

# KIM, DONGWOOK

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## CURRICULUM VITAE

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### Education

03/2019 -                      Ph.D. candidate in Bioinformatics at Seoul National University  
03/2019 - 02/2022        Completed Master's and Doctor's Integration Course in Bioinformatics at Seoul National University  
03/2015 - 02/2019        B.S. in Biological Sciences, minor in Computer Sciences at Seoul National University

### Research experience

03/2022 -                      Expert Research Personnel at the College of Natural Sciences, Seoul National University. *full-time*  
12/2021 -                      Ph.D. candidate at the Steinegger Lab., Seoul National University. *full-time*  
03/2019 - 11/2021        Ph.D. candidate at the Laboratory of Evolutionary Bioinformatics, Seoul National University. *full-time*  
06/2017 - 02/2019        Intern at the Laboratory of Evolutionary Bioinformatics, Seoul National University  
06/2014 - 07/2014        Visiting student at the Neurovascular Research Laboratory, Department of Radiology, Massachusetts General Hospital, Harvard Medical School  
03/2013 - 02/2014        Visiting student at Hyeon Soo Kim Lab., Department of Anatomy, College of Medicine, Korea University

## ACHIEVEMENTS AND QUALIFICATIONS

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### Awards, Fellowships and Achievements

2019                      Graduated *cum laude* (GPA 3.87/4.30)  
2017                      Samsung Convergence Software Course Scholarship, KRW 1,000,000  
2015                      National Science & Technology Scholarship from the National Research Foundation of Korea, KRW 24,033,000

### Certificates

2019                      Advanced english proficiency, Test of English Proficiency (Score 492/600, percentile rank 94.65%)

### Technical Strengths

Programming    Java, Rust, Python, C/C++, Linux, Shell scripting  
Databases        SQL, MySQL

### Languages

Korean            Native  
English            Fluent

## TALKS, POSTERS, AND PUBLICATIONS

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### Talks

- 07/2023 ISMB/ECCB 2023, Lyon, France, UFCG: database of universal fungal core genes and pipeline for genome-wide phylogenetic analysis of fungi
- 11/2021 IMBG Young Scientist Symposium, Seoul, Korea, EzAAI - A High-Throughput Pipeline for Prokaryotic AAI Calculations

### Posters

- 07/2024 SMBE 2024, Puerto Vallarta, Mexico, Unicore Enables Ultra-fast and Accurate Phylogenetic Reconstruction with Structural Core Genes
- 07/2023 ISMB/ECCB 2023, Lyon, France, UFCG: database of universal fungal core genes and pipeline for genome-wide phylogenetic analysis of fungi
- 06/2020 ASM Microbe Online, Virtual, UUCGf: Whole-Genome Profiling Pipeline of Fungi with Fungal Core Gene Set for High-Resolution Phylogenetics

### Publications

- [1] **Kim D.**, Gilchrist C.L.M., Chun J. and Steinegger M. (2023) UFCG: database of universal fungal core genes and pipeline for genome-wide phylogenetic analysis of fungi, *Nucleic Acids Research*, doi: 10.1093/nar/gkac894
- [2] Kim J., Na S., **Kim D.** and Chun J. (2022), UBCG2: Up-to-date bacterial core genes and pipeline for phylogenomic analysis, *Journal of Microbiology*, doi: 10.1007/s12275-021-1231-4
- [3] **Kim D.**, Park S. and Chun J. (2021), Introducing EzAAI: a pipeline for high throughput calculations of prokaryotic average amino acid identity, *Journal of Microbiology*, doi: 10.1007/s12275-021-1154-0

### Public source codes

- EzAAI <https://github.com/endixk/ezaai>
- UFCG <https://github.com/steineggerlab/ufcg>
- Unicore <https://github.com/steineggerlab/unicore>