# Chuhanwen Sun

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## EDUCATION

**Karolinska Institutet, Stockholm, Sweden**                                                          **Aug. 2023 – Present**

*Master of Biomedicine*

- Coursework taking:

**Life of sciences:** Frontiers in Biomedicine, Bioethics and Laboratory Animal Science, Applied Biomedical Communication and Professional Development, Biomedical Research Literacy, Bioentrepreneurship

**Statistics & Informatics:** Applied Biostatistics, Bioinformatics

**Tsinghua University, Beijing, China**                                                          **Sept. 2019 – Aug. 2023**

*Bachelor of Life Science, GPA:3.66*

- Second-class Prize Scholarship of Tsinghua University
- Excellent Scholarship of Comprehensive Quality at Tsinghua University
  - Coursework:

**Life of sciences:** Molecular Biology, General Biology, Genetics, Cell Biology, The General Experiment of The Biochemistry and Molecular Biology, Protein Structure in Virus Life Cycle, Current Research of Neuronal Disorders, Experiment of Cell Biology, Fundamental Neuroscience, Biology of Brain Disorders, Physiology, The magical brain

**Statistics & Informatics:** Calculus, Linear Algebra, Programming Fundamentals, Probability and Statistics, Statistics for Psychology, The Fundamentals of Computer Programming (Python), Information Retrieval

**Other core courses:** Chemical Principles, Organic Chemistry, Biochemistry, Lab. of Organic Chemistry, Lab of Inorganic and Analytical Chemistry, Physical Chemistry, Basic Practical Biochemistry.

## Internships and Summer research

**Air Tsinghua, Beijing, China**                                                          **Jul. 2022 – Aug. 2023**

*Drug repurposing: conduct computational analysis on existing patient drug response to predict the new drug efficacy*

- Analyzed and integrated RNA-Seq, methylation, SNV, and CNV data from public databases; applied deconvolution and dimension reduction for cell type estimation and tumor sub-clustering.
- Visualized repurposed drugs using Sankey diagrams and contributed to article writing with detailed figures.
- Assessed AI drug repurposing industry trends through in-depth company analysis.

*Drug sensitivity dataset  integration: employ mathematical approaches to eliminate drug sensitivity database heterogeneity*

- Integrated drug-cell line data from over 15 published databases, creating a standardized comprehensive database.
- Applied methods like MCMC for drug sensitivity curve fitting, deriving metrics for visualization to interpret data and probe database heterogeneity causes.

*Logic chain QA: extracted biological research knowledge from literature and KGs to generate a logic-based QA dataset.*

- Refined published binary outcomes to construct a knowledge graph related to biochemical and pharmaceutical fields.
- Filtered and standardized relevant published articles from PubMed for downstream use.
- Employed prompt-based and Cot methods with the GPT-3.5 model to generate QA dataset for multiple question types.

**Department of Automation, Tsinghua University, Beijing, China**                          **Jun. 2023 – Present**

*scRNA-seq analysis: identify the potential cell transformation for atherosclerotic plaque instability*

- Integrated single-cell sequencing data on several diseases including atherosclerosis and rheumatoid arthritis; identified and compared cell sub-clusters in macro/mono cells between distinct diseases.

*scRNA-seq analysis: explore the potential consistency in vascular remodeling diseases*

- Integrated multiple vascular remodeling disease sequencing data to analyze potential cell types across diseases, identifying consistencies and differences in subtypes and exploring potential disease variations and treatment methods.

# RESEARCH EXPERIENCE

**The research project,  CMB, Karolinska Institute, Stockholm, Sweden**                    **Oct. 2023 – Present**

*'Development and application of novel methods to interpret and leverage multi-organ single-cell spatial profiling data of triple-negative breast cancers' supervised by Prof. Jean Hausser*

- Develop Tumor Promoting Microenvironment Characterization method to evaluate the pro/anti-proliferative microenvironments of TNBC.

- Evaluate Niche-Phenotype Mapping and Tumor Promoting Microenvironment Characterization in immune-enriched and immune-poor TNBC and associations with recurrence.

**The capstone project,  IDG/M$^C$GOVERN INSTITUTE, Tsinghua University, Beijing, China**        **Jul. 2022 – Sept. 2023**

*'Investigation into pathophysiological roles of ATXN2/2L in neuron system' supervised by Prof. Yi Lin*

- Initiated in vivo and in vitro research on ATXN2 and ATXN2L, focusing on the effects of varying polyQ lengths.

- Constructed sixteen stable cell lines from U2OS ATXN2/2L DKO/SKO, followed by IP and IF for interaction protein differentiation; Analyzed PolyQ length impact on phase separation through in vitro protein purification. Created a cerebellum-specific ATXN2/2L knockout mouse model and evaluated its motor and balance via behavioral tests.

- Synthesized results from various experiments into comprehensive figures for academic presentation.

**The research project,  College of Life Science, Tsinghua University, Beijing, China**            **Mar. 2022 – Jul. 2022**

*'Effect of Clock protein phase isolation on rhythm' supervised by Prof. Yi Lin*

- Engineered Clock protein mutants via PCR, leading to the construction of truncated plasmids; isolated and identified proteins using in vitro phase separation assays. Developed and validated a Clock-Flag knock-in U2OS cell line through CRISPR/Cas9, confirmed with Western Blot, immunostaining, and DNA sequencing.

**The research project, Tsinghua Laboratory of Brain and Intelligence, Beijing, China**            **Sept. 2021 – Dec .2021**

*'Modeling and behavioral testing of Parkinson's disease mice,' supervised by Prof. Yichang Jia*

- Researched methodologies for chronic and subacute Parkinson's Disease (PD) mouse models.

- Innovated a reliable PD model using rotenone and MPTP, elevating its applicability for research; Validated via tissue immunofluorescence (IF) and behavioral tests; employed ImageJ for staining image quantification and conducted data analysis with SPSS, ensuring robust evaluation.

*'Study on learning and memory behavior of CX3CR1 mice' supervised by Prof. Yichang Jia*

- Engineered a CX3CR1 knockout mouse model using Cre-loxP and activated it with tamoxifen injections.

- Evaluated knockout mice's learning and memory using contextual fear conditioning tests and prepared hippocampal tissue post-stimulation and extracted RNA from RibotTag-purified samples for subsequent molecular analysis. Investigated microglia's role in learning and memory through staining techniques and ImageJ analysis.

# PUBLICATION

1. Co-authored '**Circadian clocks are modulated by compartmentalized oscillating translation', Cell.**

   **Contribution:** Three-dimensional visualization in cell staining images and quantitative comparison.

2. Co-authored '**Multi-Drug Transfer Learning Models for Efficient Pre-clinical Drug Discovery', Science Advanced (under review).**

   **Contributions:** Data Collection, Transcriptomic Deconvolution Analysis, Drug Feasibility Investigation, Public Database Utilization, Academic Figure Production.

3. Co-authored '**A new type of monocytes responsible for atherosclerotic plaque instability.', Circulation (under review).**

   **Contribution:** Preliminary Research Conduct, Public Data Integration, Initial Manuscript Drafting Participation.

# SKILLS

**Programming:** R, Python, Matlab

**Languages:** English, CET4:550 CET6:525 IETS:7.5