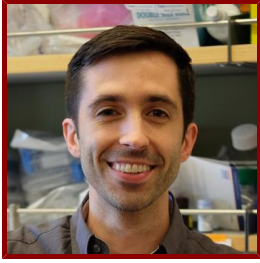


Stanford



M. Ryan Corces

Instructor, Pathology

Bio

BIO

Dr. Corces is an instructor at Stanford University in the department of Pathology. He graduated from Princeton University in 2008 with a degree in molecular biology. He began his PhD in cancer biology at Stanford University in 2009, focusing on the genomic evolution of acute myeloid leukemia (AML) under the mentorship of Dr. Ravindra Majeti. His doctoral work led to the identification of pre-leukemic hematopoietic stem cells, which serve as the reservoir for mutation acquisition in AML. He and others have demonstrated that these pre-leukemic hematopoietic stem cells are the evolutionary ancestors to AML, they persist during remission, and may represent a novel avenue for the development of relapsed disease. Dr. Corces has continued his research at Stanford as a postdoctoral fellow under the mentorship of Dr. Howard Chang and Dr. Thomas Montine. His current research focuses on the role of the epigenome in human health and disease with a focus on cancer and neurodegenerative disease.

ACADEMIC APPOINTMENTS

- Instructor, Pathology

PROFESSIONAL EDUCATION

- PhD, Stanford University , Cancer Biology (2015)
- BA, Princeton University , Molecular Biology (2008)

Publications

PUBLICATIONS

- **The chromatin accessibility landscape of primary human cancers.** *Science (New York, N.Y.)*
Corces, M. R., Granja, J. M., Shams, S., Louie, B. H., Seoane, J. A., Zhou, W., Silva, T. C., Groeneveld, C., Wong, C. K., Cho, S. W., Satpathy, A. T., Mumbach, M. R., Hoadley, et al
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- **Single-cell multiomic analysis identifies regulatory programs in mixed-phenotype acute leukemia.** *Nature biotechnology*
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- **HiChIRP reveals RNA-associated chromosome conformation.** *Nature methods*
Mumbach, M. R., Granja, J. M., Flynn, R. A., Roake, C. M., Satpathy, A. T., Rubin, A. J., Qi, Y., Jiang, Z., Shams, S., Louie, B. H., Guo, J. K., Gennert, D. G., Corces, et al
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- **Massively parallel single-cell chromatin landscapes of human immune cell development and intratumoral T cell exhaustion.** *Nature biotechnology*
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- **Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation** *CELL*
Buenrostro, J. D., Corces, M., Lareau, C. A., Wu, B., Schep, A. N., Aryee, M. J., Majeti, R., Chang, H. Y., Greenleaf, W. J.
2018; 173 (6): 1535–+
- **Transcript-indexed ATAC-seq for precision immune profiling.** *Nature medicine*
Satpathy, A. T., Saligrama, N., Buenrostro, J. D., Wei, Y., Wu, B., Rubin, A. J., Granja, J. M., Lareau, C. A., Li, R., Qi, Y., Parker, K. R., Mumbach, M. R., Serratelli, et al
2018
- **Preleukemic Hematopoietic Stem Cells in Human Acute Myeloid Leukemia** *FRONTIERS IN ONCOLOGY*
Corces, M., Chang, H. Y., Majeti, R.
2017; 7: 263
- **Rapid Chromatin Switch in the Direct Reprogramming of Fibroblasts to Neurons** *CELL REPORTS*
Wapinski, O. L., Lee, Q., Chen, A. C., Li, R., Corces, M., Ang, C., Treutlein, B., Xiang, C., Baubet, V., Suchy, F., Sankar, V., Sim, S., Quake, et al
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- **Human AML-iPSCs Acquire Leukemic Properties after Differentiation and Model Clonal Variation of Disease.** *Cell stem cell*
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- **Super-Enhancer Analysis Defines Novel Epigenomic Subtypes of Non-APL AML Including an RAR# Dependency Targetable by SY-1425, a Potent and Selective RAR# Agonist.** *Cancer discovery*
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- **Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements.** *Nature genetics*
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