

Remo Rohs

Molecular and Computational Biology Program
Departments of Biological Sciences and Chemistry
University of Southern California

New approaches to genome analysis based on the integration of DNA sequence and shape

High-throughput sequencing technologies continue to produce large amounts of DNA sequence information. The availability of whole genomes has dramatically changed biological and biomedical research and our understanding of cellular functions, biological processes, and disease. Whereas analyzing the genome as a linear one-dimensional string of letters provides answers to many biological questions, proteins recognize DNA as a three-dimensional object. Considering DNA as a double helix with sequence-dependent shape enables the biophysical characterization of protein-DNA readout. This presentation describes new approaches to genome analysis based on the integration of sequence and shape, including the evolutionary relationships between transcription factor binding sites, motif search, and de-novo motif discovery.