



KOREAN LIFE SCIENTISTS IN THE BAY AREA
STANFORD | UC BERKELEY | UC DAVIS | UCSF

2022 Annual Conference

DAVID BROWER CENTER
TAMALPAIS ROOM
Berkeley, CA

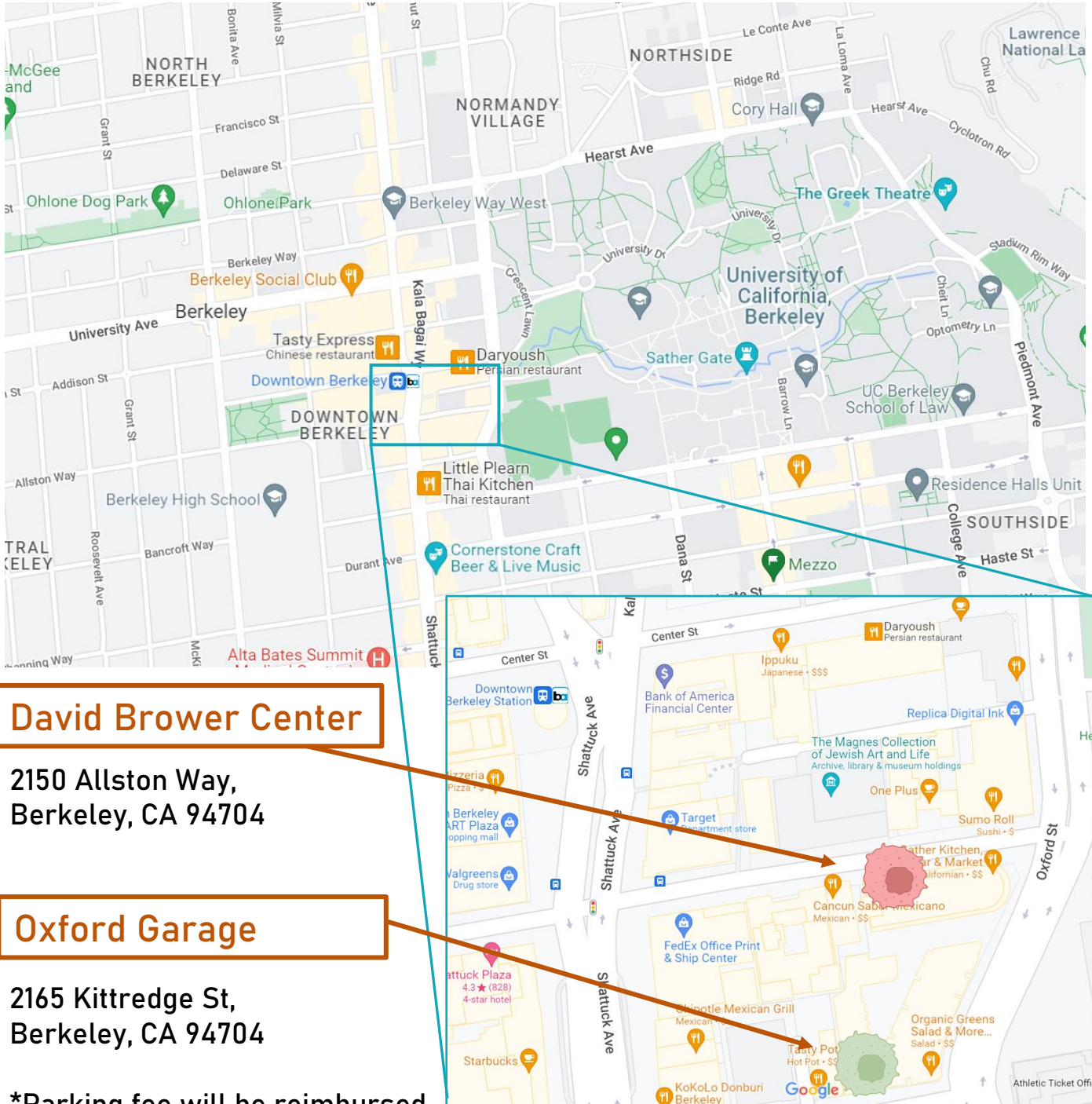
25th June 2022



KOLIS

2022 Annual Conference

DAVID BROWER CENTER TAMALPAIS ROOM
Berkeley • 25TH JUNE 2022



*Parking fee will be reimbursed

*Masks are required indoor



2022 Annual Conference

9:30 - 10:00 Registration
10:00 - 10:10 Opening remark & Raffle 1

Session 1 : Keynote & Fellowship

Moderator: Yun-Gu Jang, Ph.D.

10:10 - 10:50 Keynote 1 (Prof. Young-Wook Jun, Ph.D., UCSF)
10:50 - 11:15 Fellowship talk 1 (YeEun Kim)
11:15 - 11:40 Fellowship talk 2 (Dongjoo You, Ph.D.)
11:40 - 12:40 Group photo & Lunch
12:40 - 13:00 Sponsors

Session 2 : Career

Moderator: Kyuyoung Lee, DVM, MPVM, Ph.D.

13:00 - 13:20 한국 대학 - KENTECH (Prof. Myoung Hwan Oh, Ph.D.)
13:20 - 13:40 미국 바이오텍 - Genentech (Gyeong Jin Kang, Ph.D.)
13:40 - 14:00 미국 연구소 - Chan Zuckerberg Biohub (Yang Joon Kim, Ph.D.)
14:00 - 14:20 스타트업 창업 - MEDIC Life Science (Kyuho Han, Ph.D.)

Session 3 : Flash Talk

Moderator: Kibeom Hong, Ph.D.

14:20 - 14:50 Flash Talks
① Hyung Jun Kim ② Jaekyung Kim, Ph.D. ③ Hyunjun Yang, Ph.D.
④ Sungi Kim, Ph.D. ⑤ Juhjung Park
14:50 - 15:10 Coffee break

Session 4 : Keynote & Fellowship

Moderator: Yun-Gu Jang, Ph.D.

15:10 - 15:50 Keynote 2 (Prof. Seung-Wuk Lee, Ph.D., UCB)
15:50 - 16:15 Fellowship talk 3 (Sun Il Kwon, Ph.D.)
16:15 - 16:40 Fellowship talk 4 (JaeYoung Jung, Ph.D.)

16:40 - 17:00 Raffle 2
17:00 - 17:10 Closing Remarks
17:10 - 19:00 Banquet



2022 Annual Conference

Greetings from the KOLIS President



2022 KOLIS President
Sungi Kim, Ph.D.

안녕하십니까 KOLIS 회원 여러분,
2022년 KOLIS 회장을 맡은 UC Berkeley의 김선기입니다.

