Joha Park, Ph.D.

The Picower Institute for Learning and Memory
Massachusetts Institute of Technology (MIT)
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KEY SKILLS & EXPERIENCE

- Computational Biology, RNA Biology, Spatial Genomics
- Sequencing Data Analysis: (sc)RNA-seq, CLIP-seq, etc.
- Tissue Clearing and Expansion for Spatial Genomics
- Imaging Data Analysis: 3D Confocal/Light-sheet
- Multi-omics, Image Processing, Machine Learning

CURRENT POSITION

01/2020 – present · **Postdoctoral Associate/Fellow** · *Massachusetts Institute of Technology*
Chung Lab (webpage) (Advisor: Kwanghun Chung)
The Picower Institute for Learning and Memory
Institute for Medical Engineering and Science
Department of Chemical Engineering
Massachusetts Institute of Technology, Cambridge, MA, US

Roles
- Developing new methods for hydrogel-based tissue engineering
- Building a unified and scalable analytical framework for 3D light-sheet microscopy
- Generation of a single-cell mouse brain reference atlas

PROFESSIONAL EXPERIENCE

2019 · **Postdoctoral Researcher** · *Seoul National University*
Center for RNA Research (Director: V. Narry Kim)
Institute for Basic Science
Seoul National University, Seoul, Korea

Roles
- Leading projects on mRNA poly(A)-tail length regulations
- Conventional and custom NGS library prep & data analysis
- Wet and dry experiments related to cell and RNA biology

EDUCATION AND TRAINING

2012 – 2019 · **Ph.D. in Biological Sciences** (RNA Biology & Bioinformatics) · *Seoul National University*
RNA Biology Lab (Advisor: V. Narry Kim)
Dissertation: "Poly(A) length regulation: deadenylases and the poly(A) barricade"

2015 – 2018 · **Expert Research Personnel** · *Republic Of Korea Army*
Compulsory Military Service

2008 – 2012 · **B.S. in Biological Sciences** (*cum laude*) · *Seoul National University*

PUBLICATIONS

*: co-first author, #: co-corresponding author

1. **J. Park***, M. Kim*, H. Yi*, K. Baeg*, Y. Choi, Y.-s. Lee, J. Lim, V. N. Kim (2022) "Short poly(A) tails are protected from deadenylation by the LARP1-PABP complex" ***Nat. Struct. Mol. Biol.*** (accepted)

2   **J. Park***, S. Khan*, D. H. Yun*, T. Ku, K. L. Villa, J. E. Lee, Q. Zhang, G. Feng, J. Park, E. Nedivi#, K. Chung# (2021) "Epitope-preserving magnified analysis of proteome (eMAP)" ***Sci. Adv.*** 7(16):eabf6589

3   Y. Kim*#, **J. Park***, S. Kim*, M. Kim, M.-G. Kang, C. Kwak, M. Kang, B. Kim, H.-W. Rhee, and V. N. Kim# (2018) "PKR senses nuclear and mitochondrial signals by interacting with endogenous double-stranded RNAs" ***Mol. Cell***, 71(6):1051–1063.e6
 - Selected as "Research Highlights" in ***Nat. Chem. Biol.***, 14(11):989

4   H. Yi*, **J. Park***, M. Ha, J. Lim, H. Chang and V. N. Kim (2018) "PABP cooperates with the CCR4-NOT complex to promote mRNA deadenylation and block precocious decay" ***Mol. Cell***, 70(6):1081–1088.e5
 - Previewed in ***Mol. Cell***, 70(6):987–988

5   T. A. Nguyen*#, **J. Park***, T. L. Dang, Y.-G Choi, and V. N. Kim# (2018) "Microprocessor depends on hemin to recognize the apical loop of primary microRNA" ***Nucleic Acids Res.***, 46(11):5726–5736

6   K. T. You, **J. Park**, and V. N. Kim (2015) "Role of the small subunit processome in the maintenance of pluripotent stem cells" ***Genes Dev.***, 29(19):2004–2009

7   T. A. Nguyen, M. H. Jo, Y.-G. Choi, **J. Park**, S. C. Kwon, S. Hohng, V. N. Kim# and J.-S. Woo# (2015) "Functional anatomy of the human Microprocessor" ***Cell***, 161(6):1374–1387

