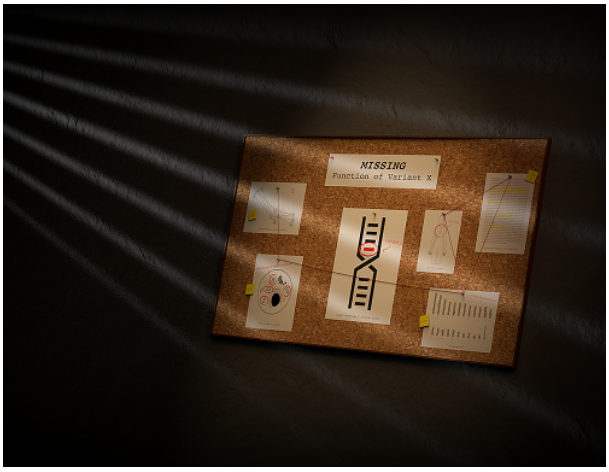
South Florida Hospital News and Healthcare Report
THE REGION'S MONTHLY NEWSPAPER FOR HEALTHCARE PROFESSIONALS & PHYSICIANS

NIH providing $185 million for research to advance understanding of how human genome functions

The newly launched Impact of Genomic Variation on Function (IGVF) consortium to include 30 U.S. sites.

September 9 2021 – The National Institutes of Health is providing approximately $185 million over five years to the Impact of Genomic Variation on Function (IGVF) consortium, initiated and funded by NIH's National Human Genome Research Institute (NHGRI). NHGRI will fund 25 awards across 30 U.S.

research sites. IGVF consortium investigators will work to understand how genomic variation alters human genome function, and how such variation influences human health and disease.



IGVF consortium investigators will work to understand how genomic variation alters human genome function, and how such variation influences human health and disease.Harry Wedel, NHGRI

The genome sequences of two different people are more than 99.9% identical. But those 0.1% differences – alternate orders of the As, Cs, Gs and Ts that make up our DNA – combined with the environment and lifestyle ultimately shape a person's overall physical features and disease risk. Researchers have identified millions of human genomic variants that differ across the world, including thousands of disease-associated ones. By integrating experimental methods with advanced computer models, the IGVF consortium will identify which variants in the genome are relevant for health and disease – information that will be of critical importance to clinicians.

"Biomedical researchers have recently made remarkable advances in the experimental and computational methods available for elucidating genome function," said Carolyn Hutter, Ph.D., director of the NHGRI Division of Genome Sciences. "The IGVF consortium will include world leaders in these areas, and together they will leverage these advances to tackle an incredibly challenging and important series of questions related to how genomic variation influences biological

function."

The IGVF consortium will develop a catalog of the results and approaches used in their studies. All information generated by the consortium will be made freely available to the research community via a web portal to assist with future research projects. Because there are thousands of genomic variants associated with disease, and it is not possible to manipulate each variant individually and in each biological setting, consortium researchers will also develop computational modeling approaches to predict the impact of variants on genome function.

The IGVF consortium includes five components: Functional Characterization Centers, Regulatory Network Projects, Mapping Centers, a Data and Administrative Coordinating Center and Predictive Modeling Projects. To view a full list of awardee sites, please visit the IGVF webpage on genome.gov.

NHGRI is one of the 27 institutes and centers at the National Institutes of Health. The NHGRI Extramural Research Program supports grants for research, and training and career development at sites nationwide. Additional information about NHGRI can be found at https://www.genome.gov.

About the National Institutes of Health (NIH): NIH, the nation's medical research agency, includes 27 Institutes and Centers and is a component of the U.S. Department of Health and Human Services. NIH is the primary federal agency conducting and supporting basic, clinical, and translational medical research, and is investigating the causes, treatments, and cures for both common and rare diseases. For more information about NIH and its programs, visit www.nih.gov.

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