올해 대면으로 진행하는 2022 KOLIS 연례 학술대회를 개최합니다.
지난 2년간 COVID-19 팬데믹 상황으로 샌프란시스코 베이 지역과 KOLIS의 교류는 굉장히 역동적이었습니다. 학교별로 이루어지던 월간 세미나를 비대면으로 전환하여 KOLIS회원들이 모두 참석할 수 있었습니다. 나아가 미국 전역의 생명과학자들과 교류하는 전미한인생명과학자의 날, 한국에서도 참석할 수 있는 비대면 연례학술대회 등을 개최해오며 오히려 거리에 제약을 벗어나 더 자유롭게 교류할 수 있었다는 장점도 누렸습니다. 하지만 그와 동시에 직접 얼굴을 보고 만나 담소를 나누며 교류하는 모임에 대한 갈증은 더욱 커지게 되었습니다. 올해는 3년만에 다시 대면행사로서의 2022 KOLIS 연례학술대회를 개최하게 되어 부담과 함께 큰 기대를 가지고 있습니다.

2022년도 KOLIS를 운영하고 연례학술대회를 개최를 준비하며 많은 분들에게 감사를 드리고 싶습니다. KOLIS의 행사가 원활이 이루어질 수 있도록 도와주시는 임원진과 각 학교 대표분들, 그리고 KOLIS를 후원해주시는 소중한 후원사 분들에게 감사의 말씀을 드리고 싶습니다. KOLIS의 선배님이시자 흔쾌히 키노트 연사로 참석을 결정해주신 이승욱 교수님과 전영욱 교수님께도 감사의 말씀을 드립니다. 또 다양한 진로로 진출하여 흥미로운 얘기를 들려주실 커리어세션의 연사분들께도 감사드립니다. 마지막으로 각자의 자리에서 묵묵히 생명과학을 연구하고 귀한 시간을 내주어 참석해주신 KOLIS의 회원 여러분들께 존경과 감사를 전합니다.

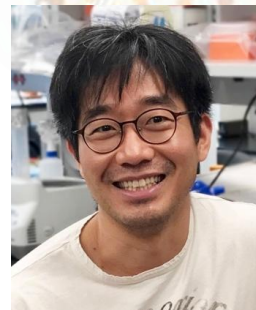
KOLIS에 관심을 갖고 2022년 다시 대면으로 개최하는 연례학술대회에 참석해 주셔서 다시 한 번 감사드립니다. 이번 학술대회를 통해 직접 교류하고 소통할 수 있는 기회가 되길 바라며 앞으로도 KOLIS를 통해 다양한 네트워킹을 진행할 수 있도록 노력하겠습니다. 감사합니다.

2022 KOLIS 회장
김선기 드림



2022 Annual Conference

Welcoming Remark from the NYKB President



2022 NYKB President
Taejin Yoon, Ph.D.

안녕하세요 KOLIS여러분,
NYKB의 2021-2022 회장단 대표를 맡고 있는 윤태진입니다.

2022년 KOLIS 연례학회를 온라인이 아닌 대면 학회를 성공적으로 진행하게 되어서 진심으로 축하를 드립니다. 지난 2년부터 현재까지 유례없는 코로나 감염으로 인해서 전세계적으로 많은 사람들이 힘들고 어려운 시간을 겪어왔고, 안타깝게도 현재까지 진행중인 상황입니다. 하지만 이러한 어려운 상황에도 불구하고, 생명과학의 눈부신 발전을 바탕으로 코로나 감염병에 대한 백신 개발기간이 획기적으로 줄여질 수 있었고, 덕분에 KOLIS 학회도 대면으로 진행될 수 있게 되었습니다. 그리고 이러한 생명과학 분야에 매진해서 연구하는 우리 생명연구자들의 헌신 및 노력과 직간접적으로 생물에 대한 퍼즐을 맞춰가는 과정이 그 어느때보다 더욱 더 중요하고 더욱 더 값진 순간이 아니라 할 수 없겠습니다.

KOLIS는 미국 서부를 대표하는 한인생명과학단체로 저희 뉴욕에 위치한 NYKB, 메릴랜드의 KLAM, 그리고 뉴잉글랜드 위치한 NEBS 와 함께 '전미한인생명과학자의 날'과 같은 학술모임을 비롯한 다양한 온라인 학술 교류를 통해, 한국과 미국에서 활발하게 연구활동을 이어가고 있는 많은 한인생명과학자들이 함께 소통할 수 있는 중요한 기회를 이끌어 가고 있습니다. 앞으로도 그리고 COVID-19 이후에도 KOLIS 와 NYKB 가 함께 더 좋은 협력적인 관계를 이룰 수 있기를 희망하며, 그럴 수 있도록 NYKB 가 노력하겠습니다. 이번 학회를 통해서 KOLIS 에 계시는 많은 연구자분들이 값지고 의미가 있는 시간을 보내실 수 있기를 진심으로 멀리서 기원드립니다.

NYKB 13대 회장
윤태진 드림



2022 Annual Conference

Welcoming Remark from the NEBS President

NEBS New
England
Bioscience
Society
뉴잉글랜드 생명과학협회



2022 NEBS President
Jae Kyo Lee, Ph.D.

안녕하십니까 KOLIS 회원 여러분,
뉴잉글랜드 생명 과학 협회 (NEBS) 이재교 회장입니다.

봄과 여름이 함께하는 이 시기에, KOLIS 회원 여러분의 가정에도 건강과 행복이 언제나
같이 하시길 바라겠습니다.

NEBS와 KOLIS는 미국의 동부와 서부에 위치한 대표적 생명과학자 협회로서, 물리적 거리로
인하여 얼마 전까지는 직접적인 교류가 쉽지는 않았다고 생각합니다. 하지만 COVID-19이라는
위기를 기회로 삼아, 올해까지 2년 연속 “전미생명과학자의 날”이라는 미국 전역의
생명과학자들을 한자리로 모아 학술적 교류를 추진한 자랑스런 역사가 있으며, 이후에도 두
단체 간의 끈끈한 협력적 관계를 유지하도록 NEBS와 KOLIS의 임원진들은 열심히 노력할
것이라 믿어 의심치 않습니다.

또한, 올해 KOLIS 학회는 대면 행사로서 진행이 될 예정이라고 들었습니다. KOLIS 회원
여러분이 고대하셨던 직접적인 네트워크와 심도 있는 학술교류가 이루어질 것이라 기대하며,
그만큼의 준비과정 또한 KOLIS 임원진들의 노고가 필요함을 알기에 감사와 존경의 말씀을
전하고 싶습니다.

그 어느 단체보다 생동감이 느껴지는 KOLIS, 그리고 2022년 연례학회를 성공적으로 준비하심을
김선기 회장님과 임원진들께 축하 드리고 싶습니다. 또한 학회에 직접 참여하시어 자리를 빛내
주시는 모든 KOLIS 회원님들께도 감사의 말씀을 전하고 싶습니다.

KOLIS와 NEBS 의 친구 같은 협력관계는 앞으로도 계속 이어지길 기원하겠으며, 저 또한
노력하도록 하겠습니다. 이번 2022년 KOLIS 연례학회를 통하여, 훌륭한 학술 교류와 함께 좋은
인연을 만들어 가시길 바라겠습니다.

NEBS 39대 회장,
이재교 드림.



2022 Annual Conference

Welcoming Remark from the Consul General



Consul General
Sangsoo Yoon

친애하는 김선기 KOLIS 회장 및 KOLIS 회원 여러분!

