

**Nicholas J. Schork, PhD**

Director of Bioinformatics & Biostatistics, Scripps Translational
Science Institute

Director of Research, The Scripps Research Institute

Dr. Nicholas Schork has the innate ability to place his talents at the right place at the right time. He was a graduate student at the University of Michigan in the late 80's, studying philosophy and statistics, when the science of genomics was being born. Dr. Francis Collins, who would later head the Human Genome Project, was on the faculty at Michigan. When Dr. Collins mapped the gene responsible for Cystic Fibrosis, it opened a new world of possibilities. However, genetic researchers soon learned that analyzing the genome produced reams of data, and that information needed to be carefully analyzed to be useful. Dr. Schork was working at Michigan's medical school when the need became apparent. While earning his Ph.D. in epidemiology, he helped provide statistical support for these early studies. Later, Dr. Schork worked with Dr. Eric Lander, MIT, another genomics pioneer. In 1994, the two co-authored a paper called "The Genetic Dissection of Complex Traits." Published in the journal *Science*, the article detailed different methods to determine the relationships between genes and disease. A milestone in the early study of human genetics, the paper is still widely cited.

Dr. Schork continued his work in both corporate and academic settings. In 2001, he was appointed to the faculty at UCSD. While this new position offered him access to excellent research facilities, what he needed most was a large genetic sample to study. "The research I wanted to pursue had to do with collecting patient data, seeing what diseases they have, seeing if we can find the mechanism, seeing if we can overcome the defects, seeing if the drugs work," says Dr. Schork.

When Dr. Eric Topol approached him with Scripps' plans to use its large patient base to facilitate genetic studies, Dr. Schork was ready. "Blockbuster drugs work in very few people," says Dr. Schork. "There's enough benefit to justify their use, but we need to identify the people they're most useful for. How can we improve the use of those existing drugs? We need to find markers that distinguish the people who will respond and won't respond. If you're looking at millions of spots on genome that may be associated with particular diseases, then how do you separate the ones that are associated from the ones that aren't? It's either a statistical nightmare or a lot of fun, depending on your outlook.



Schork Group

(back, l → r) Trygve Bakken, Andrew Schork, Ashley Scott, Ondrej Libiger, Ryan Tewhey, Vikas Bansal, Ali Torkamani, Nik Schork, Lane Votapka

(front, l → r) Rany Salem, Cinnamon Bloss, Alex Joyner, Mary Winn, Janette Lundgren Beas