

Hoon Kim

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Research Interests

Biomedical Data Science, Computational Biology, Extrachromosomal DNA, Tumor Evolution / Resistance, Genetics and Genomics

Education

Columbia University

Ph.D., Electrical Engineering

- Thesis Topic: Selection of Disease-Associated Gene Sets

- Advisor: Dr. Dimitris Anastassiou

New York, NY

2011

University of Michigan

M.Sc., Electrical Engineering-Systems

Ann Arbor, MI

2005

Korea University

B.E., Electrical Engineering

B.Sc., Genetic Engineering (Life Science)

Seoul, South Korea

2000

2000

Positions

Sungkyunkwan University

Associate Professor, Computational Biomedicine Lab, School of Pharmacy

South Korea

2021 - Present

The Jackson Laboratory for Genomic Medicine

Affiliate Scientist

Farmington, CT

2021 - Present

The Jackson Laboratory for Genomic Medicine

Senior Research Scientist

Farmington, CT

2016 - 2021

MD Anderson Cancer Center

Instructor, Department of Genomic Medicine

Houston, TX

2015 - 2016

MD Anderson Cancer Center

Postdoc Fellow, Department of Bioinformatics and Computational Biology

Houston, TX

2011 - 2015

Columbia University

Research Assistant, Genomic Information Systems Laboratory

New York, NY

2006 - 2010

Philips Research North America

Research Intern, Biomedical Informatics Dept.

New York, NY

2009

Columbia University

Teaching Assistant, Signals and Systems

New York, NY

2005

LG Electronics Inc.

System Engineer, Universal Mobile Telecommunication Systems

South Korea

2000-2002

Publications

- Johnson K*, Anderson K, [...], Hoon Kim, Estecio MRH, Tang M, Navin N, Maurya R, Ngan CY, Verburg N, Witt Hamer PC, Bulsara K, Samuels ML, Das S, Robson P, Verhaak RG. "Single-cell multimodal glioma analyses reveal epigenetic regulators of cellular plasticity and environmental stress response", *Nature Genetics*, 2021 Sep.
- Yanfen Zhu*, Amit D. Gujar*, Chee-Hong Wong*, [...], Hoon Kim, [...], Roel G.W. Verhaak, Chia-Lin Wei. "Oncogenic Extrachromosomal DNA Functions as Mobile Enhancers to Globally Amplify Chromosomal Transcription.", *Cancer Cell*, 2021 April