「2022 연례 KOLIS 학술대회」 개최를 진심으로 축하합니다.

KOLIS는 베이지역(Bay Area)의 대표적인 대학인 UC Berkeley, UC Davis, UCSF 및 스탠포드 대학의 한인 생명과학 연구자들이

결성한 학술모임으로 연례 학술대회를 포함한 다양한 활동을 통해 한인 연구자간 정보교류와 네트워크 확대에 크게 기여하고 있는 것으로 알고 있습니다. 특히, 그 동안 코로나 팬데믹 이후 처음으로 직접 대면으로 만나서 교류하는 이번 2022년 학술대회는 KOLIS가 한 단계 더 도약하는, 새로운 10년을 시작하는 계기가 될 수 있다는 점에서 큰 의미가 있다고 생각합니다.

세계 최고의 연구진들의 생명과학 연구가 진행되고 있고, 이를 산업화하기 위해 치열하게 경쟁하고 있는 베이지역에서 각자의 자리에서 혁신적 연구에 매진하면서 우리나라 생명과학 분야의 외연을 넓혀가고 있는 여러분들에게 감사의 말씀을 전합니다.

최근 4차 산업혁명 도래로 IT와 생명과학이 융합하는 새로운 바이오 산업이 급성장하고 있고, 팬데믹을 거치면서 기초 생명과학, 유전공학, 의약학 등의 중요성이 날로 커지는 가운데, 우리 정부에서도 생명공학 육성계획, 제약산업 육성지원계획 등을 통해 연구개발, 인력양성, 기업지원을 위해 노력하고 있습니다. 특히, 새 정부에서는 바이오·디지털헬스 글로벌 중심국가 도약을 중요한 국정과제로 삼고, 생명과학을 경제 재도약을 견인할 핵심전략 산업 분야 중 하나로 선정한 바 있습니다.

우리 바이오 기업들도 우수한 한인 생명과학자들을 채용하기 위해 지속적으로 샌프란시스코를 포함한 베이지역을 방문하고 있고, 최근 우리나라 바이오 산업을 대표하는 기업이 이 곳에 연구기관을 설립한 바 있으며, 무엇보다 전세계 스타트업 혁신생태계 중 기술경쟁력, 생산성, 투자유치능력, 사업화 수준에서 세계 1위인 실리콘밸리에서 성공을 꿈꾸는 창업가들이 바이오 산업 분야에서도 몰려 들고 있는 상황에서, 베이지역의 젊은 생명과학자들의 모임인 KOLIS의 역할이 더욱 기대되는 상황입니다.

오늘 KOLIS 학술행사를 통해 최신 생명과학 연구 트렌드를 공유함과 동시에 한인 연구자간 네트워킹, 한인 연구계와의 연구 협력의 좋은 기회가 되기를 바랍니다. 또한, 미국 산업계, 미국 연구소 및 한국 교수 등 다양한 커리어로 진출하신 분들의 경험을 공유하는 시간도 마련되어 있는 것으로 알고 있는데, KOLIS의 젊은 회원들의 멘토로서 진로 선택과 취업에도 많은 도움을 줄 수 있을 것이라고 기대합니다.

그 동안 베이지역을 관할하는 주샌프란시스코총영사관에서는 한인 과학자들 혹은 차세대 한인단체간 네트워킹 행사 및 교류를 지원해 왔습니다. 앞으로도 총영사관에서는 KOLIS를 포함하여 우리 과학기술자 단체들의 활동을 돕고, 새정부 출범에 발맞추어 우리나라와 현지 과학자들간 소통할 수 있는 가교 역할을 하기 위해 더욱 노력하겠습니다.

미국 유수의 대학에서 두각을 나타내며 생명과학 분야 연구를 이끌고 있는 여러분이 더욱 열심히 노력하셔서 우리나라의 생명과학, 바이오 산업 발전에도 기여해 주시길 당부드립니다. 오늘 학술대회를 준비해 주신 KOLIS 회장단의 노고를 치하하고, 오늘 참가하시는 모든 분들이 이번 학술대회에서 소기의 성과를 거두시길 기원합니다.

주샌프란시스코총영사관 윤상수 총영사



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Abstracts



Keynote 1

10:10 - 10:50

Biophysical mechanisms of signal exchanges at cellular interface

Prof. Young-Wook Jun, Ph.D.

Dept. of Otolaryngology, UC San Francisco

Dept. of Pharmaceutical Chemistry, UC San Francisco

Helen Diller Family Comprehensive Cancer Center, UC San Francisco



Juxtacrine signaling mediates communications via physical contact between neighboring cells, orchestrating development and physiology of multicellular organisms. The signal-exchange interfaces create unique microenvironments that biophysically constrain the arrangement and activity of protein, lipid, and glycan components, finally mediating the spatial organization and biochemical activity of signaling molecules, serving as the basis for wide-range of cellular functions. In this talk, I will specifically focus on spatiotemporal dynamics of Notch, a key cell communication receptor, and its signaling consequences in cells. By integrating cutting-edge nanotechnology tools including mechanogenetics¹⁻⁴ (i.e., targeted control of genetically encoded mechanosignaling), magnetically amplified protein-protein signals (MagAPPs)⁵, and single particle tracking⁶, we mapped dynamic spatial distributions of Notch receptors during the cell surface activation. We discovered that Notch undergoes dynamic spatial changes immediately after its receptor activation, choreographing downstream cell signaling sequences⁶. From these observations, we disentangled a long-standing mystery of how dynamic compartmentalization and colocalization of Notch creates enzymatically distinct environments and hence facilitates sequential proteolysis of Notch and signaling⁶.

1. Seo *et al.*, A Mechanogenetic Toolkit for Interrogating Cell Signaling in Space and Time. *Cell* 165, 1507–1518 (2016).
2. M. Kwak *et al.*, Small, Clickable, and Monovalent Magnetofluorescent Nanoparticles Enable Mechanogenetic Regulation of Receptors in a Crowded Live-Cell Microenvironment. *Nano Lett.* 19, 3761–3769 (2019).
3. Kim, J. *et al.* Magnetic Nanotweezers for Interrogating Biological Processes in Space and Time. *Acc. Chem. Res.* 51, 839–849 (2018).
4. Kim, J. *et al.* “Single cell mechanogenetics with monovalent magnetoplasmonic nanoparticles”. *Nature Protocols* 12, 1871 (2017).
5. Farlow, J. *et al.* Formation of monovalent quantum dot imaging agents by steric exclusion. *Nature Methods* 10, 1203 (2013).
6. Kwak M. *et al.* Size-dependent protein segregation creates a spatial switch for Notch and APP signaling. *bioRxiv* (2020)



Keynote 2

15:10 - 15:50

Bio-inspired Material Assembly and Applications

Prof. Seung-Wuk Lee, Ph.D.

