Xiaozhen Wen, M.S.

12133067@mail.sustech.edu.cn • [Google scholar](#)

EDUCATION

Bachelor of Science, Bioinformatics   Sept 2017 – June 2021

Southern Medical University (SMU),
Guangzhou, China

Advisors: Prof. Liang Li

Master of Science, Systems biology   Sept 2021 – June 2024

Southern University of Science and Technology (SUSTech),
Shenzhen, China

Advisors: Prof. Wei Chen

RESEARCH EXPERIENCE

Identification of TFs and ncRNAs associated with CYP3As in the liver and small intestine based on GTEx v8 data   Mar 2020 – Sept 2022

Weighted gene co-expression network analysis (WGCNA)

Screening TFs and lncRNAs related to the expression of CYP3A

Functional Enrichment Analysis

A cross-tissue investigation of molecular targets and physiological functions of Nsun6 using knockout mice   June 2021 – Mar 2022

Differential gene expression analysis of mouse datasets

Functional Enrichment Analysis

Gene Set Enrichment Analysis

Systematic characterization of RNAs associated with the cytoplasmic processing body using TRIBE-STAMP method   Mar 2022 – Present

Development of a computational pipeline for TRIBE-STAMP method analysis

Analysis of poly(A) tail length preferences in P-body associated transcripts

Determination of isoform-specific localization patterns of mRNAs by Oxford nanopore full-length cDNA sequencing

Exploring RBPs involved in mRNA localization within P-bodies using eCLIP datasets

Measurement analysis of mRNA stability with translational inhibitors

Translation efficiency calculation for polysome profiling data

Development of a computational pipeline for analyzing single-cell TRIBE-STAMP datasets

AWARDS

Outstanding volunteer, SMU (2018)
Excellent Student Cadre, SMU (2019)
National Encouragement Scholarship, SMU (2019-2020)
Outstanding student scholarship, Third prize, SMU (2020)
200m event in the graduate group, Third prize, SUSTech (2023)
Campus Running Points Competition, Third prize, SUSTech (2023)

COMPUTER SKILLS

Programming R**, shell**, Python*, Perl* (*: proficiency)

CONFERENCE

Oral presentation

Zhiyuan Sun, **Xiaozhen Wen**, liang Fang, Wei Chen. Systematic characterization of RNAs associated with the cytoplasmic processing body using TRIBE-STAMP method, The 28th Annual Meeting of the RNA Society, June 2023

PUBLICATION（1=joint first authors）

1. Chen LD, Lu HJ, Gan YL, Pang SW, Zheng Q, Ye DM, Huang XY, Qi HN, Xu WB, **Wen XZ**, Li LH, Li L. Partial thyroxine-binding globulin deficiency in a family with coding region mutations in the TBG gene. J Endocrinol Invest. 2020 Dec;43(12):1703-1710. doi: 10.1007/s40618-020-01245-1. Epub 2020 Apr 7. PMID: 32266677.

2. Huang H[1], Zhang S[1], **Wen X[1]**, Sadee W, Wang D, Yang S, Li L. Transcription Factors and ncRNAs Associated with CYP3A Expression in Human Liver and Small Intestine Assessed with Weighted Gene Co-Expression Network Analysis. Biomedicines. 2022 Nov 28;10(12):3061. doi: 10.3390/biomedicines10123061. PMID: 36551817; PMCID: PMC9775998.

3. Wang W[1], Huang H[1], Jiang H, Tian C, Tang Y, Gan D, **Wen X**, Song Z, He Y, Ou X, Fang L. A Cross-Tissue Investigation of Molecular Targets and Physiological Functions of Nsun6 Using Knockout Mice. Int J Mol Sci. 2022 Jun 13;23(12):6584. doi: 10.3390/ijms23126584. PMID: 35743028; PMCID: PMC9224068.

4. Sun Z[1], **Wen X[1]**, Li Y, Tian S, Wang M, Tan Y, Shu Y, Zhou X, Zhang M, Jiang F, Fang L, Chen W. Systematic characterization of processing body mediated RNA regulation using TRIBE-STAMP method. (Submitted, October, 2024)