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Activity Based Probes as a tool for Functional Proteomic Analysis of Proteases

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SUMMARY

Traditional proteomics methodology allows global analysis of protein abundance but does not provide information about the regulation of protein activity. Proteases in particular are known for their multilayered posttranslational activity regulation which can lead to a significant difference between protease abundance levels and their enzyme activity. To address those issues, the field of activity based proteomics has been established in order to characterize protein activity and monitor the functional regulation of enzymes in complex proteomes. In this review, we present structural features of activity based probes for proteases and discuss their applications in proteomic profiling of various catalytic classes of proteases.

Keywords

Activity based probes; proteomics; proteolysis; proteases

INTRODUCTION

All organisms express a large variety of structurally and catalytically diverse proteases. Genome sequencing projects have revealed the presence of at least 569 human proteases that can be divided into several distinct catalytical classes: metalloproteinases, serine, cysteine, threonine and aspartic proteases [1]. Interestingly, the mouse and rat genomes show even higher protease variety with 644 and 629 members respectively [2]. Proteases have the unique ability to hydrolyze peptide bonds and therefore irreversibly modify the function of target proteins. They play crucial roles in diverse physiological processes such as protein turnover, blood coagulation, apoptosis, hormone processing and bone remodeling. Because proteolytic processing is an irreversible event, it must be tightly regulated to avoid catastrophic consequences. The most common way that proteases are regulated is by expression as an inactive proenzyme that requires activation by proteolytic cleavage. The activation process can be regulated by cellular signaling as well as by changes in the microenvironment. If this regulation fails, endogenous extracellular and intracellular protease inhibitors (such as serpins and cystatins) prevent any unwanted proteolysis. This multilayered post-translational regulation can lead to significant difference between overall abundance levels and activity of proteases. Thus, methods that rely on detection of protease

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abundance rather than activity do not always provide sufficient information to allow functional assignments of specific proteases.

Traditional proteomics methodology based on 2D gel chromatograhpy coupled with mass spectrometry has recently been complemented with non-gel based methods such as MudPIT and SELDI [3,4]. Chromatography separations employed in these methods significantly increase resolving power and proteome coverage but they still lack the ability to resolve active and inactive populations of enzymes. Activity based proteomics is a relatively new sub-division of proteomics that has been developed to characterize protein activity and directly monitor the functional regulation of enzymes in complex proteomes. This method utilizes small molecule activity based probes (APBs) which covalently modify the enzyme active site and enable detection and affinity purification of a target enzyme population (Fig. 1). Activity based probes are highly selective and can be used for analysis of complex samples such as cell lysates, intact cells and even whole organisms. In this review, we will outline advances in the development of activity based probes and highlight the numerous applications of these reagents for the study of various protease classes and their roles in human disease.

STRUCTURE OF ACTIVITY BASED PROBES

All activity based probes share a similar basic design, which incorporates elements required for targeting, modification and detection of labeled proteins. Structurally, those elements can be divided into the reactive group, linker and tag (Fig 2A).

Reactive group

The reactive functional group (also termed as ‘’the warhead”) provides a covalent attachment of the probe to the catalytic residue of the protease active site. The majority of protease families have well-established catalytic mechanisms that have been defined using abundant structural and kinetic data. This data has enabled the synthesis of a large variety of specific, irreversible small molecule inhibitors, that can be transformed into activity based probes by the addition of an appropriate reporter tag [5]. Probes for serine, cysteine and threonine proteases utilize electrophile groups that form a covalent bond with their active site nucleophile (serine, cysteine or threonine residue). The electrophile has to be strong enough to react with the active site nucleophile but not with other free nucleophiles in the proteome (Fig 2B). Various reactive groups have been successfully applied to protease probe design (Table 1). The phosphonate group is highly reactive towards the hydroxyl nucleophile of serine proteases and has therefore found use a number of probes for both trypsin and chymotrypsin fold serine proteases [6]. The proteasome, on the other hand, has been targeted with probes containing a vinyl sulfone reactive group even though this class of compounds was originally designed to react with cysteine proteases [7]. Interestingly, a,b-epoxy ketones are also known to form highly selective bounds with the N-terminal threonine of the proteasome [8]. Cysteine proteases are the family most extensively studied using ABPs and probes containg a number of different reactive functional groups including epoxides, diazomethyl ketones, acyloxymethyl ketones and vinyl sulfones have been designed [9–11]. Unfortunately, the same electrophile-based approach does not work well for metalloproteinases and aspartic proteinases because they do not form covalent intermediates with their substrates. In this case, probes are designed using reversible inhibitor scaffolds coupled to a photoreactive group that provides covalent attachment upon irradiation with UV light [12,13].

