

Data available from: <http://www.hivrdi.org/what.htm>

### Background

One of the main reasons for HIV treatment failure is that the virus readily develops resistance to the drugs ranged against it. HIV replication is highly error prone and changes (mutations) in the genetic code of HIV can make it less susceptible to one or more HIV drugs.

Tests are often used to help identify drug combinations that will overcome resistance in the individual patient. The tests most commonly used (genotype tests) detect individual mutations in the genetic code of the patient's virus. Once the mutations have been detected, however, this information requires interpretation to predict what effect they will have on the susceptibility of that virus to each of the available drugs. This poses tremendous challenges because there are more than 200 different mutations that can affect drug resistance and an enormous number of possible drug combinations available. Generally, this interpretation is performed subjectively by individuals or by using sets of "rules" or algorithms based on review of the scientific literature. Many different interpretation systems are in use, which vary greatly in content and quality.

### The RDI concept

*The new approach being pioneered by the RDI involves relating HIV drug resistance and other baseline data directly to the response of patients to different drugs **in clinical practice**, using a substantial database of clinical data. Scientists and clinicians the world over believe that this approach has the potential to improve the interpretation of drug resistance information and ultimately the quality of treatment decision-making. The complete*

[RDI Concept Sheet](#)

is available to be downloaded as a pdf.

The RDI has developed and continually updates a [substantial relational database](#) of clinical data including genotypes and details of drug therapy and responses to treatment. The

development of the database is an international collaborative initiative, with data being provided by a variety of private and public research groups around the world. RDI is using this database to develop computational models to predict the virological response to different combinations of antiretroviral drugs. The output of these models is the probability that the regimen will reduce the viral load to below 50 copies.

For more information, visit RDI directly at <http://www.hivrdi.org/>

For HIV TRePS, visit <http://www.hivrdi.org/treps/login.php>