

CURRENT POSITION

School of Biological Sciences, Seoul National University Assistant Professor	2019–present
Center for RNA Research, Institute for Basic Science Research Fellow	2014–present

EDUCATION

Seoul National University Ph. D. in Biological Sciences Dissertation: Transcriptome-wide analysis of poly(A) tail and RNA-protein interaction Advisor: V. Narry Kim, D. Phil.	2009–2014
Korea Advanced Institute of Science and Technology (KAIST) M. S. E. in Bio and Brain Engineering Thesis: Evolution of animal endogenous small RNAs by gene duplication mechanisms Advisor: Dongsup Kim, Ph. D.	2007–2009
Yonsei University B. S. E. in Information and Industrial Engineering	1998–2007

PROFESSIONAL EXPERIENCE

Seoul National University Research Assistant Professor	2014–2019
LinuxKorea, Inc. Software Developer, Solution Development Team	Seoul, Korea 2001–2005

SERVICE AND AFFILIATIONS

Python Software Foundation Fellow	Oregon, USA 2004–present
Python Development Team Committer	Oregon, USA 2002–present
The FreeBSD Project Committer	Colorado, USA 2001–2010

AWARDS

Yumin Awards in Science Yumin Cultural Foundation, Korea	2020
Minister's Commendation for the Advancement of the Korean Software Industry Ministry of Information and Communications, Korea	2007

PUBLICATIONS

* Marked authors contributed equally.

- D. Kim, Y.-S. Lee, S.-J. Jung, J. Yeo, J. J. Seo, Y.-Y. Lee, J. Lim, **H. Chang**, J. Song, J. Yang, J.-S. Kim, G. Jung, K. Ahn, and V. N. Kim. (2020) "Viral hijacking of the TENT4-ZCCHC14 complex protects viral RNAs via mixed tailing." *Nature Structural & Molecular Biology*, 27:581–588.
- D. Kim, J.-Y. Lee, J.-S. Yang, J. W. Kim, V. N. Kim, and **H. Chang**. (2020) "The architecture of SARS-CoV-2 transcriptome." *Cell*, 181:914–921.e10.
- J. Won, S. Lee, M. Park, T. Y. Kim, M. G. Park, B. Y. Choi, D. Kim, **H. Chang**, V. N. Kim, and C. Justin Lee. (2020) "Development of a laboratory-safe and low-cost detection protocol for SARS-CoV-2 of the coronavirus disease 2019 (COVID-19)." *Experimental Neurobiology*, 29:107–119.
- H. Kim, J. Kim, K., Kim, **H. Chang**, K. You, and V. N. Kim. (2019) "Bias-minimized quantification of microRNA reveals widespread alternative processing and 3' end modification." *Nucleic Acids Research*, 47(5):2630–2640.
- J. Lim, D. Kim, Y. Lee, M. Ha, M. Lee, J. Yeo, **H. Chang**, J. Song, K. Ahn, and V. N. Kim. (2018) "Mixed tailing by TENT4A and TENT4B shields mRNA from rapid deadenylation." *Science*, 361:701–704.
- 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." *Molecular Cell*, 70:1081–1088.e5.
- **H. Chang***, J. Yeo*, J.-G. Kim, H. Kim, M. Lee, J. Lim, H. H. Kim, J. Ohk, H.-Y. Jeon, H. Lee, H. Jung, K.-W. Kim, and V. N. Kim. (2018) "Terminal uridylyltransferases execute programmed clearance of maternal transcriptome in vertebrate embryos." *Molecular Cell*, 70:72–82.e7.
- J. Lim, M. Lee, A. Son, **H. Chang**, and V. N. Kim. (2016) "mTAIL-seq reveals dynamic poly(A) tail regulation in oocyte-to-embryo development." *Genes & Development*, 30:1670–1682.
- J.-E. Park, H. Yi, Y. Kim, **H. Chang**, and V. N. Kim. (2016) "Regulation of poly(A) tail and translation during the somatic cell cycle." *Molecular Cell*, 62(3):462–471.
- I. Jang*, **H. Chang***, Y. Jun, S. Park, J. O. Yang, B. Lee, W. Kim, V. N. Kim, and S. Lee. (2015) "miRseqViewer: Multi-panel visualization of sequence, structure and expression for analysis of microRNA sequencing data." *Bioinformatics*, 31(4):596–598.
- M. Kampmann, M. A. Horlbeck, Y. Chen, J. C. Tsai, M. C. Bassik, L. A. Gilbert, J. E. Villalta, S. C. Kwon, **H. Chang**, V. N. Kim, and J. S. Weissman. (2015) "Next-generation libraries for robust RNA interference-based genome-wide screens." *Proceedings of the National Academy of Sciences of the U. S. A.*, 112(26):E3384–E3391.
- S. Kim, D. Seo, D. Kim, Y. Hong, **H. Chang**, D. Baek, V. N. Kim, and K. Ahn. (2015) "Temporal landscape of microRNA-mediated host-virus crosstalk during productive human cytomegalovirus infection." *Cell Host & Microbe*, 17(6):838–851.
- B. Kim, M. Ha, L. Loeff, **H. Chang**, D. K. Simanshu, S. Li, M. Fareh, D. J. Patel, C. Joo, and V. N. Kim. (2015) "TUT7 controls the fate of precursor microRNAs by using three different uridylation mechanisms." *EMBO Journal*, 34(13):1801–15.

