

Summary Experienced Senior Bioinformatics Scientist with a strong background in immunology and cancer biology research, specializing in leading bioinformatics projects from conception to completion. Extensive expertise in advanced NGS data integration, computational method design and cross-functional collaboration. Proven track record in delivering actionable insights to drive biological discovery, with first-author publications in Nature Immunology and Cell Reports. Skilled at coordinating multi-partner projects and managing pharmaceutical collaborations at Dana-Farber Cancer Institute. Recognized for exceptional analytical abilities and commitment to scientific understanding through innovative methodologies.

Education

Ph.D. in Plant Biology. University of Texas at Austin, Austin, Texas	2010 - 2017
M.S. in Biology. Seoul National University, Seoul, Korea	2007 - 2010
B.S. in Biology. Yonsei University, Seoul, Korea.	2005 - 2007

Professional Experience

Senior Bioinformatics scientist. Dana Farber Cancer Institute. Boston, MA 2022 – 2024

Informatics & Analytics, the Bioinformatics group

Research of the Belfer Center for Applied Cancer Science, Thoracic Oncology group

Team mentors: David Barbie, Cloud Paweletz

- **DGK inhibitor combinational therapy evaluation utilizing scTCR-seq:** Analyzed **scRNA-seq** and **scTCR-seq** data from combinational therapy trials of a DGK inhibitor with Pembrolizumab in NSCLC, in the platform of patient-derived cells (pDOTs). The integration of scTCR-seq with scRNA-seq. Clonotypes analysis and selection for the CAR-T cell therapy design. (BMS)
- **DS-1062a comparison with Deruxtecan:** Analyzed **scRNA-seq** data from TROP2-high cells, incorporating the tumor immune environment, and cancer-cell enriched tissue RNA-seq in two distinct NSCLC patient cohorts (responders and non-responders) with the treatment with Dxd/IgG-Dxd and DS-1062a. Comparison study of DS-1062a efficacy to standalone Dxd therapy in tumor cells and related immune cells (NK and macrophage). Studied canonical gene expressions, population shift, pathway enrichment, scoring, clustering, and feature selections using lasso regression. scRNA-seq and RNA-seq integration. (Daiichi-Sankyo)
- **TAK-676 combinational therapy in addition to NK cell injection:** Conducted **scRNA-seq** analysis across six cohorts, with combinational treatments of TAK-676 and Pembrolizumab. Rigorous data preprocessing (customized filtering, integration, normalization and annotations). CD8T+ cells-specific analysis for activated immune response by TAK-676 with Pembrolizumab. Machine learning application for NK cell sub-setting without tags. (Takeda)
- Conducted validation studies for EZH2 inhibitor candidates using ChIP-seq methodologies at Janne lab, DFCI. Developed custom processes to achieve normalization of signal peaks across samples and established a systematic approach for comparative analysis. (2023)
- **Facilitated the evaluation of STING agonist (ADU-100).** Investigated ADU-100 effects in mouse PBMCs model regarding changes in the tumor immune environment and clonotype expansion, applying scRNA-seq and TCR-seq techniques. This study, in collaboration with BMS, is being prepared for resubmission to the journal Cancer Discovery in 2024. Integration of scTCR-seq with scRNA-seq. Clonotypes selection and clonotype-associated immune cell study for population shift, DEGs, pathway enrichment, and network analysis.
- Identified target gene candidates for treatment-resistant NSCLC through PDX models, conducting gene network analysis and extensive correlation tests linked to oncogenic mutations based on bulk RNAseq data.
- **TROP2 hi/lo group analysis in TNBC-TCGA.** Data analysis on TNBC-TCGA to investigate the association of known cell types within TROP2-hi/lo subgroups. Data preprocessing, filtering, and categorization were completed, setting the stage for in-depth analysis and further exploration. (2024).

Massachusetts General Hospital Laboratory (Salvia Jain Lab)

- **Anti-CD47 therapy in Primary T cell Lymphoma model:** An integrative analysis using the unique ITK-SYK system was conducted to evaluate the efficacy of anti-CD47 therapy in PTCL models (tumor). scRNA-seq data from ITK-SYK PTCL mice analysis to determine the time-dependent effects of anti-CD47 therapy, at 2 hours and 2 weeks. Supported grant proposal writing focusing on macrophages and NK cell populations in 2024. Experiment design of subsequent RNA-seq and ATAC-seq analyses related to this project
- Supported the bioinformatics analysis for the resubmission of a manuscript detailing the KLRG1 depletion study in patients with mature T cell lymphoma, contributing to a publication in Clinical Cancer Research 2024.

