

Title (en)
METHOD AND SYSTEM FOR MICROORGANISM IDENTIFICATION BY MASS SPECTROMETRY-BASED PROTEOME DATABASE SEARCHING

Title (de)
VERFAHREN UND VORRICHTUNG ZUR BESTIMMUNG VON MIKRO-ORGANISMEN DURCH MASSENSPEKTROMETRIE UND PROTEOMDATENBANKSUCHSYSTEM

Title (fr)
PROCEDE ET SYSTEME D'IDENTIFICATION DE MICRO-ORGANISMES PAR RECHERCHE DANS UNE BASE DE DONNEES DE PROTEOMES FONDEE SUR LA SPECTROMETRIE DE MASSE

Publication
EP 1272657 A2 20030108 (EN)

Application
EP 01928435 A 20010411

Priority

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- US 19636800 P 20000412

Abstract (en)
[origin: WO0179523A2] A simple statistical model that predicts the distribution of false matches between peaks in matrix-assisted laser desorption/ionization mass spectrometry data and proteins in proteome databases is derived and validated. Given the cluttered and incomplete nature of the data, it is likely that neither simple ranking, nor simple hypothesis testing will be sufficient for truly robust microorganism identification over a large number of candidate microorganisms. In an effort to increase robust microorganism identification, the proteome databases are restricted to include data related to a given set of proteins, and not all proteins. By removing data from the proteome databases, the model is made more robust, i.e., there is a decrease in the number of false matches.

IPC 1-7
C12Q 1/00

IPC 8 full level
G01N 27/62 (2006.01); **C12Q 1/00** (2006.01); **C12Q 1/04** (2006.01); **G01N 33/48** (2006.01); **G06F 17/18** (2006.01); **G06F 19/00** (2011.01); **G16B 50/30** (2019.01)

IPC 8 main group level
C12Q (2006.01)

CPC (source: EP US)
G01N 33/569 (2013.01 - EP); **G01N 33/6851** (2013.01 - EP); **G16B 50/30** (2019.01 - EP US); **H01J 49/0036** (2013.01 - EP); **G01N 2570/00** (2013.01 - EP); **G16B 50/00** (2019.01 - EP)

Citation (search report)
See references of WO 0179523A2

Designated contracting state (EPC)
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