8   Y.-K. Kim, G. Wee, **J. Park**, J. Kim, D. Baek, J.-S. Kim#, and V. N. Kim# (2013) "TALEN-based knockout library for human microRNAs" ***Nat. Struct. Mol. Biol.***, 20(12):1458–1464

Links: <u>Google Scholar</u>, <u>PubMed</u>

HONORS AND AWARDS

04/2022 – present   Picower Postdoctoral Fellows, *The Picower Institute for Learning and Memory, MIT*

2021   AKN Outstanding Research Awards, *Association of Korean Neuroscientists*

2019   Conference Scholarship, *Keystone Symposia: Small Regulatory RNAs*

2019   Best Dissertation Awards, *School of Biological Sciences, SNU*

2008 – 2012   Presidential Science Scholarship, *Korea Science and Engineering Foundation*

INTERNATIONAL CONFERENCES

2019   Cell Symposia: Regulatory RNAs — ***short talk***
"Poly(A) barricade as a rate-limiting factor that shapes poly(A) tail length"

2018   CSHL Meeting: Regulatory & Noncoding RNAs — ***short talk***
"PKR senses nuclear and mitochondrial signals by interacting with endogenous dsRNAs"

2017   CSHL Meeting: Eukaryotic mRNA Processing — ***short talk***
"Genome-wide evaluation of the role and specificity of deadenylases"

2016   EMBL Symposium: The Complex Life of mRNA — *poster*

2016   IMBA: 11th Microsymposium on Small RNAs — *poster*

2014   Keystone Symposia: RNA Silencing — *poster*

INVITED TALKS

08/2022   Young Global Leader Symposium – *Department of Chemical and Biological Engineering, KAIST*

07/2022   Department Seminar – *Department of Pharmacology, SNU College of Medicine*

05/2022   Young Investigator Seminar Series – *Department of Biomedical Engineering, UNIST*

TEACHING EXPERIENCE

2022–2023   Kaufman Teaching Certificate Program, *Massachusetts Institute of Technology*

2014   Teaching Assistant, Advanced RNA Biology Lab, *School of Biological Sciences, SNU*

2013   Teaching Assistant, Biology Lab 2, *School of Biological Sciences, SNU*

2012   Teaching Assistant, Biology Lab 1, *School of Biological Sciences, SNU*

2011   Tutor, Basic Course for Biology, *School of Biological Sciences, SNU*

TECHNICAL EXPERTISE

Computational biology

- General skills
  - Unix/Linux environment
  - Programming languages: Python, R, Julia
  - Python scientific libraries: NumPy, SciPy, Pandas, Scikit-learn, etc.
  - Building a custom analysis pipeline: Snakemake, GNU Make
  - Efficient data visualization: Matplotlib, Seaborn, Plotly

- RNA biology
  - (sc)RNA-seq, Ribo-seq, CLIP-seq, ATAC-seq, TAIL-seq, etc.
  - Statistical analysis for genome-wide, transcriptomic studies
  - Tools: Scanpy, Squidpy, Seurat, STAR, Bedtools, Samtools, etc.

- Image processing
  - Concurrent programming for large-scale images
  - 2D/3D rigid and non-rigid biomedical image registration
  - Convolutional Neural Networks
  - Tools: PyTorch, Scikit-image, OpenCV, ImageJ/Fiji, etc.

Wet experiments

- Routine experiment
  - Molecular cloning: Gibson assembly, Golden Gate assembly
  - Mammalian & bacterial cell culture
  - DNA and siRNA transfection
  - Quantitative RT-PCR
  - Immunoprecipitation
  - Western blotting

- RNA biology
  - Custom RNA sequencing library preparation
  - Custom high-resolution poly(A)-tail length assay
  - Tet-On inducible reporter cell line generation
  - RNA co-immunoprecipitation
  - Lentiviral transduction
  - *In vitro* transcription
  - Northern blotting
  - Luciferase reporter assay

- Tissue clearing and expansion
  - SHIELD clearing
  - Expansion microscopy: eMAP