CENTER FOR THE MULTIPLEX ASSESSMENT OF PHENOTYPE

NEWSLETTER

Winter | February 1, 2021

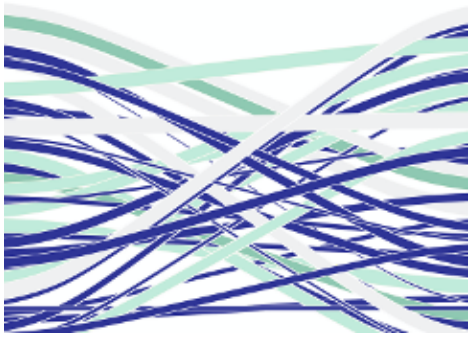
https://www.cmap.gs.washington.edu

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 meet 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

RESEARCH NEWS

RECENT PUBLICATIONS

Multiplexed Functional Assessment of Genetic Variants in CARD11. Meitlis et al *Am J Hum Genet.* Nov 2020 (Starita lab)

Cryptic transmission of SARS-CoV-2 in Washington state. Bedford et al *Science* Oct 2020 (Starita and Shendure labs)

Prioritizing genes for systematic variant effect mapping. Kuang et al *Bioinformatics.* Dec 2020 (Roth Lab)

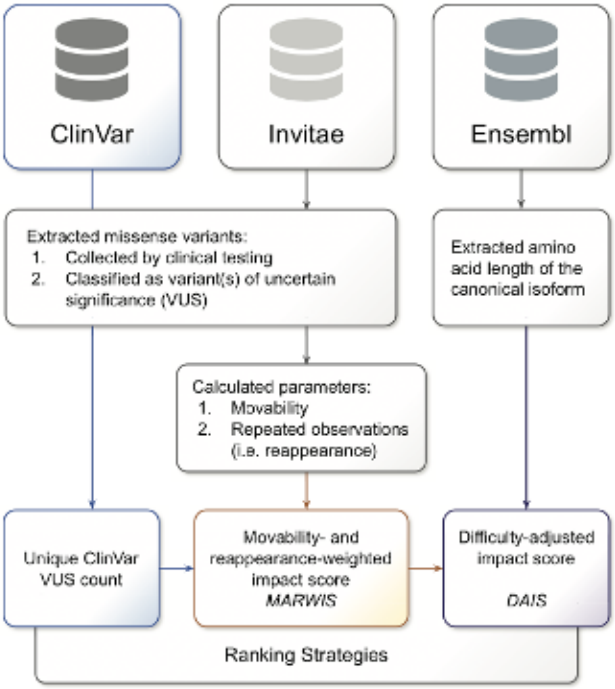
Photo Credit (UW Medicine)

"We are trying to push the limits of technology to answer very fundamental questions that are relevant to disease."

"As I have grown as a scientist, my style has turned into that of trail runner: endurance and hard work are important, and we get to enjoy running up and down the hills,"

Judit Villén

PUBLICATION HIGHLIGHT



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/

ABBYE MCEWEN

Please welcome Postdoctoral Fellow Abbye McEwen to the team!

Abbye is a cell biologist by training. During her doctoral work, she studied the basic science of cell-cell adhesion in the cadherin-catenin system. She is currently a resident physician interested in using deep mutational scanning to aid in the interpretation of clinical genetics results.