

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

- Computational Biology: NGS, Imaging, ML
- Sequencing Data Analysis: (sc)RNA-seq, etc.
- Confocal/SPIM Microscopy Imaging Data Analysis
- Python: Numpy, Pandas, Scanpy, PyTorch, etc.

Institute for Medical Engineering and Science
Picower Institute for Learning and Memory
Massachusetts Institute of Technology (MIT)
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CURRENT POSITION

2020.01 – **Postdoctoral Associate**

Chung Lab ([webpage](#)) (Advisor: Kwanghun Chung)
Institute for Medical Engineering and Science
Picower Institute for Learning and Memory
Massachusetts Institute of Technology, Cambridge, MA, US

Roles

- Building a unified analytic framework for 3D light-sheet imaging data analysis in Python
- Developing a new method for hydrogel-based tissue engineering
- Building a single-cell mouse brain reference atlas

PROFESSIONAL EXPERIENCE

2019 **Postdoctoral Fellow**

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

Roles

- Leading a project about mRNA poly(A)-tail length regulations
- Conventional and custom NGS library prep & data analysis
- Wet experiments related to cell and RNA biology

EDUCATION AND TRAINING

2012 – 2019 **Ph.D. in Biological Sciences** (RNA Biology & Bioinformatics)

Dissertation: “Poly(A) length regulation: deadenylases and the poly(A) barricade”
RNA Biology Lab (Advisor: V. Narry Kim)
Seoul National University, Seoul, Korea

2015 – 2018 **Technical Research Personnel** (Compulsory Military Service)

Republic of Korea Army

2008 – 2012 **B.S. in Biological Sciences** (*cum laude*)

Seoul National University, Seoul, Korea

PUBLICATIONS

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

- 1 **J. Park***, M. Kim*, H. Yi*, K. Baeg*, S. Lee, Y.-S. Lee, Y. Jung, J. Lim, V. N. Kim (2021)
“LARP1 decelerates deadenylation by forming a ternary complex with poly(A)-PABP”
(in preparation)

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

[PubMed link](#)

HONORS AND AWARDS

- 2019 Conference Scholarship, *Keystone Symposia: Small Regulatory RNAs*
- 2019 Best Dissertation Award, *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"
- 2019 Keystone Symposia: Small Regulatory RNAs — *conference assistant*
- 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*

FUNDING

2012 – 2018 BK21 Research Scholarship, Ministry of Education, Korea

TEACHING EXPERIENCE

2014 Teaching Assistant, Advanced RNA Biology, *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 (primary), R
 - Building a custom analysis pipeline
 - Efficient data visualization
- RNA biology
 - (sc)RNA-seq, Ribo-seq, CLIP-seq, ATAC-seq, TAIL-seq, etc.
 - Statistical analysis for genome-wide, transcriptomic studies
 - Tools: Pandas, Scanpy, STAR, Bedtools, Samtools, Snakemake, etc.
- Image processing
 - Concurrent programming for large-scale images
 - 2D/3D rigid and non-rigid biomedical image registration
 - Convolutional Neural Networks
 - Tools: Numpy, Scipy, PyTorch, Scikit-learn/image, ImageJ/Fiji etc.

Wet experiments

- Routine experiment
 - Molecular cloning
 - Mammalian & bacterial cell culture
 - DNA and siRNA transfection
 - Quantitative RT-PCR
 - Immunoprecipitation
 - Western blotting
- RNA biology
 - Custom 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