WENJIE CHEN

COMPUTATIONAL BIOLOGY | PROTEIN DESIGN | SYNTHETIC BIOLOGY

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github.com/aka-debug-jie

EDUCATION

Wuhan Institute of Technology
B.Eng. candidate in Bioengineering
Sep 2023 - Jun 2027 (expected)

Major rank: 4/72 | Comprehensive rank: 1/72
TOEFL iBT: 80/120

PROFILE

Bioengineering undergraduate moving from SERS/MOF experimental research toward computational biology and AI. Interested in protein structure prediction, sequence design and enzyme engineering, with an emphasis on connecting computational hypotheses to experimental validation.

TECHNICAL SKILLS

- Deep learning: PyTorch; dataset construction, model training, tuning and evaluation.
- Protein computation: AlphaFold2, RFdiffusion, ProteinMPNN and ESM-C.
- Molecular modelling: docking, molecular dynamics and bioinformatics workflows.
- Research: microbial experiments, scientific visualization, literature review and bilingual scientific writing.

SELECTED HONORS

- 2026 - Third Prize, National College Student Life Science Competition (Innovation & Entrepreneurship); team captain.
- 2025 - National First Prize, China Robot and Artificial Intelligence Competition.
- 2025 - Third Prize, National College Student Life Science Competition (Scientific Inquiry).
- 2024 - National Second Prize, Process Equipment Practice and Innovation Competition; team captain.
- 2024 - First Prize, Hubei Python B Group, Lanqiao Cup; Second Prize, Hubei Mathematics Competition.
- 2023-2024 - Outstanding Student Model and First-class Scholarship, Wuhan Institute of Technology.

RESEARCH EXPERIENCE

Protein Language Model Signal Analysis

First author | 2026-present | Manuscript submitted

Developed a knowledge-distillation workflow that transfers residue-level signals extracted from ESMC to a lightweight sequence model. The study tests whether compact models recover stable local sequence patterns rather than only reproducing the signal distribution.

Natural-Product Antivirulence Prioritization for P. aeruginosa PAO1

First author | 2026-present | Manuscript submitted

Built an evidence-stratified ranking framework across virulence-related targets, integrating binding evidence, target accessibility, molecular properties and structural risk, with molecular-dynamics review for candidates proposed for experimental validation.

SERS/MOF Composite Materials

Co-author | 2024-2026 | Three peer-reviewed articles

Contributed to material preparation, sample measurement, data curation, manuscript writing and selected electric-field simulations for antibiotic, pesticide and serum-biomarker detection.

PUBLICATIONS

1. Submitted. Chen, W. et al. A structured-null study of SAE-derived residue profiles in protein language models. Bioinformatics (2026). First author.
2. Submitted. Chen, W. et al. An evidence-stratified resource of natural-product candidate-target hypotheses for antivirulence discovery in Pseudomonas aeruginosa PAO1. Pharmaceuticals (2026). First author.
3. Published. Liu, Y., Chen, W., Yang, J., Cai, N. & Li, J. Exclusive core-satellite composite based on sandwich Ag-MOF-Ag nanoshell with abundant hotspots for sensitive monitoring of antibiotic and pesticide residues in milk. Colloids Surf. A 726, 138029 (2025). doi:10.1016/j.colsurfa.2025.138029
4. Published. Zhang, W., Luo, K., Chen, W., Chen, M., Cai, N. & Li, J. Highly SERS active composite of silver nanospheres-decorated Ag nanostar/ZIF-8 for determination of diquat and thiram residues. Spectrochim. Acta A 345, 126813 (2026). doi:10.1016/j.saa.2025.126813
5. Published. Gui, Y., Luo, K., Chen, W., Cai, N., You, L. & Li, J. Metal-organic framework-based SERS substrates with enrichment and sieving capability for trace detection of small-molecule biomarkers in serum. Microchem. J. 218, 115526 (2025). doi:10.1016/j.microc.2025.115526