- Hoon Kim^{*}, Nam Nguyen^{*}, Kristen Turner, [...], Sihan Wu, Jihe Liu, Sandeep Namburi, Howard Chang, Paul Mischel, Vineet Bafna, Roel Verhaak. “Extrachromosomal DNA is associated with oncogene amplification and poor outcome across multiple cancers.”, *Nature Genetics*, 2020 Aug.
- Oldrini Barbara, Nuria Vaquero-Siguero, Quanhua Mu, [...], Hoon Kim, [...], Tao Jiang, Jiguang Wang and Massimo Squatrito. “MGMT genomic rearrangements contribute to chemotherapy resistance in gliomas.”, *Nature Communications*, 2020 Aug.
- Samir Amin, Kevin J Anderson, C Elizabeth Boudreau, Emmanuel Martinez-Ledesma, [...], Hoon Kim, [...], Roel G.W. Verhaak. “Comparative molecular life history of spontaneous canine and human glioma”, *Cancer Cell*, 2020 Feb.
- Floris P. Barthel, Kevin C. Johnson, The Glioma Longitudinal Analysis Consortium (Hoon Kim included). “Longitudinal Molecular Trajectories of Diffuse Glioma in Adults”, *Nature*, 2019 Nov. (Role: Project coordination, Data preprocessing, Analytics development)
- Sihan Wu, Kristen M. Turner, [...], Hoon Kim, Julie Law, Roel Verhaak, Frank Furnari, Howard Chang, Bing Ren, Vineet Bafna, Paul Mischel. “Circular extrachromosomal DNA promotes accessible chromatin and high oncogene expression.”, *Nature*, 2019 Nov.
- Ana deCarvalho^{*}, Hoon Kim^{*}, Laila M. Poison, [...], Lynda Chin, Tom Mikkelsen, Roel G.W. Verhaak. “Discordant inheritance of chromosomal and extrachromosomal DNA elements contributes to dynamic disease evolution in glioblastoma.”, *Nature Genetics*, 2018 Apr.
- The Glioma Longitudinal Analysis Consortium^{*} (Hoon Kim included). “Glioma Through the Looking GLASS: the Glioma Longitudinal Analysis consortium, molecular evolution of diffuse gliomas”, *Neuro Oncology*, 2018 Jun.
- Javier Figueroa, Lynette Phillips, Tal Shahar, Anwar Hossain, Joy Gumin, Hoon Kim, Andrew Bean, George Calin, Juan Fueyo, Edgar Walters, Raghu Kalluri, Roel Verhaak, Frederick Lang. “Exosomes from Glioma-Associated Mesenchymal Stem Cells Increase the Tumorigenicity of Glioma Stem-like Cells via Transfer of Specific microRNA.”, *Cancer Research*, 2017 Nov.
- Wang Q, Hu B, Hu X, Hoon Kim, Nam DH, Verhaak RG. “Tumor evolution of glioma intrinsic gene expression subtype associates with immunological changes in the microenvironment.”, *Cancer Cell*, 2017 Jul.
- Hu X, Martinez-Ledesma E, Zheng S, Hoon Kim, Barthel F, Jiang T, Hess KR, Verhaak RG. “Multigene signature for predicting prognosis of patients with 1p19q co-deletion diffuse glioma.”, *Neuro Oncology*, 2017 Jun.
- Zheng S, Cherniack AD, Cancer Genome Atlas Research Network (Hoon Kim included), Verhaak RG. “Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma.”, *Cancer Cell*, 2016 May.
- Cancer Genome Atlas Research Network^{*} (Hoon Kim included). “Comprehensive, Integrative Genomic Analysis of Diffuse Lower Grade Gliomas.”, *New England Journal of Medicine*, 2015 Jun.
- Hoon Kim^{*}, Verhaak RG. “Transcriptional mimicry by tumor-associated stroma.”, *Nature Genetics*, 2015 Apr.
- Hoon Kim^{*}, Zheng S, Amini SS, Mikkelsen T, Meyerson M, Chin L, Barnholtz-Sloan JS, Verhaak RG. “Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution.”, *Genome Research*, 2015 Mar.
- Yoshihara K, Wang Q, Torres-Garcia W, Zheng S, Vegesna R, Hoon Kim, Verhaak RG. “The landscape and therapeutic relevance of cancer-associated transcript fusions.”, *Oncogene*, 2015 Sep.
- Cancer Genome Atlas Research Network^{*} (Hoon Kim included). “Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin.”, *Cell*, 2014 Aug.
- Martínez E, Yoshihara K, Hoon Kim, Mills GM, Treviño V, Verhaak RG. “Comparison of gene expression patterns across 12 tumor types identifies a cancer supercluster characterized by TP53 mutations and cell cycle defects.”, *Oncogene*, 2014 Aug.
- Zheng S, Hoon Kim, Verhaak RG. “Silent mutations make some noise.”, *Cell*, 2014 Mar.
- Cancer Genome Atlas Research Network^{*} (Hoon Kim included). “The Cancer Genome Atlas Pan-Cancer analysis project.”, *Nature Genetics*, 2013 Oct.

- Cancer Genome Atlas Research Network* ([Hoon Kim](#) included). “Comprehensive molecular characterization of clear cell renal cell carcinoma.”, *Nature*, 2013 Jul.
- Yoshihara K, Shahmoradgoli M, Martínez E, Vegesna R, [Hoon Kim](#), Verhaak RG. “Inferring tumour purity and stromal and immune cell admixture from expression data.”, *Nature Communications*, 2013.
- Cheng WY, [Hoon Kim](#), Kandel J, Anastassiou D. “Cancer invasion associated gene expression signature is present in differentially expressed genes in the reprogramming of fibroblasts into stem cells.” 2011. Available from *Nature Precedings*
- [Hoon Kim](#)*, Watkinson J, Anastassiou D. “Biomarker discovery using statistically significant gene sets.”, *Journal of Computational Biology*, 2011 Oct.
- [Hoon Kim](#)*, Watkinson J, Varadan V, Anastassiou D. “Multi-cancer computational analysis reveals invasion-associated variant of desmoplastic reaction involving INHBA, THBS2 and COL11A1.”, *BMC Medical Genomics*, 2010 Nov., Cited by 141 according to google search

Work in Progress

- Yi E., Gujar A, Guthrie M, [Hoon Kim](#), Johnson K, Amin S, Das S, Clow P, Cheng A, Verhaak RG. “Live-cell imaging shows uneven segregation of extrachromosomal DNA elements and transcriptionally active extrachromosomal DNA clusters in cancer.”, *bioRxiv*, 2010 Oct.

Awards

Caroline Ross Endowed Fellowship Award

2015

MD Anderson Cancer Center

Odyssey Fellowship Award

2012-2014

Theodore N. Law Endowment for Scientific Achievement, MD Anderson Cancer Center

The 1st recipient in the Bioinformatics/Computational Biology Dept.

