Stanford



Le Cong

Associate Professor of Pathology (Pathology Research) and of Genetics

Bio

BIO

Dr. Cong's research programs span from inventing genome engineering tools, to building agentic AI and autonomous laboratories for biomedical discovery.

On tools to program human biology, his group has pioneered advanced technologies for large-scale gene-editing and gene-cell therapy, while also leveraging these tools to study human diseases using cutting-edge stem cell models. The team's work led to one of the first CRISPR/Cas9 gene-editing tools for in vivo gene therapy. More recently, his team invented tools for cleavage-free large gene insertion using novel recombination proteins (SSAP editor) and developed machine-learning optimized single-cell methods (DAISY) for perturbing and tracking complex immune diseases. These tools are also being deployed with collaborators to study stem cell regeneration and brain aging.

On tools to accelerate biomedicine with machine intelligence, the Cong lab integrates AI foundation models with agentic AI automation. Recent innovations include RNAGenesis and UTR/IRES-LM foundation model for generative design of RNA/mRNA, CRISPR-GPT as an AI agent system that automates complex gene-editing workflows, and LabOS, an AI-XR co-scientist platform that embeds reasoning directly into physical laboratory. Alongside upcoming initiatives like AutoScreen, the group is building a vision to unify computational design with robotic execution to turn the lab into a programmable, AI-native environment.

Dr. Cong is a recipient of the NHGRI Genomic Innovator Award, and a Baxter Foundation Faculty Scholar, and the Outstanding New Investigator award from American Society for Gene and Cell Therapy (ASGCT). He has also been recognized among the Genetic Engineering and Biotechnology News (GEN) Top 10 Under 40, Clinical OMICs Pioneers Under 40, and is a Clarivate Web of Science Highly Cited Researcher.

The group is actively seeking new talents to join, please contact Dr. Cong for more information.

ACADEMIC APPOINTMENTS

- Associate Professor, Pathology
- Associate Professor, Genetics
- Member, Bio-X
- Member, Cardiovascular Institute
- Member, Stanford Medicine Children’s Health Center for IBD and Celiac Disease
- Member, Stanford Cancer Institute

- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- Outstanding New Investigator Award, American Society for Gene and Cell Therapy (ASGCT) (2026)
- Genomic Innovator Award, National Institute of Health (NIH), National Human Genome Research Institute (NHGRI)
- Donald and Delia Baxter Foundation Faculty Scholar, Baxter Foundation
- CRI Irvington Fellow, Cancer Research Institute
- HHMI International Fellow, Howard Hughes Medical Institute

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Genome Editing and New Investigator Committee Member, American Society of Gene & Cell Therapy (ASGCT) (2019 - present)
- Editorial Board, Gene and Genome Editing (2021 - present)

PROFESSIONAL EDUCATION

- PhD, Harvard University, Harvard Medical School. , Biological and Biomedical Sciences (2014)
- LHB, Harvard Medical School. , Certificate in Leder Human Biology and Translational Medicine
- B.S., Tsinghua University , Biological Sciences, Electronic Engineering (2009)

COMMUNITY AND INTERNATIONAL WORK

- Neuro-engineering and Gene-editing., Cold Spring Harbor Laboratory

PATENTS

- Feng Zhang, Le Cong, Patrick Hsu, Fei Ann Ran. "United States Patent 8,906,616 Engineering of systems, methods and optimized guide compositions for sequence manipulation"
- Le Cong, Feng Zhang. "United States Patent 8,932,814 CRISPR-Cas nickase systems, methods and compositions for sequence manipulation in eukaryotes."
- Feng Zhang, LeCong, Randall Platt, Neville Sanjana, Fei Ann Ran. "United States Patent 8,993,233 Engineering and optimization of systems, methods and compositions for sequence manipulation with functional domains"
- Cong, Egloff, Garraway, Grandis, Lander, Stransky, Tward, Zhang.. "United States Patent 9,370,551. Compositions and methods of treating head and neck cancer."
- Le Cong, Feng Zhang, Patrick Hsu, Fei Ann Ran. "United States Engineering of systems, methods and optimized guide compositions for sequence manipulation."

