

**REVIEW**

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# Retracted: Clinical and technical phosphoproteomic research

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## Abstract

An encouraging approach for the diagnosis and effective therapy of immunological pathologies, which would include cancer, is the identification of proteins and phosphorylated proteins. Disease proteomics, in particular, is a potentially useful method for this purpose. A key role is played by protein phosphorylation in the regulation of normal immunology disorders and targets for several new cancer drugs and drug candidates are cancer cells and protein kinases. Protein phosphorylation is a highly dynamic process. The functioning of new drugs is of major importance as is the selection of those patients who would respond best to a specific treatment regime. In all major aspects of cellular life signalling networks are key elements which play a major role in inter- and intracellular communications. They are involved in diverse processes such as cell-cycle progression, cellular metabolism, cell-cell communication and appropriate response to the cellular environment. A whole range of networks that are involved in the regulation of cell development, differentiation, proliferation, apoptosis, and immunologic responses is contained in the latter. It is so necessary to understand and monitor kinase signalling pathways in order to understand many immunology pathologies. Enrichment of phosphorylated proteins or peptides from tissue or bodily fluid samples is required. The application of technologies such as immunoproteomic techniques, phosphoenrichments and mass spectrometry (MS) is crucial for the identification and quantification of protein phosphorylation sites in order to advance in clinical research. Pharmacodynamic readouts of disease states and cellular drug responses in tumour samples will be provided as the field develops. We aim to detail the current and most useful techniques with research examples to isolate and carry out clinical phosphoproteomic studies which may be helpful for immunology and cancer research. Different phosphopeptide enrichment and quantitative techniques need to be combined to achieve good phosphopeptide recovery and good up- and-down phosphoregulation protein studies.

## Background

### Importance of the field

The personalized management of diseases has and is being extended and this implies the prescription of specific therapeutics best suited for the individual patient and his/her type of illness. With the combination of different proteomic strategies this can be improved, and this would imply the coupling of proteomic and clinical research.

### Areas covered in this review

Clinical and Proteomic research can be carried out in a complementary manner in order to advance and innovate therapies and diagnostics. We also point out the importance of immunology diseases including cancer, especially those which are directly connected to phosphorylated protein kinases and the way in which to isolate and methodologically analyse phosphoproteins-phosphopeptides, with their advantages and disadvantages, when using proteomic tools.

### What the reader will gain

An overview of various types of different proteomic strategy-combinations personalized for specific diseases. The principles of phosphoproteomic techniques with

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examples are also presented in a simple manner. In addition, important mass spectrometry clues will be detailed in order to identify and correctly assign a phosphate group in a phosphorylated protein.

#### Take home message

A high number of proteomic-combination-approaches are available for clinical research. It is always necessary to test different proteomic tools in order to raise a greater level of efficiency for your clinical proteomic study, especially those related to phosphorylated proteins which are poorly expressed as some kinases. Nowadays it is essential that clinicians and proteomic experts work together in order to improve the therapies and drug candidates development.

We aim to detail the current and most useful techniques with research examples to isolate and carry out clinical phosphoproteomic studies which may be helpful for immunology and cancer research. Different phosphopeptide enrichment and quantitative techniques need to be combined to achieve good phosphopeptide recovery and good up- and-down phospho-regulation protein studies.

#### (A) Phosphorylation's role in immune disorders and cancer

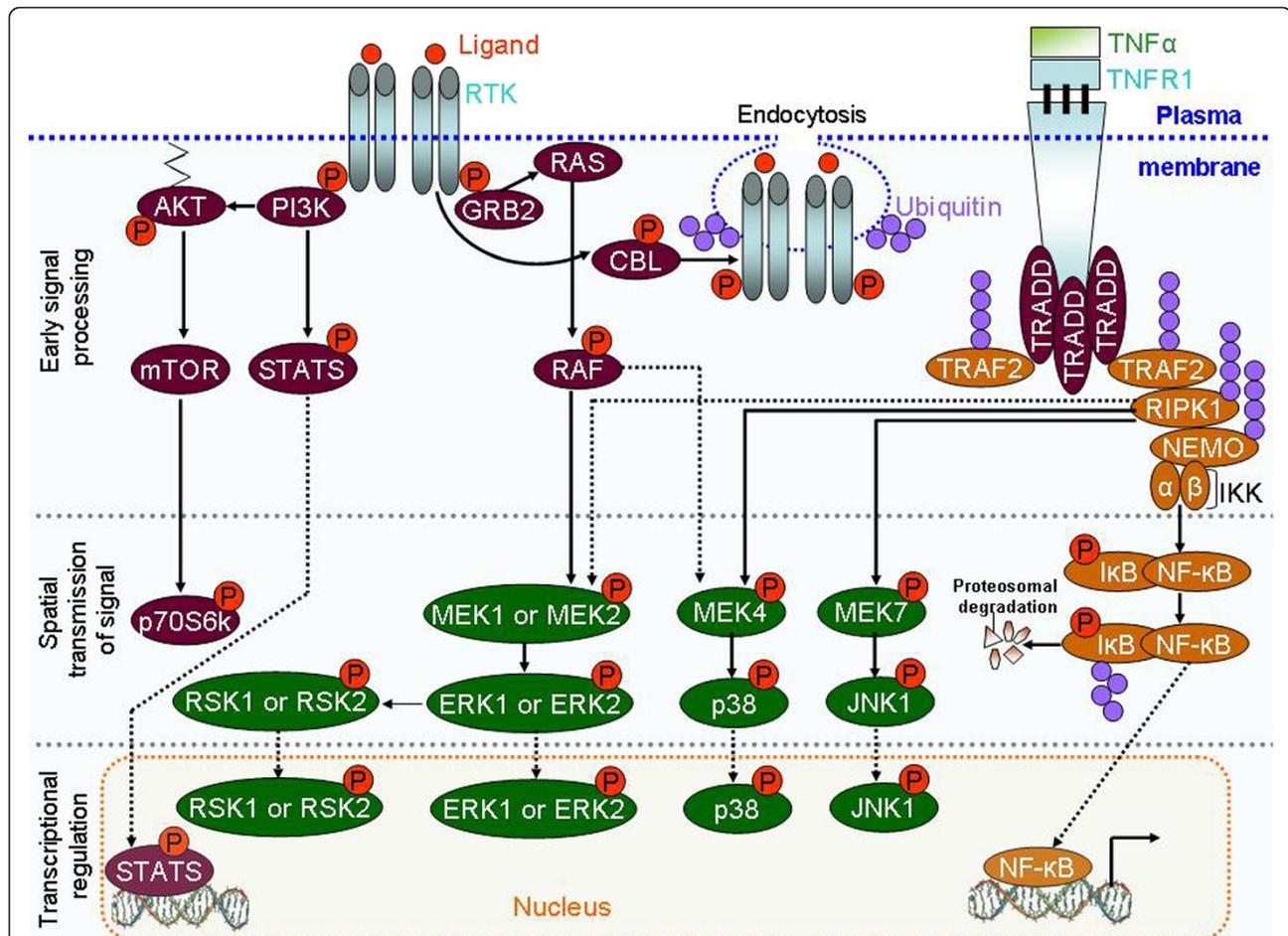
Phosphorylation and de-phosphorylation at serine, threonine and tyrosine residues are one of the most common mechanisms of activation and/or inactivation signalling pathways. A variety of cellular processes including cellular growth, proliferation, cell cycle control, cytoskeletal mobility and receptor regulation [1] are controlled by this type of modification. Phosphorylation leads to allosteric modifications that may result in conformational changes sufficient to cause activation or inactivation of various proteins and associated altered functioning. It is our hypothesis that identification of phosphoproteins associated with the various stages of different immunological disorders, including cancer, may provide information on the development of the pathology. In addition the mechanism of tumorigenesis gives us insight into the development of diagnostic and therapeutic procedures.

The mitogen activated protein kinase (MAPK) pathways are known to be deregulated in many human malignancies [2-5]. With relation to malignancy, the best studies MAPKs are the extracellular signal regulated protein kinases (ERK). ERKs phosphorylate cytoplasmic targets migrate to the nucleus where they can activate transcription factors involved in cellular proliferation. Erratic signalling in the MAPK/ERK pathways has been described in prostate, breast and colon cancers *in vitro* as well as *in vivo* models [6-9]. In cervical cancer, furthermore, a study has described decreased activation of ERK1/2 in invasive cervical carcinoma [10]. Annexin A1,

which is a calcium dependent phospholipid binding protein that has been linked to membrane trafficking through exocytosis and endocytosis [11], is a second relevant example. Other studies have evaluated the role of annexin A1 in the modulation of the MAPK/ERK [12]. In fact, many members of the Annexin family are known to undergo alternative splicing yielding a number of isoforms. The resulting variant forms may have different functions and binding capacity in comparison to the native forms [13]. The DNA-Protein Kinase catalytic subunit (DNA-PKcs) - another relevant example - a macromolecule found to be involved in the repair of double stranded DNA fractures through activation of p53, found to be expressed in cancer specimens in its tyrosine phosphorylated and cleaved form [14]. In contrast, in normal specimens DNA-PKcs existed in its whole, full length in non-phosphorylated form. This study was aimed at identifying differential expression and modification of proteins that could suggest erratic pathways which could serve as novel targets for developing new therapies in the treatment of cervical cancer and help in monitoring disease recurrence or progression. The general principles of signalling pathways are illustrated (Figure 1) and also, an example of the structure of a relevant phosphorylated protein kinase (Figure 2).

On the other hand, the CDC25 family of proteins consists of dual specificity phosphatases which regulate cell cycle transitions, and they are key targets for the checkpoint machinery to maintain genome stability during DNA damage. Three isoforms of CDC25 have been identified in mammalian cells: CDC25A, CDC25B, and CDC25C. CDC25A and CDC25B over-expression has been reported in many types of human cancers, but these are insufficient to cause cancer, and the mechanism responsible for CDC25 over-expression is unclear [15,16]. The study of dose-response effects of the anti-cancer drug rapamycin on the phosphoproteomics level has identified hundreds of novel rapamycin-targeted cellular proteins and their phosphorylation sites. This information has enabled us to identify CDC25B as the key enzyme in mediating rapamycin induced oncogenic AKT activation. It is important to point out that we can demonstrate that phosphoproteomic profiling of a certain therapeutic agent does not only identify potential drug target(s) to improve the efficiency of that therapeutic approach in disease treatment, but it can also provide cellular information about possible beneficial and adverse side effects of a specific disease therapy when treating patients [17].

