Chemical Approaches for Functionally Probing the Proteome*S

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With the availability of complete genome sequences, emphasis has shifted toward the understanding of protein function. We have developed a functional proteomic methodology that makes use of chemically reactive fluorescent probes to profile and identify enzymes in complex mixtures by virtue of their catalytic activity. This methodology allows a comparison of changes in activity of multiple enzymes under a variety of conditions using a single two-dimensional separation. The probes can also be used to localize active enzymes in intact cells using fluorescence microscopy. Furthermore, the probes enable screens for selective small molecule inhibitors of each enzyme family member within crude lysates or intact cells. Ultimately, this technology allows the rapid identification of potential drug targets and small molecule lead compounds targeted to them. Molecular & Cellular Proteomics 1:60–68, 2002.

Over the past few years the complete genome sequences of multiple organisms have been determined. These efforts have been followed by the annotation of genes that code for all proteins of a given proteome. Although this information is likely to prove valuable, a great deal of effort is still required to define the function of individual gene products. Informatics techniques have been developed to assign function to individual genes by analyzing patterns of co-inheritance throughout multiple organisms (1, 2). Furthermore, analysis of genome-wide changes in transcription in response to different stimuli allows clustering of genes of similar function based on transcriptional co-regulation (3). Although these methods help to broadly classify proteins into families, the assignment of functions to specific members within a large enzyme family remains a difficult task.

Proteomic approaches address some of the gaps in genomic methodologies by profiling and identifying bulk changes in protein levels (4, 5). However, these methodologies only provide information for abundant proteins, and proteins with difficult biochemical properties (i.e. membrane proteins) are often excluded from analysis. Moreover, for most enzymes, their activity, and therefore their function, is regulated by a complex set of post-translational controls. Therefore, even proteomic profiles in many cases provide an incomplete picture of how enzymes are functionally regulated (6).

Classical genetic approaches are tried and true methods to assign functions to specific gene products. In many biological systems it is possible to disrupt a desired gene and assess the resulting phenotype. However, this process is often tedious, and in cases where multiple related proteins have similar functions, compensation adjustments make the results difficult to interpret.

To circumvent these problems, small molecules can be used to manipulate the activity of protein targets (7, 8). This “chemical genetic” approach makes use of libraries of small molecules to screen for compounds that perturb a given biological process. The resulting “hits” can then be used to begin to assign function to specific enzyme or protein targets. However, the utility of this process is limited by the difficult task of identifying the relevant target of the small molecule.

In the case of traditional drug discovery, small molecule libraries are screened against a single pre-defined target. Lead compounds are often identified from large chemical libraries using an in vitro assay. Although many of these compounds are effective against the purified target, little is usually known about their selectivity in a crude proteome. Therefore, a method that allows screening for small molecule inhibitors in cell and tissue extracts or intact cells would allow identification of lead compounds based on multiple criteria such as potency, selectivity, and cell permeability. Furthermore, compounds could be screened against entire enzyme families thereby increasing the chances of identifying useful compounds for therapeutic intervention.

We have developed chemically reactive affinity probes that can be used to (i) identify the members of a given enzyme family within a proteome, (ii) determine the relative activity levels of individual family members, (iii) localize active enzymes within a cell, and (iv) screen small molecule libraries directly in crude protein extracts for inhibitors that can ultimately be used to determine biological functions of specific target enzymes. In this study, we have chosen to focus on the
papain family of cysteine proteases for several reasons. First, these proteases are synthesized as inactivezymogens that are activated post-translationally (9, 10). Their activity can also be regulated by interaction with macromolecular inhibitors resulting in transcription/translational profiles that provide only limited information regarding their functional regulation. Second, the papain family is composed of many closely related family members whose functions are poorly defined (11). Third, many small molecule covalent inhibitors of this class of enzyme have been developed that can be used for probe design (see Ref. 12). Finally, these enzymes have been found to play an important role in many disease conditions such as cancer (13), osteoporosis (14), asthma (11), and rheumatoid arthritis (15) making them a potential important class of enzymes for drug development.

MATERIALS AND METHODS

All chemicals used in the synthesis of the peptide epoxides were purchased from Advanced Chemtech (Louisville, KY) and Sigma-Aldrich Chemical Co. (St. Louis, MO). Purified human liver cathepsin B and H and purified turkey liver cathepsin C were purchased from Calbiochem (San Diego, CA). Purified recombinant human cathepsins K, F, and V were a kind gift of Dieter Brömmke (Mt. Sinai School of Medicine, New York, NY). Purified recombinant human cathepsin L was a kind gift of Vito Turk (Jožef Stefan Institute, Ljubljana, Slovenia).