Dept. of Bioengineering, UC Berkeley
Lawrence Berkeley National Laboratory



In nature, helical macromolecules such as collagen, chitin and cellulose are critical to the morphogenesis and functionality of various hierarchically structured materials. During morphogenesis, these chiral macromolecules are secreted and undergo self-templating assembly, a process whereby multiple kinetic factors influence the assembly of the incoming building blocks to produce non-equilibrium structures. A single macromolecule can form diverse functional structures when self-templated under different conditions. Collagen type I, for instance, forms transparent corneal tissues from orthogonally aligned nematic fibers, distinctively colored skin tissues from cholesteric phase fiber bundles, and mineralized tissues from hierarchically organized fibers. Nature's self-templated materials surpass the functional and structural complexity achievable by current top-down and bottom-up fabrication methods. However, self-templating has not been thoroughly explored for engineering synthetic materials.

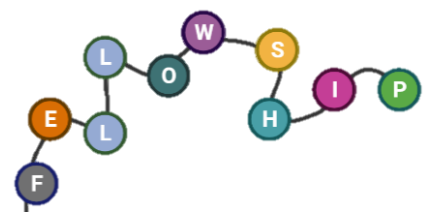
In my seminar, I will demonstrate a facile biomimetic process to create functional nanomaterials utilizing chiral colloidal particles (M13 phage). A single-step process produces long-range-ordered, supramolecular films showing multiple levels of hierarchical organization and helical twist. Using the self-templating materials assembly processes, we have created various biomimetic supramolecular structures. The resulting materials show distinctive optical and photonic properties similar to avian skin color matrices and butterfly wing nanostructures. Through the directed evolution of the M13 phages, I will also show how resulting materials can be utilized as functional nanomaterials for biomedical, biosensor and bioenergy applications.



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Fellowship 1

10:50 - 11:15

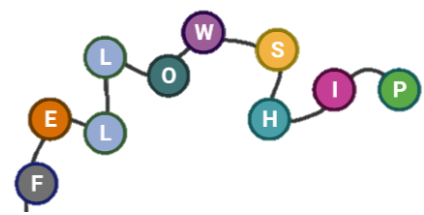
Single-cell proteomic screen reveals a new population of lymphoid-primed progenitors in human

YeEun Kim, Ph.D. Candidate

Immunology Graduate Program, Stanford University



Adult bone marrow is the major source of life-long blood production from hematopoietic stem and progenitor cells in mammals. Among different hematopoietic lineages, lymphopoiesis is poorly understood in humans despite its crucial role in adaptive immunity. To fill the gap, we assessed human bone marrow lymphoid progenitors by quantifying functional protein molecules associated with lymphoid lineage in a highly multiplexed single-cell proteomic screen. This screen revealed TdT, a specialized DNA polymerase associated with VDJ recombination, as an accurate indicator of lymphoid protein landscape. Moreover, we identify TdT⁺ cells that exhibit the surface phenotype of granulocyte-monocyte progenitors (GMPs) with open chromatin regions enriched for lymphoid-associated transcription factor motifs. We enriched TdT⁺ GMPs by sorting on CD84^{lo} GMPs and validated the robust lymphoid potential in CD84^{lo} GMPs via functional differentiation assays. This study identifies previously unappreciated lymphoid-primed progenitors and provides a single-cell level reassessment of the human lympho-myeloid axis. Furthermore, we provide a framework to redefine HSPCs via quantification of functional key players, multi-omic molecular phenotyping, identification of relevant proxy surface markers, and validation via functional assays.



2022 Annual Conference

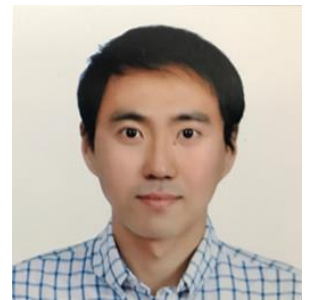
Fellowship 2

11:15 - 11:40

JMJD8 Is a Novel Molecular Nexus Between Adipocyte-Intrinsic Inflammation and Insulin Resistance

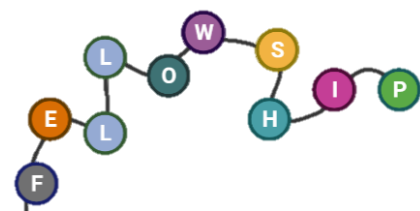
Dongjoo You, Ph.D.

Dept. of Nutritional Sciences & Toxicology, UC Berkeley



JMJD8 Is a Novel Molecular Nexus Between Adipocyte-Intrinsic Inflammation and Insulin Resistance.

Chronic low-grade inflammation, often referred to as metainflammation, develops in response to overnutrition and is a major player in the regulation of insulin sensitivity. While many studies have investigated adipose tissue inflammation from the perspective of the immune cell compartment, little is known about how adipocytes intrinsically contribute to metainflammation and insulin resistance at the molecular level. In this study, we demonstrate a novel role for Jumonji C domain-containing protein 8 (JMJD8) as an adipocyte-intrinsic molecular nexus between inflammation and insulin resistance. We determined that JMJD8 was highly enriched in white adipose tissue, especially in the adipocyte fraction. Adipose JMJD8 levels were dramatically increased in obesity associated insulin resistance models. Its levels were increased by feeding and insulin and inhibited by fasting. A JMJD8 gain-of-function was sufficient to drive insulin resistance, whereas loss-of-function improved insulin sensitivity in mouse and human adipocytes. Consistent with this, *Jmjd8*-ablated mice had increased whole-body and adipose insulin sensitivity and glucose tolerance on both chow and a high-fat diet, while adipocyte-specific *Jmjd8*-overexpressing mice displayed worsened whole body metabolism on a high-fat diet. We found that JMJD8 affected the transcriptional regulation of inflammatory genes. In particular, it was required for lipopolysaccharide-mediated inflammation and insulin resistance in adipocytes. For this, JMJD8 required interferon regulatory factor 3 to mediate its actions in adipocytes. Together, our results demonstrate that JMJD8 acts as a novel molecular factor that drives adipocyte inflammation in conjunction with insulin sensitivity.



2022 Annual Conference

Fellowship 3

15:50 - 16:15

Reconstruction-free direct Positron Emission Imaging (dPEI): Imaging at the speed of light

Sun Il Kwon, Ph.D.

Department of Biomedical Engineering, UC Davis



X-ray, gamma-ray, and optical photons are widely used for medical imaging. However, the spatial distribution of photon emission within a patient can only be recovered through a mathematical image reconstruction step, known as tomography. A large set of projections of the source distribution must be collected with sufficient linear and angular sampling for accurate image reconstruction. This is commonly done with a ring of detectors fully surrounding the patient in a cylindrical system geometry, such as CT or PET scanners. Theoretically, the back-to-back annihilation photons produced by positron-electron annihilation is a signal source that can be directly localized in 3D space using time-of-flight information without tomographic reconstruction. However, this has not yet been demonstrated due to the insufficient timing performance of current radiation detectors. Here, we develop novel ultrafast radiation detection techniques and demonstrate direct positron emission imaging (dPEI) without a need for tomographic reconstruction. This new discovery involves a compact equipment setup compared to the conventional full ring setup and could lead to inexpensive, easy, and accurate biomedical imaging scans of the patient using radioactive tracers. This presentation focuses on details of dPEI and technology roadmap for improving dPEI.

