**Curriculum Vitae**

**1. Personal Information**

Name and Contact

Jin-Wu Nam, PhD

Department of Life Science, College of Natural Sciences

Hanyang Univ. Seoul, 133-791

Tel: (82) 2-222—2428

Email: [jwnam@hanyang.ac.kr](mailto:jwnam@hanyang.ac.kr)

Homepage: http://big.hanyang.ac.kr

Academic Appointments at HYU

Associate Professor (2016.09~)

Assistant Professor (2012.09~2016.08)

Other Employment

Postdoctoral fellow, MIT, HHMI, Whitehead Institute for Biomedical Research (2008~2012)

Postdoctoral fellow, Seoul National University (SNU), MicroRNA Research Center (2007)

Researcher, Center for Bioinformation Technology (CBIT), SNU (2002-2007)

Educational Background

Sep, 2004. ~ Aug, 2007. Ph.D. in Bioinformatics, Seoul National University

Sep, 2002 ~ Aug, 2004. ME in Bioinformatics, Seoul National University

Mar, 1994 ~ Feb, 2001. BS in Biology, Yonsei University

**2. Research Activities (since 2012)**

Publications

(a) List of journal publications

[Corresponding Authorship]

**1.** Bohyun You\*, Jungho Yoon\*, Hoin Kang, Eun kyung Lee, Sangil Lee#, and **Jin-Wu Nam#,** HERES, a lncRNA that Regulates Canonical and Noncanonical Wnt Signaling Pathways via Interaction with EZH2, *Proceedings of the National Academy of Sciences*, 2019. https://doi.org/10.1073/pnas.1912126116.

**2.** Jeongyoon Park\*, Jwa-Won Seo\*, NaraeAhn, Seokju Park, Jungwook Hwang#, and **Jin-Wu Nam#**. UPF1/SMG7-dependent MicroRNA-mediated Gene Regulation, *Nature Communications*, 10:4181, 2019.

**3.** Hyeon Lee\*, Ramu Gopalappa\*, Hongjae Sunwoo\*, Seowon Choi, Suresh Ramakrishna, Jeannie Lee, Hyongbum (Henry) Kim#, **Jin-Wu Nam#**, *En bloc* and segmental deletions of human XIST reveal X chromosome inactivation-involving RNA elements, *Nucleic Acids Res.,* 47:8, 3875–3887, 07 May 2019.

**4.** Hyosun Hong\*, Han-Ha Chai\*, Kyoungwoo Nam, Dajeong Lim, Kyung-Tai Lee, Yoon Jung Do, Chang-Yeon Cho and **Jin-Wu Nam**, HSF2 Co-regulates Protein-coding and Long Non-coding RNA Genes Specific to Black Tissues of the Black Chicken, Yeonsan Ogye, *International Journal of Molecular Sciences*, 19(8),2359. 2018.

**5.** Jang-il Sohn\*, Kyoungwoo Nam\*, Hyosun Hong\*, Jun-Mo Kim\*, Dajeong Lim,Kyung-Tai Lee, Yoon Jung Do, Chang Yeon Cho, Namshin Kim, Han-Ha Chai# and **Jin-Wu Nam#** Whole genome and transcriptome maps of the entirely black native Korean chicken breed Yeonsan Ogye, *GigaSciences*, giy086, 2018.

**6.** Seo-Won Choi\*, Hyunwoo Kim\*, and **Jin-Wu Nam,** The small peptide world in long non-coding RNAs, *Briefings in Bioinformatics*, bby055, [https://doi.org/10.1093/bib/bby055, 2018](https://doi.org/10.1093/bib/bby055).

**7.** Seo-Won Choi and **Jin-Wu Nam**, TERIUS: accurate prediction of lncRNA via high-throughput sequencing data representing RNA binding protein association. *BMC Bioinformatics*, 19 (Suppl 1):41, 2018.

