

**SPECIAL SEMINAR**  
Lewis-Sigler Institute**Erez Lieberman-Aiden, Ph. D.**

Assistant Professor, Baylor College of Medicine & Rice University

**Friday, June 2**  
**Icahn Lab Rm. 101**  
**11:00am**

**“A 3D Code in the Human Genome”**

Stretched out from end-to-end, the human genome – a sequence of 3 billion chemical letters inscribed in a molecule called DNA – is over 2 meters long. Famously, short stretches of DNA fold into a double helix, which wind around histone proteins to form the 10nm fiber. But what about longer pieces? Does the genome's fold influence function? How does the information contained in such an ultra-dense packing even remain accessible? In this talk, I describe our work developing 'Hi-C' (Lieberman-Aiden et al., *Science*, 2009; Aiden, *Science*, 2011) and more recently '*in-situ* Hi-C' (Rao & Huntley et al., *Cell*, 2014), which use proximity ligation to transform pairs of physically adjacent DNA loci into chimeric DNA sequences. Sequencing a library of such chimeras makes it possible to create genome-wide maps of physical contacts between pairs of loci, revealing features of genome folding in 3D.