Fellowship 4

16:15 - 16:40

Effects of Collagen Cross-linking and Matrix Charge on Glucose Transport in the Human Cartilage Endplate

JaeYoung Jung, Ph.D.

Dept. of Orthopaedic Surgery, UC San Francisco

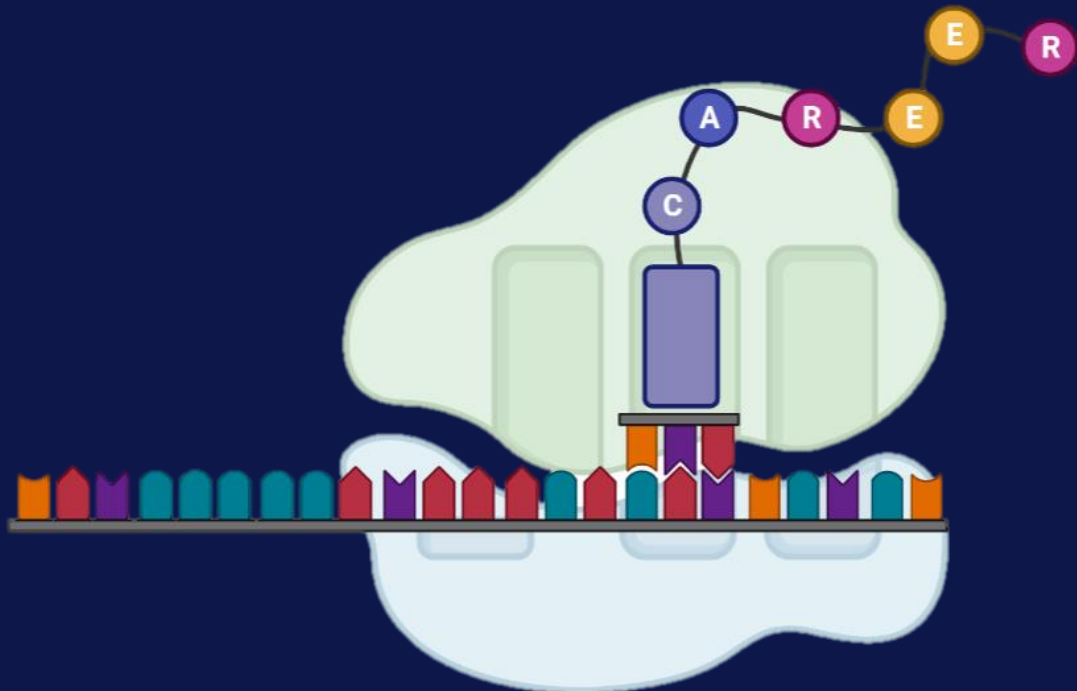


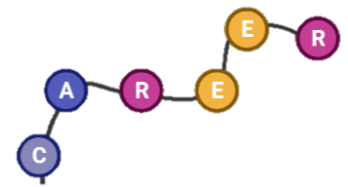
The poor nutrient environment of the avascular disc is believed to be an important reason why disc nucleus pulposus (NP) cells fail to remodel their matrix. Since nutrients entering the NP and exiting metabolites must pass through the cartilage endplate (CEP), discovering the factors that influence solute transport through the CEP may provide insight into disc degeneration etiology and inform strategies for enhancing transport to slow or reverse degeneration. A number of factors influence the transport of solutes through the CEP. For example, increased deposition of mineral, proteoglycans, and collagen in the CEP matrix limits the physical pore space available for solutes to pass. In the NP and annulus fibrosus (AF), the quality of the matrix is also important. For example, accumulation of advanced glycation endproducts (AGEs) in the NP and AF results in cross-linking of the collagen and aggrecan, and associates with lower tissue hydration, presumably by restricting the swelling capacity of those tissues. However, the effects of AGE accumulation on solute transport the human CEPs remains unknown. Therefore, the goal of this study was to determine how AGE accumulation impacts the biochemical and transport properties of the bovine NP and human CEP tissues. We hypothesized that AGEs accumulation reduces solute transport, and that the effect is independent of the amount of matrix. From 0 to 9 days of incubation in ribose, AGE concentration on the CEP samples incubated for 3-9 days significantly increased in a time-dependent manner, showing 179% (day 9) increases in AGE concentrations over the control group (day 0). These increases in AGE concentrations are equivalent to increases due to natural aging of 6.9, 15.2, and 17.9 years, respectively. We also measured glucose uptake during equilibrium partitioning experiments. Partition coefficients were negatively associated with AGE concentration ($p = 0.047$), indicating a small but significant effect. In contrast to the human CEP, partition coefficients for sodium fluorescein in the NP were significantly decreased (35%, $p < 0.0002$) by ribosylation (9 days) compared to the control group (day 0), and this also coincided with reduced tissue hydration. These findings show for the first time that AGE accumulation in the human lumbar CEP coincides with reduced glucose uptake, which suggests that matrix cross-linking in the CEP may negatively impact solute transport and disc nutrition.



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2022 Annual Conference

Career Session 1

13:00 - 13:20

Starting a University

Prof. Myoung Hwan Oh, Ph.D.

Associate Professor,
Institute for Environmental and Climate Technology
Korea Institute of Energy Technology (KENTECH)



설립도 되지 않은 대학에 임용되어 대학을 만들어가는 다사다난한 과정에서 겪은 특별한 스토리를 들려드립니다. 시작부터 새로워야 혁신적인 대학을 만들 수 있다는 믿음과 실현을 향한 끊임없는 다짐이 있었고, 그 과정에서 교원의 역할과 활동은 생각보다 크고 다양함을 깨달았습니다. 과연 스타트업 대학에서 커리어를 시작하는 건 어떤 느낌인지, 새 대학의 미래는 어떻게 전망하고 있는지 여러분과 나눠보고자 합니다.

한국에너지공과대학은 기후위기를 극복하기 위해 혁신적인 연구문화와 교육방식으로 에너지 대전환의 시대를 이끌 기술을 연구개발하고 문제해결 역량을 갖춘 인재를 육성하는 강소형 대학입니다.

Career Session 2

13:20 - 13:40

미국 인더스트리 잡서치 어디서부터 시작할까?

Gyeong Jin Kang, Ph.D.

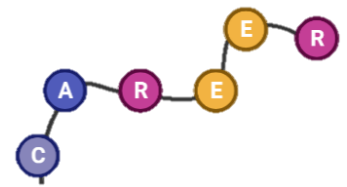
Principal Scientific Researcher, Genentech



결혼한 여성으로 박사과정을 마치고 취직을 하기까지 많은 우여곡절이 있었고 그 과정에서 받은 도움들도 많았습니다. 미국 industry로 가는 게 맞는지 아직 고민하시는 분들, industry로 가고 싶은데 어디부터 시작해야할 지 모르겠다는 분들을 위해 개인적인 경험을 바탕으로 step by step 소개해 드리고자 합니다.

나에게 맞는 포지션을 찾는 것, 레쥬메와 커버레터 작성, 인터뷰 준비, 최종 오퍼를 받고 난 후 해야할 것들 까지 모든 단계를 훑어보실 수 있도록 전달해드리겠습니다.