Synthesis Protocols

Synthesis of Ethyl (2S,3S)-oxirane-2,3-dicarboxylate and Ethyl (2R,3R)-oxirane-2,3-dicarboxylate and DCG-04—The synthesis of (2R,3R)-oxirane-2,3-dicarboxylate is identical to that reported for the (2S,3S) isomer (18). The synthesis of DCG-04 is reported elsewhere (19).

Synthesis of BODIPY558/568-DCG-04, BODIPY588/616-DCG-04, BODIPY530/550-DCG-04, and BODIPY493/503-DCG-04—All fluorophores where purchased from Molecular Probes (Eugene, OR). A free amino version of DCG-04 was synthesized by replacing the terminal biotinylated lysine with lysine using the reported synthesis protocols for DCG-04 (19). Free amino DCG-04 (6 mg, 8.8 μmol, 1.5 eq) and BODIPY558/566-OSu1 (3.0 mg, 6.0 μmol, 1.0 eq) were dissolved in 100 μl of Me2SO. Diisopropylamine was added to samples to a final concentration of 10 mM DTT, 5 mM MgCl2, 250 mM sucrose), and extracts were centrifuged at 22,000 g for 30 min at 4 °C. Cells were homogenized using glass beads in Buffer A, and supernatants were centrifuged at 22,000 g for 10 min at 4 °C. Tissues were Dounce-homogenized in Buffer B (50 mM Tris, pH 5.5, 1 mM DTT, 5 mM MgCl2, 250 mM sucrose), and extracts were centrifuged at 11,000 × g for 10 min at 4 °C, and the supernatant was centrifuged at 22,000 × g for 30 min at 4 °C. Cells were homogenized using glass beads in Buffer A, and supernatants were centrifuged for 15,000 × g for 15 min at 4 °C. The total protein concentration of the final supernatants (soluble) was determined by BCA protein quantification (Pierce).

Radiolabeling of Inhibitors

All compounds were iodinated and isolated using the protocol reported previously (18).

Preparation of Cell and Tissue Lysates

Tissues were homogenized in Buffer A (50 mM Tris, pH 5.5, 1 mM DTT, 5 mM MgCl2, 250 mM sucrose), and extracts were centrifuged at 11,000 × g for 10 min at 4 °C, and the supernatant was centrifuged at 22,000 × g for 30 min at 4 °C. Cells were homogenized using glass beads in Buffer A, and supernatants were centrifuged at 15,000 × g for 15 min at 4 °C. The total protein concentration of the final supernatants (soluble) was determined by BCA protein quantification (Pierce).

Labeling of Lysates and Purified Cathepsins with DCG-04, 125I-DCG-04, 125I-MB-074, 125I-YQ-(R,R)Eps, Yellow-DCG-04, Blue-DCG-04, Green-DCG-04, or Red-DCG-04

Lysates (100 μg of total protein in 100 μl of Buffer B (50 mM Tris, pH 5.5, 5 mM MgCl2, 2 mM DTT)) or purified cathepsins (0.1 μg in Buffer B) were labeled for 1 h at 25 °C unless noted otherwise. DCG-04 was added to a final concentration of 10 μM. Equivalent amounts of all radioactive inhibitor stock solutions (approximately 106 cpm per sample) were used for all labeling experiments. Fluorescent compounds were added to samples to a final concentration of 0.1 μM. Samples were quenched by addition of 4× SDS sample buffer (for one-dimensional SDS-PAGE) or by addition of solid urea to a final concentration of 9.5 M (for 2D SDS-PAGE). Fluorescent samples were analyzed using an ABI 377 DNA sequencer. Standard 15% SDS-PAGE gels of 0.4-mm thickness were prepared using 15-cm plates provided by the

