Hyunmin Kim, Ph.D.

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PROFESSIONAL SUMMARY

- Computational biologist with 20+ years of experience in regulomics, RNA processing, and 3D genomics.

- Author of 30+ publications, including first-author papers in Nature Structural & Molecular Biology, Genes & Development, and Molecular Cell.

- Specialized in the integrative analysis of multi-omic data—including RNA-seq, ChIP-seq, HiChIP, and CNV—to dissect gene-regulatory mechanisms and drug effects at single-cell and spatial resolution.

- Developer of multiple open-source bioinformatics pipelines for 3D genome modeling, alternative splicing, and epigenomic analysis.

- Proven experience in mentorship, cross-disciplinary collaboration, and HPC/cloud-based pipeline development (GCP, Terra, Docker, Nextflow).

EDUCATION

- Postdoctoral Research Fellow (2009–2012) **–** Biochemistry & Molecular Genetics, University of Colorado School of Medicine, Aurora, CO

- Ph.D., Bioinformatics (2004–2009) **–** University of Colorado Denver School of Medicine, Aurora, CO

- M.S., Computer Science (2000–2002) **–** Gwangju Institute of Science & Technology (GIST), Korea Full Government Scholarship Recipient

- B.S., Computer Engineering (1993–2000) **–** Inha University, Korea

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PROFESSIONAL EXPERIENCE

- **Senior Research Associate – Specialized Technical Skills (2021–Present),** *Department of Genetics and Genome Sciences, Case Western Reserve University, Cleveland, OH* :
  - Lead development of CNV-integrated and 3D chromatin–aware ChIP-seq/HiChIP pipelines for enhancer–promoter architecture analysis.
  - Conduct integrative multi-omics (WGS, ATAC-seq, RNA-seq, HiChIP) across neural differentiation and cancer models, including mCRPC and lung/COPD.
  - Mentor trainees and contribute to NIH-funded studies on transcriptomic misregulation and clonal hematopoiesis.

- **Chief Technology Officer (2021) –** *KURE.AI, Seoul, Korea :*
  - Directed development of AI-driven biomedical data-mining tools for translational genomics and disease-signature discovery single-cell splicing.
  - Built Google Cloud–based pipelines and scalable data-storage systems for multi-omics and single-cell datasets.

- **Staff Scientist (Faculty) (2020-2021) – Center for Immunotherapy & Precision Immuno-Oncology**
  Cleveland Clinic Lerner Research Institute, Cleveland, OH
  - Led computational analysis team integrating single-cell, spatial transcriptomics, and bulk RNA-seq to support immuno-oncology research and clinical translation initiatives.

- **Senior Research Instructor (2012–2020) – Core Faculty, University of Colorado Cancer Center & School of Medicine**
  - Developed computational tools for alternative splicing and polyadenylation detection; co-led multi-lab studies on transcription termination and enhancer regulation. Served as Bioinformatics Lead and Co-Investigator on NIH/NCI and V Foundation grants.

- Adjunct Professor (2015-2019), UNIST, S. Korea

- Researcher (2002-2003), KOBIC, S. Korea | 2002–2003

- Military Service (1995-1997), S. Korea

SELECTED PROJECTS & PIPELINES

- Fossil-C (2023–Present): Ultra-ancient Dinosaur DNA/peptide integration pipeline (https://github.com/hmgene/fossil-c).
- Exosome-scRNA-organoid (2025-Present): Exosome mutation effects on cerebellum development, parse-seq single-cell (https://github.com/hmgene/derrick)
- CoReA (2022–Present): Core-regulatory association framework with HiChIP-based 3D topology (https://github.com/hmgene/coreA).