현재 제넨텍의 Translational Immunology 부서에서 ocular disease treatment를 위한 연구를 진행하고 있습니다.



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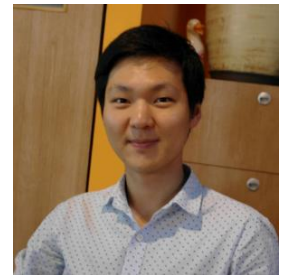
Career Session 3

13:40 - 14:00

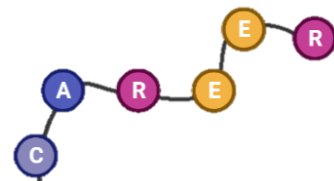
How to make a transition from a bench scientist to a data scientist?

Yang Joon Kim, Ph.D.

Chan Zuckerberg Biohub



There are many career options after PhD, probably as many as the number of PhDs. Towards the end of PhD or postdoc, you might wonder, “what do I want to do in my next job?”. I asked the same question to myself, and it took me a while to figure out what I wanted to do. One of the questions that I had was whether to stay in the wet lab or in the dry lab. As I am moving to the data science field, I want to share my experience during my transition from a wet lab to a dry lab scientist. Specifically, I will cover some tips and resources that helped me greatly.



2022 Annual Conference

Career Session 4

14:00 - 14:20

We Reveal Hidden Vulnerability in Solid Cancer –
A breakthrough platform to unmask novel drug targets for solid tumor

Kyuho Han, Ph.D.

CEO/Founder, MEDIC Life Sciences Inc.

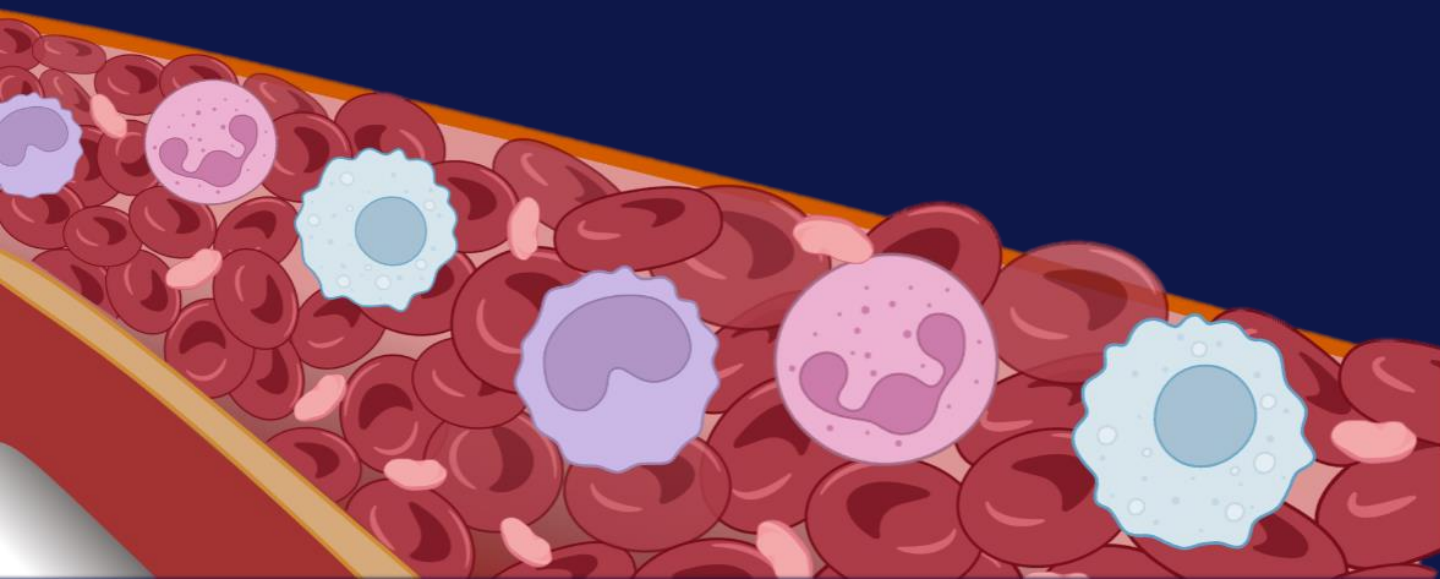


새로운 항암 치료제 개발에 있어서 좋은 표적 유전자를 찾는 것은 첫번째 단추를 잘 끼우는 것으로 비유될 수 있습니다. 문제는 기존 방법으로 찾아지는 표적 유전자들의 대부분이 잘못 끼워진 첫번째 단추와 같아서 90% 이상의 치료제 개발이 중간에서 결국 실패한다는 것입니다. 이런 문제를 본질적으로 해결하기 위하여 저희 MEDIC은 다양한 고형암들에 있어서 높은 성공 확률이 보장된 신약 표적 유전자들을 발굴할 수 있는 플랫폼을 개발하고 있습니다. MEDIC의 플랫폼은 기능 유전체학을 기반으로 하며 환자의 암과 가장 유사한 형태의 고형암 모델을 사용함으로써 기능 유전체학의 정확도를 극대화 할 수 있었습니다. 저희는 미국 내의 대형 제약사와 플랫폼 파트너십을 맺고 기술 제공을 진행하고 있으며 내부적으로도 간암과 유방암을 위한 초기 신약 개발 프로그램을 가지고 있습니다. 이번 세션에서는 저희 회사 소개와 함께 지난 2년 간의 창업 경험을 간단하게 공유하고자 합니다.



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Flash Talks



MJL-1 is a novel meiotic protein required for homolog pairing and regulation of synapsis in *C. elegans*

Interaction between chromosomes and the “linker of nucleoskeleton and cytoskeleton” (LINC) complexes in the nuclear envelope (NE) promotes homolog pairing and synapsis during meiosis. By tethering chromosomes to cytoskeletal motors, these linkages lead to rapid, processive movements of chromosomes along the NE. This activity is usually mediated by telomeres, but in *C. elegans* special chromosome regions called “pairing centers” (PCs) have acquired this meiotic function. Through a genetic screen for mutations causing meiotic nondisjunction in *C. elegans*, we discovered an uncharacterized meiosis-specific NE protein, MJL-1 (MAJIN-Like-1) that is essential for interactions between PCs and LINC complexes. MJL-1 colocalizes with PCs and LINC complexes during pairing and synapsis. Mutations in MJL-1 disrupt these interactions and eliminate processive chromosome movements. *mjl-1* mutants undergo promiscuous nonhomologous synapsis, reduced clustering of PCs, and impaired homolog pairing. Similarities of the chromosome-LINC complex attachments between *C. elegans* and other organisms suggest that these connections may play previously-unrecognized roles during meiosis across eukaryotes.



