Yoseph Barash is computational biology researcher and a Professor in the Department of Genetics and the Department of Computer and Information Science at the University of Pennsylvania.

Yoseph research focuses on predictive models to understand RNA biogenesis, its regulation, and its role in human disease. His lab, the BioCiphers lab, develops machine learning algorithms that integrate genomic and genetic data, followed by wet lab experimental verifications. Yoseph earned a B.Sc. in Physics and Computer Science at the Hebrew University, then continued to earn a Ph.D. in machine learning under Prof. Nir Friedman. Yoseph did his postdoctoral work with Prof. Ben Blencowe and Prof. Brendan Frey at the University of Toronto, focusing on alternative splicing of RNA. His work was the first to build predictive models for splicing variations as a function of the cellular condition (Barash et al Nature 2010), later extended to genetic variations (Xiong et al Science 2015). His lab was the first to offer tools for mapping, quantifying, and visualizing complex splicing variations, showing these comprise over 30% of the human transcriptome variations (Vaquero et al, Elife 2016). The tools the BioCiphers lab develops to quantify and predict aberrant splicing have been instrumental in studying RNA splicing defects in cancer, immunotherapy, and other disease (e.g. Sotillo et al Cancer Discovery 2015, Rivera et al PNAS 2021). The lab's tools have been licensed by both major pharma and startups. In addition, since 2020 Dr. Barash has been advising several companies in the RNA therapeutics space.