- 3D Chromatin Remodeling in mCRPC (2023–2024): Quantified epigenetic vulnerabilities under AR antagonist therapy using AQuA-HiChIP. PMC11621760
- 3D Peak Pipeline (peaks3D, 2022–2023): 3D Enhancer–promoter clustering and Pol2 hub mapping (https://github.com/hmgene/peaks3d).
- Aqua-tools: Collection of HiChIP pipelines and visualization (2024-2025) (https://github.com/axiotl/aqua-tools)
- EPi-Select (2021–present): Single-cell analytics for lung SCC progenitor malfunction (https://github.com/hmgene/EPIselect).
- Alternative Splicing & APA Tools integrable to single-cell: exonblox, APAchi for splicing quantification and APA regulation.

RESEARCH FUNDING & ROLES

- NIH/NCI R01CA219893 (Ghosh) | 09/01/2017 – 08/31/2022 | **Progenitor cell malfunction, mutations and changes in microenvironment**: a dynamic risk spectrum for cancer
  - Role: Key personnel : The goal of this project is to find out a common cause of cancer mortality and a neoplasm for which there is considerable evidence supporting an origin from a premalignant field on squamous cell lung cancer (SCC)

- V Foundation (Victory Over Cancer) Translational Research Award (Miller) | 11/01/2017- 10/31/2020 **Precision Chemoprevention of Lung Cancer**
  - Role : Key personnel : In this project, our patient-derived progenitor cultures will allow a patient's own progenitor cells to be tested for response before treatment even begins in the clinic, a major step towards precision chemoprevention.

- NIH/NHLBI 1R13HL142192-01 (Vandivier) | 05/01/2018 - 4/30/2019
  - Role: Co-investigator Aspen Lung Conference on COPD: **Translating Resilience and Pathogenesis to Personalized Therapy for COPD**

- NIH/NCI P30 CA046934 (Theodorescu) | 02/01/2017 – 01/31/2022
  - Role: Core Member, **Cancer Center Support Grant** – Bioinformatics Core : The goal of this development grant is to provide bioinformatics support to the University of Colorado Cancer Center Investigator.

- DOD W81XWH-18-1-0172 (Jedlicka)|07/15/2018 – 07/14/2020
  - Role:Key personnel, **Identification of Novel Epigenetic Modifiers of Metastasis Progression in Ewing Sarcoma:** The goal of this project is to execute and perform preliminary validation of an in vivo shRNA screen for novel epigenetic modifiers controlling metastasis of Ewing Sarcoma.

- NIH/NIGMS R01GM110064 (Ranish/Taatjes/Bentley) | 09/22/2016 – 05/31/2020
  - Role: Co-Investigator : **TFIIH and Transcription Regulation**. The goals of this project are to establish a structural and mechanistic understanding of how TFIIH controls basic transcriptional events such as promoter opening, pol II pausing, and mRNA processing.

- Cancer League of Colorado (Hyunmin Kim,PI) | 07/01/2017-06/30/2018
  - Role: Principal Investigator : **Systematic Alternative Splicing Analysis for Transcriptomic Misregulation in Cancer**. The goal of this project is to develop a computational system for analyzing and interpreting alternative splicing and resultant mRNA variants in cancer.

- NIH/NCI P30 CA046934   (Theodorescu, PI) | 02/01/2014 – 01/31/2017
  - Role: Core Investigator, **Cancer Center Support Grant** – Biostatistics and Bioinformatics Core. The goal of this development grant is to provide bioinformatics and biostatistics support to the University of Colorado Cancer Center Investigator in their research projects, and to facilitate collaboration.

TEACHING & MENTORSHIP

- Instructor: CANB7640 – Practical Bioinformatics for Large-Scale Genomics, Univ. of Colorado Denver, 2017

- TA: Gene520 Bioinformatics, CWRU, 2025

- TA: Introductory/Advanced Bioinformatics, Univ. of Colorado, 2005–2006

- Mentored graduate students and postdocs across multiple U.S. and international labs.