**8.** Jang-il Sohn and **Jin-Wu Nam**, The Present and Future of De Novo Whole Genome Assembly, *Briefings in Bioinformatics*, 19(1):23-40. 2018.

**9.** Bo-Hyun You, Sang-Ho Yoon, and **Jin-Wu Nam,** High-Confidence Coding and Noncoding Transcriptome Maps. *Genome Res*. 27:1050-1062, 2017.

**10.** Kyung-Tae Lee and **Jin-Wu Nam,** Post-transcriptional and translational regulation of mRNA-like long non-coding RNAs by microRNAs in early developmental stages of zebrafish embryos. *BMB Rep*. pii: 3769, 2017.

**11. Jin-Wu Nam**, Seo-Won Choi, and Bo-Hyun You, Incredible RNA: Dual Functions of Coding and Noncoding. *Mol. Cells*. 39(5):367-374. 2016.

**12.** Kyoungwoo Nam, Heesu Jeong, and **Jin-Wu Nam**. Pseudo-Reference-Based Assembly of Vertebrate Transcriptomes. *Genes*, 7:10, 2016.

**13**. Jiwon Shim and **Jin-Wu Nam**. The expression and functional roles of microRNAs in stem cell differentiation. *BMB reports,* 49(1): 3-10, 2016.

**14.** MinHyeok Kim, Bo-Hyun You, and **Jin-Wu Nam**. Global Estimation of the 3' Untranslated Region Landscape Using RNA Sequencing. *Methods*, 83:111-117, 2015.

**15.** JuneHyun Park, Soungyub Ahn, Soyoung Kim, Junho Lee, **Jin-Wu Nam#**, Chanseok Shin# Degradome sequencing reveals an endogenous microRNA target in *C.elegans*, *FEBS Letters,* [587(2013)](http://www.sciencedirect.com/science/article/pii/S0014579313001610)964-969, 2013.

[First Authorship]

**1. Jin-Wu Nam,** O. Rissland, D. Kopstein, V. Agarwal, C. Jan, M. Yildrim and D. Bartel, Global analyses of the effect of different cellular contexts on microRNA targeting, *Mol Cell*, 53(6), 1031–1043, 2014.

**2. Jin-Wu Nam** and D. Bartel, Long non-coding RNAs in *C.elegans*. *Genome Research*. 22: 2529-2540, 2012.

[Co-authorship]

**1.** Krishnamoorthy Srikanth, Nam-Young Kim, WonCheoul Park, …,Gul-Won Jang, Heebal Kim, Youn-Chul Ryu, **Jin-Wu Nam,** Jong-Eun Park, Jun-Mo Kim & Dajeong Lim. Comprehensive genome andtranscriptome analyses reveal genetic relationship, selection signature, and transcriptome landscape of small-sized Korean native Jeju horse. *Scientific Reports*, 9:16672,2019.

**2.** Jun-Bean Park, ..., Jae-Hoon Choi, **Jin-Wu Nam,** Hyung-Kwan Kim,Yun-Sang Lee, Jae Min Jeong, Yong-Jin Kim, Jin Chul Paeng, and Seung-PyoLee. Assessment of inflammation in pulmonary artery hypertension by68Ga-Mannosylated Human serum albumin. *American Journal of Respiratory and Critical Care Medicine*, 2019.

**3.** Incheol Ryu, Yeonkyoung Park, Jwa-Won Seo, Ok Hyun Park, Hongseok Ha, **Jin-Wu Nam** and Yoon Ki Kim. HuR stabilizes apolyadenylated form of replication-dependent histone mRNAs under stress conditions. [*FASEB J*.](https://www.ncbi.nlm.nih.gov/pubmed/30303743) 33(2):2680-269, 2019.

