PAUL BLAINEY is a core member of the Broad Institute of MIT and Harvard and an associate professor in the Department of Biological Engineering at MIT. An expert in microanalysis systems for studies of individual molecules and cells, Blainey is applying this technology to advance understanding of DNA-protein interaction, evolutionary processes, and functional differences between cells.

The Blainey group develops and translates microfluidic, chemical, imaging, and sequencing approaches to make high-throughput quantitative biology routine – including single-cell analysis. Such capabilities will allow scientists to determine the genomic sequences from organisms that have not been successfully cultured in the lab and examine genetic differences on a cell-to-cell basis, driving new insights into fundamental aspects of cell function and evolution. Blainey seeks to empower researchers to obtain new types of information about biological specimens and integrate different types of information, such as imaging data and next-generation sequencing-based data.

Blainey was awarded the Agilent Early Career Investigator Award in 2014, and was the recipient of a Burroughs Wellcome Fund Career Award at the Scientific Interface in 2011.

He holds a B.S. in chemistry and B.A. in mathematics from the University of Washington. He earned a Ph.D. in physical chemistry from Harvard University, where he studied how proteins interact with DNA with Xiaoliang Sunney Xie and Greg Verdine. He then completed postdoctoral research at Stanford University in the laboratory of Stephen Quake, where he pioneered novel optofluidic methods to perform single-cell microbial sequencing.