XINZHI ZOU

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EDUCATION

School of Life Sciences, Tsinghua University, Beijing, China *Sep. 2013 - Jul. 2017*
Overall GPA: 3.82/4.0 (top 3 students)
School of Medicine, Stanford University, CA, US *Jun. 2016 - Sep. 2016*
Department of Bioengineering, Stanford University, CA, US *Sep. 2017 - present*

AWARDS

- Second prize in the 2015 National Challenge Cup Innovation Competition of China
- Representative for the Tsinghua Team at the 2016 iGEM Giant Jamboree, awarded gold medal.
- UGVR Scholarship, Stanford, 2016

PUBLICATIONS

Zhang, W., Zhao, G., Luo, Z., Lin, Y., Wang, L., Guo, Y., ... & Wang, Y. (2017). *Engineering the ribosomal DNA in a megabase synthetic chromosome.* Science, 355(6329), eaaf3981.

Zhou, X. X., Zou, X., Chung, H. K., Gao, Y., Liu, Y., Qi, L. S., & Lin, M. Z. (2017). *A single-chain photoswitchable CRISPR-Cas9 architecture for light-inducible gene editing and transcription.* ACS Chemical Biology.

RESEARCH EXPERIENCE

The efficient and systematic by-step methods on the integration of Chromosome XII in the *Saccharomyces cerevisiae*.
Sep. 2015 - Sep. 2016 *Advisor: Dr. Junbiao Dai, Tsinghua University, Beijing*

· The research aims to developing an efficient and systematic method to integrate synthetic yeast chromosomes in to the genome, in order to further engineer artificial chromosome in eukaryotes.
· Integrated all 33 synthetic single chunks of Chromosome XII into wide-type *S. cerevisiae*.
· Using PCR and sequencing, identified the strains of *S. cerevisiae* in which one of the 33 single chunks of Chromosome XII is fully replaced by synthetic chunk.
· Designed a system to increase integration efficiency by DNA DSB (double-strand break) generated from Isce-I, an endonuclease native in yeast, by introducing ISce-I expression plasmid into the yeast recognition site on Chromosome XII.

A single-chain photoswitchable CRISPR-Cas9 architecture for light-inducible gene editing and transcription.
Jun. 2016 - Sep. 2016 *Advisor: Dr. Michael Lin, Stanford University, CA*

· The research project aims to achieve spatial and temporal control of gene transcription and DNA cleavage in human cell lines using a light-inducible CRISPPR/Cas9 system.
· Constructed and screened different Dronpa mutants fused sadCas9 and spdCas9 and validated light induction by mCherry expression, resulting in a 100x-increased efficiency.
· Activated endogenous gene, CXCR-4 gene in 293T cell line by ps(photo-switchable)-spdCas9. Tested the reversibility of caging and uncaging of dCas9 activity with semi-RT-qPCR.
· Compared gene transcription activation and editing function of the engineered ps-spCas9, ps-spdCas9 and ps-saCas9 to LACE(Light-activated Cas9 effector) system, proving to be better in various ways.

An inducible cell lysis system sensing population density based on pheromone-mediated cell communications in *Saccharomyces cerevisiae*.

Nov. 2016 - July. 2017 *Advisor: Dr. Junbiao Dai Tsinghua University, Beijing, China*

- The research aims to construct an inducible lytic system in *S. cerevisiae* sensing the population density.
- Constructed the over-expression of BGL-2 gene and expression of HIV-1 protease gene and compared the lytic effect in *S. cerevisiae*.
- Constructed the cell density sensing system by introduing FUS promoter to upstream of lytic gene.
- Achieved the construction of an inducible yeast lysis genetic circuit to sense cell density and finished my graduation thesis and defense.

The development and application of site-specific recombinase system in *Saccharomyces cerevisiae*.

Nov. 2014 - Aug. 2015 *Advisor: Dr. Junbiao Dai Tsinghua University, Beijing, China*

- The research aimed to construct an inducible binary gene expression system in *S. cerevisiae* using inducible DNA recombination
- Constructed the expression system in *S. cerevisiae* with recombinase Bxb1 and phiC31, and finalized the reporter system with the recognition sites and the reporter gene GFP.
- Validated the function of recombinase Bxb1 and phiC31 by PCR and sequencing.
- Uncovered a disruption in gene expression following the insertion of the recognition site of recombinase Bxb1 and phiC31 by semi-qRT-PCR.

The development of an efficiently parallel algorithm for protein design based on natural structure.

Aug. 2015 - Dec. 2015 *Advisor: Dr. Jianyang Zeng, Tsinghua University, Beijing*

- The research aimed to improve the efficiency and reliability of existing algorithms for protein design based on natural structures.
- Developed an algorithm that reduced the operation time by 20,000 times compared to the average for existing algorithms and expanded the quantity of proteins that could be designed.
- Co-authored a paper that was awarded the second prize in 2015 Challenge Cup Chinese National Undergraduate Curriculum Academic Science and Technology competition.

RESEARCH SKILLS

Molecular biology
PCR, qPCR, RT-PCR, overlap PCR, Genome extraction, RNA extraction;

Microscopy
Optical Microscopy, Fluorescent Microscopy, Confocal Microscopy

Biochemistry
ELISA, Western Blot, Protein purification, Immuno-Precipitation, FACS;

Model Organisms
E.coli, Yeast, Mammalian cell;

LEADERSHIP

Vice President, Students Association of Science and Technology in Tsinghua University

President, Traditional Chinese Calligraphy Association, Tsinghua University

SKILLS AND INTERESTS

Language: English [TOEFL: 111, GRE: V:162(90%), Q:168(95%), AW:3.5(42%)], Chinese(native)

Interests: Ultimate Frisbee, Swimming, Chinese Calligraphy, Reading, Piano.