Postdoctoral Fellow. Hackensack Meridian Health. Nutley, NJ
Center for Discovery & Innovation. Hai-Hui Xue laboratory

2021 – 2022

- **Novel Tle3 coactivator function analysis:** Led bioinformatics efforts to explore the novel role of the transcriptional cofactor Tle3 in redefining central memory CD8+ T cell fates. This pioneering research was published in Nature Immunology (2024). I developed the primary hypotheses and conducted the majority of the bioinformatic analyses. Utilized **scRNA-seq (CITE-seq)** to uncover key features of Tle3 knockout (KO) and integrated **RNA-seq, ATAC-seq, and Cut&Run** data for Tle3, Runx3, and Tbet to investigate further connections under the novel roles of Tle3. The findings were validated through extensive mouse experiments, confirming the impactful insights derived from the computational studies.

Postdoctoral Fellow. Cold Spring Harbor Laboratory. Cold Spring Harbor, NY

2020 – 2021

Dr. Janowitz Laboratory

- Conducted bioinformatic analyses on the glucocorticoid response in cancer cell models, identifying key regulatory pathways and potential therapeutic targets.
- Investigated cachexia-inducing molecules, elucidating their mechanisms and impact on metabolism within cancer progression.

Postdoctoral Fellow. University of Michigan. Ann Arbor, MI

2018 – 2020

Dr. Jun Hee Lee laboratory, co-advisor: Dr. Hyun Min Kang

- Engaged in the setup and optimization of various NGS platforms within the lab, including DROP-seq, Seq-well, BD-Rhapsody, and Seq-Scope, contributing to developments published in Cell (2021).
- Conducted a single-cell transcriptome study on colon cancer cells to investigate responses to 5FU-induced DNA damage, with findings detailed in Cell Reports (first author paper, 2020).
- Holistic characterization of single Hepatocyte transcriptome responses to high fat diet (first author paper, American Journal of Physiology, 2020)

Bioinformatics Skills

Programming language Proficient in **R, Python, Linux, custom scripting**

Linux tools Samtools, GATK, BEDTools, VCFtools, CellRanger, BWA, Bowtie, STAR, MACS2, Salmon, DeepTools, awk, VS Code

Bioconductor dplyr, ggplot2, DESeq2, Seurat, harmony, monocle, GenomicRanges, Pheatmap, doubletFinder, cellchat, scater, Rsamtools, ChIPseeker, TCGAbiolinks, MethylKit, ClusterProfiler, enrichR, ssGSEA, BiocParallel, WGCNA, STRINGdb, corrplot, maftool, scanpy, scrublet

Machine Learning application caret, keras, torch, tidymodels, glmnet, mlr3, randomForest

Public database TCGA, CCLE, GTEx, COSMIC, STRINGDB, GEO, MsigDB.

Data visualization shiny (shinyapps.io), Rmarkdown, plotly, dashboard, IGV (Genome browser)

Cloud computing HPC (PBS, SLURM), DNANexus

Code repositories maintain github, github.io and project based google drive.

Publications

The transcriptional cofactor Tle3 reciprocally controls effector and central memory CD8+ T cell fates. (Nature Immunology, 2024. X.Zhao, W.Hu, **S.R.Park**, S.Zhu, S.S.Hu, C.Zang, W.Peng, Q.Shan, H.H. Xue. *co-first (Equal contribution of all four authors) (<https://doi.org/10.1038/s41590-023-01720-w>)

SiftCell: A robust framework to detect and isolate cell-containing droplets from single-cell RNA sequence reads. (Cell Systems, 2023) Jingyue Xi, **Sung Rye Park**, Jun Hee Lee and Hyun Min Kang (<https://doi.org/10.1016/j.cels.2023.06.002>)

Sublethal whole-body irradiation induces permanent loss and dysfunction in pathogen-specific circulating memory CD8 T cell populations (PNAS,2023) Mohammad Heidarian, Isaac J Jensen, Shravan Kumar Kannan, Lecia L Pewe, Mariah Hassert, **SungRye Park**, Hai-Hui Xue, John T Harty, Vladimir P Badovinac (<https://doi.org/10.1073/pnas.23027851>)

