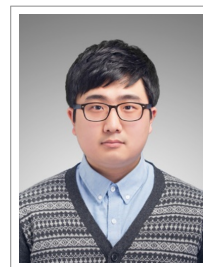# Hyunbin Kim

Curriculum Vitae

School of Biological Sciences
Seoul National University
✆ *(+82)10-9197-2561*
✉ *khb7840@gmail.com*
⌂ *hyunbinkim.com*
 Github

Education

2021–present **PhD, Interdisciplinary Program in Bioinformatics**, *Seoul National University*, Seoul, South Korea.
Protein structure, Protein structure compression, Structural motif search, Protein structure prediction, *De novo* protein design, Development of scalable bioinformatics methods

Advisor : **Dr. Martin Steinegger**, *Associate Professor, School of Biological Sciences*, Seoul National University, South Korea (*Lab web-page*)

2015–2017 : **Master of Science in Agricultural Genomics, Interdisciplinary Program in Agricultural Genomics**, *Seoul National University*, Seoul, South Korea.
Protein-protein interaction network, Fungal plant pathology, Co-expression network

Advisor : **Dr. Yong-Hwan Lee**, *Professor, Department of Agricultural Biotechnology*, Seoul National University, South Korea (*Lab web-page*)

2010–2015 : **Bachelor of Science in Biological Sciences, School of Biological Sciences**, *Seoul National University*, Seoul, South Korea.

Research Experience

2017 – 2020 **Researcher, Bioinformatics Analysis Team**, *National Cancer Center*, Goyang, South Korea, (Substitution for national service as a technical research personnel).
Developed novel computational methodologies for analysis of mutational signatures on tumors samples. Head and neck cancer, Prostate cancer, Somatic mutation analysis on WGS/WES, Bulk RNA-seq analysis

Principal Investigator : **Dr. Dongwan Hong**, *Professor, College of Medicine*, Catholic University of Korea (*Lab web-page*)

Software

2025 **Folddisco**, *Written in Rust*, A fast and scalable structural motif search tool, Repository.

2023 **Foldcomp**, *Written in C++*, Structure compression with torsion angle, Repository.

2019 **FIREVAT**, *Written in R*, A variant filtering tool using mutational signature, Repository.

Publications

First author

2023 **Hyunbin Kim**, Milot Mirdita, and Martin Steinegger. Foldcomp: a library and format for compressing and indexing large protein structure sets. *Bioinformatics*, volume 39, page btad153. Oxford University Press, 2023.

2019 **Hyunbin Kim**, **Andy Jinseok Lee**, Jongkeun Lee, Hyonho Chun, Young Seok Ju, and Dongwan Hong. Firevat: finding reliable variants without artifacts in human cancer samples using etiologically relevant mutational signatures. *Genome Medicine*, volume 11, pages 1–17. Springer, 2019.

Co-author

2025 Hyunuk Eom, Sukhwan Park, Kye Soo Cho, Jihyeon Lee, **Hyunbin Kim**, Stephanie Kim, Jinsol Yang, Young-Hyun Han, Juyong Lee, Chaok Seok, Myeong Sup Lee, Woon Ju Song, and Martin Steinegger. Discovery of highly active kynureninases for cancer immunotherapy through protein language model. *Nucleic Acids Research*, volume 53, page gkae1245. Oxford University Press, 2025.

2024 Gyuri Kim, Sewon Lee, Eli Levy Karin, **Hyunbin Kim**, Yoshitaka Moriwaki, Sergey Ovchinnikov, Martin Steinegger, and Milot Mirdita. Easy and accurate protein structure prediction using colabfold. *Nature Protocols*, pages 1–23. Nature Publishing Group UK London, 2024.

2023 Caroline Puente-Lelievre, Ashar J Malik, Jordan Douglas, David Ascher, Matthew Baker, Jane Allison, Anthony Poole, Daniel Lundin, Matthew Fullmer, Remco Bouckert, **Hyunbin Kim**, Martin Steinegger, and Nicholas Matzke. Tertiary-interaction characters enable fast, model-based structural phylogenetics beyond the twilight zone. *bioRxiv*, pages 2023–12. Cold Spring Harbor Laboratory, 2023.

2020 Seungill Kim, Kyeongchae Cheong, Jieun Park, Myung-Shin Kim, Jihyun Kim, Min-Ki Seo, Geun Young Chae, Min Jeong Jang, Hyunggon Mang, Sun-Ho Kwon, Yong-Min Kim, Namjin Koo, Cheol Woo Min, Kwang-Soo Kim, Nuri Oh, Ki-Tae Kim, Jongbum Jeon, **Hyunbin Kim**, Yoon-Young Lee, Kee Hoon Sohn, Honour C. McCann, Sang-Kyu Ye, Sun Tae Kim, Kyung-Soon Park, Yong-Hwan Lee, and Doil Choi. Tgfam-finder: a novel solution for target-gene family annotation in plants. *New Phytologist*, volume 227, pages 1568–1581. Wiley Online Library, 2020.

