Michael Snyder, J Comput Sci Syst Biol, 5:1
doi: http://dx.doi.org/10.4172/0974-7230.S1.01

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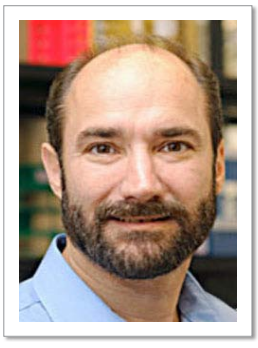

Prof. Michael Snyder

Stanford University, USA

Extensive dynamic changes in omics profiles during normal and disease states

Genomic medicine will require the integrated analysis of genomic information and omics information. We have determined the genome sequence of an individual at high accuracy and performed an integrated analysis of omics profiles during normal and virally infected states. Omics profiling of transcriptomes, proteomes, cytokines, metabolomes and autoantibody omes have revealed dynamic and broad changes in molecular components occur during infection. Analysis of heteroallelic expression suggests significant changes in differential allele expression in healthy and disease states. Analyses of information about coding and regulatory information led to predictions of disease risk; some were subsequent validation through omics and medical profiles. Our study is the first torelatepersonal genomic information to global functional omicsactivity for physiological and medical interpretation of healthy and disease states.

Biography

Michael Snyder is the Chairman of Genetics and the Director of the Center for Genomics and Personalized Medicine at Stanford. Dr. Snyder received his Ph.D. training at CalTech and carried out postdoctoral training at Stanford. His laboratory study was the first to perform a large-scale functional genomics project in any organism, and has launched many technologies in genomics and proteomics. These include the development of proteome chips, high resolution tiling arrays for the entire human genome, methods for global mapping of transcription factor binding sites, paired end sequencing for mapping of structural variation in eucaryotes, and RNA-Seq. These technologies have been used for characterizing genomes, proteomes and regulatory networks.