KLRG1 Cell Depletion as a Novel Therapeutic Strategy in Patients with Mature T-Cell Lymphoma Subtypes (Clinical Cancer Research, 2024) Bimarzhan Assatova, Robert Willim, Christopher Trevisani, Garrett Haskett, Khyati Maulik Kariya, Kusha Chopra, **Sung Rye Park**, Michael Yevgeniy Tolstorukov, Sean M McCabe, Jessica Duffy, Abner Louissaint Jr, Jani Huhtanen, Dipabarna Bhattacharya, Satu Mustjoki, Min Jung Koh, Foster Powers, Elizabeth A Morgan, Lei Yang, Brandy Pinckney, Matthew J Cotton, Andrew Crabbe, Jessica Beth Ziemba, Ian Brain, Tayla B Heavican-Foral, Javeed Iqbal, Ronald Nemec, Anna Baird Rider, Josie Germain Ford, Min Ji Koh, Nora Scanlan, David J Feith, Thomas P Loughran Jr, Won Seog Kim, Jaehyuk Choi, Juliette Roels, Lena Boehme, Tom Putteman, Tom Taghon, Jeffrey A Barnes, P Connor Johnson, Eric D Jacobsen, Steven A Greenberg, David M Weinstock, Salvia Jain. (<https://doi.org/10.1158/1078-0432.CCR-23-3504>)

Simultaneous loss of TSC1 and DEPDC5 in skeletal and cardiac muscles produces early-onset myopathy and cardiac dysfunction associated with oxidative damage and SQSTM1/p62 accumulation. (Autophagy, 2021) Chun-Seok Cho, Yongsung Kim, **Sung-Rye Park**, Boyoung Kim, Carol Davis, Irene Hwang, Susan V Brooks, Jun Hee Lee, Myungjin Kim. (<https://doi.org/10.1080/15548627.2021.2016255>)

Seq-Scope: Microscopic examination of spatial transcriptome using Seq-Scope. (Cell, 2021) Chun-Seok Cho, Jingyue Xi, Yichen Si, **Sung-Rye Park**, Jer-En Hsu, Myungjin Kim, Goo Jun, Hyun-Min Kang, Jun Hee Lee. (<https://doi.org/10.1016/j.cell.2021.05.010>)

Single cell transcriptome analysis of colon cancer cell response to 5-fluorouracil-induced DNA damage (Cell Reports, 2020) **Sung Rye Park**, Sim Namkoong, Zac Zezhi Zhang, Leon Friesen, Euisik Yoon, Chang H. Kim, Hojoong Kwak, Hyun Min Kang and Jun Hee Lee. (<https://doi.org/10.1016/j.celrep.2020.108077>) * first author

Holistic Characterization of Single Hepatocyte Transcriptome Responses to High Fat Diet (American Journal of Physiology-Endocrinology and Metabolism, 2020) **Sung Rye Park**, Chun-Seok Cho, Hyun Min Kang and Jun Hee Lee. (<https://doi.org/10.1152/ajpendo.00391.2020>) * first author

Transcriptome and epigenome analyses of vernalization in Arabidopsis thaliana (The Plant Journal, 2020) Yanpeng Xi, **Sung-Rye Park**, Dong-Hwan Kim, Eun-Deok Kim, Sibum Sung (<https://doi.org/10.1111/tpj.14817>)

Mimosine arrests the cell cycle prior to the onset of DNA replication by preventing the binding of human Ctf4/And-1 to chromatin via Hif-1 α activation in HeLa cells (Cell Cycle 2012) Soon-Young Park, Jun-Sub Im, Sung-Rye Park, Sang-Eun Kim, Hoe-Jeong Wang, Joon-Kyu Lee (<https://doi.org/10.4161/cc.11.4.19209>)

People Skills

Strong Project management Demonstrated ability to organize, manage, and track multiple complex projects simultaneously, with successful completion. **Frequently recognized by managers for effectively organizing and managing multiple complex projects, ensuring timely and successful completion**

Cross-Disciplinary Expertise Deep understanding of both biology and computational methodologies, enabling effective communication with diverse collaborators

Expertise in immunology, oncology, molecular biology, and practical experience in statistical analysis skills for bioinformatics research that were proven by first author papers.