

Ruizhe (Richard) Wang

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EDUCATION

University of North Carolina at Chapel Hill

B.S. in Biology and Computer Science | GPA: 3.86

Chapel Hill, NC

Expected May 2027

Biology Coursework: Functional Genomics & Laboratory, Molecular Genetics, Cell Biology, Developmental Biology, Immunology

Computational & Quantitative Coursework: Introduction to Machine Learning, Introduction to Computer Vision, Algorithms and Analysis, Basic Elements of Probability and Statistical Inference I, Models of Languages and Computation, Linear Algebra, Discrete Mathematics

RESEARCH EXPERIENCE

Strahl Lab, Department of Biochemistry & Biophysics, UNC Chapel Hill

Undergraduate Researcher | PI: Brian D. Strahl

Chapel Hill, NC

Mar 2024 – Present

Experimental Validation of AlphaFold 3-Predicted Histone-Recognition Proteins

Aug 2026 – Present

Collaboration with the Steven Jacobsen Lab, UCLA

- Lead experimental validation of collaborator-generated AlphaFold 3 predictions for interactions between *Saccharomyces cerevisiae* proteins and methylated histone H3 tails, with an emphasis on H3K4me3 recognition.
- Integrated predicted protein–histone interfaces with literature and database analysis to prioritize four candidate proteins—Sir2, Hst1, Swi4, and YPL245W—and develop mechanistically testable hypotheses for histone-mark recognition.
- Express and purify recombinant candidate proteins and design histone peptide pull-down assays comparing modified, unmodified, and control histone substrates to distinguish selective recognition from nonspecific binding.

Mechanisms of Histone Recognition by the Sas5 YEATS Domain

May 2025 – Present

Biology Honors Thesis; defense scheduled Oct. 30, 2026 | Mentor: Christopher “Kit” Cummins, PhD Candidate

- Investigate how the Sas5 YEATS domain recognizes histone tails and contributes to chromatin-dependent regulation by the SAS-I histone acetyltransferase complex.
- Compared wild-type and F85A YEATS domains of Sas5 and Taf14, finding that the canonical aromatic-cage mutation strongly disrupts Taf14 histone binding while preserving Sas5 binding, supporting a distinct recognition mechanism for Sas5.
- Designed and optimized histone peptide pull-down assays, varying H3/H4 modifications and salt stringency to distinguish selective histone recognition from electrostatic background.
- Troubleshoot recombinant expression and GST purification of Sas5 and Taf14 YEATS domains in *E. coli* BL21; independently applied the workflow in the Jacobsen collaboration.
- Designed an *E. coli* codon-optimized full-length SAS5 expression construct.

UNITES Lab, UNC Chapel Hill

Computer Science Honors Thesis Researcher

Chapel Hill, NC

Feb 2026 – Present

PI: Tianlong Chen | Collaborator: Yi Zhang, Duke University | Mentors: Mufan Qiu and Ruichen Zhang

Image-to-Genes Prediction from Histology at Near-Cellular Resolution

Feb 2026 – Present

- Lead an independent machine-learning project predicting spatial gene expression from H&E histology at 8- μ m resolution using 10x Visium HD colorectal cancer data containing hundreds of thousands of spatial measurements per specimen.
- Built reproducible GPU pipelines on a shared cluster to benchmark squared-error regression, flow matching, and zero-inflated negative-binomial models; identified model-selection and optimization confounds and established controlled validation procedures.
- Developed a marker-localization AUROC evaluation complementary to expression-level Pearson correlation; in one benchmark setting, predictions achieved localization AUROC 0.87 despite Pearson correlation 0.14.

RESEARCH EXPERIENCE (CONTINUED)

Strahl Lab, Department of Biochemistry & Biophysics, UNC Chapel Hill*Undergraduate Researcher | PI: Brian D. Strahl***Chapel Hill, NC***Mar 2024 – Present***RNA-seq Workflow Reproduction***Mentor: Abid Khan, Postdoctoral Fellow**Mar 2024 – Apr 2025*

- Recreated the RNA-seq workflow described in Shelsa S. Marcel's 2022 dissertation on SETD2 loss and hypoxia, applying differential-expression and pathway-enrichment analyses to existing sequencing data.
- Adapted Bash and Perl scripts and templated SLURM job submissions to implement a reusable RNA-seq workflow on UNC's Longleaf HPC.

PRESENTATIONS & RESEARCH OUTPUTS

- **Poster:** Wang, R.; Cummins, C.; Strahl, B. D. "Defining the Role of the Sas5 YEATS Domain in Histone Acetylation and Chromatin-State Regulation." *27th Annual Celebration of Undergraduate Research*, UNC Chapel Hill, Apr 2026.
- **Public research summary:** Wang, R. "How Does Sas5 Recognize Histone Proteins?" UNC Summer Undergraduate Research Fellowship, Carolina Digital Repository, Aug 2026. doi:10.17615/vt8g-1h07.

INDUSTRY & TRANSLATIONAL EXPERIENCE

AUSA Pharmed Co., Ltd.*Research Intern***Shenzhen, China***Jun 2025 – Aug 2025*

- Supported the CSPPT2 randomized controlled trial ($N = 56,000$) through participant screening, biospecimen and biomarker collection, physical assessments, ECG acquisition, and protocol-driven workflows.
- Managed electronic clinical data and performed multi-level quality-control review under Good Clinical Practice standards, connecting molecular biomarkers with large-scale precision-prevention research.

Jingke Biotechnology*Research Intern***Shenzhen, China***May 2024 – Jul 2024*

- Performed DNA extraction and whole-exome sequencing workflows from patient blood samples, including capture-based enrichment and preparation for downstream sequence analysis.
- Processed sequencing data and called variants with BWA-MEM, GATK, and bcftools to support identification of clinically relevant genetic variants.

HONORS & AWARDS

- **UNC Summer Undergraduate Research Fellowship (SURF), 2026** – Competitive award supporting independent Sas5 YEATS-domain research.
- **Dean's List**, five semesters (2023–2026).

TECHNICAL SKILLS

Molecular & Synthetic Biology: PCR, agarose gel electrophoresis, plasmid miniprep, restriction digestion and ligation, bacterial transformation, molecular cloning, yeast culture and transformation

Protein Biochemistry: Recombinant protein expression, GST/glutathione affinity purification, histone peptide pull-down assays, SDS-PAGE, Western blotting, Bradford/BCA protein quantification, TCA precipitation

Computational Biology & Genomics: RNA-seq, spatial transcriptomics, STAR, DESeq2, FastQC, Scanpy, AnnData, BWA-MEM, GATK, bcftools, Samtools

Machine Learning & Research Computing: PyTorch, probabilistic modeling, model training and evaluation, Git/GitHub, Jupyter, Docker, Apptainer/Singularity, Linux, SLURM, HPC workflows

Programming: Python, R, Bash, Perl, Java, C

Languages: Mandarin Chinese (Native), English (Fluent)