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Revised

**Intact cell MALDI-TOF Mass Spectrometry, a promising proteomic profiling method**  
**in farm animal clinical and reproduction research**

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**Abstract**

The objective of this review is to provide new insights into the possible use of a proteomic method known as Intact Cell Matrix-Assisted Laser Desorption-ionization Time-Of-Flight Mass Spectrometry (ICM-MS) in animal clinical research. Here, we give an overview of the basics of this technique, its advantages and disadvantages compared with other proteomic approaches, past applications and future perspectives. A special emphasis on its implementation in animal reproduction science is given, including examples of the reliable use of ICM-MS on fertility screening. In mammals, the ICM-MS profiles from pig epididymal spermatozoa reflect the proteome changes that they undergo during epididymal maturation and could be associated with the acquisition of fertilizing ability. In chicken, using adequate pre-processing and bioinformatics analysis tools, sperm ICM-MS profiles showed characteristic spectral features that allowed their classification according to their actual

31 fertilizing ability. The association of ICM-MS and Top-down proteomic strategies allowed the  
32 identification of chicken fertility biomarkers candidates such as protein vitelline membrane  
33 outer layer protein 1 (MVO-1) and avian beta-defensin 10 (AVB10). In female reproduction, a  
34 similar approach on ovarian follicular cells allowed the identification of specific markers of  
35 oocyte maturation in the oocyte and surrounding cumulus cells. Altogether, these results  
36 indicate that ICM-MS profiling could be a suitable approach for molecular phenotyping of  
37 male and female gametes.

38

### 39 **1. Clinical proteomics in animal sciences**

40 Clinical proteomics is a field of proteomics whose objective is the identification of  
41 biomolecules showing differential abundance in a certain body fluid, cell and/or tissue associated  
42 with a defined clinical condition. These molecules, usually denominated “biomarkers”, can be  
43 thereafter used in clinical applications for diagnosis, stratification of patients for specific treatment,  
44 or therapy monitoring. A combination of different proteomic biomarkers or “biomarker profile” can  
45 also be employed, giving a combined measure associated with the studied condition [1,2]. Biomarker  
46 profiles are potentially better at defining a complex patho-physiological condition than single  
47 biomarkers, and clinical proteomics is moving its focus to the identification of such fingerprints  
48 panels that can define a diagnostic phenotype [1]. In animal sciences, clinical proteomics has not  
49 been as widely used as in human medicine, but there is growing interest in identifying and  
50 implementing the use of disease biomarker profiles [3]. However, applications of veterinary clinical  
51 proteomics go beyond, and also include food security, quality assessment of animal products (meat,  
52 milk, eggs, wool), generation of model organisms and phenotyping of production traits [4,5]. One  
53 good example of the latter is the application of clinical proteomics in animal reproduction science,  
54 and more specifically in searching for gamete quality biomarkers. Optimization of reproduction  
55 management is actually essential in farming since keeping high productivity often relies on adequate  
56 selection of breeders as well as the use of optimal gamete handling protocols (sperm

57 cryopreservation, oocyte in vitro maturation, in vitro fertilization, etc) [6]. Actually, one of the main  
58 problems in animal breeding is that the selection for production traits, such as fast growth, egg-  
59 laying capacity or milk productivity, usually has a detrimental effect in reproductive traits [7].  
60 Breeders are therefore interested in the accurate phenotyping of the fertility of their animals to  
61 maintain high productivity [7].

62

## 63 **2. Technical approaches employed in clinical proteomics: the emergence of protein profiling** 64 **platforms**

65 Traditionally, biomarker research using proteomics starts with an initial discovery step,  
66 whose objective is untargeted screening of the whole proteome of a certain biological system in  
67 defined conditions, in search of biomarkers [8]. The initial discovery approach is usually based on the  
68 orthogonal separation of whole proteins contained in the sample either using gel electrophoresis or  
69 liquid chromatography followed by a “bottom-up” protein analysis (Figure 1). In this strategy,  
70 isolated proteins or protein mixtures are digested with a protease to obtain peptides. These  
71 fragments of proteins can be analyzed directly by mass spectrometry (MS) and identified by a  
72 peptide mass fingerprint (PMF) strategy [9]; and/or using tandem mass spectrometry (MS/MS) using  
73 a peptide fragment fingerprint (PFF) in order to obtain sequence peptides [10]. However, this  
74 method is cumbersome and complicated to be implemented in a clinical setting for routine  
75 diagnostics, since it involves complex sample preparation procedures, analytic processing of technical  
76 complexity and limited throughput. This workflow typically results in a long list of candidates  
77 (peptides/proteins showing differential relative abundance) to be integrated in order to construct a  
78 biomarker profile. These need to be verified and validated following a second analysis, this time  
79 using large cohorts, and high-throughput targeted analysis through the application of multiplexed  
80 assays [11]. One of the most recent and efficient techniques developed for the latter is known as  
81 MRM (Multiple Reaction Monitoring), which shows several advantages such as being accurate, fast  
82 and very sensitive [12]. However, the applicability of this technology in clinical settings remains to be

83 seen, since the development of such tests depends on the use of pre-existing quality MS data, is  
84 expensive, as well as the specific detection and/or quantification of some of the desired targets can  
85 be challenging [13].

86 Behind the tremendous progress and possibilities in mass spectrometry, “Bottom-up” proteomics has  
87 been and is still the driving force in proteome analysis. However, the proper assignment of  
88 proteoforms with their pattern of modifications remains a challenge for bottom-up proteomics. The  
89 real goals in proteomic analyses are knowing the functions of the intact proteins in biological  
90 processes with or without their different modifications, their locations and interactions. Many of  
91 these aspects may get lost when breaking down proteins to their corresponding peptide fragments.  
92 Beside this conventional strategy, the top-down mass spectrometry constitutes an alternative  
93 (Figure1) [14, 15]. In this approach, intact proteins are analysed by MS and MS/MS in order to obtain  
94 structural informations allowing both the identification of the proteins and the characterization of  
95 the post-translational modifications. To perform Top-down proteomics, protein fractionation  
96 combined to high-resolution mass spectrometry and specific bioinformatics tools are necessary.  
97 Despite the technical difficulty of proteome-wide analysis at the intact protein level, Top-down  
98 proteomics offers an alternative to digestion-based approaches. For several years, there is growing  
99 interest in developing untargeted methodologies based on the use of peptide/protein profiling  
100 platforms, of which the most important are based on the use of Surface Enhanced Laser Desorption  
101 Ionization Time-Of-Flight Mass Spectrometry (SELDI-TOF MS), Capillary Electrophoresis Mass  
102 Spectrometry (CE-MS, [16]) or Matrix-Assisted Laser Desorption/Ionization Time Of Flight Mass  
103 Spectrometry (MALDI-TOF MS). One of the first approaches to peptide/protein profiling is SELDI-TOF  
104 MS, which employs active coatings/surfaces with affinity for specific biomolecules. Liquid samples  
105 (biological fluids or tissue extracts) are incubated with these surfaces, thus reducing sample  
106 complexity and allowing the acquisition of readable peptide/protein profiles by applying MS analysis  
107 directly to the surface-bound molecules. These profiles are later compared between conditions, in  
108 search for diagnostic patterns [16]. Several studies have explored the possible application of SELDI-