Linker

The most basic function of the linker is to separate the reactive functional group from the tag. This improves probe accessibility and reduces steric hindrance between both groups. For this purpose, the linker can be as simple as an extended alkyl or polyethylene glycol spacer. Alternatively, the linker can be used to increase probe specificity by addition of structural elements (i.e. peptides) that enhance the specificity of the probe. For most protease probes, the linker is a short peptide sequence that mimics a true protein substrate. This peptide linker can be optimized to target distinct subfamilies of proteases by changing its aminoacid sequence [14]. A more recent improvement in linker design has been the development of a region that can be enzymatically or chemically cleaved to release probe labeled proteins. This simplifies the elution process and decreases background protein contamination during an affinity purification. Various cleavable linker elements have recently been reported. Cravatt and coworkers developed a cleavable linker that has a peptide recognition site for tobacco etch virus protease (TEV) and applied it to the identification of proteins that had been labeled with a sulfonate ester probe [15,16].

One of the first chemically cleavable linkers described makes use of a disulfide bond that is readily cleaved in mild reductive conditions [17–19] (Fig. 3A). Disulfide linkers work well in some applications, such as profiling of serine hydrolases, but they are not compatible with reductive buffers which are needed for profiling of cysteine proteases. Disulfides are also quite labile and prone to disulfide exchange, which can also lead to a premature release and nonspecific labeling of proteins containing free thiol groups [20]. These problems have been addressed with development of a novel diazo cleavable linker, which enables selective elution under mild reductive conditions [21] (Fig. 3A). The diazo linker was successfully incorporated into ABPs that were used for labeling and proteomic identification of cysteine and serine proteases [22]. As an alternative to cleavage by chemical reduction, acid cleavable linkers have been developed and are also commercially available for ICAT applications [23–25]. However, the strong acids required for cleavage (TFA) also release nonspecifically bound proteins. Finally, the linker region can be used for isotopic labeling in ICAT-like applications. Incorporation of light and heavy linkers have been demonstrated for the general papain family protease probe DCG-04 which was used for quantitative profiling of cysteine proteases by direct mass spectrometry based methods [26].

Tag

Incorporation of a tag group into an activity based probe enables the visualization and/or purification of labeled proteins. Radioisotopes are commonly used in biological applications and were also the first to be used as tags for activity based proteomics [27]. The gamma ray emitter ^{125}I can be introduced by iodination of any covalent inhibitor that has a phenol group. Labeled proteins can then be analyzed by 1D or 2D electrophoresis and visualized by autoradiography. This approach was used in activity profiling of cysteine proteases such as cathepsins [28], caspases [29] and the proteasome [30,31]. Protease probes that incorporate ^{3}H as a tag have also been reported [32]. Tritium replaces hydrogen and this modification does not affect the probe structure. However, its use is limited by low specific activity that requires long exposure times to obtain labeling profiles. Although radiolabeled probes are easy to prepare, their storage time is limited by the half-life of the radiolabel. They also require special handling and laboratory safety procedures and cannot be used to directly identify target proteins.