Grant

FUNDED

- *Characterization of extrachromosomal DNAs in tumors through computational analysis of sequencing data*
 - Role: Principal investigator
 - Grant mechanism: NIH R21
 - Top 3 %
 - Project Period: 9/1/2021 - 8/31/2023
- *Development of integrated genome analysis system*
 - Role: Principal Investigator
 - Grant mechanism: Industrial Sector
 - Funding Period: 6/1/2021 - 12/31/2025
- *Modeling Tumor Evolution in Glioma*
 - Role: Co-Investigator
 - Grant mechanism: R21 NS114873-01
 - Funding Period: 9/30/2019 - 8/31/2021
- *Extrachromosomal DNA as a Targetable Mechanism in Glioblastoma*
 - Role: Co-Investigator
 - Top 6.0th percentile
 - Grant mechanism: NIH R01

Patent

PUBLISHED

- Dimitris Anastassiou, John Watkinson, Hoon Kim, “Biomarkers based on a multi-cancer invasion-associated mechanism”, WO2011130435 A1, 2011
- Hoon Kim, Roel Verhaak, Ana Decarvalho, Tom Mikkelsen, “A Method of Targeting Patient-Specific Onco-genes in Extrachromosomal DNA To Treat Glioblastoma”, WO/2018/136837, 2018

PENDING

- Amit Gujar, Jihe Liu, Hoon Kim, Roel Verhaak, “A Method of Targeting Patient-Specific Onco-genes in Extra-chromosomal DNA To Treat Glioblastoma”, WO/2018/136837, 2018

Invited oral presentations

- “Extrachromosomal DNA in Cancer” *Lecture*, 2019 Korean Basic Medical Scientists, Korea
- “A journey to understand intratumor heterogeneity” *Lecture*, 2021, Sorak Conference, Korea
- “Extrachromosomal DNA elements are frequent in tumors and can contribute to tumor heterogeneity.” *Lecture*, 2019, Samsung Medical Center, Korea
- “Extrachromosomal DNA elements are frequent in tumors and can contribute to tumor heterogeneity.” *Lecture*, 2019, KAIST, Korea
- “Extrachromosomal DNA elements are frequent in tumors and can contribute to tumor heterogeneity.” *Lecture*, 2019, Seoul National University, Korea
- “Molecular evolution of diffuse gliomas and the Glioma Longitudinal Analysis (GLASS) consortium (on behalf of GLASS)” *The Society for Neuro-oncology*, 2018, New Orleans, LA
- “Extrachromosomal DNA elements are frequent in tumors and can contribute to tumor heterogeneity.” *Symposium: computational approaches in cancer biology*, 2018, Rotterdam, Netherlands
- “Extrachromosomal DNA elements drive disease evolution in glioblastoma.” *Scientific Symposium*, 2017, Bar Harbor, ME
- “Non-Mendelian inheritance of extrachromosomal DNA elements can drive disease evolution in glioblastoma” *The Society for Neuro-oncology*, 2016, Scottsdale, AZ
- “Whole-genome and Multisector Exome Sequencing of Primary and Post-treatment Glioblastoma Reveal Patterns of Tumor Evolution.” *Training in Brain Tumor Research*, 2015, Houston, TX
- “Alteration of the p53 pathway is associated with subclonal tumor progression in glioblastoma.” *The Society for Neuro-oncology*, 2014, Miami, FL
- “Alteration of the p53 pathway is associated with subclonal tumor progression in glioblastoma.” *AACR Annual Meeting Minisymposium session*, 2014, San Diego, CA
- “The Intratumoral Heterogeneity of Glioblastoma Suggests a Pivotal Role for Clonal Evolution.” *Advances in Genome Biology and Technology*, 2014, Marco Island, FL

Professional Service

GLIOMA LONGITUDINAL ANALYSIS CONSORTIUM

- Data Analysis Committee Member, 2014 ~ Present

PH.D. DISSERTATION COMMITTEE

- Emmanuel Martinez, Ph.D. 2015
 - Tecnologico de Monterrey, Mexico
 - Dissertation Title: “Identification of features related to cancer stages, survival, and subtypes from diverse genomics data”

PH.D. DISSERTATION COMMITTEE

- Emmanuel Martinez, Ph.D. 2015
 - Tecnologico de Monterrey, Mexico
 - Dissertation Title: “Identification of features related to cancer stages, survival, and subtypes from diverse genomics data”

GRADUATE MENTOR

- Anzhela Moskalik 2018
 - Graduate student (Neuro-Oncology), University of Connecticut School of Medicine, Farmington, CT
- Olajide Abiola 2017

- Graduate student (Neuro-Oncology), University of Connecticut School of Medicine, Farmington, CT
- Emmanuel Martinez 2012
 - Research Intern (Computer Science), MD Anderson Cancer Center, Houston, TX
- Seyed Saman Amini 2012 - 2013
 - Research Intern (Bioinformatics), MD Anderson Cancer Center, Houston, TX