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our lab develops gene-editing technologies like novel CRISPR systems and large gene insertion techniques for gene and cell therapy. We also leverage these gene-editing tools for single-cell functional screening to probe mechanisms of cancer, immunological, and aging-associated diseases. To accelerate our work, we integrate AI and machine learning to design and evolve therapeutic RNAs/proteins, and build AI-XR co-scientists like LabOS that bridge AI computation and biomedical experimentation.

Teaching

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Freja Ekman, Ronghao Zhou

Postdoctoral Faculty Sponsor

Lanqing Li, Xiaotong Wang, Guangxue Xu, Di Yin, Zhe Zhao

Doctoral Dissertation Advisor (AC)

Luna Lyu

Doctoral (Program)

Michal Gerasimiuk

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biochemistry (PhD Program)
- Bioengineering (PhD Program)
- Biology (School of Humanities and Sciences) (PhD Program)
- Biomedical Data Science (Masters Program)
- Biomedical Data Science (PhD Program)
- Biophysics (PhD Program)
- Cancer Biology (PhD Program)
- Chemical and Systems Biology (PhD Program)
- Cytopathology (Fellowship Program)
- Developmental Biology (PhD Program)
- Genetics (PhD Program)
- Hematopathology (Fellowship Program)
- Immunology (PhD Program)
- Microbiology and Immunology (PhD Program)
- Molecular and Cellular Physiology (PhD Program)
- Neuropathology (Fellowship Program)
- Neurosciences (PhD Program)
- Stem Cell Biology and Regenerative Medicine (PhD Program)
- Structural Biology (PhD Program)

Publications

PUBLICATIONS

- **Agentic AI systems for scientific discovery** *NATURE REVIEWS METHODS PRIMERS*
  Feng, B., Walther, P., Zhang, L., Coyle, R. A., Kim, S., Mandal, A., Zhang, Z., Papidocha, S. M., Kelmanson, A., Segura, D., Thakur, S., Pal, S., Bernales, et al
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- **Surfaceome CRISPR activation screening uncovers ligands regulating tumor sensitivity to NK cell killing.** *Nature communications*
  Dinesh, R. K., Wang, X., Mohammad, I. A., Gunasekaran, P., Stiklioraitis, K., Villafuerte, J. R., Rao, A., Hernandez-Lopez, R. A., Sunwoo, J. B., Cong, L.
  2026; 17 (1)

- **Autonomous biomedical research with an artificial intelligence agent.** *Science (New York, N.Y.)*
  Huang, K., Zhang, S., Wang, H., Qu, Y., Lu, Y., Li, R., Roohani, Y., Qiu, L., Cao, S., Li, G., Zhang, J., Yin, D., Wierenga, et al
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- **Optimizing microhomology-based genome editing by engineering DNA polymerase θ for improved efficiency and reduced on-target indels.** *Cell reports methods*