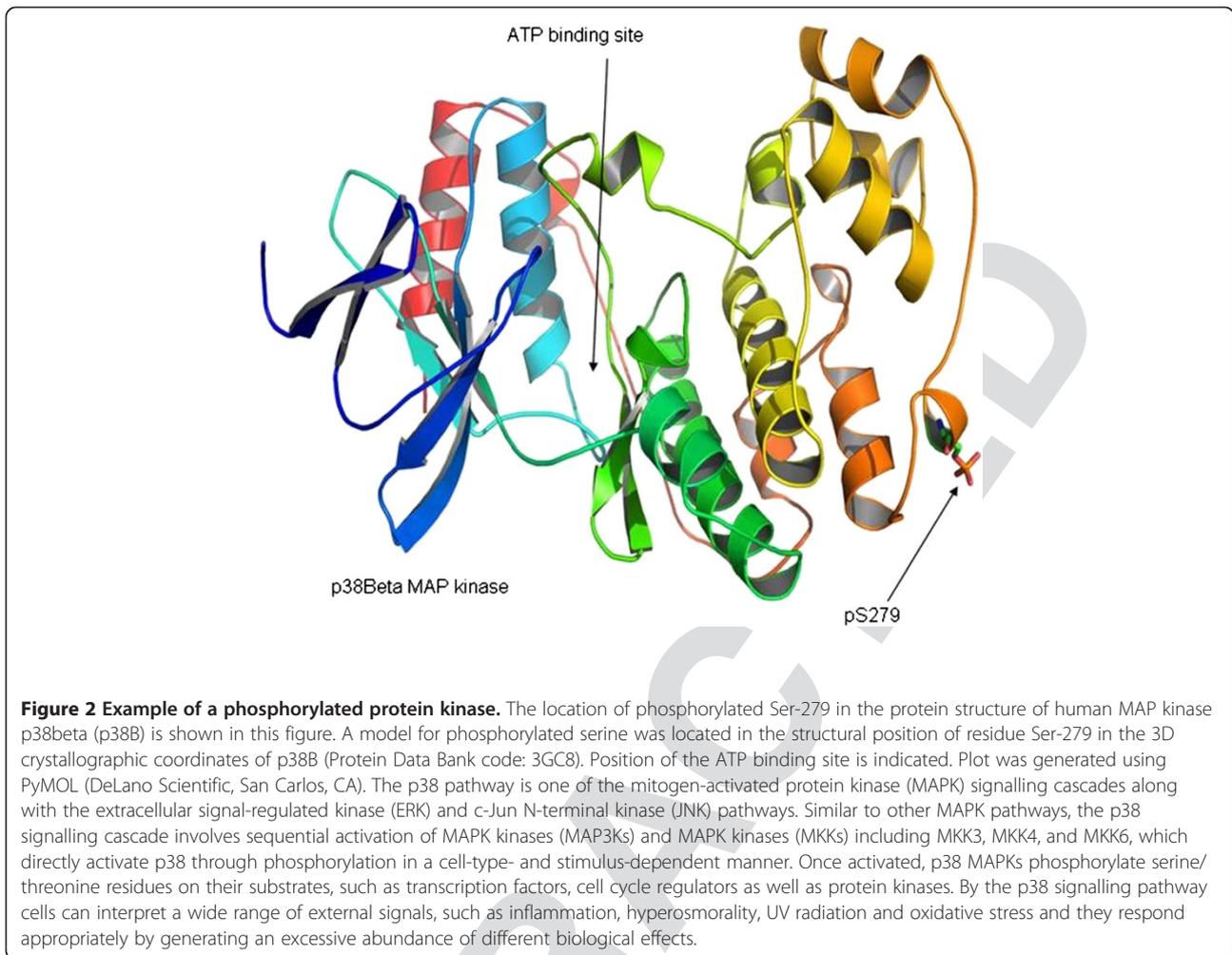
In addition, primary immunodeficiencies (PID) are "nature's experiments" which have allowed, not only the elucidation of many signalling pathways, but also their function an clinical relevance. Bruton's tyrosine kinase, is an interesting example: (Btk; member of the Tec



**Figure 1 Signalling pathways: general principles.** Followed by communication of the signal to different cellular compartments are signal processing and amplification by plasma membrane proximal events. The activation of multiple signal cascades by receptors, different protein post-translational modifications (PTMs), crosstalk between signalling pathways and feedback loops to ensure optimal signalling output are involved in this process. The binding of receptor Tyrosinases (RTKs) to their cognate ligands at the cell surface results in receptor dimerization and autophosphorylation. Phosphorylated Tyr residues subsequently serve as docking sites to recruit signalling mediators, such as growth factor receptor-bound protein 2 (GRB2). Multiple signalling cascades such as the phosphoinositide-3 kinase (PI3K)-AKT, Ras-Raf- extracellular signalregulated kinase (ERK) mitogen-activated protein kinase (MAPK), and signal transducer and activator of transcription (STAT) pathways are activated by the assembly of these signalling complexes. Casitas B-lineage lymphoma (CBL)-mediated ubiquitylation of RTKs controls their endocytosis and the duration of receptor signalling. In addition, binding of tumour necrosis factor- $\alpha$  (TNF $\alpha$ ) to its receptor, TNFR1, induces trimerization of the receptor and recruitment of the adaptor protein TNFR1-associated death domain (TRADD) This functions as a hub to assemble a multiprotein signalling complex containing TNFR-associated factor 2 (TRAF2), receptor interacting Ser/Thr protein kinase 1 (RIPK1) and nuclear factor- $\kappa$ B (NF- $\kappa$ B) essential modulator (NEMO). The result is the activation of different signalling networks, such as the ERK MAPK, p38 MAPK and NF- $\kappa$ B pathways. Proteins in the MAPK signalling pathways are activated by both RTKs and TNF $\alpha$ , which allows cells to integrate multiple signals. [Dotted lines indicate indirect activation of signalling pathways or translocation of proteins into the nucleus. I $\kappa$ B, inhibitor of NF- $\kappa$ B; IKK, inhibitor of NF- $\kappa$ B kinase; JNK1, Jun N-terminal kinase 1; MEK, MAPK ERK kinase; mTOR, mammalian target of rapamycin; p70S6K, p70 ribosomal S6 kinase- $\alpha$ ; RSK, ribosomal protein S6 kinase- $\alpha$ ].

family of kinases) [18,19], important in B-lymphocyte development, differentiation, and signalling. Btk is predominantly expressed in B lymphocytes and monocytes but not in plasma cells [20,21]. Btk expression in the B-cell lineage is also developmentally regulated, with bone marrow derived hematopoietic stem cells, common lymphoid progenitor cells, developing B and myeloid

lineages showing the highest levels, whereas the remaining mature cells prior to activation have reduced cellular Btk. What remains to be established is the physiological significance of Btk expression in other cell types as B lymphocytes are the only cells known to be affected in X-linked agammaglobulinemia (XLA). Mutations in the Btk gene lead to XLA in humans and X-



linked immunodeficiency (Xid) in mice. Activation of Btk triggers a cascade of signalling-events that culminates in the generation of calcium mobilization and fluxes, cytoskeletal rearrangements, and transcriptional regulation involving nuclear factor- $\kappa$ B (NF- $\kappa$ B) and nuclear factor of activated T cells (NFAT). In B cells, NF- $\kappa$ B was shown to bind to the Btk promoter and induce transcription, whereas the B-cell receptor dependent NF- $\kappa$ B signalling pathway requires functional Btk. In addition, Btk activation is strictly regulated by a plethora of other signalling proteins including protein kinase C (PKC), Sab/SH3BP5, and caveolin-1. Additionally, the prolyl isomerase Pin1 negatively regulates Btk by decreasing tyrosine phosphorylation and uniform state levels of Btk [22]. It is of great interest that PKC and Pin1, both of which are negative regulators of Btk, bind to the pleckstrin homology domain of Btk. For this purpose, novel mutations in the pleckstrin homology are under research, in order to design selective and novel drugs [23]. Common variable immunodeficiency (CVID) is a PID disease. CVID is the result of intrinsic deficits

affecting immunologic functions. Moreover lymphomas and neoplasms are found to be related to CVID. CVID is heterogeneous, can be present early or late in life, and it is associated with specific comorbidities [24,25]. Efforts to subcategorize CVID to predict outcomes and comorbid-condition, both clinically and based on immunologic phenotypes, are ongoing [26]. B cell-activating factor of the TNF family receptor [27], transmembrane activator, calcium modulator, cyclophilin ligand interactor (TACI) [28-30], and certain HLA haplotypes [31,32] have been identified as potential gene candidates for susceptibility to CVID. Inducible costimulator [33,34], CD81 [35], CD19 [36,37] and CD20 [38] harbour disease-causing mutations that presently explain only a small percentage of cases [39]. Recently, a genome-wide association work [40] has identified diverse causes of common variable immunodeficiency providing new mechanistic insights into immunopathogenesis based on these unique genetic variations. A highly significant number of subjects with duplications in ORC4L, a gene previously associated with

B-cell lymphoproliferative disorders was observed. All these new insights could be susceptible to phosphoproteomic analysis in order to clarify the clues of the different pathologies [41].

### **(B) Analytical techniques used in phosphoproteomics**

**B.1. Preparation of samples** The key to any successful analysis is good sample preparation; phosphorylated proteins are quite stable, chemically, but there are highly susceptible to enzymatic modification. We emphasize the importance of phosphorylation of protein kinases due to the fact that they modulate many immunology diseases and they are usually poorly expressed. Moreover, the human genome contains around 500 kinases and over 100 phosphatases [42], so that when tissues or cells are lysed and extracted, it is highly probable that further enzymatic reactions will occur. Samples have to be prepared (a) quickly, (b) generally be snap-frozen and (c) treated with phosphatase inhibitors to avoid modification of phosphopeptides during sample work-up [43,44]. Phosphopeptides generally constitute a small portion of the peptides in a given protein sample, making them difficult to detect by MS; their enrichment helps to overcome this problem. It is important (d) to avoid salts and detergents, which can decrease the recovery of phosphopeptides and/or interfere with subsequent analysis [45].