**4.** Kyeongdae Kim, Dahee Shim, Jun Seong Lee, KonstantinZaitsev, Jesse W Williams, Ki-Wook Kim, Man-Young Jang, Hyung Seok Jang, Tae Jin Yun, Seung Hyun Lee, Won Kee Yoon, Annik Prat, Nabil G Seidah ,Jungsoon Choi, Seung-Pyo Lee, Sang-HoYoon, **Jin Wu Nam** ,Je Kyung Seong, Goo Taeg Oh, Gwendalyn Randolph, Maxim N Artyomov, CheolhoCheong, and Jae-Hoon Choi, Transcriptome Analysis Reveals Non-Foamy Ratherthan Foamy Plaque Macrophages Are Pro-Inflammatory in Atherosclerotic Murine Models, *Circulation Res*. 2018.

**5.** Jung-Ho Yoon, Bo-Hyun You, ChanHyuk Park, Yeong Jin Kim, **Jin-Wu Nam**, and Sang Kil Lee. The long noncoding RNA LUCAT1 promotes tumorigenesis bycontrolling ubiquitination and stability of DNA methyltransferase 1 in esophageal squamous cell carcinoma. *Cancer Letters*, [417:47-57](https://www.sciencedirect.com/science/journal/03043835/417/supp/C), 28 March 2018[.](https://doi.org/10.1016/j.canlet.2017.12.016)

**6.** Dooyoung Lee, **Jin-Wu Nam**, and Chanseok Shin, DROSHA targets its own transcript to modulate alternative splicing. *RNA*, 23(7):1035-1047, 2017.

**7.** HuiKwon Kim, Myungjae Song, Jinu Lee, Adrussery. Vipin Menon, Soobin Jung, Young-Mook Kang, Euijeon Woo, **Jin-Wu Nam**, and Hyongbum (Henry) Kim. In vivo high-throughput profiling of CRISPR-Cpf1 activity based on target sequence composition. *Nature Methods*. 14:153-197, 2017.

**8.** Youngjune Park, Sangsoo Lim, **Jin-Wu Nam**, and Sun Kim. Measuring intra tumor heterogeneity by network entropy using RNA-seq data. *Sci. Rep.* 6, 37767; doi: 10.1038/srep37767. 2016.

**9.** Yong-HeeRhee, Tae-Ho Kim, A-Young Jo, Mi-Yoon Chang, Chang-Hwan Park, Snag-Mi Kim,Jae-Jin Song, Sang-Min Oh, Sang-Hoon Yi, Bo-HyunYou, Hyoen-Ho Kim, **Jin-Wu Nam**, and Sang-Hun Lee, Lin28a enhances the therapeutical potential of culturedneural stem cells in a Parkinson’s disease model. *Brain*, 139 (Pt10):2722-2739, 2016.

**10.** Hoin Kang, Chongtae Kim, Heejin Lee, Jun Gi Rho, Jwa-Won Seo, **Jin-Wu Nam**, Woo Keun Song,Suk Woo Nam, Wook Kim and Eun Kyung Lee, Downregulation of microRNA-362-3p and microRNA-329 promotes tumor progression in human breast cancer. *Cell Death &Diff*., 23(3):484-95. 2016.

**11.** Vikram Agarwal, George W. Bell, **Jin-Wu Nam**, David P.Bartel, Predicting effective microRNA target sites in mammalian mRNAs. *eLife*, 4:e05005. 2015.

(b) Citations and impact analysis of research output

스크린샷이(가) 표시된 사진

자동 생성된 설명

Table 1. Citation report by Google scholar, Dec. 3rd, 2019.

https://scholar.google.com/citations?user=zRXiAkEAAAAJ&hl=en

Sponsored Research (since 2012)

(a) Grants and Contracts

1. External Research Grants from Government

[Terminated]

**1.** Annotation system of long non-coding RNAs through heterogenous transcriptomic datasets, the Ministry of Science and ICT, *(2013.6.1.~2013.12.31.) ($45K)*

**2.** Identification and characterization of cancer-related mammalian long non-coding RNAs using the next-generation sequencing technology, the Ministry of Science and ICT, *(2013.6.1.~2016.5.31.) ($159K)*