Hyung Jun Kim
UC Berkeley

Roles of sleep oscillations in motor memory consolidation

Sleep has been known to contribute to brain plasticity and consolidation of both declarative and procedural/motor memories. Declarative memory is defined as our capacity to acquire and recollect facts and events, while motor memory is described as our ability to acquire a variety of skills, including motor skills such as shoe lacing or playing a musical instrument. A large body of studies has proposed the roles of sleep oscillations for declarative memories. Yet, direct evidence for the neural basis is lacking for motor memory systems. My recent studies have focused on motor memory processing to understand a sleep-dependent mechanism using multi-scale in vivo electrophysiology as well as state-of-the-art techniques such as brain-machine interface and reach-to-grasp tasks developed by our lab at UCSF. My flash talk will introduce important discoveries for motor memory processing throughout multi-regional brain areas during sleep oscillations such as slow-oscillations, delta-waves, spindles, and sharp-wave ripples (Kim et al., *Cell*, 2019; Kim et al., *Cell Rep.*, 2022; Kim et al., under revision) as well as foresight and directions for my future research.



Jaekyung Kim, Ph.D.
UC San Francisco

EMBER multi-dimensional spectral microscopy enables the quantitative determination of distinct amyloid strains



Hyunjun Yang, Ph.D.
UC San Francisco

Rapid methods to screen and quantify amyloid conformational strains are lacking. Herein, we developed EMBER (Excitation Multiplexed Bright Emission Recordings), a high-throughput and high-sensitivity method to quantify the structure sensitive nature of fluorogenic dyes by utilizing multidimensional excitation and emission on a confocal microscope. We implemented PCA and UMAP with quadratic discrimination to quantify the strain sensing properties of amyloid bound dyes. We created a novel in vitro platform to screen 145 dyes against six different amyloid fibrils, in which we identified new classes of strains sensing dyes for ex vivo application. Using EMBER in ex vivo brain slices, we first validate that in vitro discovered dyes demonstrate robust strain discrimination of A β plaque types in transgenic mouse models, and sporadic AD, familial AD, and Down syndrome patient samples in situ. Remarkably, we also discovered dyes that discriminate tau deposits from different neurodegenerative diseases, consistent with distinct cryo-EM structures found across tauopathies. EMBER is a powerful and rapid method to ascertain conformational nature of amyloid forming proteins in any biological system.

Understanding Stochasticity in T cell activation

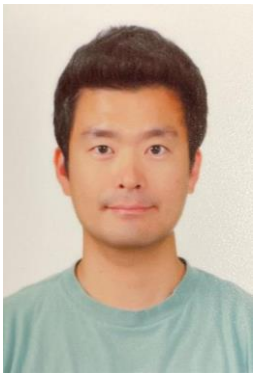


Sungi Kim, Ph.D.
UC Berkeley

T cells achieve extraordinary sensitivity and specificity on activation of immune response in binary switch-like manner. Yet, underlying molecular and cellular mechanism on stochastic T cells activation process is still unclear. Here, we simultaneously observe peptide major histocompatibility complex:T cell receptor (pMHC:TCR) signals exerted on T cells, following condensation of linker for activation of T cells (LAT), and resulting translocation of nuclear factor of activated T cells (NFAT). This real-time observation of consecutive input signals, early signaling process, and late decision making of the cells enables how T cells integrate individual pMHC:TCR binding events to determine the activation at cellular level. We found temporal overlap of multiple LAT condensates arose from pMHC:TCR complex is critical for the T cell activation. We further construct a model system by simulating dynamic LAT condensation patterns from TCR ligation to predict the stochastic activation of T cells. From our observation and simulation, we can explain stochastic activation of T cells in that only T cells which experience multiple LAT condensation at short time window over threshold can get activated. Our finding also suggests another type of noise suppression mechanism at cellular-level information processing in addition to the kinetic proofreading at molecular level.



Role of protein methylation signaling in the regulation of protein synthesis and cancer biology



Juhyung Park
Stanford

Lysine methylation of proteins has now emerged as an important post-translational modification involved in a wide range of cellular functions and disease. However, there are still many unknowns about the enzymes that catalyze disparate methylation events, the physiological functions of these modifications, and the potential role of these methylation events in human diseases.

eEF1A is referred to as eukaryotic translation elongation factor which is important for protein translational machinery and known to be highly associated with tumorigenesis. eEF1A is known to be specifically methylated at five different lysine residues. METTL10 has been shown to catalyze eEF1A methylation at lysine 318 residue. However, the physiological role of the METTL10-mediated eEF1A methylation in cancer has yet to be explored in depth. Here, we show METTL10 depletion completely abrogates eEF1AK318me in cancer cells, and eEF1AK318me is the sole product of METTL10 among the known methyl lysines of eEF1A in different type of cancer cells. To determine the functional role of METTL10 in cancer cell growth, we depleted METTL10, leading to inhibit cancer cell proliferation. We also established a robust mouse pancreatic cancer model where METTL10 showed its tumorigenic role. Thus, we suggest that METTL10 might have a role in pancreatic cancer pathogenesis which leads to its potential as a therapeutic target.



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모두가 쉬운 길을 택할 때,
아무도 가지 않는,
새로운 길만을 개척했던 한미약품!
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Hanmi



누군가 먼저 가야하는 길.

유한양행이
인류건강의 길을
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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
미래를 향한 도약과 발전의 역사를 써나가겠습니다.

우리의 도전은 이미 시작되었습니다.



유한양행

왜, 동아쏘시오그룹은 수십년 동안 끝없는 암의 비밀을 풀고있는 걸까?

아직도 완치의 희망을 놓지 않는 수많은 암환자와
가족들의 간절함을 알기에
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암보다도 더 고통스럽다는 항암 치료, 많은 좋은 약이 개발되고
있지만 암은 아직도 풀지 못한 인류의 가장 큰 숙제입니다.
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노력을 기울이고 있습니다.

2016년 애브비와 면역항암제 기술 수출 및 공동연구 계약,
2017년 아스트라제네카와 공동연구개발 계약 등
암 정복에 한발 먼저 다가가고 있습니다.

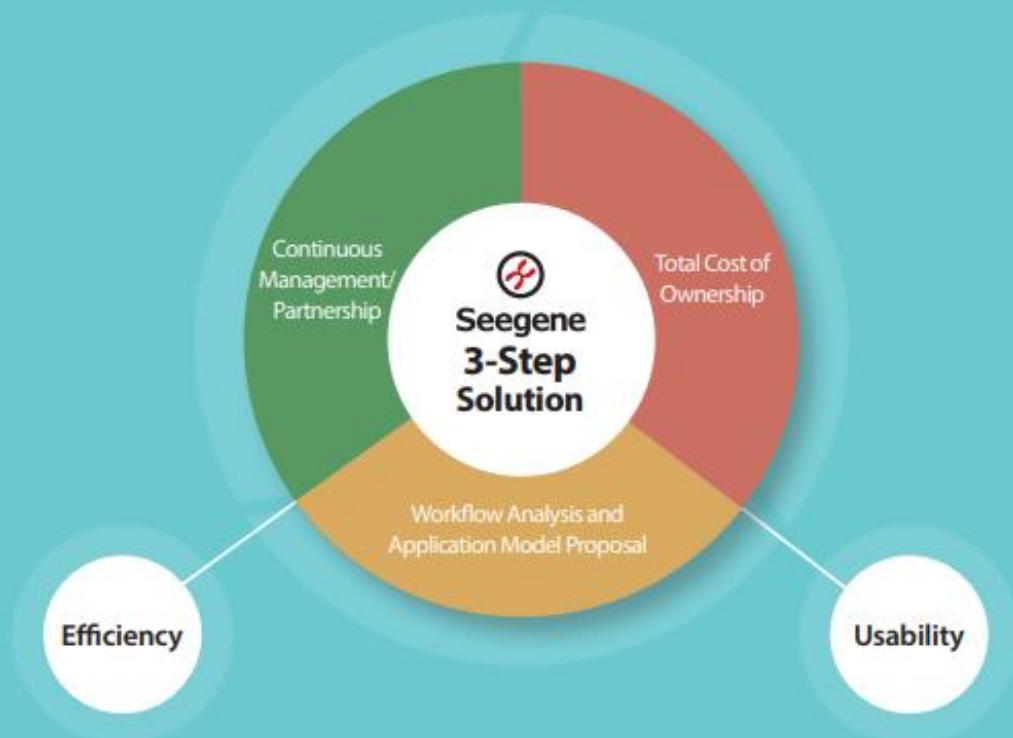
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누구나 분자진단을 시작할 수 있습니다.