### **B.2. Enrichment of phosphoprotein and phosphopeptide**

The aim in many focuses, including the study of immune disorders, is to generate a global view of serine, threonine and tyrosine phosphorylation within the sample, concentrating specifically on the selected subset of phosphopeptides. Since the detection of phosphopeptides by MS is often hindered by suppression effects, many different strategies have been established: for the removal of unphosphorylated peptides: (I) immunoprecipitation by antibodies, (II) pre-fraction systems such as ionic chromatographic exchange (SCX/SAX), calcium phosphate precipitation and hydrophilic interaction chromatography (HILIC) (III) metal affinity chromatography i.e. IMAC,  $\text{TiO}_2$ ,  $\text{ZrO}_2$ , and (IV) reverse phase chromatography (RP). (V) Immunoprecipitation of phosphotyrosine coupled or not to polyacrylamide gels, is still much more frequent [43] than immunoprecipitation using phosphoserine or threonine antibodies. This is because affinity chromatography such as IMAC or titanium dioxide has higher a capacity for phosphoserine and phosphothreonine peptide binding.

• **Antibody purification and Polyacrylamide gels** Affinity purification, a method for purifying proteins, can be used together with SDS-PAGE or alone. Antibodies raised against a protein can be used to immunoprecipitate the

protein and search for phosphorylation sites. Immunoprecipitation permits the isolation of a protein under a variety of biological conditions to assess changes in phosphorylation on that protein. In the same way, antibodies raised against a specific phosphosite on a protein can be used for immunoprecipitation. Assessment of other phosphosites on a protein is possible when one phosphosite is known (the epitope of the antibody) under this scenario. However, care must be taken when a protein is phosphorylated at multiple serines as certain phosphorylation events could be mutually exclusive and be obliterated during subsequent analysis. Phosphospecific antibodies can be used to determine the proteins that bind to a phosphoprotein (protein-phosphoprotein interactions) using phosphositespecific immunoprecipitation followed by analysis of the binding partners. Furthermore, antibodies specific for phosphotyrosines, not affected by the surrounding amino acids, have been successfully used to immunoprecipitate the “phosphotyrosinome” of cells. Since phosphoserine and phosphothreonine are much more abundant in cells and these antibodies seem to have less specificity, phosphoproteome-wide experiments are much more complicated [46].

Moreover, phospho-specific antibodies against a consensus sequence-motif for a specific kinase-motif (for example SXR, where x is any amino acid) can also be used to immunopurify all proteins that contain this motif. This form of phosphorylation has been enriched by the use of antiphosphotyrosine antibodies. It is an interesting strategy as phosphotyrosine is far less common than phosphoserine or threonine; the antibodies generally have a higher specificity and tyrosine kinases play a prominent role in human cancer. The isolated proteins are enzymatically cleaved with trypsin and analysed by MS or the phosphopeptides can be further enriched for analysis by MS. Tyrosine phosphorylated proteins are enriched by these methods to levels sufficient for detection and sequencing by MS [47-52]. Antiphosphoserine and antiphosphothreonine antibodies have been also generated [43] but have not been widely used due to their low specificity.

We would like to mention the scientific study of Kemna and co-workers (2007) [53], who used immunocapture, and tandem MS to identify and characterize hepcidin in serum and urine. In addition to diagnostic application, they investigated analytical reproducibility and biological and preanalytical variation for both serum and urine sample fluids. Samples were obtained from healthy controls and patients with documented iron-deficiency anaemia, inflammation-induced anaemia, thalassemia major, and hereditary hemochromatosis. This important proteomic technique showed that hepcidin-20, -22, and -25 isoforms are present in urine. Hepcidin-25 in serum had the same amino acid sequence as hepcidin-25 in urine, whereas hepcidin-22 was not detected in serum. In this work,

Kemna and co-workers(2007) also observed that urine hepcidin is more affected by multiple freeze-thaw cycles and storage conditions, but less influenced by diurnal variation, than serum hepcidin.

Barbey and co-workers (2009) [54] also produced another interesting scientific work where they described the results of a proteomic analysis based on SDS-PAGE, immunoblot and mass spectrometry, aimed at the identification of secreted proteins that are differently expressed at 30°C versus 37°C and at mid-exponential versus early-stationary growth phase and antigenic proteins from *Rhodococcus equi* ATCC 33701. A total of 48 proteins were identified irrespective of growth conditions. Cholesterol oxidase ChoE appears to be the major secretory protein. Four proteins, in addition, revealed high homologies with the mycolyl transferases of the Ag85 complex from *Mycobacterium tuberculosis*. 24 proteins are transported by a signal peptide-dependent pathway according to the prediction of the sequence analysis. Moreover, five antigenic proteins of *R. equi* were identified by immunoblot, including a novel, strongly immunoreactive protein of unknown function. In conclusion, the elucidation of the secretome of *R. equi* identified several proteins with different biological functions and a new candidate developing vaccines against *R. equi* infection in horses.

Radio-labelling polyacrylamide gels (P32 & 2DE) and 2D phosphopeptide mapping P32 labelling has long been used, on the other hand, for the analysis of immunoprecipitated and gel-separated signalling complexes and for quantify cation of differentially phosphorylated proteins by two-dimensional gel electrophoresis (2DE) of total cell lysates. The latter technique uses differential labelling of cells with P32 and P33 in a control and experimental group respectively. The samples are combined, and then separated by 2DE before the gels are exposed twice to radio-sensitive film. Comparison of these two exposures will reveal spots that are specifically phosphorylated under the experimental conditions tested [55,56]. It measures the incorporation of the label but not the phosphorylation level, although interesting studies can be carried out to study different isoforms of the same protein [57]. Two-dimensional (2D) phosphopeptide mapping by electrophoresis is another useful technique combined with thin-layer chromatography of peptides derived by proteolysis of a phosphoprotein. The number of spots detected indicates the number of sites of phosphorylation, but it is not easy to determine the position of the phosphorylation sites. Nevertheless, analysis of temporal and positional changes in a protein phosphorylation pattern under different physiological conditions [58] is permitted by this technique. Immunoprecipitation with specific antibodies against phosphopeptides can be used to immunoprecipitate phosphoproteins from the cell lysates [59].

• **Immobilised metal ion affinity chromatography (IMAC)** IMAC [60] is an enrichment technique that makes use of metal ions to capture and enrich negatively charged phosphopeptides prior to mass spectrometric analysis [61-66]. Simple and complex samples containing phosphopeptides and non-phosphorylated peptides are dissolved in an acidic solution to stimulate the electrostatic interactions between the negatively charged peptides, mainly phosphopeptides, and the metal ions [64]. The phosphopeptides are eluted from the stationary phase using alkaline buffers. It is also possible to bind peptides containing the acidic amino acid residues glutamic acid and aspartic acid to the metal ions. Ficarro and co-workers [67] bypassed this problem with IMAC (Fe<sup>3+</sup>) by converting acidic amino acid residues to methyl esters. They were able to purify and sequence hundreds of phosphopeptides from yeast, although there was a strong tendency towards phosphoproteins highly expressed within the cell.

Collins and co-workers (2008) [68] analyzed the mouse forebrain cytosolic phosphoproteome using sequential (protein and peptide) IMAC purifications, enzymatic dephosphorylation, and targeted tandem mass spectrometry analysis strategies (MS clues will be detailed later) which we consider a relevant biological study. To summarize, Collins *et al.*, (2008) [68] with the use of complementary phosphoenrichment and LCMS/MS strategies, 512 phosphorylation sites on 540 nonredundant phosphopeptides from 162 cytosolic phosphoproteins were characterized. Analysis of protein domains and amino acid sequence composition of this data set of cytosolic phosphoproteins revealed that it is significantly enriched in intrinsic sequence disorder, which enrichment is associated with both cellular location and phosphorylation status. The majority of phosphorylation sites found by MS were located outside structural protein domains (97%) They were mostly located in regions of intrinsic sequence disorder (86%). 368 phosphorylation sites were located in long regions of disorder (over 40 amino acids long), and 94% of proteins contained at least one such long region of disorder. In addition, it was found that 58 phosphorylation sites in this data set occur in 14-3-3 binding consensus motifs; linear motifs that are associated with unstructured regions in proteins. These results demonstrate that in this data set protein phosphorylation is distinctively depleted in protein domains and distinctively enriched in disordered protein sequences and that enrichment of intrinsic sequence disorder may be a common feature of phosphoproteomes. This goes to support the hypothesis that disordered regions in proteins allow kinases, phosphatases, and phosphorylation-dependent binding proteins to gain access to target sequences to regulate local protein conformation and activity.

• **Titanium dioxide metal-based chromatography (TiO<sub>2</sub>)** TiO<sub>2</sub> is also capable of binding negatively charged phosphate groups from aqueous solutions [65,69,70]. TiO<sub>2</sub>, like IMAC, experiences the problem of binding acidic non-phosphorylated peptides (negatively charged peptides). Heck and co-workers [65] observed a number of non-phosphorylated peptides in their analysis and recommended esterification of the acidic residues prior to the MS analysis. Larsen *et al.* [41,45,71] used 2,5-dihydroxybenzoic acid (DHB) with TiO<sub>2</sub> and achieved higher specificity and yield compared to IMAC (Fe<sup>3+</sup>) for the selective enrichment of phosphorylated peptides from model proteins. It was also demonstrated that by the use of glycolic acid in the loading buffer, more phosphopeptides are bound to the metal ions and more phosphopeptides can be eluted by using ammonium hydroxide as the eluent. TiO<sub>2</sub> binds multiphosphorylated peptides in a strong way, thus their elution is difficult. However, this is a very effective method for the isolation of singly phosphorylated peptides [72].

