

Xiaozhen Wen, M.S.

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EDUCATION

Bachelor of Science, Bioinformatics

Southern Medical University (SMU),
Guangzhou, China
Advisors: Prof. Liang Li

Sept 2017 – June 2021

Master of Science, Systems biology

Southern University of Science and Technology (SUSTech),
Shenzhen, China
Advisors: Prof. Wei Chen

Sept 2021 – June 2024

RESEARCH EXPERIENCE

Identification of TFs and ncRNAs associated with CYP3As in the liver and small intestine based on GTEx v8 data

Weighted gene co-expression network analysis (WGCNA)
Screening TFs and lncRNAs related to the expression of CYP3A
Functional Enrichment Analysis

Mar 2020 – Sept 2022

A cross-tissue investigation of molecular targets and physiological functions of Nsun6 using knockout mice

Differential gene expression analysis of mouse datasets
Functional Enrichment Analysis
Gene Set Enrichment Analysis

June 2021 – Mar 2022

Systematic characterization of RNAs associated with the cytoplasmic processing body using TRIBE-STAMP method

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

Mar 2022 – Present

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 H¹, Zhang S¹, **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 W¹, Huang H¹, 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 Z¹, **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)