The application of fluorescent tags was a big step forward in the development of activity based probes. Fluorophores are safe to use and are commercially available in a variety of excitation and emission spectral ranges. The first fluorescent APBs were demonstrated for cysteine proteases and serine hydrolases [33,34]. Various types of dyes can be used as

fluorophores but their chemical properties can significantly influence their range of applications. Fluorescein and rodamine are inexpensive, but susceptible to photobleaching which limits their imaging applications. The fluorophosphonate warhead containing a PEG linker labeled with rhoadamine tag has been demonstrated to be an effective probe for profiling of serine hydrolases in cell homogenates [33]. Fluorescein and rodamine are not cell permeable and therefore cannot be used for labeling of intracellular targets in vivo. Dansyl and NBD (nitrobenz-2-oxa-1,3-diazole) are inexpensive fluorophores that have been used for in vitro activity based profiling [34,35]. BODIPY (dipyrromethene boron difluoride) and cyanine (Cy) dyes are photostable with high absorption coefficients, high quantum yields and narrow absorption peaks. They are also cell permeable making them useful in a variety of biological applications. BODIPY labeled epoxide probes have been used for labeling of cysteine proteases in lysates and intact cells [36]. Caspase probes containing the Cy fluorophore have been reported [37]. Because of their superior chemical properties, cyanine dyes have a great potential for use in imaging applications. Unfortunately, they are also extremely expensive which limits their use for large scale synthesis.

Fluorophores are perfect for rapid determination of labeling patterns after SDS-PAGE analysis, since gels can be directly scanned using a laser scanner and there is no need for time consuming blotting procedures required for biotinylated probes. However, for the purpose of isolation and identification of proteins targeted by APBs, biotin still remains the affinity tag of choice. Strong, diffusion limited interaction between biotin and immobilized avidin provides efficient enrichment of even low abundant labeled targets. Avidin based enrichment also reduces complexity of biological samples which is extremely beneficial for proteomic applications. Unfortunately, the strong avidin-biotin interaction requires harsh elution conditions which are not directly compatible with mass spectrometry analysis. Eluted samples must first be analyzed by SDS-PAGE and proteins cut from a gel for identification. Alternatively, enriched proteins can be prepared for mass spectrometry by ‘’on bead” digestion. In this approach, proteins are reduced, alkylated and digested while they are still bound to immobilized avidin. In both approaches the final sample is contaminated with natively biotinylated proteins and abundant, nonspecifically bound proteins. This contamination can be minimized by usage of probes with cleavable linkers, which enable specific elution [22]. The biggest disadvantage of the biotin tag is its overall poor cell permeability which limits its use for *in situ* and *in vivo* applications. Since protease activity is often regulated by factors within its intracellular microenvironment, labeling of cell lysates often does not provide an accurate picture of protease activity profiles. To resolve this problem, a tandem labeling strategy which utilizes ‘’click chemistry” was developed. Çlick chemistry is based on a [2+3] cycloaddition of an azide and alkyne functional group in the presence of copper catalyst (Fig. 3B). This method was originally developed by Sharpless and coworkers but in the modified form was applied to activity based proteomics [38,39]. In this approach, intact cells are labeled with a cell permeable probe, which instead of a biotin tag carries an alkyne or azido group. After labeling, cells are homogenized and the biotin tag (which carries a complementary alkyne or azido functional group) is added by cycloaddition. Tagged proteins can than be enriched and identified by mass spectrometry [40].

APPLICATION OF PROBES FOR THE PROFILING OF PROTEASES

Cysteine, serine and threonine proteases all have an active site nucleophile that can be covalently modified by electrophiles and it is of no surprise that majority of reported activity based probes have been designed against these protease classes. Activity based probes for numerous cysteine and serine proteases are available but, so far, the proteasome is the only threonine protease to be profiled by ABPs. Probe design for proteases that do not form a

covalent intermediate with its substrate have proven to be much more challenging. Probes that target metalloproteses were reported just few years ago but ABPs that target aspartic proteases still remain elusive. In this part of the review we will outline the development and application of activity based proteomics for each of the various protease classes.