HONORS & MEMBERSHIPS

- BRIC HanBitSa Nominations: 2010, 2011, 2014

- F1000 Prime Recommendation, 2012

- Founder, Korean Bioinformatics Community (>3,900 members)

- Member: ISCB, RNA Club (CU Denver), CCTSI Bioinformatics Journal Club

CORE TECHNICAL EXPERTISE

- **Bioinformatics & Genomics: RNA-seq, scRNA-seq, ChIP-seq, HiChIP, ATAC-seq, CNV, methylation**

- **Programming: R, Python, Perl, C++, SQL, data.table, pandas**

- **Platforms: GCP, Terra, Nextflow, Docker, HPC, GitHub CI/CD**
  Statistics: GAM-NB models, differential peak analysis, covariate integration (GC, mappability)

- **Visualization: IGV, Gviz, UCSC tracks, R-based plotting**

PUBLICATIONS

(Full list: https://scholar.google.com/citations?user=-UAQUkEAAAAJ)

2025

- Chakraborty, M. et al. (including L. Morgan, Q. Scacheri, A. D'Yan, **H. Kim**, Y. Asante, and D. Chin). AQuA Tools: clear and reliable BEDPE operations for 3D genomics. *Bioinformatics* **41** (9), btaf510.

2024

- Kohrt, S. E. et al. (including E. J. Novak, S. Tapadar, B. Wu, J. Strope, Y. Asante, **H. Kim**, and D. Chin). Small-molecule disruption of androgen receptor–dependent chromatin clusters. *Proc Natl Acad Sci* **121** (48), e2406239121.
- Groves, A. et al. (including R. Poetschke, T. Wang, D. H. Chin, Y. Asante, **H. Kim**, and S. Gu). DIPG-28. CHEMOGENOMIC PROFILING OF HDAC ISOFORMS... *Neuro-Oncology* **26** (Suppl 4), 0. (Abstract)
- Wahdan-Alaswad, R. S. et al. (including S. M. Edgerton, **H. Kim**, A. C. Tan, B. R. Haugen, B. Liu, and G. A. Fincher). Thyroid hormone enhances estrogen-mediated proliferation and cell cycle regulatory pathways in steroid receptor-positive breast Cancer. *Cell Cycle* **23** (7-8), 747–766.

2023

- Asante, Y. et al. (including K. Benischke, I. Osman, Q. A. Ngo, J. Wurth, D. Laubscher, **H. Kim**, and D. Chin). PAX3-FOXO1 uses its activation domain to recruit CBP/P300 and shape RNA Pol2 cluster distribution. *Nature Communications* 14 (1), 8361.
- Miller, Y. E. et al. (including M. Ghosh, D. T. Merrick, B. Kubala, E. Szabo, L. Bengtson, and **H. Kim**). Phase Ib trial of inhaled iloprost for the prevention of lung cancer with predictive and response biomarker assessment. *Frontiers in Oncology* 13, 1204726.
- Bitler, W. Z. L. et al. (including B. G., Bailey C. A., Yamamoto T. M., McMellen A., and **H. Kim**). Targeting BRPF3 moderately reverses olaparib resistance in high grade serous ovarian carcinoma. *Mol Carcinog*.
- Kim, S. H. et al. (including M. J. Kim, M. Lim, J. Kim, **H. Kim**, C. K. Yun, Y. J. Yoo, and Y. Lee). Enhancement of the anticancer ability of natural killer cells through allogeneic mitochondrial transfer. *Cancers* 15 (12), 3225.
- Gryder, B. E. et al. (including D. Chin, **H. Kim**, and I. Osman). Histone acetylation axis in the control of RNA Pol2 clusters. *Cancer Research* 83 (7_Supplement), 3726–3726. (Abstract)
- Chin, D. H. et al. (including I. Osman, J. Porch, **H. Kim**, K. K. Buck, J. Rodriguez, and B. Carapia). BET bromodomain degradation disrupts function but not 3D formation of RNA Pol2 clusters. *Pharmaceuticals* **16** (2), 199.

