthesis pathway plays an essential role in ferroptosis; thus, this pathway potentially represents a marker for predicting the efficacy of ferroptosis-mediated cancer therapy.

Biography

Eun-Woo Lee obtained B.S., M.S. and Ph.D from Department of Food Science and Biotechnology, Sungkyunkwan University. During his PhD study, he focused on the ubiquitin-mediated regulation of intrinsic and extrinsic apoptosis pathways. During his postdoctoral fellow at Yonsei University, he studied the regulatory mechanism of necroptosis and visited Peter Vandenabeele's Lab at VIB-Ghent University, Belgium as a visiting scientist. Currently, Dr. Lee is a senior researcher at KRIBB and investigating the role of ferroptosis in cancer and metabolic diseases since 2016.

Iron overload causes a profound autophagy defect through mTORC1-UVRAG inhibition leading to insulin resistance

James Won Suk Jahng, Ph.D.

Cardiovascular Institute
Stanford University

Iron overload, a common clinical occurrence, is implicated in the metabolic syndrome and type 2 diabetes although the contributing pathophysiological mechanisms are not fully defined. I showed that iron overload in L6 skeletal muscle cells initially induced autophagy flux yet prolonged iron overload resulted in an autophagy defect associated with accumulation of dysfunctional autolysosomes and loss of free lysosomes. These autophagy defects contributed to impaired insulin-stimulated glucose uptake and insulin signaling. Mechanistically, I showed that iron overload led to a decrease in Akt-mediated repression of TSC2 and RHEB-mediated mTORC1 activation on autolysosomes, thereby inhibiting autophagic lysosomal regeneration (ALR). Constitutive activation of mTORC1 by over-expressing RHEB Q64L or iron withdrawal both replenished lysosomal pools via increased mTORC1-UVRAG signaling, which restored insulin sensitivity. Induction of iron overload via intravenous iron-dextran delivery in C57BL/6 mice also resulted in decreased insulin stimulated glucose clearance and insulin signaling accompanied with abnormal autophagosome accumulation, lysosomal loss and decreased mTORC1-UVRAG signaling in heart, muscle and liver. Collectively, my results showed that chronic iron overload leads to a profound autophagy defect through mTORC1-UVRAG inhibition and provides a new mechanistic insight into metabolic syndrome-associated insulin resistance.

Biography

James obtained B.S. from University of Toronto in Biology. During his PhD at York University (Toronto), James investigated the molecular etiology of insulin resistance in heart or skeletal muscle in various diabetic animal models. Currently, James is a postdoctoral fellow in the laboratory of Dr. Joseph C. Wu at Stanford Cardiovascular Institute since 2020. He is interested in delineating the novel autophagy regulatory mechanism in iPSC-derived cardiomyocytes or cardiac organoids from diabetic patients.

Application of helix fusion methods in structural biology

Jie-Oh Lee, Ph.D.

Department of Life Sciences
POSTECH

Methods generating fusion proteins with rigid and predictable structures have been developed in recent years. Among them, helix fusion methods that link two proteins by connecting their terminal alpha helices into a single and extended alpha helix can be particularly useful because designing fusion helices is conceptually and technically simple. These methods have been shown crucial in obtaining crystals that diffract x-rays to high resolution or attaching large and symmetrical backbone proteins to small target proteins for cryo-EM analysis. The structural rigidity of the fusion helix is critical for these applications, and the reduction of structural ambiguity and flexibility at the fusion sites will further enhance the usefulness of this method.

Biography

Jie-Oh Lee obtained B.S. and M.S. from Seoul National University in Chemistry. During the Ph.D. in Harvard and the postdoctoral study in Memorial Sloan Kettering Cancer Institute, he investigated crystal structures of Integrin, Retinoblastoma and PTEN proteins. Since he opened his lab as a professor in KAIST, 2001, he has been studying structures of TLR and TNF family receptors. Currently, he is a professor in the department of Life Science and the Director of Institute of Membrane Proteins in POSTECH.

A single cell atlas of human thymus across development and aging defines dynamics of T cell development

Jong-eun Park, Ph.D.

Graduate School of Medical Science and Engineering
KAIST

The thymus is the critical organ for T-cell development and T-cell receptor (TCR) repertoire formation, which shapes the landscape of adaptive immunity. While the thymus has been extensively studied using diverse animal models, the detailed atlas of human thymus is required to understand human immunity.

To provide a comprehensive atlas of thymic cells across human life, we performed scRNAseq using dissociated cells from human thymus during development, childhood and adult life. We identified more than 50 different cell states in the human thymus, which dynamically change in abundance and gene expression profiles across development, paediatric and adult life. We computationally predicted the trajectory of human T-cell development from early progenitors in the hematopoietic fetal liver into diverse mature T cell types. Using this trajectory, we constructed a framework of putative transcription factors driving T-cell fate determination. Among thymic unconventional T cells, we noted a distinct subset of CD8αα^{+}T cells, which is marked by *GNG4* expression and uniquely located in the peri-medullary region of the thymus. This subset expressed high levels of *XCL1* and co-localised with XCR1^{+} dendritic cells (DC1). Finally, we identified a strong bias in human VDJ usage shaped by recombination and multiple rounds of selection, including a TCRα V-J bias for CD8^{+} T cells.

