Minsoo Kim

김민수

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Education

2019 – 2026	**M.S./Ph.D. Integrated (PhD Candidate)** Sungkyunkwan University — (Biological) Physics & Bioinformatics Advisor: Jejoong Yoo Thesis: *An in silico approach of protein folding and structure prediction*
2016 – 2019	**Bachelor of Science** Sungkyunkwan University — Physics

Research Interests

Methods: Deep Learning, Protein Language Models, Molecular Dynamics Simulation, Optimal Transport, Parallel/GPU Computing
Topics: Protein Structure Prediction, Protein-Protein Interaction, Biomolecular Simulation

Academic Positions

Korea Institute for Advanced Study 2022 – Current
Research Assistant

Honors and Awards

Apr 2025	**Outstanding Presentation Award** 2025 Korean Physical Society (KPS) Spring Meeting DeepFold-PLM: Accelerating Protein Structure Prediction with Optimized Homolog Detection and Protein Language Models
Dec 2024	**2nd Place, Antibody–Antigen Targets** 16th Critical Assessment of Techniques for Protein Structure Prediction (CASP16)
Dec 2022	**4th Place, Regular Targets** 15th Critical Assessment of Techniques for Protein Structure Prediction (CASP15)

Publications

OTalign: Optimal Transport Alignment for Remote Protein Homologs Using Protein Language Model Embeddings. *Under review*, 2026.
Kim, Minsoo; Bae, Hanjin; Jo, Gyeongpil; Kim, Kunwoo; Yoo, Jejoong; Joo, Keehyoung.

Polyamine and tau: a chemical framework for understanding the hyperphosphorylated tau condensation. *International Journal of Biological Macromolecules* **365** 152366, 2026.
Lee, Jinmin; Lee, Kyubin; **Kim, Minsoo**; Kim, Min Wook; Lim, Manho; Yoo, Jejoong; Lee, Sang Hak.

DeepFold-PLM: Accelerating Protein Structure Prediction via Efficient Homology Search Using Protein Language Models. *Bioinformatics* **41**(11) btaf579, 2025.
Kim, Minsoo; Bae, Hanjin; Jo, Gyeongpil; Kim, Kunwoo; Lee, Sung Jong; Yoo, Jejoong; Joo, Keehyoung.

Web-based applications for automated generation of functionalized graphene and carbon nanotube for molecular dynamics simulations and automated three-dimensional analysis of ion flow through nanopores. *Current Applied Physics* **67** 30-37, 2024.
Jo, Gyeongpil; **Kim, Minsoo**; Lee, Jinmin; Lee, Sang Hak; Yoo, Jejoong.

DeepFold: Enhancing Protein Structure Prediction through Optimized Loss Functions, Improved Template Features, and Re-optimized Energy Function. *Bioinformatics* **39**(12) btad712, 2023.
Lee, Jae-Won; Won, Jong-Hyun; Jeon, Seonggwang; Choo, Yujin; Yeon, Yubin; Oh, Jin-Seon; **Kim, Minsoo**; Kim, SeonHwa; Joung, InSuk; Jang, Cheongjae; Lee, Sung Jong; Kim, Tae Hyun; Jin, Kyong Hwan; Song, Giltae; Kim, Eun-Sol; Yoo, Jejoong; Paek, Eunok; Noh, Yung-Kyun; Joo, Keehyoung.

Conformational changes in the human Cx43/GJA1 gap junction channel visualized using cryo-EM. *Nature Communications* **14**(1) 931, 2023.
Lee, Hyuk-Joon; Cha, Hyung Jin; Jeong, Hyeongseop; Lee, Seu-Na; Lee, Chang-Won; **Kim, Minsoo**; Yoo, Jejoong; Woo, Jae-Sung.

Cryo-EM structures of human Cx36/GJD2 neuronal gap junction channel. *Nature Communications* **14**(1) 1347, 2023.
Lee, Seu-Na; Cho, Hwa-Jin; Jeong, Hyeongseop; Ryu, Bumhan; Lee, Hyuk-Joon; **Kim, Minsoo**; Yoo, Jejoong; Woo, Jae-Sung; Lee, Hyung Ho.

Single-molecule fingerprinting of protein-drug interaction using a funneled biological nanopore. *Nature Communications* **14**(1) 1461, 2023.
Jeong, Ki-Baek; Ryu, Minju; Kim, Jin-Sik; **Kim, Minsoo**; Yoo, Jejoong; Chung, Minji; Oh, Sohee; Jo, Gyunghee; Lee, Seong-Gyu; Kim, Ho Min; Lee, Mi-Kyung; Chi, Seung-Wook.

Aggregation or phase separation can be induced in highly charged proteins by small charged biomolecules. *Soft Matter* **18**(17) 3313-3317, 2022.
Kang, Minchae; **Kim, Minsoo**; Kim, Min Wook; Shin, Yewon; Yoo, Jejoong; Lee, Sang Hak.

Matrix product wave function of the ground state and elementary excitations in the spin-1/2 chain. *Physical Review B* **103**(12) 125157, 2021.
Kim, Jintae; **Kim, Minsoo**; Padmanabhan, Pramod; Han, Jung Hoon; Lee, Hyun-Yong.

Construction of variational matrix product states for the Heisenberg spin-1 chain. *Physical Review B* **102**(8) 085117, 2020.
Kim, Jintae; **Kim, Minsoo**; Kawashima, Naoki; Han, Jung Hoon; Lee, Hyun-Yong.

Software

DeepFold-PLM — Accelerated protein structure prediction via efficient homology search using protein language models.
github.com/DeepFoldProtein/DeepFold-PLM

OTalign — Optimal transport alignment for remote protein homologs using protein language model embeddings.
github.com/DeepFoldProtein/OTalign

plmMSA — Unified MSA construction pipeline integrating the homology search of DeepFold-PLM and the optimal-transport alignment of OTalign.
github.com/DeepFoldProtein/plmMSA

Conference Presentations

Apr 2026	**Mapping the Protein Universe: Accelerated Structure Prediction via Optimal Transport and Latent Spaces** Oral Presentation, 2026 KPS Spring Meeting, Daejeon, Korea

Dec 2024	**Protein Folding: Template-based approach** Oral Presentation, 2024 APCTP-SISSA 1st Joint Workshop on AI and Natural Sciences, Pohang, Korea

Teaching

Teaching Assistant, Department of Physics, Sungkyunkwan University.

Spring 2023	Quantum Field Theory I (PHY5007) — O-Kab Kwon Computational Physics (PHY2025) — Jejoong Yoo
Spring 2022	Biophysics (PHY3033) — Jejoong Yoo
Fall 2021	Biophysics (PHY5170) — Jejoong Yoo
Spring 2021	Biophysics (PHY3033) — Jejoong Yoo
Fall 2020	Electromagnetism I (PHY2010) — Dae-Joon Kang Electromagnetism I, Problem Session (PHY2011) — Dae-Joon Kang
Spring 2020	Classical Mechanics I (PHY2001) — Jung Hoon Han Classical Mechanics I, Problem Session (PHY2002) — Jung Hoon Han

Workshops and Schools Attended

Dec 2022	The 20th KIAS Protein Folding Winter School

Skills

Programming: C, C++, Python, Rust
ML Frameworks: PyTorch, JAX
Parallel/HPC: MPI, NCCL, CUDA, OpenAI Triton, SLURM
Containers: Docker, Apptainer
Molecular Dynamics: GROMACS, OpenMM
Bioinformatics: HMMER, MMseqs2, HH-suite