JUNSOO KIM

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EDUCATION

Seoul National University, Korea 2021 - Present
Ph.D Student in Bioinformatics
Advisor: Hyeshik Chang, PhD.

University of Oxford, UK 2012 - 2013
M.Phil in Integrated Immunology
Advisor: Jan Rehwinkel, PhD.

University of Edinburgh, UK 2008 - 2012
B.Sc (Hons) in Biological Sciences (Biotechnology)

PROFESSIONAL EXPERIENCE

Macrogen, Inc., Seoul, Korea 2019 - 2020
Senior Researcher, Data Strategy Team

Seegene, Inc., Seoul, Korea 2018 - 2019
Associate Researcher, In silico Team

Macrogen, Inc., Seoul, Korea 2013 - 2017
Researcher, Bioinformatics Division

ACADEMIC AWARDS AND GRANTS

Youlchon AI for All Fellowship
Youlchon Foundation 2024

JW Basic Scientist Scholarship
JW Foundation 2023

Outstanding Oral Presentation Award
The Microbiological Society of Korea 2023

Youlchon AI Young Researcher
Youlchon Foundation 2022

3.1 Scholarship
Samil Founation 2022

Top 5 Biological Research Achievement in Korea
Biology Research Information Center 2016

Undergraduate Research Scholarship
Korea Advanced Institute of Science & Technology 2010

PUBLICATIONS

* The marked authors contributed equally

1. Seo JS*, Rhie A*, **Kim J***, Lee S*, *et al.*, De novo assembly and phasing of a Korean human genome. *Nature*. 2016 Oct 13:538(7624):243-247 (IF=64.8)
2. **Kim J***, Youn D*, Choi S*, *et al.*, SARS-CoV-2 infection engenders heterogeneous ribonucleoprotein interactions to impede translation elongation in lungs. *Exp. Mol. Med.* 55, 2541–2552 (2023). https://doi.org/10.1038/s12276-023-01110-0 (IF=12.8)

CONFERENCE PRESENTATION

The Microbiological Society of Korea (Oral) Yeosu, Korea (2023)
"SARS-CoV-2 Infection Engenders Heterogeneous Ribonucleoprotein Interactions to Impede Translation Elongation in Lungs"

Cold Spring Harbor Asia (Poster) Awaji, Japan (2023)
"Heterogeneous RNPs and impeded translation elongation in SARS-CoV-2-infected lungs"

Centre for RNA Workshop, Institute for Basic Science (Oral) Seoul, Korea (2023)
"Heterogeneous RNPs and impeded translation elongation in SARS-CoV-2-infected lungs"

Korean Society for Bioinformatics (Poster) Daejeon, Korea (2022)
"Aberrant RNA association and compromised translation manifest in the respiratory tissues of SARS-CoV-2 pathology"

Advances in Genome Biology and Technology (Poster) Marco Island, FL (2015)
"De Novo Assembly of an Asian Diploid Genome using SMRT sequencing"

RESEARCH EXPERIENCE

SARS-CoV-2 Infection: Disruption of Translation Integrity 2023
Executed a groundbreaking investigation employing tissue-optimized ribosome profiling to elucidate the translational landscape in lung tissues affected by severe SARS-CoV-2 infection. This research provided the first comprehensive temporal profile of viral and host gene translation during infection, revealing novel mechanisms of viral evasion and host response. The findings contribute to the development of therapeutic strategies targeting translational control in viral diseases.

De Novo Assembly and Phasing of a Korean Human Genome 2016
Led a collaborative effort to achieve the most contiguous diploid human genome assembly to date, focusing on the comprehensive mapping of structural variants and haplotyping of clinically relevant alleles. This work, featuring extensive analysis of previously uncharted and population-specific genetic variations, underpins future advancements in precision medicine and genomic research, particularly for Asian populations.

PA-X and RIG-I: How Flu Modulates the Innate Immune Response 2013
Conducted a seminal study on the influenza virus's strategic inhibition of the RIG-I mediated antiviral response, providing crucial insights into viral immune evasion tactics. This research delineated the molecular mechanisms employed by the influenza A virus to suppress type I interferon production, offering potential targets for antiviral drug development.

Identification of B.pseudomallei Factors That Subvert Cellular Actin Pathways 2012
Spearheaded an investigation into the molecular strategies employed by Burkholderia pseudomallei to manipulate host cell actin dynamics for cellular entry and intracellular movement. This project identified novel effector proteins implicated in the pathogen's ability to hijack cellular machinery, contributing to our understanding of bacterial pathogenesis and host-pathogen interactions.

The Induction of M1 to M2 Macrophage Transition Using IL-4 Treatment 2011
Initiated and executed a study to explore the plasticity of macrophage phenotypes in response to IL-4 stimulation, with the aim of identifying a chimeric M1/M2 macrophage subset. This research provided valuable insights into the regulatory mechanisms governing macrophage polarization, highlighting potential implications for immunotherapy and the treatment of chronic inflammatory diseases.

Differentiation of Human Embryonic Stem Cells to Dopaminergic Neurons 2010
Aimed to develop a novel protocol for the efficient differentiation of human embryonic stem cells into functional dopaminergic neurons, addressing a critical need in the study of Parkinson's disease and other neurodegenerative disorders. This project demonstrated the potential for stem cell-based therapies in regenerating damaged neuronal networks and restoring neurotransmitter function.