

Qiagen software chosen for translational genomics, 3/14

March 2014—The Mount Sinai Genetic Testing Laboratory and the Icahn Institute for Genomics and Multiscale Biology at Mount Sinai, New York City, have adopted Qiagen's Ingenuity Variant Analysis solution for research and translational genomics applications related to characterizing and identifying rare diseases. Ingenuity Variant Analysis will also serve as the genome interpretation platform for training at the Icahn School of Medicine, which gives researchers and future physicians the opportunity to sequence and perform detailed analyses of their own genomes.

The Ingenuity Variant Analysis is a Web-based software application that quickly filters genetic variants to identify those most likely to cause disease, providing researchers with a powerful platform for evaluating data generated by next-generation sequencing technologies. It is built on the Ingenuity Knowledge Base, an extensive, manually curated, integrated repository of genomic information, scientific literature, and public databases.

"In our efforts to provide answers to families who may have spent years on a frustrating and painful diagnostic odyssey, this ability to dramatically accelerate the process of getting to a medically relevant insight is invaluable," says Eric Schadt, PhD, director of the Icahn Institute for Genomics and Multiscale Biology, chair of the Department of Genetics and Genomics Sciences, and the Jean C. and James W. Crystal professor of genomics at the Icahn School of Medicine at Mount Sinai. "Our mission is to bring to bear as much information as possible to help each patient. The combination of Ingenuity Variant Analysis and the Ingenuity Knowledge Base is an essential part of achieving that goal."

[Qiagen](#), 240-686-7425