



TAEIL NOH

SOFTWARE ENGINEER

CONTACT

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SKILLS

• Programming Languages

- python, c, c++, javascript

• System and Tools

1. Bioinformatics Tools(

Gromacs, Schrodinger,
Haddock, Pymol, MMseq2,
Blast, docking tools, esm,
rdkit)

2. Software engineering(

Github, Aws, Docker, django,
Pytorch, React)

LANGUAGES

- Korean : Native
- English: Fluent (TOEFL iBT 102)

REFERENCE

Nationality : Republic of Korea

Birth : 17, Sep, 2001



PROFILE

Creative and driven undergraduate researcher passionate about AI-powered bioinformatics solutions for drug discovery.

Experienced in generative modeling, protein docking, and scalable backend systems using modern frameworks.

Always eager to challenge boundaries, build impactful tools, and contribute to the future of personalized medicine.



EDUCATION

Bachelor of Computer Engineering 2020 - 2026(expected)

School of Engineering | Hongik University, Republic of Korea

GPA : 3.68 / 4.5

MAJOR GPA : 4.24/4.5

(credits take 115/132)

Scholar ships

- 2025-1 Hongik academic creativity scholar ship
- 2024-2 Hongik academic cooperation scholar ship
- 2024-1 Hongik academic creativity scholar ship
- 2021-2 Hongik academic excellence & community spirit scholar ship
- 2021-1 Hongik academic community spirit scholar ship
- 2020-2 Hongik academic excellence scholar ship



INTERSHIP

Bio Software & Intelligent Platform Lab 2024(FEB) - PRESENT
undergraduate researcher

Antibody Sequence Optimization via Deep Generative Models

- Developed AI models (VAE, CVAE, VQ-VAE, CVQ-VAE) to generate optimized antibody binding site sequences based on experimentally measured antigen-binding affinities.
- Leveraged CNN-based classifiers to evaluate binding effectiveness of generated antibody sequences.
- Focused on identifying high-affinity variants through latent space manipulation and probabilistic sampling.

Peptide-Protein Interface Structure Prediction

- Trained large-scale generative models (Diffusion Models, VAE, VQ-VAE) using extensive peptide datasets to predict peptide-protein docking interfaces.
- Applied structure-aware learning techniques to enhance physical plausibility of predicted poses.



INTERSHIP

Modular and Parallelized Drug Discovery Pipeline under Schrodinger Licensing Constraints

- Designed and implemented a modular, reusable, and parallelized drug discovery pipeline under limited Schrodinger license resources.
- Pipeline includes: PDB fixing → protein preparation → docking → energy minimization → sequence mutation → comparative scoring using Schrodinger score, GROMACS energy, and HADDOCK metrics.

HADDOCK Docking Automation and GPU-Accelerated Parallelization

- Built a Docker-based automated pipeline for large-scale HADDOCK docking simulations.
- Developed a modular interface for HADDOCK, enabling API-level control, source code-level customization, and GPU-accelerated parallel docking.
- Conducted large-scale analysis of docking scores across multiple variants and conditions



EXTRACURRICULAR ACTIVITIES

CatchMe Web application

2023(MAR) - 2024(FEB)

Backend engineer

- Developed the backend of CatchMe, a web-based application, using the Python Django framework.
- Designed and implemented the database schema to support user interaction and application logic.database design
- Deployed the application using AWS infrastructure, ensuring scalability and reliability in production environments.

Laidd drug discovery development bootcamp

2024(AUG) - 2024(AUG)

- AI Drug Discovery Bootcamp Completion Certificate Hosted by Korea Pharmaceutical and Bio-Pharma Manufacturers Association (KPBMA)

Military Service, Republic of Korea Army

2021(SEP) - 2023(MAR)

Signal platoon &

Confidential document Specialist

- Appointed as squad leader(for 9 months) in the Signal Platoon and awarded commendations from the division commander, regiment commander, and battalion commander.

Band Khalua

2020 - PRESENT

- drummer (2020 - PRESENT)
- president (2021-2022)

Certification

- Network Advisor 2 (Certificate No : NT2062879)

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