CYSTEINE PROTEASES

The main catalytical feature of cysteine proteases is the use of a Cys residue that is activated for nucleophilic attack by a nearby His residue. Cyteine proteases are further divided into six clans based on the structure of their active site. The two most abundant and intensively studied clans are the CA and CD clans. Clan CA includes papain and calpain families of cysteine proteases as well as various families of the ubiquitin processing peptidases. E-64 is a well known natural product inhibitor of this family of cysteine proteases and its structure and reactive epoxide were a logical choice for the use in the design of cysteine protease activity based probes [41]. The general epoxide probe DCG-04 has a wide specificity toward calpains and cysteine cathepsins and was used to determine their roles in various physiological and pathological processes. DCG-04 was used to identify m-calpain and the related Lp82 as the main active cysteine proteases present in the eye lens that mediate γ-crystalin cleavage during cataract formation [42]. Activity based labeling and affinity purification with DCG-04 was also used for identification of the papain-like protease cathepsin L as the prohormone processing enzyme responsible for cleaving proenkephalin [43]. This probe was also successfully used to identify cysteine proteases involved in host cell invasion by the parasite Plasmodium falciparum and in the proteomic identification of papain-like proteases in plants [44,45]. Papain-like cathepsins were also found to be involved in various stages of cancer progression. Fluorescent versions of DCG-04 were used to profile up-regulation of cathepsin activity in various stages of tumorigenesis in several mouse cancer models [46,47]

Mammalian deubiquitinating enzymes (DUBs) are another important group of clan CA cysteine proteases. Many of these enzymes act as oncogenes, tumor suppressors or have some other connection to cancer and therefore represent important target for drug development. The first DUB-specific activity based probes were designed based on a full length ubiquitin (Ub) derivatized at the C-terminus with a reactive vinyl sulfone. Fluorogenic substrates for DUBs such as Ub-7-amido-4-methyl coumarin (UbAMC) as well as DUB inhibitors Ub-aldehyde and Ub-nitrile were also developed [48–51]. Development of the irreversible DUB inhibitor UbVS (ubiquitin vinyl sulfone) represented an important advancement in the study of DUB function. UbVS binding is SDS resistant and also enables radioiodination with subsequent autoradiographic visualization of labeled enzymes [52]. However, this probe still lacks the ability to enrich and isolate targets for the purpose of proteomic identification. To achieve this goal an intein-based chemical ligation method was introduced. Here, an N-terminally epitope tagged ubiquitin derivative with a C-terminal electrophile was prepared by combination of recombinant protein expression and synthetic chemistry [53]. This probe allowed activity based profiling and proteomic identification of previously uncharacterized DUBs in complex biological samples [54]. In a more complex study, DUB activity was monitored in tumor cell lines and was found to be increased as a direct consequence of cell transformation [55]. Activity based probes have also been used for proteomic identification of DUBs in various pathogenic organisms such as herpes simplex virus, human cytomegalovirus, chlamydia, *Plasmodium falciparum* and *Escherichia coli* [56–59].

Clan CD is the second most abundant clan of cysteine proteases. Its members include caspases, gingipains, legumains, clostripains and separases. Caspases are of particular interest due to their crucial role in apoptosis and it is not surprising that they were targets of

the first generation of APBs for the CD clan. Caspase probes utilizing acyloxymethyl ketone (AOMK) and aldehyde reactive groups coupled to a specific peptide sequence and a biotin tag have been designed. In fact, the first caspase (caspase 1, β-interleukin converting enzyme- ICE) was identified using a biotinylated AOMK activity based probe [60]. Recently, a small molecule positional scanning library was used for the development of highly specific AOMK based probes for caspases 3, 7, 8 and 9. These probes could then be used for monitoring caspase activation kinetics upon stimulation of apoptosis in cell-free extracts and intact cells [61]. APBs were also designed for separases and legumain. Acyloxymethyl and chloromethyl ketone based probes were used to study the role of separase in cell division [62]. Legumain is thought to play a role in lysosomal protein degradation although its exact role still remains elusive. Legumain can participate in the processing of antigenic peptides and in generation of double chain forms of the papain-like cathepsins [63,64]. A highly specific set of AOMK based probes for legumain was recently developed that could provide key insight into its physiological role [65].

