teristics, in particular already at an early state of up scaling, being additionally time-saving and cost-reducing, but having a high prediction accuracy for said performance in a large volume scale cultivation and/or under high productivity conditions, in particular in a bioreactor scale.

This problem is solved by the independent claims of the present invention.

In one aspect, there is provided a process for the prediction of cell culture performance data of at least one sample cell comprising the steps:

(a) providing a sample of the at least one sample cell, cell culture performance data from a standard cell and raw standard MS (mass spectrometric) data from the standard cell,

(b) subjecting the sample of the at least one sample cell to a MS analysis to obtain raw sample MS data thereof,

(c) subjecting the raw standard and the raw sample MS data to at least one first MS signal processing method to obtain pre-treated standard and sample MS profiles and

(d) subjecting the cell culture performance data from the standard cell of step (a) and the pre-treated standard and sample MS profiles obtained in step (c) to a second MS signal processing method including a PLS-DA (partial least squares discriminant analysis) based comparative evaluation so as to predict the cell culture performance data of the at least one sample cell, wherein the cell culture performance data are cell specific productivity, integral viable cell count or cell product concentration data.

In another aspect, there is provided a device that is adapted to provide a prediction of cell culture performance data when supplied with a sample of at least one sample cell comprising the following technical features:

(a) a means adapted for subjecting a sample of the at least one sample cell to a MS (mass spectrometric) analysis to obtain a raw sample MS data thereof,

(b) a means adapted for subjecting a raw standard and the raw sample MS data to at least one first MS signal processing method to obtain pre-treated standard and sample MS profiles and

(c) a means adapted for subjecting cell culture performance data from a standard cell and the pre-treated sample and standard MS profiles to a second MS signal processing method including a PLS-DA (partial least square discriminant analysis) based comparative evaluation so as to predict the cell culture performance data of the sample cell, wherein the cell culture performance data are cell specific productivity, integral viable cellcount or cell product concentration data.

~~Thus, t~~The present invention also provides a process, preferably an in vitro process, for the prediction of cell culture performance data of at least one sample cell comprising the steps:

a) providing a probe of the at least one sample cell, preferably cultivated in a low volume of a medium, cell culture performance data from a standard cell and raw standard MS (mass spectrometry) data from a standard cell,

b) subjecting the probe of the at least one sample cell to a MS analysis to obtain a raw sample MS data thereof,

c) subjecting the raw standard and the raw sample MS data to at least one first MS signal processing method to obtain pre-treated standard and sample MS profiles and

d) subjecting the cell culture performance data from the standard cell from step a) and the pre-treated sample and standard MS profiles obtained in step c) to a second MS signal processing method including, preferably to a data analysis comprising of, a PLS-DA (partially least squares-discriminant analysis) based comparative evaluation so as