Chem; Robbins Scientific). Each library was constructed using a constant amino acid at the P2 position and an isokinetic mixture of all natural amino acids (minus cysteine and methionine plus norleucine) at the variable position. The isokinetic mixture was created using a ratio of equivalents of amino acids based on their reported coupling rates (24). The total mixture was adjusted to 10-fold excess total amino acids over resin load. For constant positions, a single amino acid was coupled using 10-fold excess. In addition to the natural amino acids, a set of 42 non-natural hydrophobic amino acids were used for the constant P2 position (see Table I in Supplemental Material). Couplings were carried out using disopropylcarbodiimide and hydroxybenzotriazole under standard conditions for solid phase peptide synthesis. Libraries and single components were cleaved from the resin by addition of 90% trifluoroacetic acid, 5% water, 5% triisopropylamine for 2 h. Cleavage solutions were collected, and products were precipitated by addition of cold diethyl ether. Solid products were isolated, and the crude peptides were dissolved in Me2SO (50 μM stock) based on average weights for each mixture. Libraries and single compounds were stored at −20 °C and further diluted to 10 μM stock plates for use in experiments.

Synthesis of YQ-(R,R)Eps and YG-(R,R)Eps—All single component peptide epoxides were synthesized on the solid support using the protocols reported for DCG-04 (19). The inhibitors were cleaved from the resin by addition of 90% trifluoroacetic acid, 5% water, 5% triisopropylamine for 2 h. Ice-cold ether (15 ml) was used to precipitate the products. The crude products were purified on a C18 reverse phase HPLC column (Waters) using a linear gradient of 0–100% water-acetonitrile. Fractions containing the product were pooled, frozen, and lyophilized to dryness. The identity of the product was confirmed by mass spectrometry. The electrospray mass spectrum was as follows: [M + H] calculated for YG-(R,R)Eps C17H21N3O7 380.1, found 380.1; YQ-(R,R)Eps C20H26N4O8 451.2, found 451.2.

The abbreviations used are: OSu, O-succinimide ester; ABP, activity-based probe; CD, collision-induced dissociation; E-64, trans-Epoxyysuccinyl-L-leucylamido(4-guanidino)butane; HPLC, high pressure liquid chromatography; IF, isoelectric focusing, MS, mass spectrometry; PSL, positional scanning library; DTT, dithiothreitol; 2D, two-dimensional.
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manufacturer. Samples were loaded and electrophoresed for 3–4 h at a constant current of 55 mA with voltage limited to 750 V. Gel images were created using the Gene Scan software provided by the manufacturer. In some experiments, fluorescent samples were analyzed by standard SDS-PAGE followed by scanning with a Molecular Dynamics Typhoon laser scanner.

In Situ Fluorescence Labeling

Dendritic cells (DC2.4) were plated on a 24-well dish (10⁵ cells/well) embedded with sterile microscope coverslips, in RPMI medium containing 10% fetal bovine serum. After 16 h, cells were washed with 1 ml of TC-199 medium and incubated with 1 μM Green-DCG-04 in TC-199 for 12 h at 37°C. Cells were washed three times with 1 ml of TC-199 and incubated for 5 h in probe-free medium. Subsequently, cells were either lysed in Buffer A and analyzed on a 12.5% SDS-PAGE using a fluorescent scanner or viewed under a fluorescent microscope.

Gel Electrophoresis

One-dimensional SDS-PAGE and two-dimensional IEF were performed as described (25).

Competition Labeling and Analysis of Data

Rat liver lysates (100 μg of total protein in 100 μl of Buffer B (50 mM Tris, pH 5.5, 5 mM MgCl₂, 2 mM DTT)) or purified cathepsins (1 μg of protein in 100 μl of Buffer A) were pre-incubated with 10 μM of each library member (diluted from 10 mM Me₂SO stocks) for 30 min at room temperature. Samples were then labeled by addition of 125-I-DCG-04 to each sample followed by further incubation at room temperature for 1 h. Samples were quenched by the addition of 4X sample buffer, resolved by SDS-PAGE, and analyzed by phosphorimaging (Molecular Dynamics). Bands corresponding to each labeled protease were quantitated. Inhibitor-treated samples were compared with an untreated control sample. Numerical values for percent competition were analyzed as described previously (26) using the programs Tree View and Cluster written by Eisen and co-workers (3). These programs can be obtained from www.microarrays.org.