SERINE PROTEASES

Serine proteases are part of the larger serine hydrolase family which represents approximately 1% of all genes in the human genome. Besides proteases, the serine hydrolase family also includes numerous lipases, esterases, amidases and transacylases. All of them share the same catalytical mechanism which involves a serine nucleophile, that is activated by a proton relay involving an acidic residue (aspartate or glutamate) and basic residue (usually histidine). The majority of serine hydrolases are irreversibly inhibited by the fluorophosphonate (PF) reactive group. Thus probes containing PEG or aliphatic linkers and various tags attached to this warhead have been developed as broad specificity serine hydrolyase ABPs [66]. These probes have been used in a range of profiling experiments, most notably in studies of serine hydrolase biomarkers in cancer. Cravatt and coworkers used fluorescent PF-Rhodamine probes to profile serine hydrolase activities in a series of cancer cell lines [67]. Samples were labeled, analyzed by SDS-PAGE and the labeled protein profile was visualized by laser scanning. In a parallel experiment, a biotinylated version of the probe was used to directly isolate targets by affinity chromatography for identification by mass spectrometry. The identified serine hydrolase profiles were used to classify cancer cell lines into functional subtypes based on tissue of origin and state of invasiveness, thus demonstrating the diagnostic power of the probes for disease classification.

A similar approach was also used to profile hydrolases found in different stages of breast cancer [68]. Serine hydrolase specific probes (fluorophosphonate and sulfonate ester reactive groups) were used to study the differences in activity profiles of MDA-MB-231 human breast cancer cells, when grown in cell culture and after tumor formation in mouse mammary fat pads. These studies showed that cancer cells exhibited distinct activity profiles when grown in vitro (in culture) and in vivo (xenograft tumors). More than seven types of enzyme activities with unique activity profiles were identified. These findings suggest that studies using human cancer cell lines grown in culture may not be predictive of the behaviour of these same cells *in vivo*. It was also noted that many dramatic alterations in enzyme activities occurred as a result of posttranscriptional events, again confirming the value of activity based profiling methods.

This cancer profiling methodology was soon enhanced by incorporation of non-gel methods for proteomic analysis of labeled samples. A two-phase functional proteomic platform was reported, where in the first phase serine hydrolases were labeled by fluorogenic FP-probe and an activity profile was determined by 1D SDS-PAGE analysis. This stage required a minimal amount of sample and could be applied to a wide range of primary human

specimens. In the second phase, labeled targets were identified by multidimensional LC-MS/MS (MudPIT). Thus, the sensitivity and resolution of MudPIT was coupled to the high-content functional information obtained by activity based profiling. Using this approach, more than fifty enzyme activities were identified in breast tumor samples [69]. Comparison of activity based proteomics data with cDNA microarray analysis showed that for some enzymes, activity and mRNA levels were largely uncorrelated. This finding additionally emphasizes the importance of activity based proteomics, which can detect low abundance disease-associated enzymes, that might evade other molecular profiling methods. As an alternative to the FP probe, which shows broad reactivity with serine hydrolyases, the diphenylphosphonate warhead has been used to design serine protease specific probe. P1 basic amino acid probes were found to target only trypsin family serine proteases and proved valuable for the profiling of serine protease activity in the mast cells [70].

METALLOPROTEASES

Perhaps the most critical difference between metalloproteases and the serine and cysteine classes of proteases is that they do not use an aminoacid sidechain as a nucleophile for direct covalent attack on the substrate. Instead, they utilize a zinc ion in their active site to deprotonate a water molecule which then mediates hydrolysis of the peptide bond [71]. Since metalloproteases do not form acyl-enzyme intermediates they cannot be labeled using simple electrophiles fused to a peptide that mimics a protein substrate. To overcome this problem, probes containing a hydroxamate scaffold linked to a benzophenone crosslinking group have been developed [72]. The hydroxamate is a strong zinc chelating agent, which tightly binds in the protease active site. While this is a high affinity interaction, it is not irreversible and the benzophenone photocrosslinking group is required for the attachment of the probe to the protease active site. The main disadvantage of this type of ABPs is that they are not suitable for use in living cells and whole animals. Hydroxamate probes for metalloproteases were successfully applied in the search for diagnostic markers in an invasive melanoma cell line [72]. In this study, a trifunctional hydroxamate probe (with fluorescent and biotin tag) was used for detection, affinity isolation and identification of neprilysin. This metallo protease was also found to be highly upregulated in melanoma cell lines. Neprilysin is a membrane associated metalloprotease which is considered to be a negative regulator of tumorigenesis since it is known to degrade several mitogenic peptides [73]. The results reported with the metallo protease ABPs suggest that, in some tumor types, it may also promote cancer progression.