109 TOF profiling in veterinary sciences in the past, e.g for the detection of porcine diseases [17] or  
110 bovine paratuberculosis [18]. However, it is nowadays generally accepted that its low reproducibility  
111 (inter-laboratory CV% values above 40%) and lack of analytical robustness (difficulties with  
112 calibration and mass accuracy) impair its routine use in the clinic [13]. Capillary electrophoresis mass  
113 spectrometry (CE-MS) appeared later as an alternative to SELDI-TOF MS profiling using biofluids. This  
114 technique employs biomolecule separation through capillary electrophoresis as a method to reduce  
115 sample complexity. Separated molecules are then directly analyzed by MS to obtain a profile [19].  
116 While CE-MS shows improved reproducibility and sensitivity compared to SELDI-TOF MS, it requires  
117 laborious sample preparation and shows low throughput, which are negative aspects in clinical  
118 proteomics [20]. CE-MS has been successfully applied in animal sciences [21,22], although it is  
119 recognized that its application to clinical proteomics is hampered by its low throughput, the need to  
120 standardize and simplify the sample preparation, as well as the development of accurate methods  
121 for calibration and data extraction/processing .

122         Along with CE-MS, Matrix-assisted laser desorption/ionization time of flight mass  
123 spectrometry (MALDI-TOF MS) profiling is an emerging approach in clinical proteomics. This  
124 technique has theoretically a higher potential for clinical application than CE-MS due to its high  
125 throughput, ease of operation, simple sample preparation and the existence of established data-  
126 processing platforms . MALDI-TOF MS has the ability to detect the most intense intact molecular ions  
127 present directly in the biological sample over a relatively wide mass range (typically 1,000 – 30,000  
128 Da), with a high sensitivity (from the picomolar to the femtomolar concentrations) and a high  
129 tolerance for contaminants such as salts [23]. Consequently, MALDI-MS constitutes a powerful tool  
130 for the direct analysis of complex peptide/protein mixtures within biological specimens such as crude  
131 extracts and intact cells. It is in fact, the possibility of using whole, untreated cells what makes this  
132 technique particularly promising for clinical applications. In spite of this, this platform has been rarely  
133 used in medicine and even less in animal sciences. In this review, we will focus on the technical  
134 aspects of the platform MALDI-TOF MS using intact cells (known as Intact cell MALDI-TO MS or ICM-

135 MS), as well as the past applications and possibilities of this technique especially in animal sciences.  
136 Particularly, we will provide with a more in-deep overview on the past use of this platform in animal  
137 gametes.

138

### 139 **3. Intact cell MALDI-TOF MS: the basics**

140 In the following paragraphs we will describe the typical ICM-MS protocol workflow (Figure 2).

141

#### 142 *3.1. Sample preparation*

143 An important application of ICM-MS is to detect endogenous peptides and proteins (intact  
144 forms unmodified by any chemical treatments) directly in whole cells using MALDI-TOF profiling  
145 without previous sample pre-fractionation, protein extraction or treatment. In this context, “intact  
146 cell” means that whole cells are subjected to analysis without any preparatory steps, although they  
147 can be cryopreserved or kept frozen prior to analysis. Direct analysis of cells by MALDI-TOF MS thus  
148 avoids the problems associated with extraction procedures (lost or degraded biological material),  
149 avoids the variability introduced by sample preparation and allows significant increase of a number  
150 of conditions to compare (up to several hundred). Samples susceptible of being analyzed through  
151 ICM-MS must consist of homogenous cellular populations, thus derived from cell culture or being  
152 isolated from a cell mix. Pre-treatment of such cells only requires the removal of the biological matrix  
153 where cells are contained, such as biological fluids or culture media. Usually, cells are harvested,  
154 rinsed and centrifuged, discarding after the supernatant containing biological matrix proteins. Wash  
155 buffers must keep cell integrity, promote crystallization and ionization, and ideally chelate salts.  
156 Good examples of the latter are Tris HCl-sucrose buffer (osmolarity at  $\approx 300$  mOsm/L) [24,25] or  
157 ammonium acetate [26,27]. It is important to avoid buffers containing phosphate-buffered saline  
158 (PBS), since the salts and the negative charge provided by PBS can interfere with the analysis.

159

#### 160 *3.2. Matrix deposition*

161           Although sample deposition on the MALDI plate is a simple process, the protocol followed at  
162 this stage can have a significant effect on the outcome of the analysis [28], and so this has to be  
163 optimized for each sample type. A known amount of cells (usually  $2 \times 10^3$  to  $1 \times 10^6$  cells) is deposited  
164 on the target of a conductive MALDI metallic plate and mixed with an adequate matrix solution. The  
165 matrix consists of crystallized molecules, the three most commonly used being 3,5-dimethoxy-4-  
166 hydroxycinnamic acid (sinapinic acid) [24-27,29-33],  $\alpha$ -cyano-4-hydroxycinnamic acid (CHCA, alpha-  
167 cyano or alpha-matrix) [34,35] and 2,5-dihydroxybenzoic acid (DHB) [36]. A solution of one of these  
168 molecules is made, often in a mixture of highly purified water and UV-absorbing weak organic acid  
169 such as acetonitrile (ACN), which is present in a concentration ranging 40-60%. A counter ion source  
170 such as Trifluoroacetic acid (TFA) is usually added to generate the ions, in a concentration ranging  
171 0.1-3%. The ratio of analyte to matrix is important, and must be optimized for each sample type.  
172 There are multiple ways of performing the mix of samples and matrix. Among these methods, the  
173 'dried droplet' method is the most usually employed [24-26, 29, 32-34,36]. It consists of depositing  
174 the sample and subsequently the matrix on the plate and then allowing co-crystallization. However,  
175 the thin layer [30-31] (a saturated matrix layer + mix of sample/matrix) or the sandwich [27] (a  
176 saturated matrix layer + dried droplet) methods can provide better results on a qualitative level. The  
177 resulting mixture is then allowed to completely dry at room temperature.