Purification and Identification of Affinity-labeled Proteases from Rat Liver

Protein lysates prepared in Buffer C (50 mM Acetate buffer, 5 mM DTT, 0.1% Triton X-100) were incubated with 5 μM DCG-04 for 1.5 h at room temperature. After incubation the protein lysate was passed through a PD10 column pre-equilibrated with Buffer D (50 mM Tris, pH 5.5, 5 mM MgCl₂, 2 mM DTT) or purified cathepsins (1 μg of protein in 100 μl of Buffer A) and incubated for 5 min at a flow rate of −250 nI/min. Mass spectrometry detection was performed on a QSTAR quadrupole orthogonal acceleration-time-of-flight tandem mass spectrometer (Applied Biosystems/MDS Sciex, Foster City, CA) in information-dependent acquisition mode; 2-s survey acquisitions were followed by 5-s CID acquisitions, in which the most abundant ion of each survey scan was selected as the precursor. All the singly charged ions, as well as some trypsin autolysis products, were excluded from the precursor ion selection. The collision energy was optimized and adjusted automatically depending on the charge state and the m/z value of the precursor ions selected. The mass range recorded in survey acquisitions was m/z 300–1400. For CID experiments the lower mass limit was changed to m/z 60. All the data were measured using a two-point external calibration. The instrument affords ~8000 resolution and 30 ppm mass accuracy with external calibration in both MS and CID mode. Proteins were identified automatically by Mascot database search using the MS/MS data (Matrix Science Ltd., London, UK).

RESULTS AND DISCUSSION

Probe Design and Application to Crude Homogenates and Intact Cells—Several laboratories have developed small molecule electrophiles that show class-specific reactivity toward nucleophilic active site residues of several different enzyme families. These include serine (16, 17) and cysteine (18–20) hydrolases, as well as aldehyde dehydrogenases (21). In each case, electrophiles have been designed that exhibit broad irreversible reactivity for enzyme family members, while remaining relatively inert toward free-circulating nucleophiles such as thiols, hydroxyls, and amines. The resulting activity-based probes (ABPs) can be used to covalently label specific target enzymes within the complex mixture of proteins from a cell or tissue sample. Our laboratory has developed probes based on the structure of the general cysteine protease inhibitor trans-epoxysuccinyl-L-leucylamido(4-guanidino)butane (E-64) (19). These ABPs can be used to affinity-label papain family cysteine proteases. They also allow rapid purification of labeled proteases by incorporation of a biotin affinity tag. Here we have used the core peptide epoxide analog of E-64 to create four fluorescently labeled ABPs for papain family cysteine proteases (Fig. 1).

These probes incorporate four different fluorescent moieties, each with non-overlapping excitation and emission spectra, allowing for multiplexing of probes. Four BODIPY analogs were chosen based on the excitation and emission wavelengths of fluorophores commonly used in DNA sequencing protocols. We reasoned that it should be possible to visualize and quantify fluorescently labeled proteins using a standard DNA sequencing apparatus equipped with a high intensity laser. Fig. 2A shows the gel image that results from incubation of eight different purified or recombinant papain family cysteine proteases with each of the four fluorescent ABPs followed by analysis on an ABI 377 DNA sequencer (see “Materials and Methods”). Using these probes, it is possible to load all eight proteases in a single gel lane and distinguish each, based on differences in molecular weight and emission
wavelength of fluorescent labels. The same four probes were next used to profile the repertoire of papain family proteases within a complex protein mixture derived from a tissue homogenate. Fig. 2B shows the profiles of cysteine proteases in total rat liver homogenates obtained by labeling with the biotinylated probe DCG-04, the radiolabeled version of DCG-04, and the four fluorescent analogs of DCG-04. All ABPs labeled the same four predominant protease (bands 1–4) species with only slight differences in relative intensities observed for each probe. These results suggest that the presence of structurally diverse labeling groups at the distal affinity site of the molecules had little effect on the ability of a compound to covalently modify its targets.

Because covalent modification of target proteases by the ABPs requires modification of the active site thiol nucleophile, labeling intensities can be used as an indirect measure of enzymatic activity. Thus, unlike antibodies that can only be used to monitor bulk levels of specific proteins, these reagents allow analysis of changes in levels of enzymatic activity. In the past, our laboratory has used these reagents to follow activity of cysteine proteases during processes such as tumor progression/cell invasion and cataract formation (18, 22). These newly developed ABPs therefore provide an efficient method for monitoring changes in protease activities within a proteome.

