

Hyeon Gu Kang

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Objective

JAX scholar award application

Education and Training

2023 – Present	Postdoctoral Associate in JAX Genome Medicine Farmington, CT, USA
2022 – 2023	Post-Doc researcher in Information & Electronics Research Inst KAIST, Daejeon, Korea
2019 – 2022	Ph.D. in Bio & Brain engineering KAIST, Daejeon, Korea
2017 – 2019	M.S. in Bio & Brain engineering KAIST, Daejeon, Korea
2011 – 2014	B.S. in Biomedical engineering Dongguk University, Seoul, Korea

Research interests

Transcriptome data analysis, RNA splicing mechanism, and Human aging and disease

Research Experiences

	Spatial transcriptome analysis of young and old mice breast tissue to identify an association aging and transcriptome changes
	Refinement of the Pacbio long-read pipeline and development of RNA splicing consequence estimation tool
Present	Single cell Cut & Tag analysis of luminal epithelial cells of young and old mice
	Exploring transcriptome changes in longitudinal samples to elucidate PARPi resistance mechanism in ovarian cancer patients
	Large-scale isoform analysis to find cancer-specific isoform expression patterns (Long/short read RNA seq)
2018 – 2022	Aberrant transcript usage analysis in breast, ovarian cancer for predicting drug response
2017 – 2018	Splicing QTL (sQTL) analysis in breast cancer

Presentation and Poster

11/03/2023	Discovering Biological Targets: A High-Throughput and Accurate Splicing interpreter, Poster, Yale RNA center.
11/27/2019	Genome-wide methylation pattern predicts clinical benefit of immune checkpoint blockade therapy in NSCLC patients, Poster, AACR.

- 6/11/2019 DNA repair defects by aberrant transcript usage in wildtype BRCA tumors, Presentation, GIGS.
- 9/8/2018 Alternative splicing in normal tissues as a primary risk factor of breast cancer, Poster, ECCB.

Honors and Awards

- 2/17/2023 Best paper of the year, KAIST
- 8/21/2014 Early graduation with honors, Dongguk Univ

Publications

Junghoon Shin*, **Hyeon Gu Kang***, Jin Ok Yang, Jung Kyoon Choi. Integrative analysis of 26,848 human transcriptomes reveals cancer-defining transcriptional architecture at the isoform resolution. (Expected to submit by Feb 2024).

Brittany L. Angarola, Siddhartha Sharma, Neerja Katiyar, **Hyeon Gu Kang**, Djamel Nehar-Belaid, SungHee Park, Rachel Gott, Giray N. Eryilmaz, Mark A. LaBarge, Karolina Palucka, Jeffrey H. Chuang, Ron Korstanje, Duygu Ucar, Olga Anczuków. Comprehensive single cell aging atlas of mammary tissues reveals shared epigenomic and transcriptomic signatures of aging and cancer (Under review 2024).

Hyeon Gu Kang, Haeun Hwangbo, Myung Ji Kim, Sinae Kim, Eun Ji Lee, Min Ji Park, Jae-Weon Kim, Byoung-Gie Kim, Eun-Hae Cho, Suhwan Chang, Jung-Yun Lee and Jung Kyoon Choi. Aberrant transcript usage is associated with homologous recombination deficiency and predicts therapeutic response. *Cancer Res.* 2022.
(*co-first author)

Patent

Method for Determining Sensitivity to PARP inhibitor or genotoxic drugs based on non-functional transcripts. **Hyeon Gu Kang**, Jung Kyoon Choi, Eun-Hae Cho. PCT/KR2021/015800. 2021. WO/2022/098086, 2022.