178

### 179 *3.3. Spectra acquisition*

180           Once the MALDI sample plate is prepared and placed within the mass spectrometer, a laser  
181 pulse hits the cells-matrix mixture. The matrix absorbs the laser energy, causing its own desorption  
182 and protonation, and subsequent sample protonation and vaporization. The generated ions are then  
183 accelerated by an applied high voltage (15-25 kV), separated in a linear field-free tunnel and  
184 detected as an electrical signal at the end of the TOF analyzer. Peptides and proteins of different  
185 masses and charges (mostly under the single-charged ions form) then fly at different speeds through  
186 the TOF analyzer. Their arrival times at the detector are distributed according to the square root of



187 the mass-to-charge ratio ( $\sqrt{m/z}$ ). The result is a spectrum in the range of 1,000-30,000 m/z, whose  
188 components (peaks) show a degree of intensity that correlates with their abundance in the original  
189 sample. Each spectrum is produced by averaging several hundred to thousand laser shots that are  
190 spread over the entire sample spot surface. Several replicate spectra (a minimum of 6, up to 12) are  
191 taken for each biological sample under the same experimental conditions and a minimum of three  
192 reads per spot are recommended to be performed. Spectral acquisition is performed using an  
193 automated MS mode, thus increasing the speed and throughput of this technique. External mass  
194 calibration must be performed, using a peptide and protein known mixture whose masses must  
195 cover the analytical mass range. A high degree of mass accuracy is desired, and typical calibration  
196 error should not be higher than 0.5%. In order to optimize mass accuracy, it is recommended to  
197 apply an additional internal calibration (by superposing sample and calibration standard) as well as a  
198 lock-mass correction using a high-intensity mass at the middle of the mass range (error of 0.05%).

199

#### 200 *3.4. Spectra pre-processing*

201 Raw MALDI data usually contain a large set of spectra, each containing thousands of  
202 measurements composed by m/z-intensity pairs, most of which correspond to noisy signals. In order  
203 to distinguish true from noise signals as well as to reduce experimental variance within the data set,  
204 several spectral treatments (known as pre-processing) must be carried out. This pre-processing  
205 includes the following steps: (1) internal lock-mass calibration using a mass of known or unknown  
206 identity, to provide with a higher mass accuracy, (2) baseline correction to remove the effect of noise  
207 introduced by the matrix, (3) filtering to smooth the signal, (4) alignment of all spectra using common  
208 m/z, (5) automatic peak detection on average spectra (area and/or intensity), and (6) normalization.  
209 The criteria followed for this pre-processing can drastically change the outcome of analysis, and so it  
210 is essential to pay attention to this stage in order to perform a rigorous study [37].

211

#### 212 *3.5. Statistical analysis and pattern matching algorithms*

213           Once this is accomplished, applying statistical methods and/or machine-learning techniques  
214 is often desired in order to identify those spectral features (peaks) associated with a given condition  
215 (candidate biomarkers or biomarker profiles), sample grouping (through hierarchical classification or  
216 principal component analysis) and classification (through the constructions of class-predictive models  
217 based on the use of data-dependent algorithms or through comparison with reference spectra  
218 contained in a database). While processing and data analysis were initially based on the use of  
219 general tools like R or SPSS (Statistical Package for the Social Sciences) softwares, requiring  
220 programming skills and implying a lack of uniformity in the criteria followed for this process, a  
221 number of user-friendly tools specific for MALDI profiling data are currently available. In general,  
222 there are two kinds of tools regarding the type of post-processing analysis: those based on the use of  
223 a reference spectra database to which test spectra are compared, and those in which the user sets  
224 examples of the different studied classes. The first group of tools includes commercial software  
225 packages containing reference databases, and its use is mainly restricted to microorganism  
226 identification (e.g. MALDI Biotyper from Bruker Daltonics or Anagnostec SARAMIS from Shimadzu).  
227 The second group entails tools that allow both supervised and unsupervised techniques to analyze  
228 data following a clinical approach. In general, the biomarker research-oriented analysis starts with  
229 performing a statistical analysis (parametric or non-parametric) using quantitative values (normalized  
230 peak height or area). The  $m/z$  peaks presenting significant differences between the different studied  
231 conditions are selected and relative data are then utilized to perform additional analysis such as  
232 Receiver Operating Characteristic curves, cluster analysis, Principal Component Analysis, etc. It is  
233 important to set a statistical stringency adequate to the desired statistical power (usually set at 0.8),  
234 especially in studies using a reduced sample number. This statistical analysis can be completed with  
235 machine-learning techniques. In this case, the diagnostic performance of the ICM-MS-based  
236 predictive model for a given condition should be compared with that of traditional diagnostic tests of  
237 the same condition. In the recent years, different open-source tools (e.g. Mass-up, MALDIquant) and

238 commercial tools (e.g. ProgenesisMALDI-Nonlinear Dynamics, ClinProTools-Bruker Daltonics.  
239 MarkerView™- AB Sciex) specifically designed for MALDI profiling analysis have been released.

240

#### 241 **4. Top-Down MS for identification of proteins detected by ICM-MS**

242 The progress in the general use of MS-based profiling has been somewhat hampered by the  
243 difficulties in confidently identifying diagnostic MS signatures [38]. ICM-MS analyses (in general all  
244 profiling methods) are ideally completed with the identification of the  $m/z$  peaks present in the  
245 spectra. As aforementioned, these masses correspond to native, endogenous molecules present in  
246 the sample. Of all the mass spectrometry-based identification approaches currently available (Figure  
247 3), Top-Down proteomics represents the best approach to identify endogenous peptidofoms and  
248 proteofoms, as involves the detection of an intact molecular species and its direct fragmentation,  
249 thus providing with a complete description of the primary structure of the protein and of its  
250 modifications [39].