Our single-cell transcriptome profile of the thymus across human lifetime and across species provides a high-resolution census of T-cell development within the native tissue microenvironment. Systematic comparison between human and mouse thymus highlights human-specific cell states and gene expression signatures. Our detailed cellular network of the thymic niche for T-cell development will aid the establishment of *in vitro* organoid culture models that faithfully recapitulate human *in vivo* thymic tissue.

Biography

Jongeun Park obtained B.S. from Seoul National University in Biological Sciences. During his PhD in Prof. Narry Kim's lab in Seoul National University, he studied molecular mechanisms for diverse post-transcriptional regulators. After PhD, he joined Sarah Teichmann's group in Wellcome Sanger Institute, where he participated in Human Cell Atlas Initiative. Main focus of his research is to understand the development of human immune system by applying single-cell omics and designing computational methods. He just started his own lab in KAIST Graduate School of Medical Sciences and Engineering, where he will expand his focus to diverse immune diseases.

Airway Innate Lymphoid cells in the Induction and Regulation of Lung Diseases

Hye Young Kim, Ph.D.

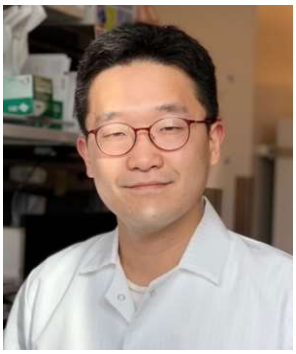
Department of Biomedical Sciences, College of Medicine
Seoul National University

Our understanding of innate lymphoid cells (ILCs) marked an increase in the recent ten years. Since their identification as a separate family of leukocytes, innate lymphoid cells (ILCs) have emerged as critical effector cells of the innate immune system. It is clear that ILCs contribute to the maintenance of lung homeostasis; however, there are growing pieces of evidence to support the contribution of ILCs to several lung pathogenesis. Here, we will discuss recent advances in the understanding of ILC biology in chronic respiratory disorders, including asthma and COPD (Chronic Obstruction Pulmonary Disease) in humans and experimental models using mice. We have found the dysregulation of the ILC function correlated with the severity and phenotype of diseases. Also, changing the lung microenvironment affect the sensitivity and features of respiratory ILCs. Therefore, further studies should aim to uncover these complex relationships, particularly in the setting of chronic lung disease, which may reveal potential treatment targets.

Biography

Hye Young Kim obtained a B.S. from Ewha Womans University in Biology and M.S. and a Ph.D. degree from Seoul National University in genetics and immunology, respectively. During her post-doctoral period at Harvard Medical School, she conducted in-depth researches on asthma and allergic diseases. In particular, her research interest was innate immunity such as NKT and innate lymphoid cells. Currently, Dr. Kim is an associated professor at Seoul National University College of medicine since 2014. Currently, we are conducting experiments by expanding the scope of our research to the mechanisms of developing various chronic diseases such as allergic diseases and autoimmune diseases.

Targeted Transcriptomics Identifies Neddylation as a Novel Therapeutic Target in Multiple Sclerosis



Kicheol Kim, Ph.D.

Weill Institute for Neurosciences, Department of Neurology
University of California, San Francisco

Multiple sclerosis (MS) is an autoimmune disease of the central nervous system in which both genetic and environmental factors are involved. Genome-wide association studies revealed more than 200 risk loci, most of which harbor genes primarily expressed in immune cells. However, whether genetic differences are translated into cell-specific gene expression profiles and to what extent these are altered in MS patients are still open questions in the field. To assess cell-type-specific gene expression in a large cohort of MS patients, we sequenced the whole transcriptome of FACS-sorted T cells (CD4+ and CD8+) and CD14+ monocytes from treatment-naive MS patients (n=106) and healthy subjects (n=22). We identified 479 differentially expressed genes (DEGs) in CD4+ T cells, 435 in monocytes, and 54 in CD8+ T cells. Importantly, in CD4+ T cells, we discovered up-regulated transcripts from the *NAE1* gene, a critical subunit of the NEDD8 activating enzyme (NAE), which activates the neddylation pathway, a posttranslational modification analogous to ubiquitination. Finally, we demonstrated that inhibition of NAE using the specific inhibitor Pevonedistat (MLN4924) significantly ameliorated disease severity in murine experimental autoimmune encephalomyelitis (EAE). Our findings provide novel insights into MS-associated gene regulation unraveling neddylation as a crucial pathway in MS pathogenesis with implications for the development of tailored disease-modifying agents.

