07/04/03
20030193 12

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

162162

(43) International Publication Date
8 August 2002 (08.08.2002)

PCT

(10) International Publication Number
WO 2002/061661 A3

(51) International Patent Classification[7]: G06F 19/00, H01J 49/00, G01N 33/68, C12Q 1/68

(21) International Application Number: PCT/US2001/049491

(22) International Filing Date: 19 October 2001 (19.10.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/242,165 19 October 2000 (19.10.2000) US
60/242,398 19 October 2000 (19.10.2000) US

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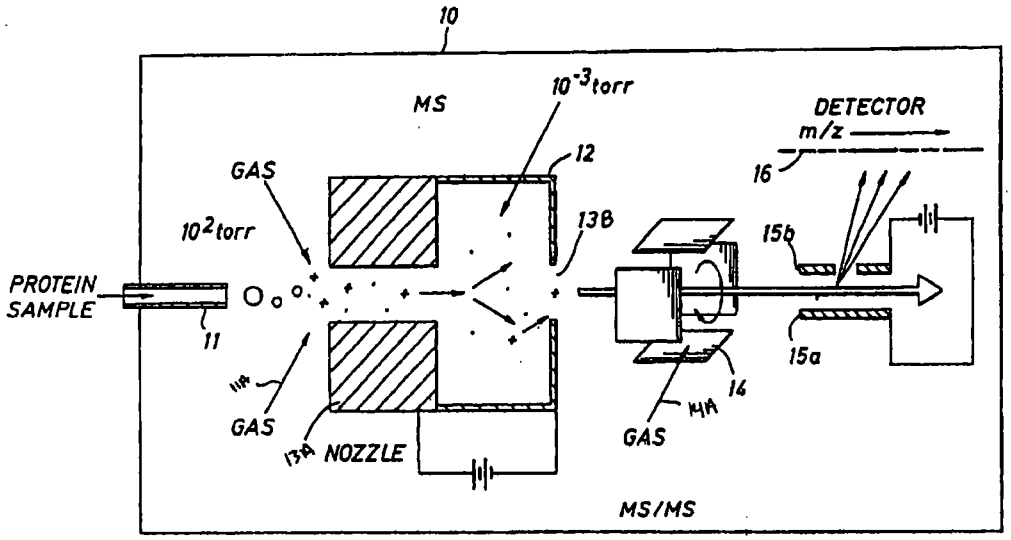
(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— with international search report

[Continued on next page]

(54) Title: METHODS FOR DETERMINING PROTEIN AND PEPTIDE TERMINAL SEQUENCES



(57) Abstract: Methods and apparatuses for deriving the sequence of an oligomer. In one exemplary method for deriving the sequence of a polypeptide, a predetermined set of mass/charge values for amino acid sequences is stored. An abundance value from mass spectrum data for each mass/charge value in the predetermined set is determined to produce a plurality of abundance values. A first ranking, based on the plurality of abundance values, is calculated for each sequence of a set of amino acid sequences having a first number of amino acids. A second ranking, based on the plurality of abundance values, for each sequence of a set of amino acid sequences having a second number of amino acids is calculated. A cumulative ranking, based on the first ranking and the second ranking, is calculated for each sequence of a set of amino acid sequences having at least the second number of amino acids.

WO 2002/061661 A3

ACTION

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

(88) Date of publication of the international search report:
8 April 2004

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.