Claims

1. 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.

2. The process according to claim 1, wherein the cell culture performance data are cell specific productivity, integral viable cell count or cell product concentration data.

3. The process according to any one of the preceding claims, wherein the cell is selected from the group consisting of human cell lines, animal cell lines, plant cell lines, cells from fungi, cells from bacteria, cells from yeast and stem cells.

4. The process according to any one of the preceding claims, wherein the cell is a CHO cell line, a CHO-K1 cell line or a modified CHO-K1 cell line.

5. The process according to any one of the preceding claims, wherein the MS analysis in step (b) is MALDI-TOF.

6. The process according to any one of the preceding claims, wherein the sample of the sample cells subjected to step (b) comprises from 0.015×10^6 to 0.0625×10^6 cells.

7. The process according to any one of the preceding claims, wherein the raw sample MS data obtained in step (b) and the raw standard MS data provided in step (a) are signal processed by an operation selected from the group consisting of baseline correction, normalisation, alignment, filtering and cropping.

8. The process according to any one of the preceding claims, wherein the pre-treated standard and sample MS profiles obtained in step (c) are optically analysed.

9. The process according to any one of the preceding claims, wherein the sample cell with the predicted cell culture performance data evaluated in step (d) is cultivated in a cell culture so as to verify its cell culture performance data.

10. The process according to any one of the preceding claims, wherein the raw sample MS profiles obtained in step (b) and the verified cell culture performance data of the sample cell are used in step (a) as standard MS data and cell culture performance data from a standard cell.

11. A process for the production of a cell product from a cell comprising the steps:

a) predicting the cell culture performance data according to claims 1 to 10,

b) identifying the sample cells with the desired cell culture performance data,

c) cultivating said sample cells identified in step b) and

d) obtaining the cell product produced by the cultivation in step c).

12. The process according to claim 11, wherein the sample cell which cell culture performances data are predicted in step a) is cultivated in a low volume of a medium.

13. A process for the isolation of a cell with desired cell culture performance data, wherein a process according to any one of the preceding claims is performed and the desired cell is isolated.

14. A cell isolated by the process according to claim 13.

15. The cell according to claim 14, which is characterised by a protein productivity of above 10 g/l.

16. A device for the prediction of cell culture performance data 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.

Claims

1. 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.

2. The process according to claim 1, wherein the cell is selected from the group consisting of human cell lines, animal cell lines, plant

cell lines, cells from fungi, cells from bacteria, cells from yeast and stem cells.

3. The process according to any one of the preceding claims, wherein the cell is a CHO cell line or a CHO-K1 cell line.

4. The process according to any one of the preceding claims, wherein the MS analysis in step (b) is MALDI-TOF.

5. The process according to any one of the preceding claims, wherein the sample of the sample cells subjected to step (b) comprises from 0.015×10^6 to 0.0625×10^6 cells.

6. The process according to any one of the preceding claims, wherein the raw sample MS data obtained in step (b) and the raw standard MS data provided in step (a) are signal processed by an operation selected from the group consisting of baseline correction, normalisation, alignment, filtering and cropping.

7. The process according to any one of the preceding claims, wherein the pre-treated standard and sample MS profiles obtained in step (c) are optically analysed.

8. The process according to any one of the preceding claims, wherein the sample cell with the predicted cell culture performance data evaluated in step (d) is cultivated in a cell culture so as to verify its cell culture performance data.

9. The process according to claim 8, wherein the raw sample MS profiles obtained in step (b) and the verified cell culture performance

data of the sample cell are used in step (a) as standard MS data and cell culture performance data from a standard cell.

10. A process for the isolation of a cell with desired cell culture performance data, wherein a process according to any one of the preceding claims is performed and the desired cell is isolated.

~~11. A cell isolated by the process according to claim 10, which is characterised by a protein productivity of at least 10 g/l/h.~~

~~12~~11. 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 per-

formance data are cell specific productivity, integral viable cellcount or cell product concentration data.