Biocatalysis offers the ability to carry out important synthesis and production of valuable chemicals at benign conditions. In the development of new processes, enzymes are being engineered towards specific products with great success. Currently, mutations are introduced into enzymes, and mutants are formed thereof and a search among these is conducted. High throughput screening can deliver screening of mutants in the order of millions a day. Enzyme mutants with increased performance are therefore likely to be found. Here, the enzyme amine transaminases is evaluated since it offers a unique way of producing chiral amines. These amines are important as building blocks for pharmaceuticals and agrochemicals. A promising enzyme has been found, but it has been a problem to assess its performance and give process development direction. Common limitations are substrate and product solubility, unfavourable thermodynamics, inhibition and stability. It is a difficult task to assess where the current bottle neck is for a desired process. Moreover, it cannot be expected that a single solution to the limitations can be found and rather an integrated solution of all of the problems should be the future aim. All the limitations surround the reactor of a process, and with the performance of this being unknown, it is almost impossible to direct development. A focal point must therefore lie in the determination of kinetic models and how kinetic data can be obtained in a robust and generic way. Models for many enzymes already exist and can be found in common text books. These models do however require mutant specific data and must be collected with the target reaction. In this thesis a novel way of collecting kinetic data is created, this is carried out by combining existing technology and enables the analysis of aqueous solutions on-line. Furthermore, the use of a size exclusion column enables the simultaneous detection of enzymes and UV/VIS active compounds. The size exclusion chromatography does not provide baseline separated results, nor is this required. The application of chemometric tools enable detection of compounds in the collected retention time wavelength data. A major improvement over traditional techniques is the quantification of enzyme concentration and this makes it possible to use specific activities for model fitting. The setup takes advantage of microfluidic features and delivers semi-automatic experimentation, overall reducing both consumption of precious materials and costly labor.