2022

- Boe, D. M. et al. (including H. J. Hulsebus, K. M. Najarro, J. E. Mullen, **H. Kim**, and A. C. Tan). Advanced age is associated with changes in alveolar macrophages and their responses to the stress of traumatic injury. *J Leukoc Biol* **112** (6), 1371–1386.
- Dastpak, M. et al. (including **H. Kim**, C. L. Paraggio, C. E. Leonard, S. Yin, B. Chi, and K. W. Nassar). Chemokine Receptor 1 and its associated immune pathway are downregulated in SF3B1MT blood and non-blood cancers. *bioRxiv*, 2022.03.31.485699. (Pre-print)
- Shull, L. C. et al. (including E. S. Lencer, **H. Kim**, S. Goyama, M. Kurokawa, and J. C. Costello). PRDM paralogs antagonistically balance Wnt/β-catenin activity during craniofacial chondrocyte differentiation. *Development* **149** (4), dev200082.
- Pollyea, D. A. et al. (including **H. Kim**, B. M. Stevens, F. F. Y. Lee, C. Harris, and B. R. Hedin). MDS-associated SF3B1 mutations enhance proinflammatory gene expression in patient blast cells. *J Leukoc Biol* **110** (1), 197–205.

2021

- Shull, L. C. et al. (including **H. Kim**, E. S. Lencer, S. Goyama, M. Kurokawa, and J. C. Costello). PRDM proteins control Wnt/β-catenin activity to regulate craniofacial chondrocyte differentiation. *bioRxiv*, 2021.05.21.445211. (Pre-print)
- Chavez, J. S. et al. (including J. L. Rabe, D. Loeffler, K. C. Higa, G. Hernandez, T. S. Mills, and **H. Kim**). PU.1 enforces quiescence and limits hematopoietic stem cell expansion during inflammatory stress. *J Exp Med* **218** (6), e20201169.
- Wahdan-Alaswad, R. S. et al. (including S. M. Edgerton, H. Salem, **H. Kim**, and A. C. Tan). Exogenous thyroid hormone is associated with shortened survival and upregulation of high-risk gene expression profiles in steroid receptor–positive breast cancers. *Clin Cancer Res* **27** (2), 585–597.

- Chavez, J. S. et al. (including J. L. Rabe, D. Loeffler, K. C. Higa, G. Hernandez, T. S. Mills, and **H. Kim**). PU.1 enforces quiescence and limits hematopoietic stem cell expansion during inflammatory stress. *bioRxiv*, 2020.10.19.345517. (Pre-print)

2020

- Watson, Z. L. et al. (including T. M. Yamamoto, A. McMellen, **H. Kim**, C. J. Hughes, and L. J. Wheeler). Histone methyltransferases EHMT1 and EHMT2 (GLP/G9A) maintain PARP inhibitor resistance in high-grade serous ovarian carcinoma. *Clinical epigenetics* **11** (1), 165.

2019

- Chavez, J. et al. (including J. L. Rabe, K. Higa, D. Loeffler, A. Nouraiz, T. Mills, B. M. Idler, and **H. Kim**). PU.1 Enforces Hematopoietic Stem Cell Quiescence during Chronic Inflammation. *Blood* **134**, 822. (Abstract)
- Yamamoto, T. M. et al. (including A. McMellen, Z. L. Watson, J. Aguilera, R. Ferguson, and **H. Kim**). Activation of Wnt signaling promotes olaparib resistant ovarian cancer. *Molecular carcinogenesis* **58** (10), 1770–1782.
- Wheeler, L. J. et al. (including Z. L. Watson, L. Qamar, T. M. Yamamoto, B. T. Sawyer, K. D. Sullivan, and **H. Kim**). Multi-omic approaches identify metabolic and autophagy regulators important in ovarian cancer dissemination. *Iscience* **19**, 474–491.
- Yoo, M. et al. (including J. Shin, **H. Kim**, J. Kim, J. Kang, and A. C. Tan). Exploring the molecular mechanisms of Traditional Chinese Medicine components using gene expression signatures and connectivity map. *Computer methods and programs in biomedicine* **174**, 33–40.
- Powell, M. P., Young, A. J., & **Kim, H.** A journey in capacity building: revisiting the mullins framework for meaningfully engaging patients in patient centered outcomes research. *Frontiers in Public Health* **6**, 343.

