Treatment for HIV/AIDS has proven difficult due to the high mutation replication rate of the HIV virus as well as the high mutation rate of the HIV genome. Current treatments for HIV consist of multiple drugs, generally all targeted at the enzyme reverse transcriptase, but these treatments are far from perfect; and the discovery of new drug targets could lead to more effective treatments or even a cure for HIV/AIDS. To this end, we have used computational models to predict binding between the HIV virus proteins and the human body proteins, and we have utilized other such methods to select an unknown interaction that we believe may be crucial to the HIV life cycle, the GP-41-LCK interaction. We have ordered these proteins and are testing in the lab to determine the pattern of interaction between these two proteins, which holds promise to lead to new HIV drug targets.