

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

- RNA Biology & Tissue Engineering
- Sequencing Data Analysis: (sc)RNA-seq, etc.
- Confocal/SPIM Microscopy Image Data Analysis
- Python: Pandas, PyTorch, Scikit-learn, etc.

Institute for Medical Engineering and Science  
Picower Institute for Learning and Memory  
Massachusetts Institute of Technology (MIT)  
43 Vassar St, 46-6265, Cambridge, MA 02139, US  
email: [johapark@mit.edu](mailto:johapark@mit.edu)  
webpage: [johapark.github.io](http://johapark.github.io)

**CURRENT POSITION**

2020.01 – **Postdoctoral Associate**  
Chung Lab ([webpage](#)) (Supervisor: Kwanghun Chung)  
Institute for Medical Engineering and Science  
Picower Institute for Learning and Memory  
Massachusetts Institute of Technology, Cambridge, MA, US

**PROFESSIONAL EXPERIENCE**

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

**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 (Supervisor: 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: Scikit-learn/image, PyTorch, Numpy, Scipy, 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