The research work of Craft and co-workers (2007) [73] is an interesting example of the application of TiO<sub>2</sub> technique coupled to other proteomic tools. Amphiphysin I (amphI) is dephosphorylated by calcineurin during nerve terminal depolarization and synaptic vesicle endocytosis (SVE). Some amphI phosphorylation sites (phosphosites) have been identified with *in vitro* studies or phosphoproteomics screens. A multifaceted strategy including 32P tracking to identify all *in vivo* amphI phosphosites and determine their relative abundance and potential relevance to SVE was used. AmphI was extracted from 32Plabeled synaptosomes; phosphopeptides were isolated from proteolytic digests using TiO<sub>2</sub> chromatography, and mass spectrometry revealed 13 sites: serines 250, 252, 262, 268, 272, 276, 285, 293, 496, 514, 539, and 626 and Thr-310. These were distributed into two clusters around the proline-rich domain and the C-terminal Src homology 3 domain. Hierarchical phosphorylation of Ser-262 preceded phosphorylation of Ser-268, -272, -276, and -285. Off-line HPLC (High-performance liquid chromatography or high-pressure liquid chromatography separation and two-dimensional tryptic mapping of 32P-labeled amphI revealed that Thr-310, Ser-293, Ser-285, Ser-272, Ser-276, and Ser-268 contained the highest 32P incorporation and were the most stimulus-sensitive. Individually Thr-310 and Ser-293 were the most abundant phosphosites, incorporating 16 and 23% of the 32P. The multiple phosphopeptides containing Ser-268, Ser-276, Ser-272, and Ser-285 had 27% of the 32P. Evidence for a role for at least one proline-directed protein kinase and one non-proline-directed kinase was obtained. Four phosphosites predicted for non-prolinedirected kinases, Ser-626, -250, -252, and -539, contained low amounts of 32P and were not depolarization-responsive. At least one alternatively

spliced amphI isoform was identified in synaptosomes as being constitutively phosphorylated because it did not incorporate 32P during the 1-h labeling period. Multiple phosphosites from amphIco- migrating synaptosomal proteins were also identified, including SGIP (Src homology 3 domain growth factor receptor bound 2 (Grb2)-like (endophilin)-interacting protein 1), AAK1, eps15R, MAP6, α/β-adducin, and HCN1. Their results revealed two sets of amphI phosphosites that are either dynamically turning over or constitutively phosphorylated in nerve terminals and they improve the understanding of the role of individual amphI sites or phosphosite clusters in synaptic SVE.

• **IMAC (SIMAC) Sequential elution** Sequential elution from IMAC is useful for purifying, detecting and characterising phosphorylated peptides from complex biological samples [72]. It makes use of the observation that monophosphorylated peptides tend to elute from IMAC (Fe<sup>3+</sup>) under acidic conditions whereas multiphosphorylated peptides elute at high basic pH. TiO<sub>2</sub> is used to capture and purify the unbound monophosphorylated peptides in the combined IMAC flowthrough and washings. SIMAC has been used successfully in the study of human stem cells (~300 μg) with more than 300 phosphopeptides, including the identification of mono and multiply phosphorylated peptides [74].

This technology was developed by Tine E. Thingholm and co-workers (2007) [74]. They reported a simple and rapid strategy, SIMAC (sequential elution from IMAC), using stem cells as a sample to be studied, for sequential separation of monophosphorylated peptides and multiply phosphorylated peptides from highly complex biological samples. This research study, allowed individual analysis of different pools of phosphorylated peptides using mass spectrometric parameters differentially optimized due to their unique properties. They compared the phosphoproteome identified from 120 μg of human mesenchymal stem cells using SIMAC and an optimized titanium dioxide chromatographic method. More than double the total number of identified phosphorylation sites was obtained with SIMAC, primarily from a 3-fold increase in recovery of multiply phosphorylated peptides.

• **Zirconium dioxide (ZrO<sub>2</sub>)** The utility of ZrO<sub>2</sub> for phosphopeptide isolation prior to mass spectrometric analysis has been demonstrated [75]. When compared with TiO<sub>2</sub> using α and β casein as protein models, ZrO<sub>2</sub> was capable of isolating singly phosphorylated peptides more selectively than TiO<sub>2</sub>. An interesting research study was carried out by Houjiang Zhou *et al.* (2007) [76] where the high specificity of this approach was also demonstrated by the isolation of phosphopeptides from the digests of model phosphoproteins. The strong

affinity of  $ZrO_2$  nanoparticles to phosphopeptides enables the specific enrichment of phosphopeptides from a complex peptide mixture in which the abundance of phosphopeptides is two orders of magnitude lower than that of nonphosphopeptides.  $ZrO_2$  nanoparticles were further applied to selectively isolate phosphopeptides from the tryptic digestion of mouse liver lysate for phosphoproteome analysis by nanoliter LC MS/MS (nano-LC-MS/MS) and MS/MS/MS. Manual validation, using a series of rigid criteria, identified a total of 248 defining phosphorylation sites and 140 phosphorylated peptides. Therefore,  $ZrO_2$  has been successfully used in the large-scale characterisation of phosphoproteins from mouse liver samples (~1 mg) [76]. A total of 248 phosphorylation sites and 140 phosphorylated peptides were identified in this study.

• **Calcium phosphate precipitation** This is a strategy providing a useful pre-fractionation step to simplify and enrich phosphopeptides from complex samples. Zhang and co workers [77] have demonstrated that phosphopeptide precipitation by calcium phosphate combined with a two step IMAC ( $Fe^{3+}$ ) procedure resulted in the observation of an increased number of phosphopeptides. This method consists of precipitating phosphopeptides by adding 0.5 M  $NaHPO_4$  and 2 M  $NH_3OH$  to the peptidemixture followed by 2 M  $CaCl_2$ . The sample is vortexed and centrifuged, and, subsequently, the supernatant is removed before washing the pellet with 80 mM  $CaCl_2$ . The washed pellet is dissolved in 5% of formic acid and the resulting peptide mixture is desalted through reversed phase chromatography before isolating the phosphopeptides by IMAC ( $Fe^{3+}$ ).

Zhang and co workers [77] point out that even with very complex biological samples such as the total enzymatic digest of rice embryo proteins, high enrichment of the phosphopeptides can be achieved with minimal contamination with non-phosphopeptides. In addition, it could be possible to reduce the complexity of the samples by successive IMAC enrichments using a limited amount of IMAC material at each step. This technique demonstrates that serial phosphopeptide enrichment initiated by a precipitation step improves the selectivity of phosphopeptide enrichment and allows identification of more phosphopeptides. In addition, Zhang and co workers say that further analyses to examine the rice phosphoproteome in detail are now underway. Moreover, it can be applied for clinical phosphoproteomics clinical research.

• **Strong cation and anion exchange (SCX and SAX)** The principle of SCX/SAX phosphopeptide enrichment is based on the negative charged phosphate group ( $PO_4^-$ ) of the phosphopeptides. In cation exchange chromatography,

a positively charged analyte is attracted to a negatively charged solid-support; whilst in anion exchange chromatography negatively charged molecules are attracted to a positively charged solid-support. SAX has previously been successfully combined with IMAC [66] and has resulted in greater recovery and identification by MS of monophosphorylated peptides originating from membrane proteins. In a similar way, SCX has been combined with IMAC ( $Fe^{3+}$ ) and MS analysis, allowing the identification of thousands of phosphorylated residues from complex biological samples [78]. Moreover, Gruhler and co-workers [78] demonstrated that use of the SCX/IMAC combination is consistent with their previous study where strong anion exchange chromatography/IMAC was used. Thus, either strong anion exchange chromatography (SAX) or SCX can be used to reduce the sample complexity prior to IMAC enrichment of phosphopeptides in large scale phosphoproteomics.

As practical issues, Nuhse *et al.*, 2003 [66], investigated and presented a scheme for two-dimensional peptide separation using SAX chromatography prior to IMAC ( $Fe^{3+}$ ) in order to decrease the complexity of IMAC-purified phosphopeptides, obtaining a wide coverage of monophosphorylated peptides. Nuhse and co-workers did, in fact, obtain a high yield in identifying phosphopeptides from membrane proteins. SCX has also been successfully used coupled to IMAC ( $Fe^{3+}$ ) and MS analysis allowing the identification of thousands of phosphorylated residues from biological complex samples [78,79]. Gruhler and co-workers showed that performing SCX at low pH (2.7-3.0), phosphorylated peptides are separated from nonphosphorylated species according to the charge difference associated with the negatively charged phosphate group. Therefore, net charged peptides (+1) were collected in the first fractions of the SCX pre-fractionation step containing mainly single phosphorylated peptides. These first fractions were then loaded onto IMAC ( $Fe^{3+}$ ) micro tips in order to recover a large number of phosphopeptides from biologically complex samples.

• **Hydrophilic interaction chromatography (HILIC)** Hydrophilic interaction chromatography (HILIC) is a less commonly used method for peptide fractionation despite the fact that it is often used to fractionate small metabolites. HILIC is commonly described as partition chromatography or liquid/liquid extraction system between the mobile and stationary phase. A water-poor layer of mobile phase versus a water-rich layer on the surface of the polar stationary phase is formed. Thus, a distribution of the analytes between these two layers will occur. In addition, HILIC includes weak electrostatic mechanisms as well as hydrogen donor interactions between neutral polar molecules under high organic

elution conditions. This distinguishes HILIC from ion exchange chromatography - the main principle for HILIC separation is based on the compound's polarity and degree of solvation. More polar compounds will have stronger interaction with the stationary aqueous layer than less polar compounds - resulting in a stronger retention. In addition, HILIC shows a very good separation and peak shape for critical compounds like adenosine and its phosphate derivatives.

It is of interest to note that Albuquerque and co-workers (2008) [80] carried out a study related to the separation of unphosphorylated peptides using SCX, HILIC, and RP-HPLC, indicating that a better orthogonal separation could occur between HILIC and RP-HPLC for unphosphorylated peptides. The observed orthogonal separation between HILIC and RP-HPLC is probably a reflection of their different mechanisms of separation. Although RP-HPLC depends on interaction with the hydrophobic amino acid side chains, HILIC depends on interaction with those hydrophilic and possibly charged amino acid residues via hydrogen bonding and ionic interactions. Moreover, because phosphopeptides are generally hydrophilic and charged, one would expect that phosphopeptides should interact more strongly with HILIC than do unphosphorylated peptides. Thus, it should be possible to separate phosphopeptides using HILIC.