Because the fluorescent probes are cell-permeable they make ideal tools for imaging of protease activity in intact cells or tissue sections. Fig. 3 shows the dendritic cell line DC2.4 either directly labeled in situ with Green-DCG-04 or pre-treated with E-64 and then labeled with the fluorescent probe. Cells directly treated with the green ABP showed a fluorescence staining pattern characteristic of lysosomal compartments. Cells that had been pre-treated with E-64 showed

**Fig. 1.** Structures of the fluorescent ABPs DCG-04, Yellow-DCG-04, Red-DCG-04, Green-DCG-04, and Blue-DCG-04.

**Fig. 2.** Affinity labeling of papain family proteases using fluorescent ABPs. A, purified cathepsins (as indicated) were diluted into pH 5.5 buffer and labeled with 100 nM Yellow-DCG-04, Red-DCG-04, Green-DCG-04, or Blue-DCG-04 for 1 h. Samples were separated on a 15% SDS-PAGE gel, and labeled bands were visualized using an ABI 377 DNA sequencer as described under “Materials and Methods.” B, total cell extracts from rat liver were diluted into pH 5.5 buffer and labeled with 10 μCi DCG-04, 125I-DCG-04 (approximately 1 × 10⁶ cpm), or 100 nM Red-, Blue-, Green-, and Yellow-DCG-04. Samples were separated on a 15% SDS-PAGE gel, and labeled bands were visualized (as indicated at bottom) by affinity blotting or autoradiography or using a Molecular Dynamics Typhoon laser fluorescence scanner.
diffuse fluorescence throughout the cytosol, likely because of residual free probe that failed to be washed away. The cells were collected after imaging, lysed, and analyzed by SDS-PAGE and fluorescence detection. The resulting profiles indicated that multiple protease species were labeled by the fluorescent probe and that these proteases were completely inhibited by pre-treatment of cells with E-64. Thus the fluorescent staining observed in the non-pretreated cells represents the localization of active papain family cysteine proteases. This method is likely to be applicable to tissue samples and may serve as a convenient way to image protease activities in tissues derived from important clinical samples such as solid tumors.

Using ABPs to Screen for Selective Inhibitors of Papain Family Cysteine Proteases in Crude Tissue Extracts—Perhaps the most powerful attribute of ABPs is their ability to facilitate screening of small molecule inhibitors against complete enzyme families without the need to first identify, clone, and express individual targets. Furthermore, the data that is obtained from the screening process provides information not only regarding potency of the potential lead compounds but also regarding selectivity of the compounds in a physiologically relevant sample that contains many closely related family members.

To demonstrate the utility of this approach a series of small molecule inhibitor libraries were designed based on a core peptide backbone coupled to the epoxide electrophile contained in the DCG-04 probes (Fig. 4A). Initially, PSLs were synthesized in which a single amino acid position was scanned through a series of natural and non-natural amino acids, whereas the remaining two positions were coupled with a mixture of all possible natural amino acids (minus cysteine and methionine and including norleucine). The resulting sub-libraries were composed of 361 members each. Scanning of constant amino acids at the P3 and P4 positions through all natural amino acids indicated that these elements did not significantly contribute to selectivity of inhibitor binding to protease targets (data not shown). Therefore, only data compiled for scanning of the constant P2 position are presented.

To increase the diversity of the small molecules in the PSLs we included 42 hydrophobic non-natural amino acids as building blocks (see Table I in Supplemental Material). In addition, each of the natural amino acids was coupled to the mirror-image enantiomeric form of the epoxide (2R, 3R versus 2S, 3S). Previous work indicates that this change in stereochemistry favors binding of the inhibitors on the prime side of the active site resulting in more diversity in our libraries (23).

PSLs were first screened against the primary protease targets of DCG-04 in rat liver homogenates (bands 1–4 from Fig. 2B; see Fig. 4B). Potency was assessed by pretreatment of total cell extracts with each library followed by labeling with 125I-DCG-04 and analysis by SDS-PAGE and autoradiography. The ability of each library to block active site labeling by DCG-04 was measured as a percentage competition relative to an untreated control. The resulting values were visualized using software developed by Eisen and co-workers (3) designed to analyze data generated from microarray analysis. This software assigns a color to numerical competition values and allows clustering of profiles based on similarities across diversity positions (x axis) and enzyme family members (y axis). The resulting “clustergram” is shown in Fig. 4B.

