

Mo Sun

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INTERESTS

My current research focus on genetics, epigenetics and genome instability by utilizing bioinformatics methods and techniques. My research work is about: 1) Gene regulation and Single-cell genomics 2) RNA roles in genome instability 3) DNA repair and CRISPR screening.

EDUCATION

Georgia Institute of Technology

Ph.D. Student in Bioinformatics

Advisor: Prof. Francesca Storici

Aug. 2021 - 2026 (expected)

Atlanta, GA

Worcester Polytechnic Institute

M.S. in Bioinformatics & Computational Biology

Advisor: Prof. Dmitry Korkin

Aug. 2019 - May. 2021

Worcester, MA

Henan University of Chinese Medicine

Bachelor of Science in Pharmacy

Sep. 2015 - Jun. 2019

CHINA

SELECTED PUBLICATIONS

(*Equally contributed) (Full list: [Google scholar profile.](#))

- [1] Xu, Penghao, Taehwan Yang, Deepali L. Kundnani, **Mo Sun**, Stefania Marsili, Alli L. Gombolay, Youngkyu Jeon et al. "Light-strand bias and enriched zones of embedded ribonucleotides are associated with DNA replication and transcription in the human-mitochondrial genome", **Nucleic Acids Res.** **2024**
- [2] *Jingcheng Yang, ***Mo Sun**, Zihan Ran, Taewhan Yang, Deepali L. Kundnani, Francesca Storici, Penghao Xu. "rNMPID: a database for ribonucleoside Mono-Phosphates In DNA", **Bioinformatics Advances.** **2024**
- [3] Zhao Cui, Caifeng Li, Wei Liu, **Mo Sun**, Shiwen Deng, Junxian Cao, Hongjun Yang and Peng Chen. "Scutellarin activates IDH1 to exert antitumor effects in hepatocellular carcinoma progression", **Cell Death & Disease.** **2024**
- [4] *Yu, Gengyuan, ***Mo Sun**, Tonghua Zhang, Haoran Xu, Jiaqi Wang, Wanting Ye, Peng Wang, Shiyun Zhang, Chenning Zhang, and Yikun Sun. "Lanhuashen stimulates the positive cross-regulation mediated by the S1P axis to ameliorate the disorder of glucolipid metabolism induced by the high sucrose diet in *Drosophila melanogaster*", **Journal of Ethnopharmacology.** **2023**
- [5] Srinivasan, Suhas, Hongzhu Cui, Ziyang Gao, Ming Liu, Senbao Lu, Winnie Mkandawire, Oleksandr Narykov, **Mo Sun** and Dmitry Korkin. "Structural genomics of SARS-CoV-2 indicates evolutionary conserved functional regions of viral proteins", **Viruses.** **2020**

RESEARCH EXPERIENCE

Georgia Institute of Technology

Sep. 2022 - Present

• Genome-wide ribonucleotides embedment and R-loops in Aicardi-Goutières Syndrome

- Analyzed ChIP-seq, ATAC-seq, DRIPc-seq, DNA-seq and Ribose-seq data to reveal rNMPs distribution patterns and Epigenetic signatures in Aicardi-Goutières Syndrome patients.
- Explored the role and function of rNMPs and R-loops in transcription-replication conflict.
- Developed deep learning model for de novo mutation detection using Nanopore sequencing.

Emory University

Jan. - May. 2022

• Multi-omics analysis of the Gene-Environment interactions in Autism spectrum disorder

- Performed scRNA-seq and scATAC-seq to analysis the effect of BPA of neural cell differentiation using cerebral cortical organoids.
- Functional analysis of BPA-responsive non-coding variants using massively parallel reported assays.
- Analysis of BPA-responsive SNPs using scarless genome editing in iPSCs and chromatin accessibility in post-mortem brains from bulk and snATAC-seq

Worcester Polytechnic Institute

Sep. 2019 - May. 2021

• Prediction of Protein-ligand binding effect by Population-specific Variants

- Analyzed WGS data in gnomAD and GWAS to determine the functional diversities among populations.
- Co-localization analysis of Protein-ligand binding patterns on mutation sites.
- Development of Semi-supervised machine learning methods to predict large-scale effects of genetic variants on protein-ligand interaction

• Structural Genomics and Interactomics of SARS-CoV-2

- Modeling structure characterization of SARS-CoV-2 protein.
- Inferring SARS-Cov-Host protein-protein interaction network.

HONORS

Outstanding Graduates of Henan University of Chinese Medicine

2020

SKILLS

- **Programming:** Python, R, Matlab, Bash, Git, SQL, L^AT_EX.
- **Machine Learning and Deep Learning:** PyTorch, Keras, Scikit-learn, Tensorflow.
- **Bioinformatics and Computational Biology:** DNA sequencing, RNA-seq, epigenomics, functional genomics, single-cell multi-omics.
- **Biology skills:** Flow cytometry, Mass spectrometry, qPCR, Cell Transfection, Cell Culture, Western Blot.