Dean E. McNulty and Roland S. Annan (2008) [81] reported the use of hydrophilic interaction chromatography (HILIC) as part of a multidimensional chromatography strategy for proteomics. Analysis of tryptic digests from HeLa cells yielded numbers of protein identifications comparable to those obtained using strong cation exchange. They also demonstrate that HILIC represents a significant advance in phosphoproteomics analysis. In fact, they exploited the strong hydrophilicity of the phosphate group to selectively enrich and fractionate phosphopeptides based on their increased retention under HILIC conditions. In addition, in this study IMAC enrichment of phosphopeptides from HILIC fractions showed more than 99% selectivity. This was achieved without the use of derivatization or chemical modifiers. In a 300 µg equivalent of HeLa cell lysate over 1000 unique phosphorylation sites were identified. More than 700 novel sites were added to the HeLa phosphoproteome.

• **Reverse phase chromatography** All the phosphorylated proteins and phosphopeptides isolations can be coupled to reverse phase chromatography. Subsequently, most phosphoprotein-phosphopeptide analyses are performed nowadays by MS. As the MS technique is sensitive to contaminants such as salts, it is necessary to clean the samples prior to analysis, generally by reversed phase chromatography combining POROS R3 with C18 Disks and also graphite powder [82-84]. Poros R3, C18

Disks and graphite powder are materials containing long hydrocarbon chains, proven to be effective for the desalting and cleaning of very hydrophilic peptides, including phosphopeptides [71,85]. In 1999, Gobom and co-workers [82] introduced a micro column purification method in which a chromatographic resin was packed in the tip of a small constricted GELoader tip, creating a micro-column. With GELoader tips packed with R3, C18 or graphite material, contaminants like salts can be separated from the phosphopeptides using a chromatographic approach. In fact, using RP chromatography, molecules such as proteins, peptides and nucleic acids are separated according to their hydrophobicity. In addition to the removal of salts, these techniques also facilitate a concentration of the sample by the use of a low elution volume. This is an additional improvement for the sensitivity and quality of the subsequent mass spectrometric analysis. RP chromatography is usually coupled to all the phosphoproteins and phosphopeptides enrichment-methods previously described.

• **Current methodologies for the detection of phosphorylated proteins - advantages and limitations**

There are several analytical techniques for the analysis of phosphorylation, i.e., Edman sequencing and  $^{32}\text{P}$ -phosphopeptide mapping for localization of phosphorylation sites; however, these methods do not allow high-throughput analysis or imply very high-labour operations [86], whereas with the use of Mass Spectrometry (MS) high-throughput analysis of phosphorylated protein residues can be developed [67,78]. On the other hand, phosphospecific antibodies are routinely used to immunoprecipitate and therefore enrich in phosphorylated proteins from complex mixtures [87], but, currently, no commercial antibodies are available which are suitable for enriching all proteins that are phosphorylated, and thus, these proteins must be purified or enriched from complex mixtures using alternative methods [88]. By carrying out in-gel or in-solution trypsin digestion of protein complex mixtures, the resulted phosphopeptides and non-phosphopeptides can be loaded into different metal ion chromatographies (i.e. Immobilized Metal ion Affinity Chromatography IMAC ( $\text{Fe}^{3+}$ ), and Titanium Dioxide  $\text{TiO}_2$  [71] in order to enrich in phosphopeptides. The enriched solution can also be submitted into different reverse-phase chromatographies (i.e. Graphite powder [89], POROS R3 [88] in order to clean and desalt those phosphopeptides previously eluted. In addition these kinds of chromatographies will reduce the suppression of phosphorylated peptides in the mass spectra.

Using IMAC ( $\text{Fe}^{3+}$ ) and also ( $\text{TiO}_2$ ) [71] and ( $\text{ZrO}_2$ ) [1], the negatively charged phosphopeptides are purified by their affinity to positively charged metal ions, but

some of these methods experience the problem of binding acidic, non-phosphorylated peptides. Ficarro and co-workers [67] bypassed this problem on IMAC ( $\text{Fe}^{3+}$ ) by converting acidic peptides to methyl esters but increased the spectra complexity and requiring lyophilization of the sample, which causes adsorptive losses of phosphopeptides in particular [90]. Ficarro *et al.*, were able to sequence hundreds of phosphopeptides from yeast, including Slp2p kinase, but the level of phosphorylated residues identified from kinases were low compared to those from phosphoproteins highly expressed within the cell. Recently,  $\text{TiO}_2$  chromatography using 2,5-dihydroxybenzoic acid (DHB) was introduced as a promising strategy by Larsen *et al.*, [71].  $\text{TiO}_2$ /DHB resulted in a higher specificity and yield as compared to IMAC ( $\text{Fe}^{3+}$ ) for the selective enrichment of phosphorylated peptides from model proteins (i.e. lactoglobulin bovine, casein bovine). Moreover, SIMAC has been developed in order to get a higher efficiency than IMAC and  $\text{TiO}_2$  for the isolation of as many phosphopeptides as possible [74].

The fact that mainly phosphopeptides from highly expressed proteins within cells can be purified, while those from phosphorylated proteins with low level expression (i.e. kinases) do not bind so well to those resins, constitutes another important limitation concerning phosphoenrichment methods. This is due to the low proportion of this kind of protein, or, on the other hand, their available amount binds to metal ions although it is not sufficient to be detected by MS. The combination of SCX with IMAC ( $\text{Fe}^{3+}$ ) has been proven on yeast, resulting in a huge number of phosphorylated residues identified (over 700 including Fus3p kinase) [78]. Although more than 100 signalling proteins and functional phosphorylation sites, including receptors, kinases and transcription factors, were identified, it was clear that only a fraction of the phosphoproteome was revealed [78]. In addition, recent combinations of HILIC with IMAC ( $\text{Fe}^{3+}$ ) have been proven in clinical studies (HeLa samples), with the result of the identification of a large number of phosphorylated residues (1000) [81].

Improvement in methodologies to enrich for phosphorylated residues from kinases is clearly necessary. However, this is not straightforward for several reasons: (a) The low abundance of those signalling molecules within cells, (b) The stress/stimulation time-duration, as only a small fraction of phosphorylated kinases are available at any given time as a result of a stimulus. The time adaptation over signalling pathways is also a relevant and fast factor for kinases phosphorylation [91].

♦ **Summary - phosphoprotein and phosphopeptide enrichments based on electrostatic interactions** The most common techniques for enrichment for individual and/or global phosphorylation are IMAC and Titanium

Dioxide ( $\text{TiO}_2$ ) [45], which are based on the high affinity of positively charged metal ions. However, conversion of carboxylate groups to esters effectively eliminates nonspecific retention of non-phosphorylated peptides, although this constitutes a drawback due to increased complexity in the subsequent MS analysis.

During the last five years, titanium dioxide ( $\text{TiO}_2$ ) has emerged as the most common of the metal oxide affinity chromatography (MOAC) based phosphopeptide enrichment methods. This technique offers increased capacity compared to IMAC resins in order to bind and elute mono-phosphorylated peptides.  $\text{TiO}_2$  exploits the same principle as IMAC, and is similarly prone to nonspecific retention of acidic nonphosphorylated peptides. However, when loading peptides in 2, 5-dihydroxybenzoic acid (DHB) [71], glycolic and phthalic acids, nonspecific binding to  $\text{TiO}_2$  is reduced, thereby improving phosphopeptide enrichment without a chemical modification of the sample. In addition,  $\text{TiO}_2$  is often considered to be interchangeable with IMAC. It works on similar levels of sample amounts (e.g., micrograms of protein) for the identification of phospho-sites by MS analysis. Recently, SIMAC [72,74] appeared as a phosphopeptide enrichment tool which exploits the properties of IMAC coupled to  $\text{TiO}_2$ , making it possible to carry out more refined studies. Another phosphopeptide enrichment prior to mass spectrometric analysis is  $\text{ZrO}_2$  [75] and its principle is based on metal affinity chromatography like IMAC and  $\text{TiO}_2$ .  $\text{ZrO}_2$  permits the isolation of single phosphorylated peptides in a more selective manner than  $\text{TiO}_2$ . It has, in fact, been successfully used in the large-scale characterization of phosphoproteins [66,78-80]. Furthermore, strategies which consist of fractionating and subsequently enriching phosphopeptides on a proteome wide scale are based on strong cation/anion exchange (SCX and SAX) chromatography and HILIC interaction chromatography. Calcium phosphate precipitation is also a useful pre-fractionation step to simplify and enrich phosphopeptides from complex samples which can be coupled to IMAC [77].

**B.3. Phosphopeptides isolated by proteomic techniques -MS analysis** Phosphorylation on serine and threonine residues are labile and conventional fragmentation CID (Collision Induced Dissociation) typically results in the partial neutral loss of phosphoric acid ( $\text{H}^3\text{PO}_4$ , 98/z) in MS2 mode, due to the gas phase  $\beta$ -elimination of the phosphor-ester bond. Therefore, dehydroalanine and dehydroaminobutyric acid are generated. When peptide ions are fragmented by CID, series of  $\gamma$ - and  $b$ - ions are formed [92,93]. By correlating mass difference between peaks in the  $\gamma$ -ion series or between peaks in the  $b$ - ion series with amino acid residue masses the peptide sequence is obtained. The CID

