

**Joha Park, Ph.D.****KEY SKILLS & EXPERIENCE**

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

Intellia Therapeutics, Inc.  
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**CURRENT POSITION**

03/2023 – present **Senior Computational Scientist** *Intellia Therapeutics*  
Computational Sciences  
Genomic Innovation  
Intellia Therapeutics, Inc., Cambridge, MA, US (Remote)

**PROFESSIONAL EXPERIENCE**

01/2020 – 03/2023 **Postdoctoral Associate/Fellow** *Massachusetts Institute of Technology*  
3 yrs 3 mos 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  
• Develop methods for hydrogel-based tissue clearing and expansion  
• Build a scalable computational framework for 3D light-sheet microscopy  
• Generate a single-cell mouse brain reference atlas

03/2019 – 12/2019 **Postdoctoral Researcher** *Seoul National University*  
10 months Center for RNA Research (Director: V. Narry Kim)  
Institute for Basic Science  
Seoul National University, Seoul, Korea  
  
Roles  
• Lead projects on mRNA poly(A)-tail length regulations  
• Perform conventional and custom NGS library prep & data analysis  
• Carry out wet and dry lab experiments for 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 (2023) "Short poly(A) tails are protected from deadenylation by the LARP1-PABP complex" **Nat. Struct. Mol. Biol.**, 30(3):330–338
- 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: [Google Scholar](#), [PubMed](#)**HONORS AND AWARDS**

- 2022 – 2023 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

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- 11/2022 Special Seminar – *Yonsei University College of Medicine*
- 08/2022 Young Global Leader Symposium – *Dept. of Chemical and Biomolecular 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

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- 2022 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

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### Computational biology

- General skills
  - Unix/Linux environment
  - Programming languages: Python, R, Rust
  - Python scientific computing libraries: NumPy, SciPy, Pandas, Scikit-learn, etc.
  - Building a custom analysis pipeline: Docker, Snakemake
  - 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, Imaris, etc.

### Wet experiments

- Routine experiment
  - Molecular cloning: Gibson, 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