**3.** Analyses of Genomic/Transcriptomic Characteristics of Native Domestic Animals Using Next-Generation Sequencing, the Rural Development Administration, Co-PI *(2014.3.1.~2017.12.31.), ($720K)*

**4.** Development of Standard Operating Procedures for Cancer Transcriptome and Epigenome Analyses, Public Health Administration, Co-PI *(2016.12.1.~2018.11.30.), ($325K).*

**5.** Investigation of the liver disease mechanism based on bioinformatics, the Ministry of Science and ICT,, Co-PI, *(2014.11.30.~2017.11.29.), ($300K).*

[Ongoing]

**1.** Development of Bioinformatics Platform for Genome Analyses, the Ministry of Science and ICT,, Co-PI, *(2014.1.1.~2021.12.31.), ($560K)*

**2.** Convergence Research of Echo-Biology, Education Program, Education Administration *(2014.3.1.~2021.6.30.), ($240K).*

**3.** Development of high-precision and high-performance multiomics cancer genome analysis software for targeted therapeutics and certification for clinical application, Public Health Administration, Co-PI, *(2015,12.1~2021.11.30.), ($830K).*

**4.** Development of the Next-Generation Genomic Cytometry, the Ministry of Science and ICT, Co-PI, *(2017.11.1.~2022.12.31.), ($900K).*

**5.** Studying alternative splicing of long non-coding RNAs that causes cancers, the Ministry of Science and ICT,, PI, *(2018.3.1.~2021.2.28.), ($500K).*

Patents (since 2012)

**1.** Detection Method And Detection Apparatus for DNA Structural Variations Based On Multi-reference Genomes, 2018. PCT.

**2.** Marker predicting liver cancer recurrence in patients with liver transplantation prescription and uses thereof, 2019. Korea.

**3.** Markers for diagnosticor prognosis predictive of squamous cell carcinoma and uses thereof, 2019. Korea.

**4.** Pharmaceutical composition for preventing or treating squamos cell carcinoma containing expression inhibitor of HERES, 2019. Korea.

**3. Teaching, Mentoring, and Advising**

Teaching Philosophy

***“Constructive criticism and questions will challenge current beliefs but build new knowledge in the future.”***

My main teaching principle is to promote the development of critical thinking through a series of steps: (1) motivate students with real-world problems; (2) help students understand complex ideas with simplified, concrete examples; (3) facilitate the acquisition of critical-thinking skills in the context of these problems; (4) help students develop new ideas about how to solve problems and then implement these ideas; and (5) assess their outcomes and provide feedback.

These teaching steps have several advantages: (1) they allow students to actively engage in the class; (2) they promote a deeper understanding of how theories are utilized in real-world contexts; and (3) they help develop a student’s abilities to think scientifically in future careers.

Courses Taught

[Undergraduate program]

Bioinformatics (2014-2, 2015-2, 2016-2, 2017-2, 2018-2), 3 credits, (PBL)

Computational Biology (2015-1, 2016-1, 2017-1, 2018-1), 2 credits, (PBL)

Genetics (2014-2, 2015-1), 3 credits

Molecular Biology (2018-2), 2 credits

Biochemistry (2014-1), 3 credits

General Biology (2014-2, 2015-2, 2016-1, 2017-2), 1 credit

[Graduate program]

Programming in Bioinformatics (2014-1, 2016-1, 2018-1), 3 credits

Advanced Bioinformatics (2016-1, 2018-1), 3 credits

Next-Generation Genome Data Analysis (2012-2, 2013-2, 2014-2, 2015-2, 2017-2), 3 credits