251 As it is generally desired to employ the same platform for both profiling and sequencing,  
252 following an on-line approach, there is big interest in the scientific community in advancing in  
253 technology and data-processing systems that would allow MALDI Top-Down analysis in complex  
254 samples (such as protein extracts, whole cells or tissue slides). Post-Source (PSD) [40] or In-Source  
255 Decay (ISD) [41] MS methodologies can be used for de novo sequencing of the whole proteins, with  
256 the condition of these being enriched or purified, since their main limitation is the inability of dealing  
257 with complex samples, and the MS/MS strategy is routinely restricted to small peptides with  $m/z <$   
258 5,000 [42,43]. Thus, the *in-situ* targeted identification of peaks of interest observed by MALDI  
259 remains challenging. Sample complexity can be decreased through fractionation (e.g. using  
260 chromatography, gel separation, depletion of abundant proteins, etc), and fractions are later re-  
261 analyzed by MALDI-TOF/TOF. This approach indeed increases the number of positively identified  
262 biomolecules, but still shows a low throughput. Alternatively, Top-Down proteomics combining liquid  
263 chromatography separations and high resolution tandem mass spectrometry (LC-HR-MS/MS) with

264 electrospray (ESI) source seems to be the most appropriate approach to identify endogenous  
265 peptido- and proteoforms [36,41]. ESI generates multiply charged ions and is the preferred MS  
266 method for the analysis of both peptides and intact proteins, especially on a proteome-wide scale  
267 (global approach). Nowadays, Top-Down proteomic studies have largely been implemented using ESI  
268 coupled to either Fourier transform ion cyclotron resonance (FT-ICR) or Orbitrap mass analyzers to  
269 obtain high resolution ( $R > 100,000$ ) and mass accuracy ( $< 5$  ppm). Thus, a large number of whole,  
270 intact biomolecules can be directly identified, whose masses can be matched with MALDI  $m/z$  peaks,  
271 with a mass accuracy tolerance  $< 0.05\%$ . As described in the literature, the combination of ICM-MS  
272 and Top-Down HRMS is therefore a convenient analytical strategy [44, 45].

273

#### 274 **5. Intact Cell MALDI-TOF Mass Spectrometry – from bacteria to mammalian cells**

275 The use of ICM-MS was firstly reported in 1996 by Holland et al., and was applied to bacterial  
276 chemotaxonomy [46]. In this study, it was described that ICM-MS protein profiles contained species-  
277 specific signatures, so they could be used as a taxonomic tool [47]. In effect, the analysis of  
278 endogenous peptidoforms and proteoforms can be considered as a functional genomics analysis and  
279 therefore useful for phenotyping [48]. ICM-MS has been applied in different studies for bacterial  
280 identification, aiding at the development of the field of phyloproteomics [46,49,50]. Identification of  
281 the microorganisms was based on the identification of species-specific signatures in the ICM-MS  
282 spectra using bioinformatic tools and in the subsequent construction of reference spectral databanks  
283 [51]. Thereafter, comprehensive and curated databases were constructed using rigorous  
284 standardization procedures and commercialized together with tools that allowed a robust  
285 identification analysis [52, 53]. Nowadays, ICM-MS has become a valuable tool for the identification  
286 and the classification of microorganisms, including bacteria [47] or yeast [54-56], and it has been  
287 introduced in clinical routine microbiological diagnostics. Thus, this approach assists clinicians to  
288 provide a fast, accurate diagnosis associated with an adequate antimicrobial treatment in infectious  
289 diseases. Furthermore, this approach can also be applied to detect specific bacterial biomarkers, such

290 as antibiotic resistance, and may potentially predict infectious complications or/and being used for  
291 the development of novel virulence factor-based therapies [57].

292         Theoretically, ICM-MS could be applied to any cell type including superior eukaryotes, with  
293 the sole condition of cells being isolated (not in a tissue). Even if this approach is not yet routinely  
294 applied to the analysis of mammalian cells, there is sufficient evidences in the literature showing that  
295 ICM-MS spectra from “whole cells” or “intact cells” are sufficiently characteristic to address biological  
296 questions in human and animal clinical research (Table 1). In fact, ICM-MS has been applied mostly in  
297 cultured cells as a phenotyping tool in order to differentiate similar cell lines including glial [27] or  
298 cancer [58] lines. It has also been employed to evaluate the response of established cell lines to  
299 different treatments, like toxic chemicals [30]. Another series of studies have isolated different  
300 circulating white blood cells like monocytes or neutrophils to evaluate their differential response to  
301 different conditions [29, 59-62].

302

## 303 **6. ICM-MS proteomic analysis in animal sciences**

304         ICM-MS is a promising diagnostic tool, showing several advantages such as being cost-  
305 effective, simple and showing a high throughput. As it is based on the comparison of peptide and  
306 small proteins profiles rather than the comparison of single biomarkers, it is theoretically more prone  
307 to identify phenotypic differences associated with a certain physiological, pathological or  
308 experimental condition [5]. Bearing that in mind, multiple applications of ICM-MS in animal sciences  
309 could be foreseen. As it could be easily applied in cultured cells, it might be useful in screening  
310 studies in toxicology and infectious diseases, thus helping evaluate in a fast way the effect of single  
311 and combined substances (toxic compounds, pathogens, immuno-reactive substances, etc) in order  
312 to establish similarities, for instance, in their mechanisms of action, evaluating the nature of their  
313 response, etc. There are several examples in the literature describing how ICM-MS can be easily  
314 implemented in cellular toxicology tests. For instance, it has been shown in a fish cell model that  
315 proteome changes induced by copper sulfate, acridine, and  $\beta$ -naphthoflavone were reflected in the

316 ICM-MS profiles [30]. Similar results were obtained in human cell lines treated with hydrogen  
317 peroxide and aflatoxin B1 [26].

318         The use of ICM-MS for disease diagnostics in animals could be implemented in blood  
319 circulating cells, where the presence of pathognomonic ICM-MS spectra patterns could be  
320 researched. This could be particularly interesting in the course of infections often leading to sub-  
321 clinical symptoms (e.g. paratuberculosis), and/or those involving intracellular pathogens in blood  
322 cells (ehrlichiosis, anaplasmosis, babesiosis etc.). Several studies carried out in human samples have  
323 actually evidenced that ICM-MS analysis of human monocytes evidenced proteome changes  
324 occurring upon microbial stimulation [29]. ICM-MS spectra from M1 and M2 macrophage subtypes  
325 were also significantly different , as well as those obtained from macrophages in contact with  
326 extracellular (group B Streptococcus, *Staphylococcus aureus*) and intracellular (*Mycobacterium bovis*,  
327 *Orientia tsutsugamushi*, *Coxiella burnetii*) bacteria [60]. The ability of ICM-MS-based analysis to  
328 detect molecular differences linked to specific phenotypes has allowed the discovery of several  
329 markers. For instance, whole cell MALDI profiling analysis of peripheral chicken cells evidenced that  
330 thymosin beta-4 was an abundant peptide present in avian monocytes/macrophages (and not in  
331 granulocytes) and that it was regulated by bacterial lipopolysaccharides and peptidoglycans [63]. The  
332 same approach helped to put in evidence that  $\beta$ -defensin 2 is an important anti-microbial peptide in  
333 chicken and turkey heterophils [63].

