The pursuit of identifying efficient cell factory candidates for production of pharmaceutically relevant products and commodity chemicals relies heavily on the successful selection of process suitable microorganisms. Hence the selection of efficient cell factories is paramount for successful scale-up to economically viable industrial processes. Accurate quantitative assessment of cellular performance is required for the evaluation of the overall suitability of a microorganism as an industrial cell factory, ensuring that not only product, but also process parameters are optimised. With the increasing number of strains generated through genetic engineering programmes, the traditionally applied methods for strain characterisation, which are typically labour intensive and time consuming, have become somewhat limited due to throughput capacity. Unfortunately, most high throughput methods only provide low levels of information compared to larger scale cultivations, explaining why these systems have not been broadly implemented. The overall aim of the thesis was, therefore, to shift this paradigm towards higher throughput systems for assessment of cellular performance with a higher level of information. This was pursued through development and validation of small, scalable microtiter based systems, for cultivating yeast and filamentous fungi, validated by comparable results from bioreactors. The experimental work was performed using *Saccharomyces cerevisiae* (yeast) and *Aspergillus nidulans* (filamentous fungus) strains producing the heterologous model polyketide, 6-methylsalicylic acid (6-MSA). An automated methodology for high throughput screening focusing on growth rates, together with a fully automated method for quantitative physiological characterisation in microtiter plates, was established for yeast. Full scalability was demonstrated through comparative physiological characterisation of yeasts, cultivated in both microtiter plates and bioreactors, revealing that the growth rate and yield coefficients of all non-volatile products including biomass could be correlated. The highly correlated results were taken as an indication of comparable growth physiology in both microtiter plates and bioreactors, which was substantiated by metabolic flux analysis resulting in identical flux distributions over micro-scale and lab scale cultivations. The thesis further presents a novel automated high throughput method for cultivating filamentous fungi in microtiter plates, without compromise to morphology and with product yields and growth rates identical to bioreactors. This was made possible by the dispersive effect on morphology of the anionic polymer carboxypolymethylene, enabling the application of optical density measurements as a means to evaluate growth rates. Again full scalability was demonstrated for a heterologous 6-MSA producing *A. nidulans* strain, cultivated in both microtiter plates and bioreactors, displaying identical growth rates and 6-MSA yields on glucose. This versatile and robust method was shown to be applicable for a wide range of different filamentous fungi and conditions, with growth rates comparable with those reported in the literature. A final comparative study of cell factory potential, involving the heterologous 6-MSA producing *S. cerevisiae* and *A. nidulans* strains, applied throughout the thesis, demonstrated superior yields and productivities for an *A. nidulans* strain where two copies of the 6-MSA gene had been chromosomally integrated. Implementation of a chemostat cultivation strategy for *A. nidulans* proved successful for conditional comparison, while metabolic oscillations and low productivities in continuous cultivations of *S. cerevisiae* rendered it less favorable for production of 6-MSA. Overall the methods developed and validated during the course of this study, have contributed to a progression towards higher throughput, together with an improved level of detail in physiological characterisation of cultivations at micro-scale. This paves the way for further advances in detailed quantitative physiology based on omics analyses, which would further increase the possibilities for advanced quantitative physiology at different scales.