

Introducing the NIDA Core Center of Excellence in Omics, Systems Genetics, and the Addictome

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Addiction is a highly complex heterogeneous disease with risk factors that include genetic variants and differences in development, sex, and environment. The long-term potential of precision medicine to improve treatment and prevention depends on gaining a better understanding how genetics, drugs, brain cells, and neuronal circuitry interact to influence behavior. There are serious technical barriers that prevent researchers and clinicians from incorporating more powerful computational and predictive methods in addiction research. The purpose of the *NIDA P30 Core Center of Excellence in Omics, Systems Genetics, and the Addictome* is to empower current and future researchers supported by NIDA and NIAAA to analyze the interwoven roles of genetic, epigenetic and environmental variation on drug abuse risk, relapse, and treatment. We will do this by assembling sophisticated analytic/synthetic omics resources—primarily for rat models—that will give investigators mechanistic and behavioral insights and by providing training in omics, systems genetics, and advanced computational/statistical modeling. In the *Transcriptome Informatics and Mechanisms* research core, we will assemble hundreds of large genome and transcriptome datasets for rodent models of addiction and upgrade methods and tools for quantitation and integration of these data to uncover molecular mechanisms of addiction. In the *Systems Analytics and Modeling* research core, we will use innovative systems genetics methods (gene mapping) to understand the linkage between DNA differences, environmental risks, and the differential risk of drug abuse and relapse. Our *Pilot* core will catalyze new collaborations among early career investigators in the field of addiction research. As we built this national resource for reproducible research in addiction, we are seeking input from the research community on how to best meet their needs and wants. Our vision is that the Center can be used a catalyst for building an NIDA Addictome Portal that will include all genomic data relevant to addiction research.