For complex biological systems, how do we characterize the effects of many experimental conditions on many possible behaviors? This type of problem has not typically been addressed, since common approaches either address a single behavior for many conditions or a few behaviors for one or a few conditions. Furthermore, these have been almost exclusively studied under very strong assumptions, namely having quantitative measures of similarity for different conditions, or with the set of possible phenotypes known ahead of time, or with other structural, simplifying assumptions. We have shown that, for a broad range of simulated data, incrementally choosing informative experiments based on repeated phenotype estimation and model building can learn accurate models with fewer experiments than by randomly sampling experiments even when possible phenotypes are not known in advance. Furthermore for this active learning method it is also possible to form a stopping rule by which a practitioner may estimate the probability that an actively learned model is approximately correct. The method was applied to determine how a collection of 48 proteins in CD-tagged NIH-3T3 altered their subcellular localizations in response to 48 perturbagens. This required extensive laboratory automation, and produced a system which achieved 92% predictive accuracy after having only performed 28% of the possible experiments; it is unlikely that random sampling would have led to better coverage of the experiment space ($P<10^{-86}$). The final model correctly predicted novel translocations different than those observed. To the best of our knowledge, this is the first tabula rasa active learning experiment for a biological problem.