Bioinformatics Seminar (2014-2, 2016-2, 2018-2), 3 credits

Sequence Analysis Algorithm (2013-1, 2013-2), 3 credits

Course or Curriculum Development

Course Introduction: <https://coya75.wixsite.com/biglab/courses>

(A) *Computational Biology:* Intended for undergraduate students, this class introduces topics of general interest and challenging real-world problems in computational biology and medicine. (B) *Bioinformatics:* Intended for senior undergraduate and junior graduate students, this class introduces the basic skills needed to deal with discrete numerical values, categorical values, and sequences in biology and medicine using Python and R programming. The class covers core bioinformatic topics, such as distance metrics, similarity metrics, clustering, classification, sequence alignment, gene prediction, RNA structure, and protein structure. (C) *Analysis of Next-Generation Genomic Data*: Intended for graduate students at all levels in the program, this is a project-based class in which each student tackles a specific problem in medical, genomic, or transcriptomic data analysis. The course begins with lectures that cover statistical methods for combining heterogeneous data, classifying labeled data, and clustering unlabeled data. (D) *Sequence Analysis Algorithms:* This course is intended for graduate students at all level and covers sequence-alignment algorithms, motif-finding algorithms, secondary-structure prediction algorithms, and high-throughput sequencing data analyses. (E) *Programming in Bioinformatics*: This course provides opportunities for students to learn shared concepts, languages, and skills that biologists must have to operate in a collaborative, inter-disciplinary mode. The goal is to educate students studying bio-related topics (including biology, biotechnology, and medicine) who have little or no experience in bioinformatics, computational biology, or computer programming. The prerequisite for this class is at least a basic knowledge of biology and genomics.

Individual Student Guidance

*Past Master’s students:*

Hyunjoo Lee (Seegen, inc), Jwawon Seo (Univ. of Maryland, PhD course), Hyosun Hong (Medical School, Korea Univ., Researcher), Kyungwoo Nam (LabGenomics, inc), HyeonYoon Cho (KNIH, Researcher).

*Past Postdoctoral fellows:*

Youngmook Kang, PhD (KBSI, Researcher)

MinHyeok Kim, PhD (LG CTO)

*Current Master’s students:*

Seongjin Pyo, Eunkyung Park, Youxi Cui

*Current Doctoral students:*

Bo-Hyun You, Seowon Choi, Vipin Menon, Minhak Choi, Sangho Yoon, Seokju Park, Dohun Lee, Kyeongtae Lee, Hyeonwoo Kim

*Current Postdoctoral fellows:*

Jangil Sohn, PhD (current member)

*Undergraduate interns:*

Twenty four students have attended our research intern program so far.

**4. Service and Outreach**

Editorships, Editorial Boards, and Reviewing Activities

(a) Editorships

*Genes and Genomics*, Associate Editor (2018~)

*Animal Cells and Systems*, Editor (2018~)

(b) Reviewer for Journals and Presses (ad hoc review)

*Nature Genetics*

*Cell*

*Cell Reports*

*eLife*

*Genome Research*

*Nature Communications*

*Nucleic Acids Research*

*Molecules and Cells*

*Oncogene*

*Scientific Reprots*

*Briefings in Bioinformatics*

*Bioinformatics*

*BMC Bioinformatics*

External Service and Consulting

(a) Technology review for biotechnology company IPOs (three companies)

(b) Review board for biology text book (middle and high schools)

Committees, Professional, and Campus Service

(a) Committee

CSBio program committee (2013~2016)

TBC program committee (2013~)

GIW/BIOINFO committee (2017)

TBC/BIOINFO program chair (2018)

KSMCB program chair (2016, 2017)

APBC2020 program committee (2020)

(b) Compus service

Graduate Fair Management Committee

Invited Lectures (International)