2019 Ki-Tae Kim, Jaeho Ko, Hyeunjeong Song, Gobong Choi, **Hyunbin Kim**, Jongbum Jeon, Kyeongchae Cheong, Seogchan Kang, and Yong-Hwan Lee. Evolution of the genes encoding effector candidates within multiple pathotypes of magnaporthe oryzae. *Frontiers in Microbiology*, volume 10, page 2575. Frontiers Media SA, 2019.

2017 Seungill Kim, Jieun Park, Seon-In Yeom, Yong-Min Kim, Eunyoung Seo, Ki-Tae Kim, Myung-Shin Kim, Je Min Lee, Kyeongchae Cheong, Ho-Sub Shin, Saet-Byul Kim, Koeun Han, Jundae Lee, Minkyu Park, Hyun-Ah Lee, Hye-Young Lee, Youngsill Lee, Soohyun Oh, Joo Hyun Lee, Eunhye Choi, Eunbi Choi, So Eui Lee, Jongbum Jeon, **Hyunbin Kim**, Gobong Choi, Hyeunjeong Song, JunKi Lee, Sang-Choon Lee, Jin-Kyung Kwon, Hea-Young Lee, Namjin Koo, Yunji Hong, Ryan W Kim, Won-Hee Kang, Jin Hoe Huh, Byoung-Cheorl Kang, Tae-Jin Yang, Yong-Hwan Lee, Jeffrey L Bennetzen, and Doil Choi. New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. *Genome biology*, volume 18, pages 1–11. Springer, 2017.

2017 Jongbum Jeon, Ki-Tae Kim, Hyeunjeong Song, Gir-Won Lee, Kyeongchae Cheong, **Hyunbin Kim**, Gobong Choi, Yong-Hwan Lee, Jane E Stewart, Ned B Klopfenstein, et al. Draft genome sequence of the fungus associated with oak wilt mortality in south korea, raffaelea quercus-mongolicae kacc44405. *Genome announcements*, volume 5, pages 10–1128. American Society for Microbiology 1752 N St., NW, Washington, DC, 2017.

Presentations

Oral presentations

2024 **Hyunbin Kim**, Rachel Seongeun Kim, Milot Mirdita, and Martin Steinegger. Structural motif detection on the scale of the protein universe with folddisco. In *APBJC2024, 1st Asia&Pacific Bioinformatics Joint Conference JSBi, GIW, InCoB, APBC, and ISCB-Asia*. ISCB, 2024.

2023   **Hyunbin Kim**, Milot Mirdita, and Martin Steinegger. Foldcomp: scalable solution for compressing huge protein structure database. In *ISMB/ECCB 2023, The 31st Annual Intelligent Systems For Molecular Biology and the 22nd Annual European Conference on Computational Biology, Lyon, France*. ISCB, 2023.

2017   **Hyunbin Kim**, K. Cheong, K.T. Kim, J. Jeon, G. Choi, and Y.H. Lee. Magnet: the integrated gene network of the rice blast fungus *Magnaporthe oryzae*. In *29th Fungal Genetics Conference Asilomar 17, Pacific Grove, CA*. Genetics Society of America, 2017.

Poster presentations

2024   **Hyunbin Kim**, Rachel Seongeun Kim, Milot Mirdita, and Martin Steinegger. Structural motif detection on the scale of the protein universe with folddisco. In *APBJC2024, 1st Asia&Pacific Bioinformatics Joint Conference JSBi, GIW, InCoB, APBC, and ISCB-Asia*. ISCB, 2024.

2023   **Hyunbin Kim**, Milot Mirdita, and Martin Steinegger. Foldcomp: scalable solution for compressing huge protein structure database. In *ISMB/ECCB 2023, The 31st Annual Intelligent Systems For Molecular Biology and the 22nd Annual European Conference on Computational Biology, Lyon, France*. ISCB, 2023.

2022   **Hyunbin Kim**, Johannes Söding, and Martin Steinegger. Fast lossy protein structure compression algorithm. In *ISMB 2022, The 30st Annual Intelligent Systems For Molecular Biology, Madison, Wisconsin*. ISCB, 2022.

2017   **Hyunbin Kim** and Yong-Hwan Lee. Deciphering protein-protein interaction network in the rice blast fungus, *Magnaporthe oryzae*. In *2017 APS Annual Meeting, San Antonio, Texas*. American Phytopathological Society, 2017.

2017   **Hyunbin Kim**, K. Cheong, K.T. Kim, J. Jeon, G. Choi, and Y.H. Lee. Magnet: the integrated gene network of the rice blast fungus *Magnaporthe oryzae*. In *29th Fungal Genetics Conference Asilomar 17, Pacific Grove, California*. Genetics Society of America, 2017.

Computer skills

Programming languages   **C++, Rust, R, Python,** C, Go, Shell script

Web technologies   HTML 5, Javascript, Typescript

Design software   Illustrator, Figma, Affinity designer

Teaching Assistant

Fall, 2021 :   **Advanced Bioinformatics**, Seoul National University.
Feedback to the student presentation materials for improvement

Spring, 2021 :   **Introduction to Bioinformatics**, Seoul National University.
Assignment & exam design

Certificate

2019   **Certificate of competency in Fundamental of Deep Learning for Natural Language**, *NVIDIA Deep Learning Institute*, Seoul, South Korea.