fragmentation occurs on the peptide backbone, and only limited sequence information is obtained. This event can also compromise the identification of phosphorylation sites. In relation to phosphotyrosine residues, partial neutral loss is also observed ( $\text{HPO}_3$ , 80/z) in MS2 mode, but the phosphate group on tyrosine residues is more stable than on serine and threonine residues. In addition, the phospho-fingerprint characteristic of phosphotyrosine, is the phosphotyrosine immonium ion (~216 Da), this being a positive indicator for the presence of a peptide phosphorylated on tyrosine [94,95]. The ion originating from neutral loss of phosphoric acid ( $\text{H}^3\text{PO}_4$ ) can be selected for further fragmentation by MS3 mode. After neutral loss fragmentation, the selected ion is automatically selected for further fragmentation. This makes it possible to add extra energy for the fragmentation of peptide backbone. However, the MS3 mode requires that the phosphorylation on serine and threonine residues are labile and conventional fragmentation CID (Collision Induced Dissociation) typically results in the partial neutral loss of phosphoric acid ( $\text{H}^3\text{PO}_4$ , 98/z) in MS2 mode, due to the gas phase  $\beta$ -elimination of the phosphor-ester bond. Therefore, dehydroalanine and dehydroaminobutyric acid are generated. When peptide ions are fragmented by CID, series of y- and b- ions are formed [92,93]. The peptide sequence is obtained by correlating mass difference between peaks in the y-ion series or between peaks in the b-ion series with amino acid residue masses. The CID fragmentation occurs on the peptide backbone, and only limited sequence information is obtained. This event can also compromise the identification of phosphorylation sites. In relation to phosphotyrosine residues, partial neutral loss is also observed ( $\text{HPO}_3$ , 80/z) in MS2 mode, but the phosphate group on tyrosine residues is more stable than on serine and threonine residues. In addition, the phospho-fingerprint characteristic of phosphotyrosine, is the phosphotyrosine immonium ion (~216 Da), which is a positive indicator for the presence of a peptide phosphorylated on tyrosine [94,95]. The ion originating from neutral loss of phosphoric acid ( $\text{H}^3\text{PO}_4$ ) can be selected for further fragmentation by MS3 mode. The selected ion, after neutral loss fragmentation, is automatically selected for further fragmentation. This makes it possible to add extra energy for the fragmentation of peptide backbone. However, the MS3 mode requires that the selected ion is abundant in order to observe the fragmented ions. A pseudo-MS3 development is MultiStage Activation (MSA) [96], which was implemented on quadrupole-IT and linear IT-orbitrap. In MSA, the fragmentation of the precursor ion occurs simultaneously with the fragmentation of the ion originating from the neutral loss. The MS2 and MS3 massdata are then combined in a hybrid spectrum, resulting in improved sequence information and also in an improvement of reliability for the phosphorylation site assignment. Alternative

fragmentations to CID are ECD (electron capture Dissociation) and ETD (Electron transfer dissociation). By ECD, radical peptide ions are obtained when multiplycharged peptide ions are rationally with low-energy thermal electrons. In addition, this fragmentation occurs in the peptide between the backbone amide and the alpha carbon, generating c- and z-ions [97]. An advantage of ECD is that it only occurs on the peptide backbone, and labile phosphate groups remain intact on the resulting c- and z- fragment ions, thus enabling the identification of the specific phosphorylation sites. Therefore, it is extremely useful for the analysis of multiply-phosphorylated peptides. A disadvantage of ECD is its selectivity for disulfide bonds, due to the high radical affinity of the bond [98,99]. The main drawback of ECD is that it is solely used in the Fourier transform-Ion Cyclotron Resonance (FT-ICR) instruments due to the requirement of a static magnetic field for the thermal electrons, meaning high costs and high specialization. c- and z- ions are also generated by ETD. This fragmentation was actually developed in order to carry out ECD-like dissociation experiments, in a Quadrupole Linear Ion Trap [96,100]. ETD is a chemical process in which reaction with fluoranthene radical anions disrupts the peptide backbone at regular intervals. ETD preserves the intact information about labile modifications, which are not observed directly when using CID. For instance, phosphate groups are good leaving groups, which mean that they are easily lost in the excitation process. However, by using ETD one can directly observe fragments that contain the intact phosphopeptides. The drawback of ETD is that it is less sensitive compared to CID, because of lower ionization efficiency. As a result, we recommend using CID to start with, and would recommend switching to ETD in case you are not able to determine the phosphorylation site.

### ***(C) Quantitative proteomic methodologies used in clinical research; examples of relevant phosphorylated proteins studied***

For phosphopeptides proteins containing amino acids with one or more of the stable isotopes of  $^2\text{H}$ ,  $^{13}\text{C}$ ,  $^{15}\text{N}$  or  $^{18}\text{O}$  can be used as internal standards by addition, at an early stage of the analysis, of a complex protein sample. There are two approaches for introducing a stable isotope into proteins or peptides: metabolic labelling using whole cells grown in culture (e.g. SILAC) or chemical labelling (e.g. iTRAQ, ICAT). Since protein phosphorylation is very dynamic and constantly changing throughout the life of a cell, measuring the changes in phosphorylation is critical for understanding the biology of a phosphorylation event. We restrict the discussion here to four MS based quantitation strategies which have direct utility towards measuring changes in protein phosphorylation extensively: SILAC, iTRAQ, AQUA and

MRM. Other chemical labelling techniques which rely on stable isotope incorporation using e.g.  $^{18}\text{O}$  labelled water during trypsin digestions and stable isotope incorporation ICAT can also be considered to contain relevant information, but will not be described here. In addition, we will also include the explanation and examples of 2-D Fluorescence Difference Gel Electrophoresis (2D\_DIGE) quantification methodology, which nowadays also provides interesting research studies.

**C.1. Stable Isotope Labelling with Amino acid in cell Culture (SILAC)** Stable isotope labelling by amino acids in cell culture (SILAC) is a quantitative method based on in vivo labelling of proteins in cell cultures with amino acids that contain stable isotopes (non radioactive, e.g.  $^2\text{H}$ ,  $^{13}\text{C}$  and  $^{15}\text{N}$ ) [57,101]. In its simplest form, two separated cell cultures are grown in a pairwise fashion; for example, culture A might be yeast cells grown under “normal” conditions (light conditions) while culture B might be yeast cells grown in the presence of a stress condition. The growth conditions of the cells are identical (except for the presence of the stress stimuli), but the growth media of culture B has an essential amino acid (one not synthesized by the cell) replaced with an isotopically “heavy” form of that amino acid (e.g.  $^{13}\text{C}_6$ -arginine). A number of cell lines have been used for SILAC experiments, and the growth and morphology of the cells have not been affected by the isotopically labelled amino acid [78,101,102].

After approximately five rounds of doubling, cellular proteins are essentially 100% labelled with the selected amino acid. After culturing, the light and heavy cell populations are combined (1:1) into one pool and the proteins are isolated. The protein pool is then digested with a protease, typically trypsin, to form a peptide pool that is analyzed by MS. Each peptide analyzed will be present in two forms: the light and the heavy form. They are distinguishable based on the mass difference due to the heavy isotope incorporation in the selected amino acid. The SILAC method is compatible with the above mentioned enrichment of phosphoproteins/phosphopeptides including the immunoprecipitation of a target protein [103]. One of the first research studies which carried out this technology was provided by Gruhler and co-workers (2005) [78]. In this study, more than 700 phosphopeptides from *Sacharomyces cerevisiae* were identified, 139 were differentially regulated at least 2-fold in response to mating pheromone. Components belonging to the mitogen-activated protein kinase signaling pathway and to downstream processes including transcriptional regulation, the establishment of polarized growth, and the regulation of the cell cycle were among these regulated proteins.

### C.2. Isobaric Tag for Relative and Absolute (iTRAQ)

The second method for the global quantification of proteins and protein modifications is an in vitro chemical labelling procedure called iTRAQ. The iTRAQ reagent consists of two to eight isobaric tags that can be used to label two to eight separate protein samples. The iTRAQ tags contain three regions: a peptide reactive region, a reporter region, and a balance region [104]. The peptide reactive region of the tag consists of an NHS ester and is designed to react with the N-termini and lysines of peptides after protease digestions. In the case of 4-plex iTRAQ, the four reporter groups appear in the tandem mass spectrum at  $m/z$  114, 115, 116, and 117. The attached balance groups are designed to make the total mass of the balance and reporter group 145 Da for each tag, which results in balance groups of 31 Da, 30 Da, 29 Da, and 28 Da, respectively. Protein samples for quantification are separately isolated and digested proteolytically, and each sample is chemically labelled with one of the iTRAQ reagents. After labelling, the samples are combined and subsequently analyzed by MS. Identical peptides from each sample will have identical masses as the iTRAQ reagents are isobaric. The iTRAQ reagent labels phosphopeptides to the same degree as nonphosphorylated peptides and it does not affect the stability of phosphopeptides. Enrichment strategies, such as IMAC [44,105] or immunoprecipitation with anti-phosphotyrosine antibodies [44], have been used to remove non-phosphorylated peptides to focus the analysis on site-specific phosphorylation. Since iTRAQ is an in vitro labelling procedure it can also be applied to clinical samples such as tumour tissues and fluids (e.g. serum, urine, blood). iTRAQ has been described as a very powerful method for the quantification of phosphorylation on a proteomic scale. As a relevant example we mention that Boja and co-workers (2009) [106] successfully monitored phosphorylation sites of mitochondrial proteins including adenine nucleotide translocase, malate dehydrogenase and mitochondrial creatine kinase, etc. Among them, four proteins exhibited phosphorylation changes with these physiological stimuli: (a) BCKDH-E1 $\alpha$  subunit increased phosphorylation at Ser337 with DCA and de-energization; (b) apoptosis-inducing factor phosphorylation was elevated at Ser345 with calcium; (c) ATP synthase F1 complex  $\alpha$  subunit and (d) mitofilin dephosphorylated at Ser65 and Ser264 upon de-energization. This screening validated the iTRAQ/HCD technology as a method for functional quantitation of mitochondrial protein phosphorylation as well as providing insights into the regulation of mitochondria via phosphorylation.

**C.3. Absolute Quantitation (AQUA)** The AQUA strategy provides an absolute quantification of a protein of

interest [107]. In the AQUA method, a peptide from the protein of interest is constructed synthetically containing stable isotopes, and the isotopically labelled synthetic peptide is called AQUA peptide. The synthetic peptides can be synthesized with modifications such as phosphorylation to allow for the direct, quantitative analysis of posttranslationally modified proteins. The stable isotopes are incorporated into the AQUA peptide by using isotopically "heavy" amino acids during the synthesis process of the interesting peptide (native peptide). In this way, the synthetic peptide has a mass increase of e.g. 10 Daltons, due to the incorporation of a  $^{13}C_6$  and  $^{15}N_4$ -arginine into the synthetic peptide, compared to the native peptide. Although the mass difference between the native and the synthetic peptide allows the mass spectrometer to differentiate between the two forms, both forms have the same chemical properties, resulting in the same chromatographic retention, ionization efficiency, and fragmentation distribution. In AQUA experiments, a known amount of the isotopically labelled peptide is added to a protein mixture, which is proteolytically digested, and later analyzed by MS. Since the native peptide and its synthetic counterpart have the same chemical properties, the MS signal from the quantified synthetic peptide can be compared to the signal of the native peptide. The absolute quantification of the peptide to be determined [108] is thus finally permitted. Multiple AQUA peptides can be used to quantify multiple proteins in a single experiment.