Keystone Symposia, Long Noncoding RNAs, Speaker (Whistler), 2019

IBS RNA Symposium, Speaker (Seoul), 2018

KSMCB RNA Symposium, Speaker (Kyeongjoo), 2018

Ewha-Jax Joint Symposium, Speaker (Seoul), 2018

East Asia Genomics Symposium, Speaker, (Jeonjoo), 2017

Univ. of Bern, Invited speaker (Bern), 2017

Korea-China-Japan Tri-Bioinformatics Symposium, Speaker, (Seoul), 2017

IBS-CNRS Joint Symposium on RNA Biology, Speaker, (Seoul), 2016

KOGO international conference, Speaker (Seoul), 2014

  PAGGI Conference, Speaker (Kwanggyu), 2013

KSMCB International Conference, Speaker, (Seoul), 2013

BMS/Illumina Symposium, Speaker (Seoul), 2012

Keystone Symposia, Noncoding RNAs, Speaker (Utah), 2012

**5. Awards, Honors, and Recognition**

BlueRibbon Lecture Award, Korea Society for Molecular Cell Biology, 2020

Interactional Exchange Program Award, LG YeonAm Foundation, 2018

Outstanding Research Award, Korea Society for Bioinformatics, 2018

RNA meeting Poster Award (UC Berkeley), 2018

Outstanding Research Award, Research Center for Natural Sciences at HYU, 2016

**6. Representative Achievement Summary**

My team has developed machine-learning-based methods to identify non-coding transcripts (Choi and Nam, 2018, *BMC Bioinfo.*; Choi et al., 2018, *Briefings in Bioinfo.*) and to predict the 3'-end of transcripts (Kim et al., *Methods*, 2015); we have also focused on reconstructing coding and non-coding transcriptome maps for humans (You et al., *Genome Res*. 2017) and other vertebrates (Hong et al.,*IJMS*, 2018). To further understand the interaction between coding and non-coding elements and the associated regulatory mechanisms, we have developed an efficient CRISPR/Cas system (Kim et al., 2017, *Nature Methods*), which was applied in a study of human *XIST*, a non-coding RNA that acts in X chromosome inactivation, and led to the identification of functional elements in human *XIST* (Lee et al., *Nucleic Acids Res*. 2019). We also identified a novel long non-coding RNA gene that regulates Wnt signaling pathways during the development of squamous cell-type carcinoma (You et al., 2019 *PNAS*), and uncovered a novel UPF1-dependent microRNA-mediated mRNA decay pathway (Park et al., 2019, *Nature Comm*.). Recently, my team has expanded our research interests to genome assembly (Sohn et al., 2018, *GigaScience; Sohn et al., 2018, Briefings in Bioinfo.)*, detection of genomic variations (*in preparation*), and single-cell transcriptome studies (*in preparation*).

List of Representative Publications

**1.** HERES, a lncRNA that Regulates Canonical and Noncanonical Wnt Signaling Pathways via Interaction with EZH2, *Proceedings of the National Academy of Sciences*, 2019.

**2.** UPF1/SMG7-dependent MicroRNA-mediated Gene Regulation, *Nature Communications*, 10:4181, 2019.

**3.** *En bloc* and segmental deletions of human XIST reveal X chromosome inactivation-involving RNA elements, *Nucleic Acids Res.,* 47:8, 3875–3887, 2019.

**4.** Whole genome and transcriptome maps of the entirely black native Korean chicken breed Yeonsan Ogye, *GigaSciences*, giy086, 2018.

**5.** The small peptide world in long non-coding RNAs, *Briefings in Bioinformatics*, bby055, [https://doi.org/10.1093/bib/bby055, 2018](https://doi.org/10.1093/bib/bby055).

**6.** HSF2 Co-regulates Protein-coding and Long Non-coding RNA Genes Specific to Black Tissues of the Black Chicken, Yeonsan Ogye, *International Journal of Molecular Sciences*, 19(8),2359. 2018.

**7.** TERIUS: accurate prediction of lncRNA via high-throughput sequencing data representing RNA binding protein association. *BMC Bioinformatics*, 19 (Suppl 1):41, 2018.

**8.** High-Confidence Coding and Noncoding Transcriptome Maps. *Genome Res*. 27:1050-1062, 2017.

**9.** The Present and Future of De Novo Whole Genome Assembly, *Briefings in Bioinformatics*, 19(1):23-40. 2018.

**10.** Pseudo-Reference-Based Assembly of Vertebrate Transcriptomes. *Genes*, 7:10, 2016.