Actvity based probes usually only target a limited number of members within a specific enzyme class. This is problematic when trying to globally profile large and structurally diverse protease families such as metalloproteases. To overcome this problem, Cravatt and coworkers developed a profiling strategy using small libraries of structurally diverse photoreactive hydroxamate probes. By using libraries that were designed to have complementary metalloprotease selectivity it was possible to increase the overall coverage of the metalloproteases. The probes in the library were designed to be cell permeable by incorporating the alkyne group, so that a tag of choice (fluorophore or biotin) could be added after labeling using ‘’click” chemistry. Initial SDS-PAGE analysis enabled the selection of a ‘’cocktail” of optimal probes, that provided the greatest coverage of the family. This mixture of probes was used for more extensive ABPP-MudPIT analysis of cancer cell lines [74]. With this approach, the authors were able to identify over 20 metalloproteases in various human and mouse samples. Among the identified metalloproteases were members of all of the main branches of this enzyme family. Other examples of hydroxamate probes for matrix metalloproteases using ‘’click” chemistry have also been reported [75]. Metalloprotease probe libraries have also been created and used for

the rapid determination of metalloprotease inhibitor specificity fingerprints using a microarray approach [76,77].

THREONINE PROTEASES

So far the only threonine protease extensively studied using activity based proteomics is the proteasome. This multi-subunit complex is the central protease activity involved in ubiquitin mediated protein degradation. It degrades old and damaged proteins and fulfills several vital regulatory functions. The proteasome has six proteolytic sites in the central core particle that possess three distinct substrate specificities: chymotrypsin-like, trypsin-like and peptidyl-glutamyl peptide hydrolyzing [78]. The proteasome is a threonine protease since it uses the N-terminal threonine of the catalytic β-subunits as a nucleophile for the attack on the peptide bond. Although initially designed to target cysteine proteases, carboxy-terminal vinylsulfones have proven effective as irreversible inhibitors of active site N-terminal threonine and are now widely used as warheads for design of ABPs [30]. The first probes developed for characterization of catalytical proteasome β subunits made use of the vinylsulfone warheads coupled to a peptide that could be labeled with a radioisotope or biotin tag [79]. In addition, cell permeable proteasome probes have also been prepared by incorporation of azido linker (‘’click chemistry”) or hapten tag [80,81]. Finally, cell permeable fluorescent probes were recently developed for visualization of labeled proteasomes in living cells and animals [82,83]. The natural product epoxomicin was also found to be a highly selective, irreversible covalent inhibitor of the proteasome. This natural product contains a reactive a,b epoxyketone that forms a stable six member ring with the N-terminal threonine. A labeled version of this natural product was used as an ABP to identify the target as the proteasome [84]. Thus, this class of compounds is likely to find use as a highly specific ABP of the proteasome.

Expert Opinion and five-year view

The authors believe that the next five years will see a continued growth in the development and application of activity based probes for not only proteases but also for additional classes of important regulatory enzymes. The past five years has already seen a dramatic expansion in the diversity of enzyme families that can be studied using activity based proteomic methods. Creative work by chemists has lead to the development of probes for kinases, histone deacetylases, phosphatases and glycanases to name just a few [85–88]. The development of activity based probes that target diverse enzyme families has led to a range of applications for activity based proteomics. Probes can be applied to a large collection of complex biological samples and enable global profiling of enzyme activities. Comparison of enzyme activity profiles from healthy and disease samples can lead toward identification of novel biomarkers and drug targets. Important advantage of activity based probes is also in profiling of enzyme activities *in vivo*. Last year Blum and coworkers developed protease probes that enable monitoring of enzyme activities by whole body imaging. Furthermore, those probes also allow subsequent *ex vivo* identification and biochemical characterization of labeled targets [89]. Those results show that ABPs have a potential to become an important imaging tools used for disease diagnosis and for preclinical and clinical testing of therapeutic agents *in vivo*. ABP based *in vivo* assays significantly improve high throughput inhibitor screens needed for discovery of novel therapeutic agents. They enable screening of more than one target in a single experiment and because protein targets are screened in their native environment there is a better chance of detecting any unanticipated off-target inhibition or activation [90,91].

