# Feng Yang

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## EDUCATION

**Sichuan University**
Sichuan, China
September 2014-June 2018
Degree: Bachelor of Software Engineering
Degree: Bachelor of Biological Science
Specialty: Bioinformatics
GPA: 3.4/4.0

**Institute of Neuroscience**
Shanghai, China
September 2018-April 2021

**The Chinese University of Hong Kong**
Hong Kong, China
September 2021-July 2025
Degree: PhD
Specialty: Bioinformatics

## PUBLICATIONS

1. Xiaona Chen*, **Feng Yang***, Suyang Zhang*, Xiaofan Guo, Jieyu Zhao, Yulong Qiao, Liangqiang He, Yang Li, Qin Zhou, Michael Tim Yun Ong, Chun Kit Kwok, Hao Sun and Huating Wang. “DNA G-quadruplex Profiling Reveals Functional and Mechanistic Role of G-quadruplexes in Skeletal Muscle Stem Cells” **BioRxiv**, 2025 https://doi.org/10.1101/2025.02.10.637367
2. Jieyu Zhao*, **Feng Yang***, Yuwei Zhang, Huating Wang and Chun Kit Kwok. “TDP-43 binds to RNA G-quadruplex structure and regulates mRNA stability and translation” 2025 (In revision, Nucleic Acids Research)
3. Yanwang Huang, Shangyi Wang, Qingxiu Wang, Chaowen Zheng, **Feng Yang**, Lei Wei, Xintong Zhou and Zuoren Wang. "Glutamatergic Circuits in the Pedunculopontine Nucleus Modulate Multiple Motor Functions" **Neuroscience Bulletin**, 2024 https://doi.org/10.1007/s12264-024-01314-y

4. Yuwei Zhang, Jieyu Zhao, Xiaona Chen, Yulong Qiao, Jinjin Kang, Xiaofan Guo, **Feng Yang**, Kaixin Lyu, Yiliang Ding, Yu Zhao, Hao Sun, Chun-Kit Kwok and Huating Wang. "DHX36 binding induces RNA structurome remodeling and regulates RNA abundance via $m^6A$ reader YTHDF1" **Nature Communications**, 2024
   https://doi.org/10.1038/s41467-024-54000-y
5. Zhiming He, Xiaona Chen, Li Yuying, **Feng Yang**, Hao Sun and Huating Wang. "Sugt1 loss in skeletal muscle stem cells impairs muscle regeneration and causes premature muscle aging", **Life Medicine**, 2023
   https://doi.org/10.1093/lifemedi/lnad039
6. Suyang Zhang, **Feng Yang**, Yile Huang, Liangqiang He, Yuying Li, Yi Ching Esther Wan, Yingzhe Ding, Kui Ming Chan, Ting Xie, Hao Sun and Huating Wang."ATF3 induction prevents precocious activation of skeletal muscle stem cell by regulating H2B expression" **Nature Communications**, 2023
   https://doi.org/10.1038/s41467-023-40465-w
7. Qiming Lv, Mingchao Yan, Xiangyu Shen, Jing Wu1, Wenwen Yu, Shengyao Yan, **Feng Yang**, Kristina Zeljic, Yuequan Shi, Zuofu Zhou, Longbao Lv, Xintian Hu, Ravi Menon and Zheng Wang."Normative Analysis of Individual Brain Differences Based on a Population MRI-Based Atlas of Cynomolgus Macaques" **Cerebral Cortex**, 2021
   https://doi.org/10.1093/cercor/bhaa229

## Research EXPERIENCE

**ATF3 induction prevents precocious activation of skeletal muscle stem cell by regulating H2B expression**

**December 2021 - September 2022**

- By analyzing RNA-Seq in FISCs collected from the Ctrl and iKO muscles, we found that the ATF3 loss induced global transcriptional activation, and we found ATF3 loss decreases H2b gene expression.
- By analyzing H2B CUT&Run and comparing the H2B binding difference after ATF3 KO, we found that decreased H2B level could mediate the precocious SC activation following the ATF3 loss.

**TDP-43 promotes enhancer-promoter loop interaction via binding and stabilizing DNA G-quadruplexes**

**December 2021 - present**

- By harnessing and integrating a variety of high-throughput sequencing datasets, including Hi-C, DNA G4(dG4) ChIP-seq, TDP-43 ChIP-seq, ATAC-seq, etc., from K562 and HepG2 cells, we demonstrate that dG4 and TDP-43 signals are highly enriched at enhancer-promoter (E-P) loop anchors. dG4 enrichment at the E-P loop anchors is associated with increased loop interaction.
- Moreover, dG4 formation at the E-P loop anchors is positively associated with chromatin openness, TF binding, and promoter expression.
- Further analysis reveals that TDP-43 binding at the E-P loop anchors is associated with a higher dG4 enrichment and increased interaction frequency. And increased chromatin openness, TF binding, and gene expression are observed on the TDP-43 bound dG4 enriched E-P anchors.

**DNA G-quadruplex Profiling Reveals Functional and Mechanistic Role of G-quadruplexes in Skeletal Muscle Stem Cells**

**April 2022 - present**

- Analyzed G4 CUT&Run-seq to map the G4 landscapes in adult skeletal muscle stem cells (MuSCs) which are essential for injury induced muscle regeneration. we uncover dynamic endogenous G4 formation with a pronounced G4 induction when MuSCs activate and proliferate.
- Combined with RNA-seq, we further demonstrate that the G4 induction promotes MuSC activation thus the regeneration process.
- By integrating Micro-C and HiC data, histone ChIP-seq, we found that promoter associated G4s regulate gene transcription through facilitating chromatin looping.
- By integrating public transcription factor (TF) ChIP-seq results, we found that G4 sites are enriched for TF binding events in activated MuSCs; And we found MAX binds to G4 structures to synergistically facilitate chromatin looping and gene transcription thus promoting MuSC activation and regeneration.

**TDP-43 binds to RNA G-quadruplex structure and regulates mRNA stability and translation**

**April 2022 - present**

- Analyzed RNA Bind-n-Seq, we show that TDP-43 exhibits a preference for binding to the rG4 structure under K+ condition.
- By analyzing the SHALiPE-seq data, we found that the loss of TDP-43 contributes to a decrease in mRNA structure in the transcriptome by using the newly developed SHALiPE-seq technology.
- Combined with TDP-43 iCLIP-seq, we demonstrate that the reduction in structural complexity is likely due to the loss of TDP-43 binding to the RNA targets, especially in the 3'UTR.
- We further revealed that TDP-43 binds to a novel rG4 structure in the 3'UTR of SLC1A5 mRNA, promoting its mRNA stability and translation.

**Functional study of JunB in skeletal muscle regeneration a tale of muscle stem cell-niche crosstalk**

**April 2022 - present**

- After analyzing bulk RNA-seq, we found that JunB is rapidly induced upon MuSC activation.
- By combined multi omics analysis, we found JunB binds and suppresses the transcription of factors mediating the extrinsic MuSC-niche crosstalk; JunB ablation leads to increased expression of niche factors and alters niche cell composition and cell crosstalk.
- Combined with HiC, Micro-C data, we found that JunB may orchestrate gene transcription by regulating EP looping.

## Laboratory Skills

- **Programming:** Python, R, Perl, C, Bash
- **Analyze sequencing data:** Bulk RNA-seq, Single cell RNA-seq, ChIP-seq, CUT&Run, CUT&Tag, HiC, Micro-C, SHALiPE-seq, rG4-seq, RBNS-seq