

# **Qiyang Hong**

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## **EDUCATION**

- **Ph.D. in Biomedical Engineering (Medical AI)**, Peking Union Medical College & Tsinghua University School of Medicine, Beijing, China (Sept 2023–Present)  
**Advisor:** Prof. Erping Long (Researcher; National Overseas Young Talent)  
**Core Expertise:** Foundation models, LLMs, multimodal learning, temporal modeling; deep phenotyping, clinical AI; model interpretability; high-performance computing (4×A6000, 2×H100)
- **M.S. in Biochemistry and Molecular Biology**, Xiamen University, Xiamen, China (Sept 2014–July 2017)  
**Advisor:** Prof. Ning-Shao Xia (Academician, Chinese Academy of Engineering)  
**Specialization:** Transcriptomics, viral immunology, structural biology, computational molecular analysis
- **B.Eng. in Bioengineering**, Jimei University, Xiamen, China (Sept 2010–July 2014)

## **TECHNICAL SKILLS**

- **Artificial Intelligence & Machine Learning:**  
Neural networks, Transformer architectures, foundation models, LLMs, multimodal learning, temporal modeling, representation learning, model interpretability.
- **Model Training & High-Performance Computing:**  
PyTorch, CUDA, distributed training, GPU cluster management (Linux HPC, A6000 nodes), job scheduling, system optimization, large-scale data preprocessing, performance profiling.
- **Bioinformatics & Genomic Analysis:**  
WES/WGS pipelines, RNA-seq, SNP/Indel/CNV detection, variant annotation and ACMG classification, immunogenomics, neoantigen prediction, clinical diagnostics workflow development.
- **Programming & Data Engineering:**  
Python, NumPy, pandas, scikit-learn; workflow automation; reproducible pipelines; Django-based web applications.

- **Data Visualization & Network Analysis:**

matplotlib, seaborn, igraph, networkx; interactive visualization for clinical and genomic datasets.

## **PROFESSIONAL EXPERIENCE**

- **Group Leader, Molecular Diagnostics**

Affiliated Hospital of Putian University, Prenatal Diagnosis Center  
Aug 2020 – Jul 2023

- **Senior Bioinformatics Engineer (Part-time)**

Jinfeng Biotechnology Co., Ltd., Data & Information Department  
Nov 2020 – Jan 2022

- **Bioinformatics Supervisor**

Berry Genomics Co., Ltd.  
Jul 2017 – Aug 2020

## **PUBLICATIONS**

\*Equal contributor, #Corresponding author, 'first-author student

### **In revision/ review/ preparation:**

1. **Qiyang H\***, Long E#. A foundational model encodes deep phenotyping data and enables diverse downstream applications. *npj Digital Medicine*. 2025. (Revision 1)
2. **Qiyang H**, Long E#. Multi-Omics Mendelian Randomization Identifies SERPING1 as a COPD Modulator. 2025. (Submitted)
3. **Qiyang H\***, Long E#. Cough, sputum, and CD164: Novel risk factors/biomarkers for COPD and lung function decline. 2025. (Submitted)
4. **Qiyang H\***, Long E#. Proteo-metabolomic insights into the progression of COPD and lung function decline. 2025. (Submitted)
5. **Qiyang H**, Long E#. GWAS meta-analyses with a new Chinese population expand the genetic architecture and improve ancestry-specific genetic risk prediction of chronic obstructive pulmonary disease. 2025. (Submitted)

### **Published/ accepted:**

6. Xinti Sun\*, **Qiyang H\***, Long E#. Model confrontation and collaboration: a debate intelligence framework for enhancing medical reasoning in large language models. *Cell Reports Medicine*. 2025. (Cover Highlights)
7. Lin K\*, **Qiyang H\***, Mingqiao Chen#. Cervical HPV infection and related diseases among 149,559 women in Fujian: an epidemiological study from 2018 to 2023. *Frontiers in Microbiology*. 2024.
8. Yang H\*, Zizhen L\*, **Qiyang H**, Ningshao X#. A stepwise docking molecular dynamics approach for simulating antibody recognition with substantial conformational changes. *Computational and Structural Biotechnology Journal*. 2022.

9. **Qiyang H**, Ningshao X<sup>#</sup>. Identification of strategic residues at the interface of antigen–antibody interactions by in silico mutagenesis. *Interdisciplinary Sciences: Computational Life Sciences*. 2018.
10. **Qiyang H**, Ningshao X<sup>#</sup>. Atomic structures of Coxsackievirus A6 and its complex with a neutralizing antibody. *Nature Communications*. 2017.
11. **Qiyang H**, Ningshao X<sup>#</sup>. The C-terminal arm of the human papillomavirus major capsid protein is immunogenic and involved in virus-host interaction. *Structure*. 2016.
12. **Qiyang H**, Ningshao X<sup>#</sup>. A shared N-terminal hydrophobic tail for the formation of nanoparticulates. *Nanomedicine*. 2016.

## **PROFESSIONAL ACTIVITIES**

**Reviewer (ad-hoc):**Nature Medicine, Nature Biomedical Engineering, Frontiers in Aging Neuroscience

## **RESEARCH PROJECTS & TECHNOLOGY DEVELOPMENT**

- **Temporal Foundation Models for COPD Progression**

National Science and Technology Major Project (Youth Scientist Program), 2025–2028

Developing longitudinal multi-omics integration and temporal neural networks to decode COPD progression, identify molecular signatures, and support early risk prediction.

- **Biomedical Foundation Model (UK Biobank)**

Built a Transformer-based foundation model trained on deep phenotyping data from >500,000 participants, enabling disease prediction, multimorbidity analysis, and patient stratification across 289 conditions.

- **Automated Clinical WES Analysis Pipeline**

Developed an end-to-end workflow from FASTQ to SNP/Indel/CNV detection, annotation, ACMG classification, and automated reporting; deployed in clinical settings with version-controlled pipelines.

- **Neoantigen Prediction and Immunogenomics Pipeline**

Integrated WES and RNA-seq pipelines with NetMHC/MHCflurry to identify candidate neoantigens for immunotherapy and tumor profiling.

- **WES Clinical Interpretation and Visualization Platform**

Implemented a Django-based interactive web platform enabling clinicians to visualize variants, coverage, CNVs, and Sanger traces, supporting clinical genetic diagnosis.

- **Consumer Genomics Analysis Framework**

Contributed to the development and maintenance of large-scale production pipelines for SNP genotyping and ancestry/trait reporting in collaboration with consumer genomics companies.

- **Inherited Disease and Metabolic Panel Pipelines**

Designed and optimized pipelines for thalassemia, SMA, mitochondrial disorders, and mtDNA variant detection to support clinical molecular diagnostics.

- **Custom WES Probe Design Optimization**

Improved exome capture efficiency by designing probe sets enriched for pathogenic ClinVar regions, enhancing diagnostic yield.

- **High-throughput Transcriptomics Analysis**

Performed differential expression and KEGG/GO enrichment analysis for bacterial and human datasets under diverse physiological conditions.