Clustering data throughout the constant amino acid resi-
dues grouped the data such that residues that showed overall poor binding to all targets were positioned to the right, and residues that showed universal strong binding were positioned to the left. The remaining residues in the middle of the clustergram showed some degree of selectivity for individual enzymes. The results from the clustering indicate that the non-natural amino acids and natural amino acids linked to the (R, R) enantiomer of the epoxide provided the greatest target selectivity. Specificity profiles for each of the major protease species labeled by DCG-04 also identified several residues that clustered to the center of the profile that confer unique specificity for an individual protease species in the extract. Therefore, this method yielded interesting lead compounds using a relatively small number of libraries (~80) with limited structural diversity. A similar screen of a larger, more structurally diverse small molecule library is likely to provide a greater number of inhibitor leads. Given the relative ease of screening and the abundance of the protein extracts, such a large-scale screen is clearly accessible using this methodology.

Profiling Changes in Protease Activities upon Addition of Selective Small Molecule Inhibitors—Analysis of the library data from screening of liver extracts indicated that several PSls showed selective binding to a single protease. We chose to focus on the constant P2 glutamine (R, R) epoxide library because of its high degree of selectivity for protease 2 in the extract. Liver extracts were either directly labeled with the Red-DCG-04 probe or treated with the library and then labeled with the Blue-DCG-04 probe. The samples were then combined and subjected to a first dimension of isoelectric focusing followed by analysis by SDS-PAGE in the second dimension using the DNA sequencer (Fig. 5A). This method allowed analysis of multiple channels of data in a single gel that could be merged to determine changes in activity of each protease species in the presence of the inhibitor library. The resulting 2D profile unambiguously demonstrated that the glutamine (R, R) library specifically binds to the active site of a single protease (spot 2) as indicated by loss of labeling in the blue channel.

To determine the identity of the protease selectively targeted by the small molecule library, we used the biotin-tagged DCG-04 to perform a single-step affinity purification of all labeled proteases from liver extracts. The resulting silver-
stained 2D profile shows that all fluorescently labeled protease could be rapidly purified from the crude extract and correlated with the labeling profiles (Fig. 5B). The silver-stained spot corresponding to band 2 was excised and identified as cathepsin B by liquid chromatography-MS-time-of-flight CID sequencing (Fig. 6). Furthermore, several other cathepsin family members including cathepsins Z, H, C, and J were identified by this method.

**Design of Selective Inhibitors Based on Library Screening Data**—Using information from the scanning of our PSLs, we synthesized several individual compounds designed to validate the library approach. In all cases a P3 tyrosine was included as a site for radioiodination, and the P2 residue was chosen based on target selectivity. P2 glutamine attached to the (R, R) epoxide inhibitor (YQ-(R, R)-Eps) was chosen because of its selectivity for cathepsin B in the extract, and P2 glycine was chosen as a negative control. The cathepsin B-specific ABP MB-074 (18) was used as a control for comparison with YQ-(R, R)-Eps. Compounds were added to extracts over a wide concentration range, and activity for each target was assessed by labeling with 125I-DCG-04 (Fig. 7A). As expected, YQ-(R, R)-Eps and MB-074 selectively blocked labeling of the cathepsin B band (number 2) whereas YG-(R, R)-Eps showed little or no inhibition of all of the proteases.

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The newly developed cathepsin B inhibitor was also radiiodinated and used to label liver homogenates (Fig. 7B). The labeling profile was compared with the profiles for the cathepsin B-specific probe \(^{125}\text{I}-\text{MB-074}\) and the generally reactive probe \(^{125}\text{I}-\text{DCG-04}\). YQ-(R, R)-Eps, like MB-074, showed selective labeling of the band identified as cathepsin B.

We conclude that it is possible to rapidly identify a structurally distinct class of cathepsin B-selective inhibitors by screening of libraries of limited complexity. The resulting lead compound, although not excessively potent, now serves as a template for the design of optimized inhibitors that are distinct from the CA-074 class of cell-impermeable cathepsin B inhibitors. No doubt this approach could also be used to selectively target other cathepsin family members through a more extensive library screening effort.

In summary, we have developed tools to identify families of related enzymes within a complex proteome. These tools can be used to determine relative activity levels of these enzymes and to visualize their localization in live cells. These tools also allow rapid design and screening of small molecule inhibitors for select targets. In the current study we successfully identified a new cathepsin B-selective inhibitor by screening of a small set of libraries in crude liver extracts. Furthermore, we have developed a general method for rapid analysis of large data sets generated from library screening of multiple targets in crude cell extracts. This approach allows rapid comparison of inhibitors, as well as targets based on similarities in structure-function relationships. This general functional proteomic method, although applied here to papain family proteases, can also be used for a wide range of enzyme families through design and synthesis of new families of class-specific affinity probes.

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