Wang, W., Zhou, M., Ji, T., Jiang, Q., Zhao, J., Xu, Z., Liu, R., Luo, Y., Han, F., Cong, L., Fan, L., Chen, C., Wang, et al
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- **HDR-GPT: An agentic AI platform for optimized homology-directed repair in primary human cells using HiFi Cas9**
  Ekman, F., Hui, S., Ghanim, H., Selvaraj, S., Russkamp, N., Cong, L., Porteus, M.
  CELL PRESS.2026: 3265-3268
- **Programmable RNA translation through deep learning-driven IRES discovery and de novo generation** *NATURE MACHINE INTELLIGENCE*
  Chu, Y., Yin, D., Yu, D., Xu, G., Zhang, J., Wang, X., Shen, Y., Li, Y., Zhao, N., Zhu, Y., Zhang, J., Goodarzi, H., Wang, et al
  2026; 8 (4)
- **Minimizing far-extending chromatin perturbation in genome editing preserves stem cell identity.** *Cell stem cell*
  Zhu, M., Yuan, J., Meng, Q., Yu, J., Xu, X., Xu, M., Ren, X., Hu, Y., Wei, G., Jia, Z., Yuan, G., Zang, L., Liu, et al
  2026
- **Compact bacterial recombination complexes drive efficient kilobase-scale knock-in in mammalian cells.** *Nucleic acids research*
  Luo, Y., Jiang, Q., Qu, Y., Li, W., Liu, R., Zhu, Y., Xie, Y., Jiang, C., Chen, C., Cong, L., Han, F., Bao, J., Wang, et al
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- **Publisher Correction: CRISPR-GPT for agentic automation of gene-editing experiments.** *Nature biomedical engineering*
  Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H. C., Johnson, W. A., Wang, X., Shah, M., Altman, R. B., Zhou, D., Wang, et al
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- **Autonomous AI Agents Discover Aging Interventions from Millions of Molecular Profiles.** *bioRxiv : the preprint server for biology*
  Ying, K., Tyshkovskiy, A., Moldakozhayev, A., Wang, H., De Magalhães, C. G., Iqbal, S., Garza, A. E., Tskhay, A., Poganik, J. R., Huang, K., Qu, Y., Glubokov, D., Jin, et al
  2025
- **CRISPR-GPT for agentic automation of gene-editing experiments.** *Nature biomedical engineering*
  Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H. C., Johnson, W. A., Wang, X., Shah, M., Altman, R. B., Zhou, D., Wang, et al
  2025
- **Membrane-wide screening identifies potential tissue-specific determinants of SARS-CoV-2 tropism.** *PLoS pathogens*
  Dinesh, R. K., Wang, C., Qu, Y., Rustagi, A., Cousins, H., Zengel, J., Wang, X., Barnard, T. R., Johnson, W. A., Xu, G., Zhang, T., Magazine, N., Beck, et al
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- **Biomni: A General-Purpose Biomedical AI Agent.** *bioRxiv : the preprint server for biology*
  Huang, K., Zhang, S., Wang, H., Qu, Y., Lu, Y., Roohani, Y., Li, R., Qiu, L., Li, G., Zhang, J., Yin, D., Marwaha, S., Carter, et al
  2025
- **Efficient and multiplexed somatic genome editing with Cas12a mice.** *Nature biomedical engineering*
  Hebert, J. D., Xu, H., Tang, Y. J., Ruiz, P. A., Detrick, C. R., Wang, J., Hughes, N. W., Donosa, O., Siah, V. P., Andrejka, L., Karmakar, S., Aboiralor, I., Tang, et al
  2025
- **A call for built-in biosecurity safeguards for generative AI tools.** *Nature biotechnology*
  Wang, M., Zhang, Z., Bedi, A. S., Velasquez, A., Guerra, S., Lin-Gibson, S., Cong, L., Qu, Y., Chakraborty, S., Blewett, M., Ma, J., Xing, E., Church, et al
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- **CRISPR-GPT: LLM Agents for Automated Design of Gene-Editing Experiments**
  Qu, Y., Huang, K., Yin, M., Zhan, K., Liu, D., Yin, D., Cousins, H., Johnson, W., Wang, X., Altman, R., Zhou, D., Wang, M., Cong, et al
  CELL PRESS.2025
- **Surfaceome CRISPR Activation Screens to Delineate Determinants of Natural Killer Cell Killing towards Cancer Cells**
  Wang, X., Dinesh, R., Mohammad, I., Sunwoo, J., Cong, L.
  CELL PRESS.2025
- **FoldMark: Protecting Protein Generative Models with Watermarking.** *bioRxiv : the preprint server for biology*
  Zhang, Z., Jin, R., Fu, K., Cong, L., Zitnik, M., Wang, M.