334         However, clinical research in animal science is not only focused in finding disease biomarkers,  
335 but also in finding molecular tools that could help in animal production. Reproduction management  
336 represents one of the most important aspects of animal production, and very few molecular tools are  
337 available to monitor the implementation of new management methods in farm animals. In this  
338 sense, ICM-MS has been proven useful to follow cell-specific peptidome/proteome changes in the  
339 cells related to the animal reproductive system. In the following sections, we will discuss how ICM-  
340 MS profiling has been implemented for the analysis of male and female gametes in farm animals.

341

## 342 **7. ICM-MS proteomic analysis of male gametes**

343 Evaluation of sperm quality is usually based on the assessment of individual sperm  
344 parameters (motility, morphology), which is cumbersome and sometimes not well correlated with  
345 the actual fertilizing ability of tested sperm. Thus, the development of a fast, accurate tool for  
346 fertility screening is largely needed in human and veterinary medicine. From all possible molecular  
347 biology techniques applicable, proteomics seems to be one of the most adequate to study sperm  
348 biology. Numerous proteomic studies aiming to identify sperm markers of fertility were recently  
349 performed in several mammalian species (reviewed in [64-66]). However these approaches are not  
350 directly applicable for their routine use and the use of individual biomarkers has not been yet  
351 successfully implemented in fertility clinics to stratify sperm according to their quality. Sperm peptide  
352 and small protein profiling through ICM-MS has been recently proven useful to identify proteome  
353 patterns linked with fertility in chicken [45, 67]. The method included only a few and simple  
354 preparatory steps namely cell counting, washing sperm cells to eliminate seminal plasma proteins,  
355 and resuspension in the same buffer at a known concentration. The plating procedure was simple:  
356 sperm suspension was spotted onto a MALDI plate, overlaid with an adequate matrix and allowed to  
357 dry. Further MS analysis can be automated, this increasing the throughput of the method. Using  
358 adequate pre-processing and bioinformatics analysis tools, sperm ICM-MS profiles showed  
359 characteristic spectral features that allowed their classification according to their actual fertilizing  
360 ability [67]. This method was successfully employed in different chicken genetic lines, as well in other  
361 livestock species, thus showing a high versatility. Moreover, several peaks of chicken sperm ICM-MS  
362 spectra corresponding to peptidoforms (due to specific or non specific proteolytic activities) or  
363 proteoforms were identified using HRMS, including some fertility biomarkers candidates, such as  
364 protein vitelline membrane outer layer protein 1 or different forms of the avian beta-defensin 10. It  
365 has been also shown that the ICM-MS profiles from pig epididymal spermatozoa reflect the  
366 proteome changes that they undergo during epididymal maturation, mostly those related with a  
367 differential activity of sperm intracellular proteases and peptidases [68]. Moreover, it was observed

368 that the analysis of whole cells allowed a better discrimination of different maturation stages  
369 compared with sperm cell extracts as obtained with neutral detergents [68]. In short, these results  
370 indicate that ICM-MS profiling could be a suitable approach for molecular phenotyping of male  
371 gametes.

372

### 373 **8. ICM-MS proteomic analysis of female gametes**

374 Today, it is possible to initiate early embryonic development of just about any mammalian  
375 species by co-incubating oocyte with spermatozoa following a protocol known as *in vitro* fertilization  
376 (IVF). The original process includes the administration of high levels of gonadotropins to stimulate  
377 oocyte maturation and ovulation [69]. Oocyte maturation is a transition from immature germinal  
378 vesicle (GV) transcriptionally silenced oocyte to metaphase-II stage (Meta-II) which is accompanied  
379 by polar body extrusion, reorganization of the organelles through the ooplasm and molecular  
380 modifications including changes in protein abundance and post-translational modifications. Oocyte  
381 maturation plays an important role in the acquisition of oocyte developmental competence, referred  
382 as oocyte quality, which, at the same time, is crucial for embryo quality [70]. Maturation can be  
383 accomplished *in vitro* starting from the oocytes recovered from small antral follicles at the stage prior  
384 to selection and dominance, by using specific culture media, following a protocol known as *in vitro*  
385 *maturation* (IVM). IVM requires little or no use of *in vivo*-administered gonadotropins and has been  
386 proposed as an alternative to conventional IVF with ovulated oocytes in humans since it reduces the  
387 primary adverse effects caused by controlled ovarian stimulation, including the ovarian  
388 hyperstimulation syndrome [71]. IVM is actually a routine technique in animal reproduction  
389 biotechnologies, used especially in dairy cows of high genetic merit, where the success rate after  
390 artificial insemination is often low. In cattle, immature oocytes can be obtained from the ovaries  
391 either by ovum pick up or after slaughter, then subjected to IVM, fertilized and developed to  
392 transferable embryos. This technique of *in vitro* embryo production allows the use of less semen (this  
393 is important in the case of expensive and rare sperm), as well as increasing the progeny of oocyte



394 donors [72]. However, proteomic changes that occur in the oocyte during maturation and that define  
395 the quality of *in vitro* matured oocytes are mostly unknown, and so there is no accurate way of  
396 evaluating/monitoring how different IVM protocols can affect the process. Classic proteomics has  
397 been employed in the past with this objective. In fact, by using 2D-DIGE or 2DE coupled with nano-  
398 liquid chromatography and high resolution tandem MS, proteomes were established for bovine,  
399 porcine and murine oocytes identifying numerous proteins including putative markers of oocyte  
400 developmental competence including proteins needed for fertilization, reprogramming, embryo  
401 genome activation and first cleavages during early embryogenesis [73-75]. However, these proteomic  
402 approaches require a high amount of oocytes to be performed. In cows, only 8-10 oocytes fully-  
403 grown oocytes can be collected per ovary, so the amount of material is limited. The bovine oocyte is  
404 about 120  $\mu\text{m}$  in diameter, but it contains a relatively low intra-cellular protein content, about 80-  
405 100 ng per oocyte. ICM-MS was recently adapted to bovine ovarian cells from the individual antral  
406 follicles to obtain the protein/peptide signatures (<17kDa) of single oocytes, surrounding cumulus  
407 cells and granulosa cells [76]. It was demonstrated, that this technology could be applied to single  
408 bovine oocytes, and that single-oocyte ICM-MS spectra are characteristic of each stage of oocyte  
409 meiotic maturation from prophase-I in immature oocytes to metaphase-II in mature ones [76]. In  
410 this study, ICM-MS coupled to an optimized Top-down HR-MS proteomic approach on ovarian  
411 follicular cells allowed the identification of specific markers of oocyte meiotic maturation including  
412 IGF2 binding protein 3 and hemoglobin B in the oocyte and thymosins beta-4, and beta-10, histone  
413 H2B and ubiquitin in surrounding cumulus cells.

