WELCOME

The Center for the Multiplexed Assessment of Phenotype, (CMAP) is a Center of Excellence in Genome Sciences, supported by the National Human Genome Research Institute. Our goal is to develop technologies to assess the functional impact of variants in human genes. Linking phenotype to genotype is one of the most pressing problems in biology and our goal is to facilitate variant interpretation to enable genome-guided precision medicine in clinical decision making. We are based at the University of Washington and at the University of Toronto.

MUTATIONAL SCANNING SYMPOSIUM

Multiplex Assays of Variant Effects (MAVEs) are key to variant interpretation and are transforming our understanding of the human genome. Experts in the field of mutational scanning come from around the world to present their work and provide insights on the future of this science for this three-day event which will be held virtually April 5th-7th 2021. Our keynote speakers this year will be Ben Lehner, PhD (CRG Barcelona) and Kim Reynolds, PhD (UTSW Dallas). Registration is free! To learn more please visit the url below.

REGISTRATION IS NOW OPEN!

https://www.varianteffect.org/aveevents/mutational-scanning-symposium
In their recent paper "Prioritizing genes for systematic variant effect mapping," Kuang et al. lay out an approach for prioritizing genes for systematic variant effect mapping. Their results could be used to guide systematic functional testing of missense variation towards greater impact on clinical variant interpretation. To learn more about their approach visit: https://pubmed.ncbi.nlm.nih.gov/33300982/