20년의 분자진단 제품 개발 노하우를 가진 선도기업 씨젠이
분자진단 실험실 구축을 위한 다양한 요소들을 모두 고려하여
**최소한의 공간과 인력만으로도 최대의 효과를 낼 수 있는
솔루션을 제안합니다.**

여러분은 **씨젠이 자랑하는 맞춤형 3-Step Solution**을 통해
내 상황과 조건에 맞는 최적의 실험실을 제안받으실 수 있으며
3-Step Solution을 통해 구축되는 실험실에서는 완전 자동화 분자진단 장비인
STARlet-AIOS와 다양한 호흡기 검사 제품들을 통해
효율성과 활용성이라는 두 마리 토끼를 모두 잡을 수 있습니다.



GC Biopharma to the world right now! We bring new hope to patients around the world

1983 - The world's 3rd hepatitis B vaccine

1988 - The world's 1st epidemic hemorrhagic fever vaccine

1993 - The world's 2nd varicella vaccine

2010 - The world's 6th WHO prequalified
pandemic (H1N1) influenza vaccine

2011 - The world's 4th WHO prequalified
seasonal trivalent influenza vaccine

2016 - The world's 2nd WHO prequalified
seasonal quadrivalent influenza vaccine



Since its establishment in 1967, GC Biopharma has consistently maintained a philosophy of taking the difficult but essential path, rather than the easier path. Now, GC Biopharma is going that extra mile by aiming to give new hope to people all around the world, not just those living in Korea. By combining its outstanding R&D capability for developing globally-recognized vaccines and blood derivatives with its differentiated solutions, GC Biopharma has set itself a new challenge to discover novel and much needed medicines and to become a trusted name, synonymous with protecting the health and happiness of people across the world.

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PharmAbcine's fully human antibody libraries and innovative selection systems are our priceless proprietary assets. We also provide co-development opportunities with novel therapeutic antibodies.

PharmAbcine possesses core technologies such as Dual or Multiple Target Antibody Platform Technology / Immuno Oncology-based Therapeutic Agents / ADC-based & CAR-T/NK Cell-based Therapeutic Agents. We will constantly develop pipelines for sustainable growth with a vision to become a global biopharmaceutical company.

Recently, we appointed legendary pathologist Dr. David Cheresh and a world-leading molecular biologist Dr. Napoleone Ferrara. Also, Prof. Soohyeon Lee from Dept. of medicinal oncology at Korea University School of Medicine to Scientific Advisory Board.

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Applications

- Cell monitoring
- Wound healing assay
- Cell proliferation
- Apoptosis
- Coculture monitoring
- Cytotoxicity assay
- Transfection efficiency
- Reactive oxygen species detection

Key features

- One color fluorescence (Green or Red) and bright field imaging
- Compact size that easily fits into a standard CO₂ incubator
- Fully motorized stages allow multi-point imaging up to 96 wells
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'크리스탈지노믹스'를 검색하세요!

크리스탈지노믹스



About SML Genetree

SML Genetree is a leading developer of multiplex molecular technologies and multiplex clinical molecular diagnostics based in South Korea. SML Genetree is recognized as a premier partner in developing technology and on-time delivery, providing both basic research in molecular biology and applied research in molecular diagnosis. SML Genetree has succeeded in commercializing the Ezplex HPV NGS Kit, gaining global recognition.

In 2020, SML Genetree developed Ezplex COVID-19 RT PCR test kits and founded SML Genetree Sciences to expand into the US market. SML Genetree was one of the first companies with a COVID-19 test to obtain emergency use approval from the South Korean Ministry of Food and Drug Safety (MFDS).

About SML

SML Genetree is an affiliate of Samkwang Medical Laboratories (SML), one of the largest diagnostic commercial labs in South Korea since 1985. SML has continued to provide diagnostic results to customers across 3,000 government medical institutions in South Korea, including the Military Manpower Administration (MMA), university hospitals, and local medical institutions. In 2020, SML conducted approximately 3 million clinical trial tests for COVID-19. Meditree and Labtree, affiliates of SML, also support SML Genetree through related projects, such as Central Lab Service/CRO and vaccine R&D.

Our Vision & Mission

SML Genetree strives to be a leader in the industry through continuous challenge, innovation and customer value. SML Genetree has world-class genome research competence and abundant experience leading to research and customer value. It is considered as one of the top molecular diagnostic companies in South Korea through efficiency and a value-based business system establishment and performance in the global market. SML Genetree seeks to develop a new driving force in the bio-industry by taking on the role of a pioneer in preventive and precision medicine.

Core Capabilities

NGS
(Next Generation
Sequencing Analysis)

Sequencing

**Real-time
PCR**

PCR

Key Products

- COVID-19, including VOC kit
- Respiratory pathogen diagnostic kits (up to 19 respiratory viruses and 6 types of pneumonia-causing bacteria, including SARS-CoV-2 (COVID-19)/Flu A/Flu B/RSV diagnostic kit)
- Sexually Transmitted Infections diagnostic kits
- Tuberculosis & Non-TB diagnostic kit
- *H. pylori* and resistance diagnostic kit
- HPV genotyping diagnostic kits (NGS)
- HLA diagnostic kits for organ transplant (NGS)
- Other viral infections: HBV, HCV, HIV, SFTS



Bacterial disease



Viral disease



Drug resistance



Precision medicine
for cancer



Human leukocyte
antigen (HLA) typing

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01 /

NIW (National Interest Waiver)
EB-1(a) (Alien of Extraordinary Ability)
EB-1(b) (Outstanding Professors/Researchers)
EB-1(c) (Multinational Manager or Executive)

02 /

O Visa
E1/E2 (Treaty Trader/ Treaty Investor)
L-1 (Intra-company Transferees)
H-1B (Specialty Worker)
J-1 waiver



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THANK YOU

We hope to see you again soon in the June Seminar!