414

## 415 **9. Conclusions**

416 ICM-MS is a peptide/protein profiling platform widely used for phyloproteomics that has been  
417 recently revealed as a promising tool for molecular phenotyping in clinical proteomics. The  
418 applicability of this technique has been already shown in clinical microbiology and it is starting to  
419 bring some attention in biomedicine. Indeed, specific characteristic features present in ICM-MS

420 profiles in a given condition can be considered as biomarker profiles, and individual differential  
421 features can be identified following Top-Down proteomics. Although still not widely used, ICM-MS  
422 profiling can have multiple applications in animal research, ranging from basic sciences - as for  
423 example, in newly established primary cell lines phenotyping or in vitro toxicological studies - to  
424 applied sciences for use in disease diagnostics, male fertility classification according to semen  
425 profiling or monitoring of oocyte quality, among others.

426

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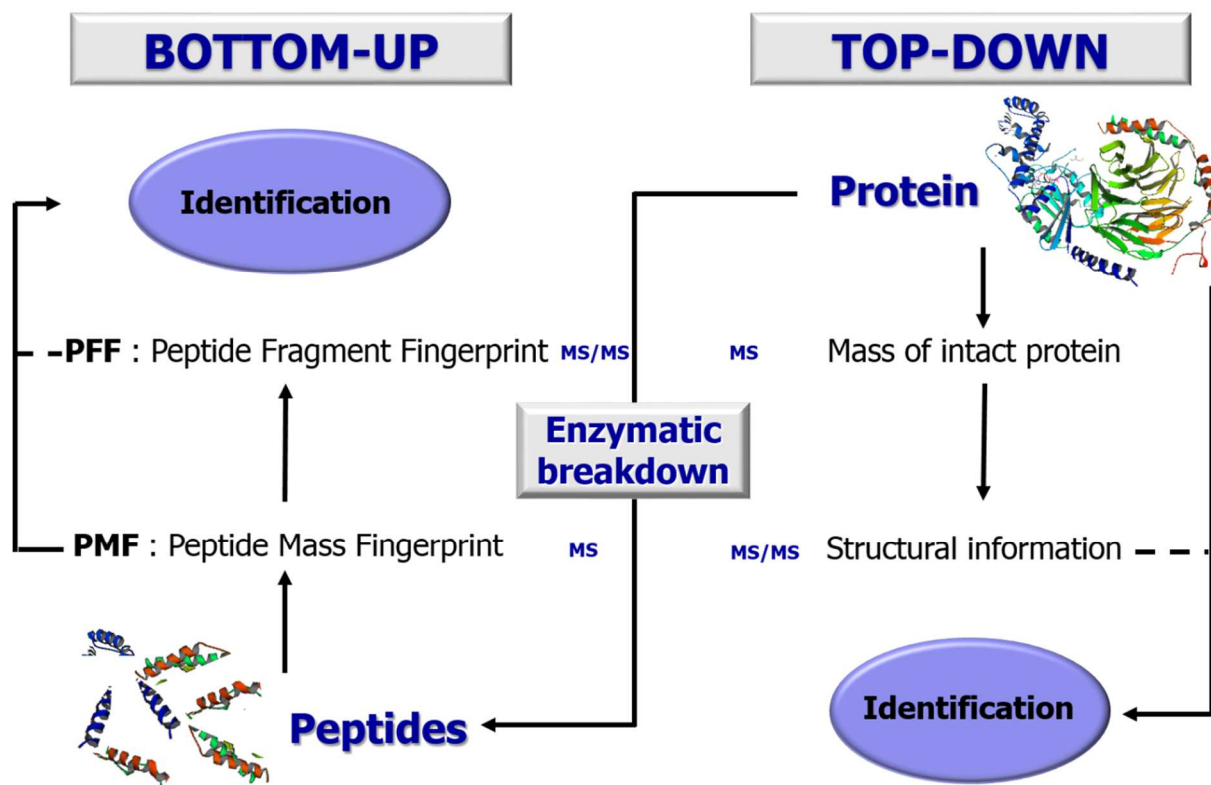
## 655 **Figure Legends**

656 Figure 1: Proteomic approaches distinguishing traditional bottom-up strategies and no-classical top-  
657 down strategy

658 Figure 2: Typical ICM-MS workflow

659 Figure 3: Top-Down protein identification workflow adapted for ICM-MS spectra characterization. 1.  
660 Fractionation can be done using chromatographic separation, gel separation or any other sample  
661 treatment aiming at decreasing sample complexity. 2. Top-Down protein identification can be  
662 performed from whole cells, crude protein extracts, or pre-fractionated protein extracts. Analysis can  
663 be based on the use of MALDI (A,B) or ESI (C,D) source ionisation m and fragmentation can be  
664 performed using PSD/ISD (A,B), or HCD (B,C,D).

