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HIV Resistance Algorithm

The Stanford HIV Drug Resistance Database maintains a frequently updated expert system for interpreting HIV-1 genotypic resistance tests. The system accepts user-submitted protease, reverse transcriptase (RT), and or integrase sequences or lists of mutations in these genes. The system uses the sequences or mutations to infer the extent of susceptibility of the sequenced virus to seven nucleoside RT inhibitors (NRTIs), four nonnucleoside RT inhibitors (NNRTIs), eight protease inhibitors (PIs), and three integrase strand transfer inhibitors (INSTIs). Sequences or mutations can be submitted on a web page or via a web service.

Applications

- HIV drug resistance evaluation for determining therapy effectiveness

Advantages

- Addresses every possible mutation, not just the most commonly reported mutations
- By assigning scores to individual mutations, it prevents the possibility that a pattern of mutations will arise in a virus sequence that is not specifically addressed by the algorithm
- Performs quality control and returns warnings when a sequence contains poor quality regions that interfere with reliable drug resistance interpretation

Innovators

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