Ziwei Yu and co-workers (2007) [109] using AQUA as a novel system of *in situ* quantitative protein expression analysis, studied the protein expression levels of phosphorylated Akt (p-Akt). Activation of Akt in tumours is mediated via several mechanisms, including activation of cell membrane receptor tyrosine kinases such as EGFR and loss of phosphatase PTEN with dephosphorylation of phosphoinositol triphosphate. Ziwei and co-workers (2007) discovered that Akt activation in oropharyngeal squamous cell carcinoma (OSCC) is associated with adverse patient outcome, indicating that Akt is a promising molecular target in oropharyngeal squamous cell carcinoma.

**C.4. Multiple Reaction Monitoring (MRM)** MRM is a very sensitive method for detecting phosphorylated peptides on a hybrid triple quadrupole linear ion trap mass spectrometer (qTRAP). This method requires that the sequence of the protein be known in order to calculate precursor and fragment ion values, which can be used to trigger dependent ion scans in a qTRAP instrument [110,111]. This technique can also be used to perform a precursor ion and neutral loss scan, to identify unknown phosphopeptides from a complex mixture, and is a powerful method for the identification and quantification of post-

translational modifications in proteins. MRM has recently been used by White and co-workers [112,113] to identify and quantify tyrosine phosphorylated kinases for hundreds of nodes within a signalling network and across multiple experimental conditions. Moreover, White and co-workers [112,113] applied iTRAQ combined with MRM for phospho quantitative analysis of signalling networks, identifying and quantifying 222 tyrosine phosphorylated peptides, obtaining an extremely high percentage of signalling nodes covered. They defined the mechanisms by which EGFRvIII protein alters cell physiology, as it is one of the most commonly mutated proteins in GBM and has been linked to radiation and chemotherapeutic resistance. They performed a phosphoproteomic analysis of EGFRvIII signalling networks in GBM cells. The results of this study provided important insights into the biology of this mutated receptor, including oncogene dose effects and differential utilization of signalling pathways. In addition, clustering of the phosphoproteomic data set revealed a previously undescribed crosstalk between EGFRvIII and the c-Met receptor. Treatment of the cells with a combination using both EGFR and c-Met kinase inhibitors dramatically decreased cell viability *in vitro*.

**C.5. 2-D Fluorescence Difference Gel Electrophoresis (DiGE)** In DiGE, proteins extracted from a control extract are labelled with one CyDye (Cy3 or Cy5 conjugated), and proteins isolated from a test extract labelled with the other colour of CyDye fluorophore, which are size and charge matched. These labelled protein extracts are mixed and co-resolved (often with the addition of an internal standard, which can be labelled with Cy2) on large-format two-dimensional gels for analysis of expression changes in the resulting pattern of spots ('spot maps') [114]. In comparison with two-dimensional gel electrophoresis, DiGE offers the advantage that multiple samples could be compared on a single gel ('multiplexing'), and made it possible to stain control and test samples with different fluorescent dyes prior to electrophoresis. This advance alleviated issues of gel-to-gel comparison and decreased the number of gels required. The capability to include an internal standard, composed of an equal fraction of all the samples in an experiment, also improved intergel matching and facilitated normalization of matched spots in replicate samples on multiple gels. The use of CyDyes to label proteins, in place of non-fluorescent post-stains, can give a large enhancement of sensitivity for protein detection [115] and constitutes the crucial advantage of the DiGE approach for biomaterial applications. This enables analysis of even very scarce protein samples, including small areas of laser-microdissected tissue [116,117]. Twodimensional difference gel electrophoresis (2D-

DIGE) with novel ultra high sensitive fluorescent dyes (CyDye DIGE Fluor saturation dye) enables the efficient protein expression profiling of laser-microdissected tissue samples. The combined use of laser microdissection allows accurate proteomic profiling of specific cells including tumour tissues [118].

As an example, differential protein analysis was performed using 2-dimensional differential in-gel electrophoresis (2D-DIGE) by Yefei Rong and co-workers (2010) [119]. They found that 16 protein spots were differently expressed between the two mixtures (a comparison was made with serum samples from five individuals with pancreatic cancer and five individuals without cancer). Yefei Rong and co-workers [119] demonstrated that eight proteins from these fluids were up-regulated and 8 were down-regulated in cancer. Mass spectrometry and database searching allowed the identification of the proteins corresponding to the gel spots. Up-regulation of mannosebinding lectin 2 and myosin light chain kinase 2, which had not previously been implicated in pancreatic cancer, were observed. In an independent series of serum samples from 16 patients with pancreatic cancer and 16 non-cancerbearing controls, increased levels of mannose-binding lectin 2 and myosin light chain kinase 2 were confirmed by western blot.

Moreover, Nagano (2010) [120] has recently developed the technology named “antibody proteomics technology”. This technology can screen for biomarker proteins by isolating antibodies against each candidate in a rapid and comprehensive manner. He applied “antibody proteomics technology” to breast cancer-related biomarker discovery and evaluated the utility of this novel technology. Cell extracts derived from breast tumour cells (SKBR3) and normal cells were analyzed by two-dimensional differential gel electrophoresis (2D-DIGE) in order to identify proteins over-expressed in the tumour cells. Candidate proteins were extracted from the gel pieces, immobilized onto a nitrocellulose membrane using a dot blot apparatus and then used as target antigens in scFv-phage enrichment and selection. scFvs binding to 21 different over-expressed proteins in tumor cells were successfully isolated within several weeks following this *in vitro* phage selection procedure. The expression profiles of the identified proteins were then determined by tissue microarray analysis using the scFv-phages. Consequently, three breast tumour-specific proteins were identified. His data demonstrated the utility of an antibody proteomics system for discovering and validating tumour-related proteins in pharmaceutical proteomics. Currently, he and other related groups are analyzing the functions of these proteins in order to be able to confirm and use them as diagnostic markers or therapeutic targets.

#### **(D) Phosphorylated proteins related to different diseases and the benefits of proteomic strategies in such clinical studies**

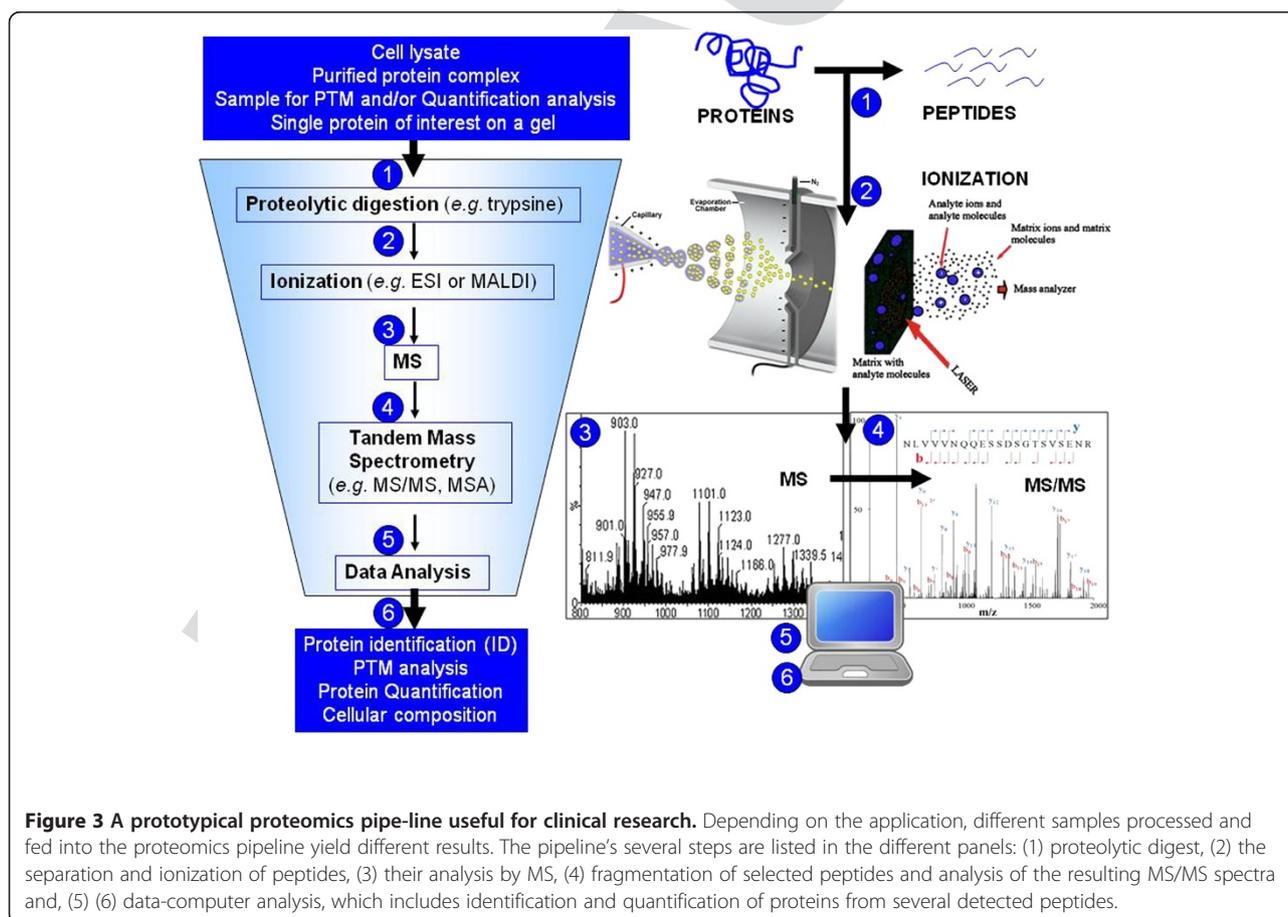
In a recent study Steen *et al.* examined the role of phosphorylation in the dynamics of the anaphase promoting complex (APC) [121]. Some drugs that bind to microtubules and block mitosis are ineffective in cancer treatment; others show inexplicable focal efficacy. For example, the vinca alkaloids are useful for treating lymphoma, neuroblastoma and nephroblastomas, whereas taxol is useful for advanced breast cancer and ovarian cancer. It is not known why these drugs are not all equally effective, nor why they have different therapeutic value against different cancers. The authors observed distinct phosphorylation states of the APC in response to different antimitotic drugs and suggest they may explain some of these differences. They also propose it is possible that cells from different tissues, or cells harbouring different mutations, or cells under different physiological stresses, such as hypoxia, may differ in their response to spindle poisons and would thus reflect those differences in different sites of phosphorylation. Differences in spindle checkpoint phosphorylation may reveal new features of the mitotic state. The categorisation of drugs, the discrimination of the response of tumours to drugs and the identification of new means of checkpoint control may be facilitated by the ability to characterise drug candidates based on the spectrum of APC phosphorylations. The authors further suggest that the results of the study indicate that the term mitotic arrest is a misnomer: arrest is a dynamic state in which some cells enter apoptosis and other cells revert to interphase. The ability to observe biochemical events during arrest could be very important for understanding antiproliferative treatments. The exploration of the dynamics of phosphorylation, however, makes great demands on the accuracy of quantitation. Most mass spectrometric based quantitative approaches, including stable isotope labelling with amino acids in cell culture (SILAC) and isobaric tag for relative and absolute quantitation (iTRAQ), give relative data, meaning that one state of phosphorylation is determined relative to another phosphorylation state [122-124]; these data can help to establish the kinetics of a pathway. The method used in this work offers a significant advance over earlier techniques. It allowed the measurement of specific quantitative changes in APC phosphorylation in cells arrested in nocodazole for varying periods. If these dynamics can be correlated with the process by which the arrested state is resolved, we may be provided with new tools to understand the mitotic process and to find more effective drug targets in cancer.