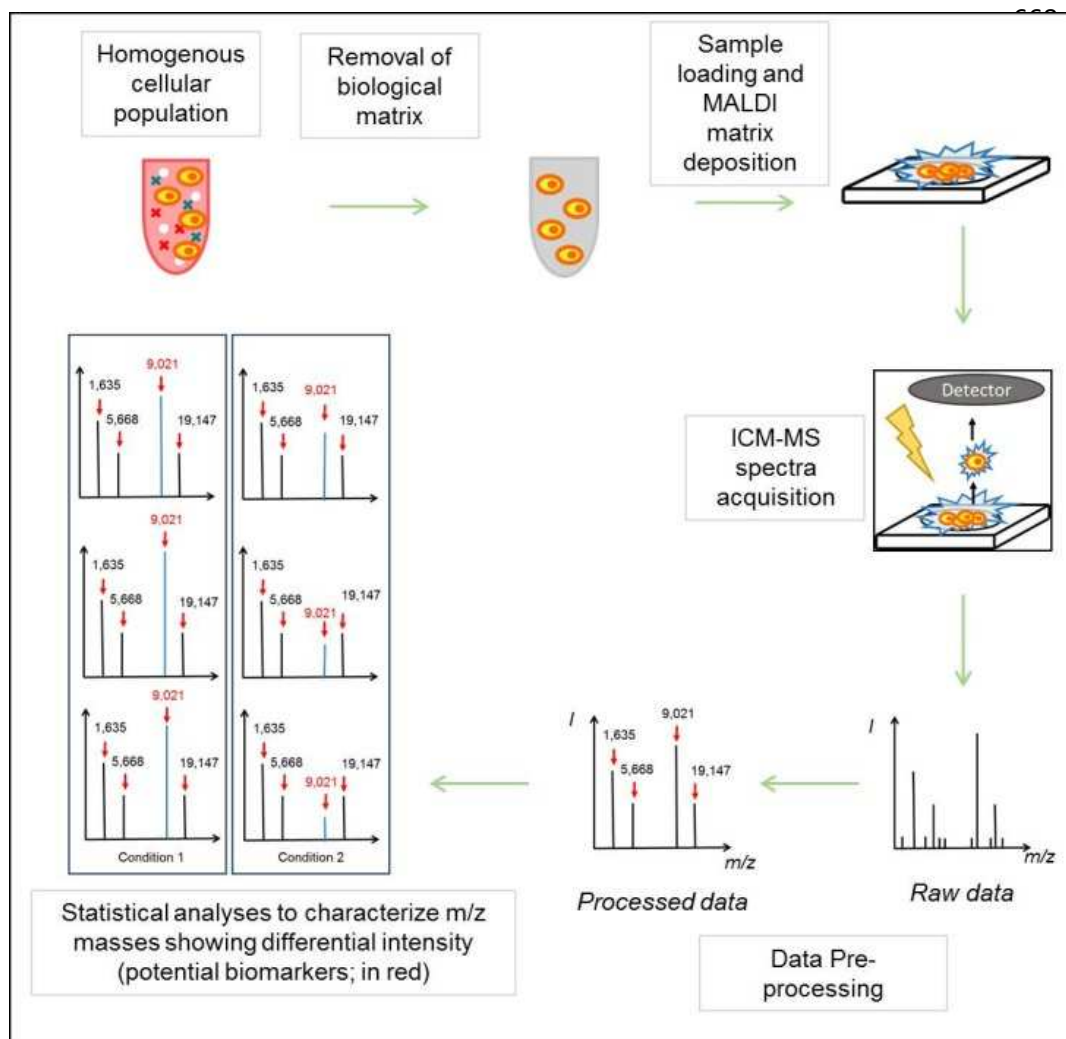




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667 Figure 1.



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Figure 2

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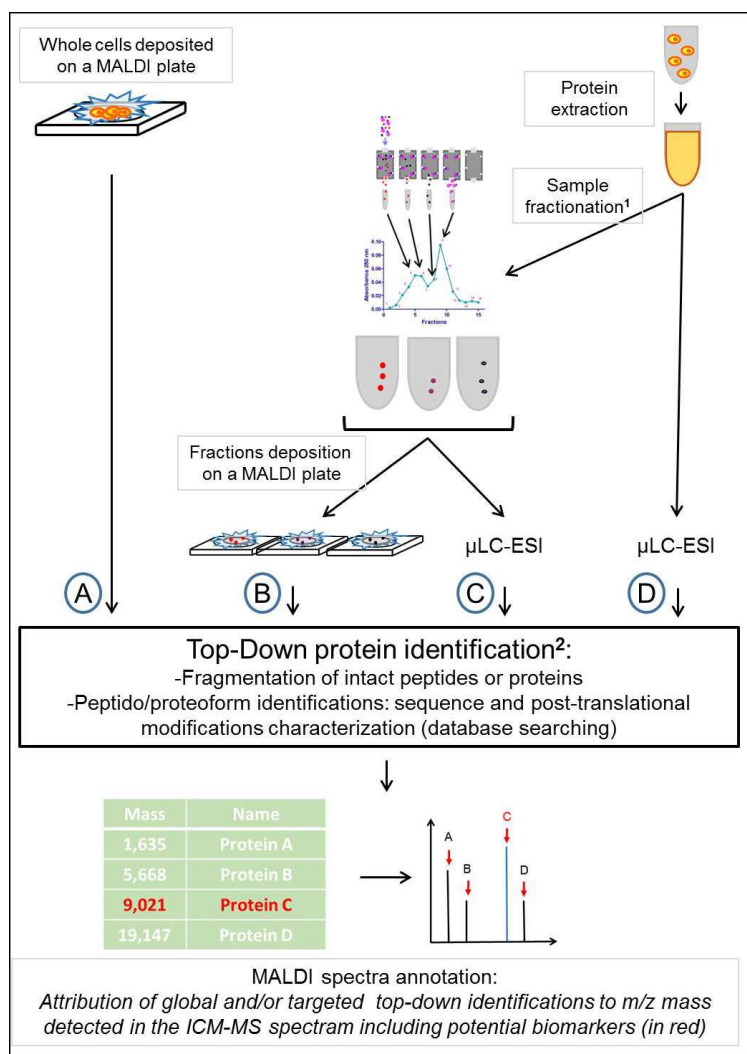


Figure 3

Year	Model	Objectives	Proteomic approach	m/z mass identification approach	Reference
2019	Neuroblastoma cell lines	Authentication of Drug-Adapted Cancer Cell Lines.	Targeted	no	58
2019	macrophages	Characterization of activation of macrophages	Targeted	no	60
2018	Bovine oocytes	Impact of meiotic maturation on single oocytes, cumulus cells and granulosa cells.	Global	Top-Down HRMS	76
2016	Chicken spermatozoa	Diagnosis of avian male fertility	Global	Top-Down HRMS	67
2015	Chicken spermatozoa	Phenotyping of semen to discriminate avian males on their reproductive capacity	Global	Top-Down HRMS	45
2015	Porcine Spermatozoa	Characterization of epididymal sperm maturation process	Global	Top-Down HRMS	68
2015	Human monocytes	Distinction of human monocyte subpopulations and monitorization of activation profiles of monocytes exposed to distinct microbial ligands	Global	No	29
2015	Fish cell line RTL-W1	Characterization of toxic effects and identification of toxins in complex environmental samples	Global	No	30
2015	HepG2 and THP-1 cells	Characterization of <i>in vitro</i> cellular responses to toxic chemicals	Global	No	26
2014	Cancer cells (chronic myelogenous leukemia cell line K562)	Label-free quantification of histone acetylation to measure the tumor-selective pharmacodynamic responses to drug in a mouse model of gastrointestinal cancer	Targeted	No	31
2012	Human macrophages	Monitorization of the various activation patterns of immune cells (macrophage)	Global	No	34
2012	Human monocytes and polymorphonuclear neutrophils	Phenotyping of mammalian primary cells and cell lines (HL-60, THP-1 and Hela S3)	Global	No	62
2011	Mammalian and insect cell lines	Cell line identification	Global	No	29
2011	Rodent glial cells	Brain cells phenotyping (astroglial, microglial, and oligodendroglial cells)	Global	Bottom-up using one-dimensional sodium dodecyl sulfate-polyacrylamide gel electrophoresis followed by LC-MS/MS	27
2011	Chinese hamster ovary cells	Selection of stable and high-producing cell lines for monoclonal antibody (mAb) IgG	Global	No	33
2011	Sea slug neurons	Characterization of D-amino acid-containing peptides	Targeted	Top-Down MALDI-TOF-TOF	6