- J. Lim*, M. Ha*, **H. Chang***, S. C. Kwon, D. K. Simanshu, D. J. Patel, and V. N. Kim. (2014) "Uridylation by TUT4 and TUT7 marks mRNA for degradation." *Cell*, 159(6):1365–1376.
- **H. Chang***, J. Lim*, M. Ha, and V. N. Kim. (2014) "TAIL-seq: genome-wide determination of poly(A) tail length and 3' end modifications." *Molecular Cell*, 53(6):1044–1052.
- M. Lee*, S. Han*, **H. Chang***, Y.-S. Kwak, D. M. Weller, and D. Kim. (2013) "FitSearch: a robust way to interpret a yeast fitness profile in terms of drug's mode-of-action." *BMC Genomics*, 14(Suppl 1):S6.
- S. Han, M. Lee, **H. Chang**, M. Nam, H.-O. Park, Y.-S. Kwak, H. Ha, D. Kim, S.-O. Hwang, K.-L. Hoe, and D.-U. Kim. (2013) "Construction of the first compendium of chemical-genetic profiles in the fission yeast *Schizosaccharomyces pombe* and comparative compendium approach." *Biochemical and Biophysical Research Communications*, 436(4):613–618.
- J. Cho*, **H. Chang***, S. C. Kwon, B. Kim, Y. Kim, J. Choe, M. Ha, Y. K. Kim, and V. N. Kim. (2012) "LIN28A is a suppressor of ER-associated translation in embryonic stem cells." *Cell*, 151(4):765–777.
- S. Cho, I. Jang, Y. Jun, S. Yoon, M. Ko, Y. Kwon, I. Choi, **H. Chang**, D. Ryu, B. Lee, V. N. Kim, W. Kim, and S. Lee. (2012) "miRGator v3.0: a microRNA portal for deep sequencing, expression profiling and mRNA targeting." *Nucleic Acids Research*, 41(D1):D252–D257.
- I. Heo, M. Ha, J. Lim, M.-J. Yoon, J.-E. Park, S. C. Kwon, **H. Chang**, and V. N. Kim. (2012) "Mono-uridylation of pre-microRNA as a key step in the biogenesis of group II let-7 microRNAs." *Cell*, 151(3):521–532.
- J.-E. Park, I. Heo, Y. Tian, D. K. Simanshu, **H. Chang**, D. Jee, D. J. Patel, and V. N. Kim. (2011) "Dicer recognizes the 5' end of RNA for efficient and accurate processing." *Nature*, 475(7355):201–205.
- **H.-S. Chang**, K. Hwang, and D. Kim. (2007) "Discovering *cis*-regulatory elements by combining multiple predictors." *Bioinformatics and Biosystems*, 6(2):57–64.