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- **Computationally guided high-throughput engineering of an anti-CRISPR protein for precise genome editing in human cells.** *Cell reports methods*
  Marsiglia, J., Vaalavirta, K., Knight, E., Nakamura, M., Cong, L., Hughes, N. W.
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- **Systematic Discovery, In Vivo Delivery, and DNA Repair Mechanism of Single-Strand Annealing Protein for Precision Integration of Large DNA Sequences**
  Cong, L., Yin, D., Xu, G., Qu, Y., Wang, C., Wang, X., Johnson, W., Filsinger, G., Wannier, T., Church, G. M., Phoon, L., Gao, B., Lan, et al
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- **A 5′ UTR language model for decoding untranslated regions of mRNA and function predictions** *NATURE MACHINE INTELLIGENCE*
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- **A 5' UTR Language Model for Decoding Untranslated Regions of mRNA and Function Predictions.** *Nature machine intelligence*
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- **Long sequence insertion via CRISPR/Cas gene-editing with transposase, recombinase, and integrase** *CURRENT OPINION IN BIOMEDICAL ENGINEERING*
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- **Gene set proximity analysis: expanding gene set enrichment analysis through learned geometric embeddings, with drug-repurposing applications in COVID-19.** *Bioinformatics (Oxford, England)*
  Cousins, H., Hall, T., Guo, Y., Tso, L., Tzeng, K. T., Cong, L., Altman, R. B.
  2022
- **Single-cell transcriptome analysis of regenerating RGCs reveals potent glaucoma neural repair genes.** *Neuron*
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- **Machine-learning-optimized Cas12a barcoding enables the recovery of single-cell lineages and transcriptional profiles.** *Molecular cell*
  Hughes, N. W., Qu, Y., Zhang, J., Tang, W., Pierce, J., Wang, C., Agrawal, A., Morri, M., Neff, N., Winslow, M. M., Wang, M., Cong, L.
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- **dCas9-based gene editing for cleavage-free genomic knock-in of long sequences.** *Nature cell biology*
  Wang, C., Qu, Y., Cheng, J. K., Hughes, N. W., Zhang, Q., Wang, M., Cong, L.
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- **Bandit Theory and Thompson Sampling-Guided Directed Evolution for Sequence Optimization**
  Yuan, H., Ni, C., Wang, H., Zhang, X., Cong, L., Szepesvari, C., Wang, M.
  edited by Koyejo, S., Mohamed, S., Agarwal, A., Belgrave, D., Cho, K., Oh, A.
  NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2022
- **Neural Bandits for Protein Sequence Optimization**
  Wang, C., Kim, J., Cong, L., Wang, M., IEEE
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- **The role of p53 in the development of pancreatic ductal adenocarcinoma.**
  Hanson, K. J., Flowers, B. M., Hughes, N., Vogel, H., Cong, L., Attardi, L. D.
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- **Deciphering pathogenicity of variants of uncertain significance with CRISPR-edited iPSCs.** *Trends in genetics : TIG*
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- **Conventional type I dendric cells maintain a reservoir of proliferative tumor-antigen specific TCF-1+ CD8+ Tcells in tumor-draining lymph nodes.** *Immunity*
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- **Cleavage-Free dCas9 Knock-In Gene-Editing Tool Leveraging RNA-Guided Targeting of Recombineering Proteins**
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- **A CRISPR Landing for Genome Rewriting at Locus-Scale.** *The CRISPR journal*
  Hughes, N. W., Cong, L.
  2021; 4 (2): 163–66
- **Microbial single-strand annealing proteins enable CRISPR gene-editing tools with improved knock-in efficiencies and reduced off-target effects.** *Nucleic acids research*
  Wang, C., Cheng, J. K., Zhang, Q., Hughes, N. W., Xia, Q., Winslow, M. M., Cong, L.
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- **A functional taxonomy of tumor suppression in oncogenic KRAS-driven lung cancer.** *Cancer discovery*
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- **Adeno-associated viral vector-mediated immune responses: Understanding barriers to gene delivery.** *Pharmacology & therapeutics*
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