We can expect that the number and types of applications for ABPs will continue to expand. This rapidly growing field is likely to have a significant impact on a number of disciplines of research with proteomics being perhaps the most directly impacted. Besides profiling of

protease activities and target identification, chemical labeling has also become a powerful tool for proteomic identification of protease substrates. In this approach, complex proteomes are directly treated with specific proteases and newly formed N-terminal ends of cleaved substrates are chemically modified by biotinylated reagent. After affinity purification, substrates and their exact cleavage sites are identified by mass spectrometry [92]. Cleavage sites can also be quantitatively evaluated by incorporation of quantitative proteomic techniques such as iTRAQ [93,94]. Determination of whole complement of cellular protease substrates (degradome) remains one of the main challenges that field of proteolysis faces today.

As the quality of instrumentation improves and we are able to analyze more and more complex, biologically relevant samples, we anticipate that APBs will help to siphon off the most relevant and important information from these large data sets. This will require a wide-spread integration of the probes and continued efforts from chemist to develop probes with enhanced functionality. We are confident that the early developments in this field have created the necessary positive momentum to see these goals realized.

KEY ISSUES

- The main advantage of activity based proteomics is that it detects enzyme activity instead of abundance and therefore provides more accurate information about the biological roles of these enzymes in a given biological process.
- Activity based proteomics makes use of small molecules probes that are designed to target specific enzyme classes.
- Activity based probes are composed of a functional group (warhead), linker and tag, which enable specific labeling and enrichment of target proteins.
- Activity based probes for all the main protease classes of proteases (serine, cysteine, threonine and metalloproteases) have been successfully developed and are in use for global functional studies of proteases.

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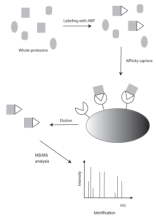

Figure 1. Workflow of activity based proteomics

Target proteins in the complex proteome are labeled with activity based probes. Labeled proteins are enriched by affinity purification and identified by mass spectrometry.

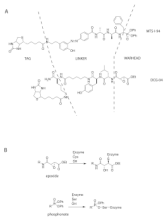

Figure 2. Structure and binding of activity based probes

A: Structural features of two types of activity based probes are shown. Probe MTS-I-94 targets serine proteases. It is composed of phosphonate warhead, a cleavable diazo linker and a biotin tag. DCG-04 is a cysteine protease probe with epoxide warhead.

B: Probes that target serine and cysteine proteases irreversibly and covalently bind to the active site nucleophile (serine or cysteine).

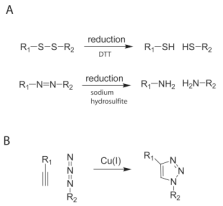

Figure 3. Cleavable and ‘’click” chemistry linkers

A: Reduction cleavage of disulfide and diazo cleavable linkers.

B: Mechanism of ‘’click” chemistry. Cycloaddition of an azide and alkyne functional group is used for the tag attachment after protein labeling.

Table 1

Types of reactive groups used for targeting of various protease classes.

Reactive group	Targeted protease class	References
phosphonate	serine proteases	6,67–70
sulfonate	serine proteases	68
vinyl sulphone	cysteine proteases threonine proteases (proteasome)	7,11,30,79
epoxide	cysteine proteases	10,41–47
diazomethyl ketone	cysteine proteases	5
acyloxymethyl ketone	cysteine proteases	9,89
hydroxamate	metalloproteases	13,72–77