



Patrick David Hsu

Assistant Professor of Pathology

Bio

BIO

Patrick Hsu is Co-Founder of the Arc Institute and Assistant Professor of Pathology at Stanford University. The Hsu lab works at the intersection of biology and machine learning to develop technologies for biological and therapeutic design. Recent contributions include the Evo series of genome foundation models and the first universally programmable DNA recombinases. Patrick received A.M. and Ph.D. degrees from Harvard University and the Broad Institute of MIT and Harvard, where he was an early pioneer of CRISPR-Cas9 technologies for genome editing. His research has been recognized by awards from the New York Times, The Atlantic, Forbes, MIT Technology Review, Rainwater Foundation, and Amgen. He serves on the scientific advisory board of Amgen and the board of Stylus Medicine, and cofounded Fast Grants for rapid science funding.

ACADEMIC APPOINTMENTS

- Assistant Professor, Pathology

Publications

PUBLICATIONS

- **Genome modelling and design across all domains of life with Evo 2.** *Nature*
Brix, G., Durrant, M. G., Ku, J., Naghipourfar, M., Poli, M., Sun, G., Brockman, G., Chang, D., Fanton, A., Gonzalez, G. A., King, S. H., Li, D. B., Merchant, et al
2026
- **Rapid directed evolution guided by protein language models and epistatic interactions.** *Science (New York, N.Y.)*
Tran, V. Q., Nemeth, M., Bartie, L. J., Chandrasekaran, S. S., Fanton, A., Moon, H. C., Hie, B. L., Konermann, S., Hsu, P. D.
2026: eaea1820
- **Megabase-scale human genome rearrangement with programmable bridge recombinases.** *Science (New York, N.Y.)*
Perry, N. T., Bartie, L. J., Katrekar, D., Gonzalez, G. A., Durrant, M. G., Pai, J. J., Fanton, A., Martins, J. Q., Hiraizumi, M., Ricci-Tam, C., Nishimasu, H., Konermann, S., Hsu, et al
2025: eadz0276
- **Sequence modeling and design from molecular to genome scale with Evo.** *Science (New York, N.Y.)*
Nguyen, E., Poli, M., Durrant, M. G., Kang, B., Katrekar, D., Li, D. B., Bartie, L. J., Thomas, A. W., King, S. H., Brix, G., Sullivan, J., Ng, M. Y., Lewis, et al
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- **Bridge RNAs direct programmable recombination of target and donor DNA.** *Nature*
Durrant, M. G., Perry, N. T., Pai, J. J., Jangid, A. R., Athukoralage, J. S., Hiraizumi, M., McSpedon, J. P., Pawluk, A., Nishimasu, H., Konermann, S., Hsu, P. D.
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- **A combinatorial domain screening platform reveals epigenetic effector interactions for transcriptional perturbation.** *Nature communications*
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2026
- **Generalist biological artificial intelligence in modeling the language of life.** *Nature biotechnology*
Rao, V. M., Zhang, S., Plosky, B. S., Hsu, P. D., Wang, B., Zou, J., Zitnik, M., Topol, E. J., Rajpurkar, P.
2026
- **Rewriting endogenous human transcripts with dual CRISPR-guided 3' trans-splicing.** *Cell systems*
Chandrasekaran, S. S., Tau, C., Fu, B. X., Nemeth, M., Bartie, L., Pawluk, A., Konermann, S., Hsu, P. D.
2026: 101487
- **Site-specific DNA insertion into the human genome with engineered recombinases.** *Nature biotechnology*
Fanton, A., Bartie, L. J., Martins, J. Q., Tran, V. Q., Goudy, L., Kernick, C., Durrant, M. G., Wei, J., Armour-Garb, Z., Pawluk, A., Konermann, S., Marson, A., Gilbert, et al
2025
- **Virtual Cell Challenge: Toward a Turing test for the virtual cell.** *Cell*
Roohani, Y. H., Hua, T. J., Tung, P. Y., Bounds, L. R., Yu, F. B., Dobin, A., Teyssier, N., Adduri, A., Woodrow, A., Plosky, B. S., Mehta, R., Hsu, B., Sullivan, et al
2025; 188 (13): 3370-3374
- **How to build the virtual cell with artificial intelligence: Priorities and opportunities.** *Cell*
Bunne, C., Roohani, Y., Rosen, Y., Gupta, A., Zhang, X., Roed, M., Alexandrov, T., AlQuraishi, M., Brennan, P., Burkhardt, D. B., Califano, A., Cool, J., Dernburg, et al
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- **How to Build the Virtual Cell with Artificial Intelligence: Priorities and Opportunities.** *ArXiv*
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- **Structural mechanism of bridge RNA-guided recombination.** *Nature*
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- **Bridge RNAs direct modular and programmable recombination of target and donor DNA.** *bioRxiv : the preprint server for biology*
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2024
- **Deep learning and CRISPR-Cas13d ortholog discovery for optimized RNA targeting.** *Cell systems*
Wei, J., Lotfy, P., Faizi, K., Baungaard, S., Gibson, E., Wang, E., Slabodkin, H., Kinnaman, E., Chandrasekaran, S., Kitano, H., Durrant, M. G., Duffy, C. V., Pawluk, et al
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- **The KDM6A-KMT2D-p300 axis regulates susceptibility to diverse coronaviruses by mediating viral receptor expression.** *PLoS pathogens*
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Strine, M. S., Cai, W. L., Wei, J., Alfajaro, M. M., Filler, R. B., Biering, S. B., Sarnik, S., Chow, R. D., Patil, A., Cervantes, K. S., Collings, C. K., DeWeirdt, P. C., Hanna, et al
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- **Systematic discovery of recombinases for efficient integration of large DNA sequences into the human genome.** *Nature biotechnology*
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- **What are the current bottlenecks in developing and applying CRISPR technologies?** *CELL SYSTEMS*
Kellogg, E. H., Gootenberg, J., Abudayyeh, O., Wong, A. S. L., Dahlman, J. E., Lapinaite, A., Myhrvoid, C., Liu, C. C., Hsu, P. D., Mali, P., Qi, L.
2022; 13 (8): 589-593
- **Genome-wide bidirectional CRISPR screens identify mucins as host factors modulating SARS-CoV-2 infection.** *Nature genetics*
Biering, S. B., Sarnik, S. A., Wang, E., Zengel, J. R., Leist, S. R., Schafer, A., Sathyan, V., Hawkins, P., Okuda, K., Tau, C., Jangid, A. R., Duffy, C. V., Wei, et al
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- **GENOME-WIDE, BIDIRECTIONAL CRISPR SCREENS IDENTIFY MUCINS AS CRITICAL MODULATORS OF SARS-COV-2 INFECTION**
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- **Pairwise library screen systematically interrogates Staphylococcus aureus Cas9 specificity in human cells** *NATURE COMMUNICATIONS*
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- **Twinfilin 2 Regulates Actin Filament Lengths in Cochlear Stereocilia** *JOURNAL OF NEUROSCIENCE*
Peng, A. W., Belyantseva, I. A., Hsu, P. D., Friedman, T. B., Heller, S.
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