The long-held belief in the cancer research community that a precise molecular understanding of cancer can

result in cancer therapy is validated by the development of drugs for specific biological pathways with increased specificity and reduced toxicity. The development of Herceptin, a monoclonal antibody against the HER2 receptor for breast cancer therapy is one of the most successful recent examples of cancer-specific drugs. HER2 is an important target in cancer because its overexpression increases tumour cell proliferation, vessel formation and invasiveness, and predicts poor prognosis. Wolf-Yadlin and other scientists [111,112,121-124] have used phosphoproteomics and MS to investigate the role of phosphorylation in the effects of HER2 overexpression on EGF- and HRG-mediated signalling of erbB receptors. Identification was possible of specific combinations of phosphorylation sites that correlate with cell proliferation and migration and that potentially represent targets for therapeutic intervention. Unfortunately, owing to sensitivity limitations, only 68 out of 322 phosphorylation sites could be analysed kinetically, so the study does not provide a comprehensive analysis of the multitude of effects produced by HER2 overexpression. It does, however, mark an important breakthrough in the characterisation of the erbB receptor signalling network in

tumours and illustrates the importance of understanding protein phosphorylation.

A central role is played by mitochondria in energy metabolism and cellular survival, and consequently mitochondrial dysfunction is associated with a number of human pathologies. Moreover, mitochondrial dysfunction is linked to insulin resistance in humans with obesity and type 2 diabetes. Recently, Zhao and co-workers (2011) [125], studied the phosphoproteome of the mitochondria isolated from human skeletal muscle. Zhao and coworkers revealed extensive phosphorylation of inner membrane protein complexes and enzymes combining titanium dioxide (TiO<sub>2</sub>) protocols with reverse phase chromatography coupled to MS analysis. 155 distinct phosphorylation sites in 77 mitochondrial phosphoproteins, including 116 phosphoserine, 23 phosphothreonine, and 16 phosphotyrosine residues were identified. Phosphorylation sites in mitochondrial proteins involved in amino acid degradation, importers and transporters, calcium homeostasis, and apoptosis were also assigned. Furthermore, many of these mitochondrial phosphoproteins are substrates for protein kinase A, protein kinase C, casein kinase II and DNA-dependent protein kinase.



**Figure 3 A prototypical proteomics pipe-line useful for clinical research.** Depending on the application, different samples processed and fed into the proteomics pipeline yield different results. The pipeline's several steps are listed in the different panels: (1) proteolytic digest, (2) the separation and ionization of peptides, (3) their analysis by MS, (4) fragmentation of selected peptides and analysis of the resulting MS/MS spectra and, (5) (6) data-computer analysis, which includes identification and quantification of proteins from several detected peptides.

The high number of phosphotyrosine residues suggests that tyrosine phosphorylation has an important role in mitochondrial signalling. Many of the mitochondrial phosphoproteins are involved oxidative phosphorylation, tricarboxylic acid cycle, and lipid metabolism, i.e. processes proposed to be involved in insulin resistance. It is well known that mitochondria dysfunction is centrally involved in a number of human pathologies, such as type 2 diabetes, parkinson's disease and cancer [126]. In this study, the most prevalent form of cellular protein posttranslational modifications (PTMs), reversible phosphorylation [127-134][135-139], emerges as a central mechanism in the regulation of mitochondrial functions [130,131]. The steadily increasing numbers of reported mitochondrial kinases, phosphatases and phosphoproteins also imply the important role of protein phosphorylation in different mitochondrial processes [132-134]. The prototypical proteomics pipe-line useful for clinical research is illustrated (Figure 3).

#### **(E) Observations and future needs**

Cancer and immune disorders are still among the leading causes of death worldwide. Therefore, there is still a need for the identification of useful biomarkers and the improvement of the understanding of the development of these diseases. The immune system is readily affected by the existence of cancer in the body, even at a preclinical stage, and these studies should be expanded and extended in the future to answer the numerous questions concerning (a) the roles of immune cells in cancer surveillance (b) the characteristics of inflammation in association with cancer development, (c) the effects of environment/lifestyle factors on the immune system, and (d) the interaction between aging diseases. The importance of protein kinase-regulated signal transduction pathways in immunology disorders and cancer has led to the development of drugs that inhibit protein kinases at the apex or intermediary levels of these pathways. Protein phosphorylation assignment studies of these signalling pathways will provide important insights into the operation and connectivity of these pathways that will facilitate the identification of the best targets for cancer therapies and immunology diseases (e.g. the identification of a phosphate group on a specific serine, threonine or tyrosine by phosphoenrichments combined with MS). Phosphoproteomic analysis of individual tumours, blood, sera, tissues will also help match targeted therapeutic drugs to the appropriate patients. It is now generally accepted that no single proteomic method is comprehensive, but combinations of different enrichment methods produce distinct overlapping phosphopeptide datasets to enhance the overall results in phosphoproteome analysis. During the last decade, phosphopeptide sequencing by mass spectrometry has

seen tremendous advances. For example, MS/MS product ion scanning, multistage activation and precursor ion scanning are effective methods for identifying serine (Ser), threonine (Thr) and tyrosine (Tyr) phosphorylated peptides.

The current phosphoproteomic goals imply the identification of phosphoproteins, mapping of phosphorylation sites, quantitation of phosphorylation under different conditions, and the determination of the stoichiometry of the phosphorylation. In addition, knowing when a protein is phosphorylated, which kinase/s is-are involved, and how each phosphorylation fits into the signalling network, are also important challenges for researchers in order to understand the significance of different biological events. The new MS technologies are fundamental for cataloguing all this information, and it is heading towards the collection of accurate data on phosphopeptides on a global scale. In addition, the possible difficulties to get sufficient amount of specific phosphorylated proteins of specific low abundant protein-kinases *in vivo* which might limit the usability of the phosphoproteome analysis, must be pointed out.

Finally, it is important to state that to develop clinical proteomic applications using the identified proteins and phosphoproteins, collaboration between research scientists, clinicians and diagnostic companies, and proteomic experts is essential, particularly in the early phases of the biomarker development projects. The proteomics modalities currently available have the potential to lead to the development of clinical applications, and channelling the wealth of the information produced towards concrete and specific clinical purposes is urgent.

#### **Abbreviations**

Note: These abbreviations are useful proteomic abbreviations some of them are mentioned and described in this Review and they are also described in the References of this article.; AQUA: Absolute Quantitation; CID: Collision-Induced Dissociation; Da: Dalton (molecular mass); DIGE 2-D: Fluorescence Difference Gel Electrophoresis; ECD: Electron Capture Dissociation; ESI: Electron Spray Ionization; ETD: Electron Transfer Dissociation; FT-ICR: Fourier transform-Ion Cyclotron Resonance; HILIC: Hydrophilic interaction chromatography; HPLC: High-performance liquid chromatography or high-pressure liquid chromatography; H<sub>3</sub>PO<sub>4</sub>: Phosphoric acid; ICR: Ion Cyclotron Resonance; IMAC: Immobilized Metal Affinity Capture; IT: Ion Trap; iTRAQ: Isobaric Tag for Relative and Absolute Quantitation; kDa: kilodalton (molecular mass); LC: Liquid Chromatography; MALDI: Matrix-Assisted Laser Desorption/Ionization; MOAC: Metal Oxide Affinity Chromatography; Mr: Relative molecular mass (dimensionless); MRM: Multiple reaction monitoring; MS: Mass Spectrometry; MSA: MultiStage Activation; MS/MS: tandem mass spectrometry; m/z: Mass to charge ratio; PID: Primary Immunodeficiencies; PTM: Post-Translational Modification; SILAC: Stable Isotope Labelling with Amino acid in cell Culture; SIMAC: Sequential Elution from IMAC; TiO<sub>2</sub>: Titanium dioxide; TOF: Time of Flight; ZrO<sub>2</sub>: Zirconium dioxide.

#### **Competing interests**

The authors declare that they have no competing interests.

#### **Authors' contributions**

EL carried out the proteomics, phosphoproteomics and mass spectrometry studies for this review. IL, AF, JS carried out the clinical studies for this

review. EL, IL, AF and JS carried out these complementary studies in order to develop clinical phosphoproteomics research and publish this article. All authors read and approved the final manuscript.

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