Biography

Kicheol Kim is a scientist specialized in human genetics and transcriptomics research. His research seeks to characterize the genetic architecture and identify the genes associated with human diseases and phenotypes. He earned a Ph.D. in biological science, with a concentration in human genetics, from Dankook University. During his Ph.D. study, he contributed several human population genetics research including 1,000 genomes project and forensic genetics with national forensic service of South Korea. He expanded his specialty from genetics to transcriptomics during a postdoctoral scholar in Baranzini Lab at UCSF. This is his postdoc research and just accepted in Brain. In this study, using cell-type-specific gene expression profiling, he revealed post-translational modification pathway related to T cell activation is crucial in multiple sclerosis pathogenesis and its' small molecule inhibitor as a new therapeutic drug. He is currently seeking early cancer biomarkers as a bioinformatics scientist at Everest Detection.

Career Development Session 2

How to land your first faculty job in Korea

나는 이 물음을 이어갈 수 있을까?

Joon-Yong An, Ph.D.
Assistant Professor
School of Biosystem and Biomedical Science, College of Health Science
Korea University

"커리어의 다음 단계에서 나는 좋은 연구를 할 수 있을까?", "한국 대학에서 연구 커리어는 지속될 수 있을까?" 등은 지난 임용을 준비하며 스스로에게 가장 많이 한 질문이었습니다. 정답지는 없겠지만, 지원 과정 중 느꼈던 개인적인 경험과 지원 절차 별 준비 과정을 공유하고자 합니다. 또한 대학 임용 과정에서 커리어 전환기에 필요한 부분들, 그리고 (아직은 진행중인) 한국 대학의 정착기를 전달하고자 합니다.

21 세기 유전학은 고처리량의 유전체 기술과 데이터 공유가 만나, 형질과 질병의 유전적 조성을 보다 포괄적으로 설명하는 기회를 제공합니다. 이 흐름에 잇대어, 저희 인간유전체 연구실 (https://joonanlab.github.io/) 은 발달장애 및 난치성 질환의 밑절미가 되는 유전적 원인을 연구합니다. 전장 유전체, 싱글셀 전사체 등을 활용하여 질병의 유전적 조성을 포괄적으로 기술하기 위한 연구 및 분석 방법론 개발을 하고 있습니다.

지원하기 전에 알았다면 좋았을 것들

Jaecheol Lee, Ph.D.
Assistant Professor
School of Pharmacy
Sungkyunkwan University

제가 임용 시장에 뛰어 들었을 때 저는 마치 아무것도 할 수 없는 캄캄한 우주를 떠돌고 있는 느낌을 받았습니다. 제 스스로 할 수 있는 것이 거의 없고, 자신의 인생이 다른 사람에 의해 평가받고 결정된다는 점은 참 낯설고 어려운 경험이었습니다. 비록 제가 임용에서의 경험이 많지 않지만 적어도 어떠한 것을 이해하고 있어야 좀 더 편안한 마음으로 임용에 임할 수 있는지, 또한 어떠한 점이 가장 중요한 결정이였는지에 대하여 말씀드리고자 합니다.

저는 성균관대학교 약학대학에서 2018 년도부터 근무하고 있습니다. 저희 연구실은 유도만능줄기세포 및 유전자 가위 기술을 이용하여 질환을 모델링하고 이를 통하여 새로운 메커니즘을 제시하고자 합니다. 또한 이러한 질환 모델 시스템을 이용하여 다양한 약물을 스크리닝 할 수 있는 HCS(high content screening) 플렛폼을 개발하고 있습니다.
(http://pharm.skku.edu/intro/professor_detail.php?pr_id=78&target=03#subcon)

Research career in KIST

Sanghee Lee, Ph.D.
Senior Researcher
Center for Neuromedicine
Korea Institute of Science & Technology (KIST)

KIST 등 한국 내의 정부 출연 연구소에서의 연구 환경, 연구실, 채용절차 등에 대해 소개 드리고자 합니다

저희 실험실 (https://sangheelee85.wixsite.com/kist)은 KIST 뇌과학연구소 내 뇌의약연구단의 Chemical Biology & Therapeutics Lab 으로 뇌종양 및 신경염증, 자폐 등의 뇌 질환 분야에서 다양한 Chemical tool 을 이용한 생명현상 연구를 진행하고 있습니다.


Hanmi 한미약품
Hanmi
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개척하겠습니다!
모두가 쉬운 길을 택할 때,
아무도 가지 않는,
새로운 길만을 개척했던 한미약품!
인류건강을 위한
혁신신약 연구개발로
삶의 가치를 높이는데 앞장서겠습니다

유한이 가야 하는 길.

국민이 사랑하고, 국민과 함께 자란 기업 유한양행
지난 90여년 동안 이어진 정직과 성실의 기업문화와
기업의 사회적 책임에 대한 확고한 신념이 지금의 유한을 만들었습니다.

지금껏 걸어온 길을 돌아보며, 앞으로 가야 할 길을 생각합니다.
혁신적 신약개발을 통한 글로벌 제약사로의 도약, 대한민국을 넘어
모든 인류가 건강하고 행복한 길을 걸어가려 합니다.

다가올 100년에는 창업자 유일한 박사의 숭고한 정신을 바탕으로
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왜, 동아쏘시오그룹은 글로벌 제약사도 포기한 치매치료에 최선을 다하는 걸까?

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