2018

- Oweida, A. et al. (including M. K. Hararah, A. Phan, D. Binder, S. Bhatia, S. Lennon, and **H. Kim**). Resistance to radiotherapy and PD-L1 blockade is mediated by TIM-3 upregulation and regulatory T-cell infiltration. *Clinical Cancer Research* **24** (21), 5368–5380.
- Pei, S. et al. (including M. Minhajuddin, B. Adane, N. Khan, B. M. Stevens, S. C. Mack, S. Lai, and **H. Kim**). AMPK/FIS1-mediated mitophagy is required for self-renewal of human AML stem cells. *Cell stem cell* **23** (1), 86–100.e6.
- **Kim, H.** Personal health records and their impact on breast cancer screening among women. (The University of Memphis, 2018). (Dissertation/Thesis)
- Kim, J. et al. (including M. Yoo, J. Shin, **H. Kim**, J. Kang, and A. C. Tan). Systems pharmacology‑based approach of connecting disease genes in genome‑wide association studies with traditional Chinese medicine. *International Journal of Genomics* **2018**, 7697356.

- Kim, H. et al. (including D. Y. Kim, K. I. Joo, J. H. Kim, S. M. Jeong, E. S. Lee, J. H. Hahm, and K. Kim). Coherent Raman imaging of live muscle sarcomeres assisted by SFG microscopy. *Scientific Reports* **7** (1), 9211.

2017

- Ebmeier, C. C. et al. (including B. Erickson, B. L. Allen, M. A. Allen, **H. Kim**, N. Fong, and J. R. Jacobsen). Human TFIIH kinase CDK7 regulates transcription-associated chromatin modifications. *Cell reports* **20** (5), 1173–1186.
- Fusby, B. et al. (including S. Kim, B. Erickson, **H. Kim**, M. L. Peterson, and D. L. Bentley). Coordination of RNA polymerase II pausing and 3′ end processing factor recruitment with alternative polyadenylation. *Molecular and cellular biology* **36** (2), 295–303.

2016

- Fong, N. et al. (including K. Brannan, B. Erickson, **H. Kim**, M. A. Cortazar, and R. M. Sheridan). Effects of transcription elongation rate and Xrn2 exonuclease activity on RNA polymerase II termination suggest widespread kinetic competition. *Molecular cell* **60** (2), 256–267.

2014

- Fong, N. et al. (including **H. Kim**, Y. Zhou, X. Ji, J. Qiu, T. Saldi, K. Diener, and K. Jones). Pre-mRNA splicing is facilitated by an optimal RNA polymerase II elongation rate. *Genes & development* **28** (23), 2663–2676.

2013

- Perales, R. et al. (including B. Erickson, L. Zhang, **H. Kim**, E. Valiquett, and D. Bentley). Gene promoters dictate histone occupancy within genes. *The EMBO journal* **32** (19), 2645–2656.

2012

- Brannan, K. et al. (including **H. Kim***, B. Erickson, K. Glover-Cutter, S. Kim, N. Fong, and L. Kiemele). mRNA decapping factors and the exonuclease Xrn2 function in widespread premature termination of RNA polymerase II transcription. *Molecular cell* **46** (3), 311–324.

