Curriculum Vitae

Personal Information

Title	**Dr.**
Name	**Kwangwoo Kim**
Degree	**PhD**
Country	**1. USA** **2. Korea**
Affiliation	**1. National Institute of Arthritis and Musculoskeletal and Skin Diseases, National Institutes of Health** **2. Department of Biology, Kyung Hee University**
E-mail	**1. kwangwoo.kim(at)nih.gov** **2. kkim(at)khu.ac.kr**

Educational Background

Ph.D. **Korea Advanced Institute of Science and Technology (KAIST)** **2007-2011**
Human Genetics at the Department of Biological Sciences *(Advisor: Changwon Kang, PhD)*

M.Sc. **Korea Advanced Institute of Science and Technology (KAIST)** **2005-2007**
Human Genetics at the Department of Biological Sciences *(Advisor: Changwon Kang, PhD)*

B.Sc. **Pusan National University** **2000-2005**
Department of Molecular Biology

Professional Career

Special Volunteer (Government Visitor) **2023-Present**
National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS)
National Institutes of Health (NIH; MD, USA)

Associate Professor **2020-Present**
Department of Biology & Department of Biomedical and Pharmaceutical Sciences
Kyung Hee University (Seoul, Korea)

Assistant Professor **2016-2020**
Department of Biology, Kyung Hee University (Seoul, Korea)

Research Assistant Professor **2015-2016**
Hanyang University Hospital for Rheumatic Diseases (Seoul, Korea)
(Mentor: Sang-Cheol Bae, MD, PhD, MPH)

Research Fellow **2013-2014**
Harvard Medical School | Brigham & Women's Hospital | Broad Institute (MA, USA)
(Mentors: Robert M. Plenge, MD, PhD; Elizabeth W. Karlson, MD; Soumya Raychaudhuri, MD, PhD)

Senior Engineer **2011-2012**
Bio Tech Group, Advanced Tech Center, Samsung Techwin (Seongnam, Korea)

Research Field

His research has the overall theme of understanding genomic variants associated with common complex inflammatory diseases including rheumatoid arthritis, systemic lupus erythematosus, and inflammatory bowel disease by using a tremendous amount of genomic, transcriptomic, epigenetic, and metagenomic data through a number of research projects that employ cutting edge Omics technologies, including next-generation sequencing, along with various statistical and bioinformatic methods. Human genetic studies on common complex diseases have uncovered a number of genetic loci associated with disease susceptibility, highlighting HLA variants and many other variants in noncoding elements that may have allele-specific regulatory effects in relevant tissues. He takes advantage of emerging publicly available multi-Omics data as well as actual patients' Omics data and computational approaches, which are enabling him to leverage genetic variants in

order to comprehend disease genes, functionally relevant cell types, and biological pathways involved in impaired immune processes and disease phenotypes. Consequently, his work suggests potential drug targets and identifies potentially repurposable drugs. Prof. Kim obtained his PhD at Korea Advanced Institute of Science and Technology (KAIST; Daejeon, Republic of Korea). He received training at Hanyang University (Seoul, Republic of Korea), Harvard Medical School (Boston, Massachusetts, USA), Brigham & Women's Hospital (Boston, Massachusetts, USA) and Broad Institute of MIT and Harvard (Cambridge, Massachusetts, USA).

Keywords: Immunogenomics, Computational Genomics, Bioinformatics, Multi-Omics Big Data Mining

Main Scientific Publications

[Corresponding/First author papers only]

1. Regulatory Variants on the Leukocyte Immunoglobulin-Like Receptor Gene Cluster are Associated with Crohn's Disease and Interact with Regulatory Variants for TAP2. ***J Crohns Colitis.*** 31;jjad127. Online ahead of print. [July, 2023] [IF=8.0]

2. Higher genetic risk loads confer more diverse manifestations and higher risk of lupus nephritis in systemic lupus erythematosus. ***Arthritis Rheumatol.*** 75(9):1566-1572. [September, 2023] [IF=15.5]

3. Biological insights into systemic lupus erythematosus through an immune cell-specific transcriptome-wide association study. ***Ann Rheum Dis.*** 24;81(9):1273-80. [May, 2022] [IF=28.0]

4. Recent advances in understanding the genetic basis of systemic lupus erythematosus. ***Semin Immunopathol.*** 44(1):29-46. [January, 2022] [IF=11.8]

5. Genetic variants shape rheumatoid arthritis-specific transcriptomic features in $CD4^+$ T cells through differential DNA methylation, explaining a substantial proportion of heritability. ***Ann Rheum Dis.*** 80(7):876-883. [July, 2021] [IF=28.0]

6. Large-scale meta-analysis across East Asian and European populations updated genetic architecture and variant-driven biology of rheumatoid arthritis, identifying 11 novel susceptibility loci. ***Ann Rheum Dis.*** 80(5):558-565. [May, 2021] [IF=28.0]

7. Meta-analysis of 208370 East Asians identifies 113 susceptibility loci for systemic lupus erythematosus. ***Ann Rheum Dis.*** 80(5):632-640. [May, 2021] [IF=28.0]

8. Allele-specific quantification of HLA-DRB1 transcripts reveals imbalanced allelic expression that modifies the amino acid effects in HLA-DRβ1. ***Arthritis Rheumatol.*** 73(3):381-391. [March, 2021] [IF=15.5]

9. Genome-wide association study in a Korean population identifies six novel susceptibility loci for rheumatoid arthritis. ***Ann Rheum Dis.*** 79(11):1438-1445. [November, 2020] [IF=28.0]

10. Massive false-positive gene–gene interactions by Rothman's additive model. ***Ann Rheum Dis.*** 78(3):437-439. [March, 2019] [IF=28.0]

11. Update on the genetic architecture of rheumatoid arthritis. *Nat Rev Rheumatol.* 13(1):13-24. [January, 2017] [IF=32.3]

12. Identification of a systemic lupus erythematosus risk locus spanning ATG16L2, FCHSD2, and P2RY2 in Koreans. ***Arthritis Rheumatol.*** 68(5):1197-209. [May, 2016] [IF=15.5]

13. High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. ***Nat Genet.***, 48(3):323-30. [March, 2016] [IF=41.4]

14. Interactions between amino-acid-defined MHC class II variants and smoking for seropositive rheumatoid arthritis. ***Arthritis Rheumatol.*** 67(10):2611-23. [October, 2015] [IF=15.5]

15. High-Density Genotyping of Immune Loci in Koreans and Europeans Identifies 8 New Rheumatoid Arthritis Risk Loci. ***Ann Rheum Dis.*** 74(3):e13. [May, 2015] [IF=28.0]

16. The HLA-DRβ1 Amino Acid Positions 11-13-26 Explain the Majority of SLE-MHC Associations. ***Nat Commun.*** 5:5902. [December, 2014] [IF=17.7]

17. Variation in the ICAM1-ICAM4-ICAM5 locus is associated with systemic lupus erythematosus susceptibility in multiple ancestries. ***Ann Rheum Dis.*** 71 (11), 1809-1814. [October, 2012] [IF=28.0]