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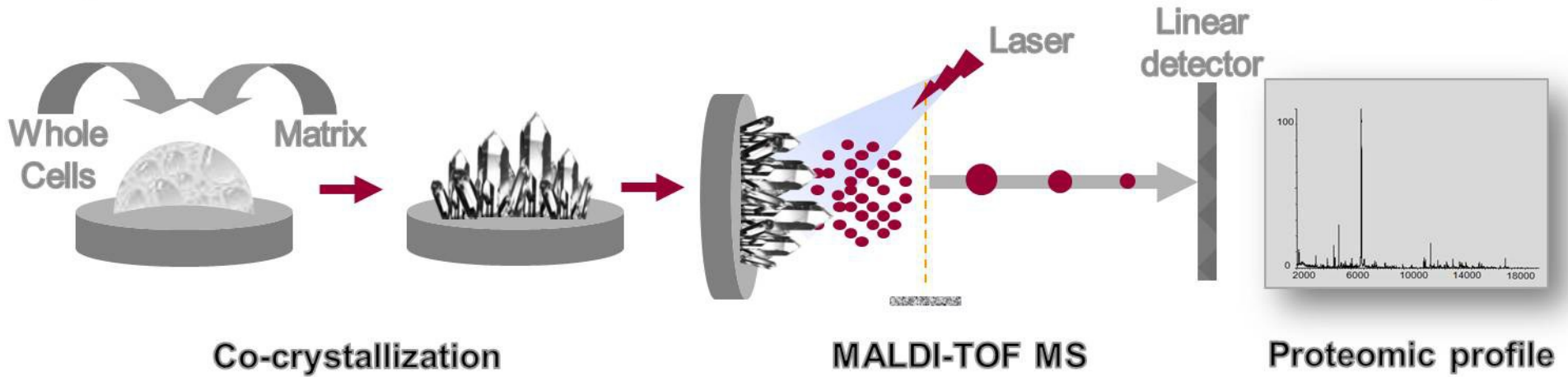
2010	Human and murine immune cells	Immune cells (monocytes, T lymphocytes and polymorphonuclear cells) phenotyping	Global	No	58
2010	Insects and animal cells	Cell lines phyloproteomics	Global	No	35
2010	Chinese hamster ovary cells	Characterization of low/high-producing cell lines for the production of recombinant biotherapeutics	Global	No	33
2009	Avian heterophils	Direct identification of mature $\beta$ -defensin 2 in avian heterophils	Targeted	Edman sequencing and bottom-up	63
2008	Human colon epithelial carcinoma T84 cell line	Identification of cell differentiation markers	Global	Bottom-up using GeLC-MS/MS	77
2007	Chicken macrophages	Identification and characterization of thymosin beta-4	Target	Purification by HPLC and Bottom-up using MALDI-TOF	78
2007	Mouse pancreatic islet alpha and beta cells	Identification of secretory products (hormones) in endocrine cells	Global	No	79
2006	Human myelomonocytic and lymphoblast, rodent BHK-21	Identification of mammalian cell lines	Global	Top-Down HRMS, MALDI-TOF-TOF and PSD, bottom-up using nanoLC-MS/MS	80
1999	Rat adrenal pheochromocytoma PC 12 cells)	Profiling of mammalian cell line after stimulation with neurotrophic factor (nerve-growth factor)	Global	No	81

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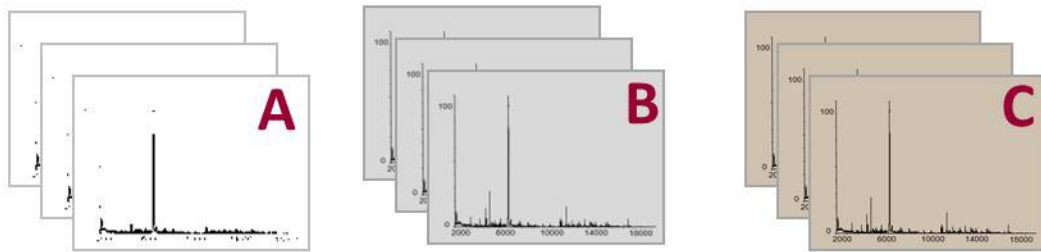
721 Table 1. Literature on superior eukaryotic Intact Cell MALDI-TOF MS studies.

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# Intact Cell MALDI-TOF Mass Spectrometry



## Differential analysis



## Informatic treatments

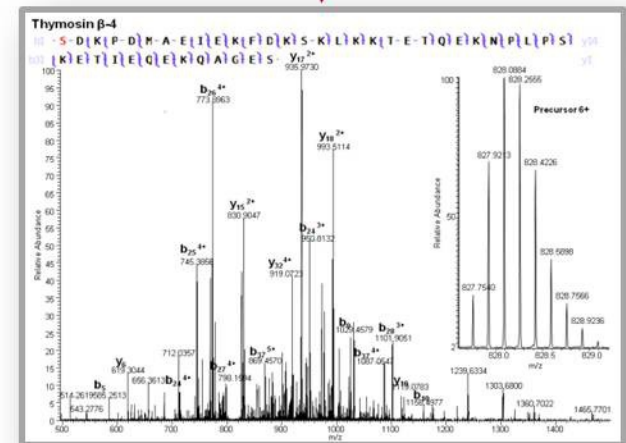
Internal calibration, Baseline subtraction, Smooth, Spectra alignment, Peak detection, Normalization

## Statistical analyses for marker characterization

ANOVA, PCA, hierarchical clustering...

## Top Down MS

Fragmentation of intact endogenous peptides/proteins



Sequence and PTM identifying pepti/proteoforms of interest