2011

- Kim, J. & A. C. Tan (including **H. Kim**). BiNGS! SL-seq: a bioinformatics pipeline for the analysis and interpretation of deep sequencing genome-wide synthetic lethal screen. *Next Generation Microarray Bioinformatics: Methods and Protocols*, 389–398. (Book Chapter)
- Pollock, D. D. et al. (including A. P. J. de Koning, **H. Kim**, T. A. Castoe, M. E. A. Churchill, and K. J. Kechris). Bayesian analysis of high-throughput quantitative measurement of protein-DNA interactions. *Plos one* **6** (11), e26105.

- Johnson, S. A. et al. (including **H. Kim**, B. Erickson, and D. L. Bentley). The export factor Yra1 modulates mRNA 3′ end processing. *Nature structural & molecular biology* **18** (10), 1164–1171.
- Kim, S. et al. (including **H. Kim**, N. Fong, B. Erickson, and D. L. Bentley). Pre-mRNA splicing is a determinant of histone H3K36 methylation. *Proc Natl Acad Sci* **108** (33), 13564–13569.
- Kim, H. et al. (including A. Herzing, C. A. Michaels, G. W. Bryant, and S. J. Stranick). Coherent stokes scattering from gold nanorods: Critical dimensions and multicolor near-resonant plasmon excitation. *Nanoscale* **3** (10), 4290–4295.
- **Kim, H.** et al. (including J. Kim, H. Selby, D. Gao, T. Tong, T. L. Phang, and A. C. Tan). A short survey of computational analysis methods in analysing ChIP-seq data. *Human genomics* **5** (2), 117. (Review)
- Gao, D. et al. (including J. Kim, **H. Kim**, T. L. Phang, H. Selby, A. C. Tan, and T. Tong). A survey of statistical software for analysing RNA-seq data. *Human genomics* **5** (1), 56. (Review)

2010

- **Kim, H.** et al. (including B. Erickson, W. Luo, D. Seward, J. H. Graber, D. D. Pollock, and P. C. Megee). Gene-specific RNA polymerase II phosphorylation and the CTD code. *Nature structural & molecular biology* **17** (10), 1279–1286.
- Castoe, T. A. et al. (including A. P. J. de Koning, **H. M. Kim**, W. Gu, B. P. Noonan, and G. Naylor). Evidence for an ancient adaptive episode of convergent molecular evolution. *Proc Natl Acad Sci* **106** (22), 8986–8991.

Pre-2010

- Mant, C. T. et al. (including J. M. Kovacs, **H. M. Kim**, D. D. Pollock, and R. S. Hodges). Intrinsic amino acid side-chain hydrophilicity/hydrophobicity coefficients determined by reversed-phase high-performance liquid chromatography... *Peptide Science* **92** (6), 573–595.
- Castoe, T. et al. (including A. P. J. de Koning, **H. M. Kim**, W. Gu, B. Noonan, and Z. Jiang). An ancient adaptive episode of convergent molecular evolution confounds phylogenetic inference. *Nature Precedings*, 1–1. (Pre-print)
- **Kim, H.** et al. (including K. J. Kechris, and L. Hunter). Mining discriminative distance context of transcription factor binding sites on ChIP enriched regions. *International Symposium on Bioinformatics Research and Applications*, 338–349. (Conference Proceeding)
- Caporaso, J. G. et al. (including W. A. Baumgartner Jr, **H. Kim**, Z. Lu, and H. L. Johnson). Concept recognition, information retrieval, and machine learning in genomics question-answering. *TREC*. (Conference Proceeding)
- Johnson, H. L. et al. (including K. B. Cohen, J. R. WILLIAM A. BAUMGARTNER, Z. Lu, and M. Bada). Evaluation of lexical methods for detecting relationships between concepts from multiple ontologies. *Pacific Symposium on Biocomputing*, 28. (Conference Proceeding)
- Bitler, B. G. et al. (including T. M. Yamamoto, A. McMellen, **H. Kim**, Z. L. Watson, and Z. L. Watson). BRPF3 knockdown or inhibition moderately reverses olaparib resistance in high grade serous ovarian carcinoma. (Unknown/Duplicate Entry)