

Global Sequencing of Proteolytic Cleavage Sites in Apoptosis by Specific Labeling of Protein N Termini

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SUMMARY

The nearly 600 proteases in the human genome regulate a diversity of biological processes, including programmed cell death. Comprehensive characterization of protease signaling in complex biological samples is limited by available proteomic methods. We have developed a general approach for global identification of proteolytic cleavage sites using an engineered enzyme to selectively biotinylate free protein N termini for positive enrichment of corresponding N-terminal peptides. Using this method to study apoptosis, we have sequenced 333 caspase-like cleavage sites distributed among 292 protein substrates. These sites are generally not predicted by *in vitro* caspase substrate specificity but can be used to predict other physiological caspase cleavage sites. Structural bioinformatic studies show that caspase cleavage sites often appear in surface-accessible loops and even occasionally in helical regions. Strikingly, we also find that a disproportionate number of caspase substrates physically interact, suggesting that these dimeric proteases target protein complexes and networks to elicit apoptosis.

INTRODUCTION

Apoptosis is a noninflammatory form of cell death that regulates tissue differentiation and homeostasis in higher eukaryotes (for a review, see Taylor et al., 2008). Since apoptotic turnover of cells lies in direct opposition to the uncontrolled growth of tumor cells, a strong link exists between apoptosis and cancer. Indeed, the terminal cellular effect of most chemotherapeutic compounds is induction of apoptosis (Kaufmann and Earnshaw, 2000). The widespread intracellular proteolysis that is a hallmark of apoptosis is predominantly mediated by a family of dimeric aspartate-specific proteases termed caspases. Apoptosis can be induced by extracellular death ligands, such as Fas ligand,

TNF- α , or TRAIL, via the extrinsic pathway to activate caspase-8. It can also be induced by agents such as cytotoxic compounds, radiation, and other environmental stresses via the intrinsic pathway with release of proapoptotic factors from mitochondria to activate caspase-9. Initiator caspases-8 and -9 in turn activate executioner caspases, among them caspases-3 and -7. Caspases then catalyze a multitude of proteolytic events to inactivate prosurvival and/or antiapoptotic proteins and activate antisurvival and/or proapoptotic proteins. This proteolysis results in apoptotic cell death and clearance of apoptotic bodies by phagocytes.

Because the study of apoptotic pathways has ramifications for development of therapies for treatment of cancer, there is significant interest in gaining a better understanding of caspase activity during apoptosis. For example, identification of new targets of proteolysis in apoptosis can lead to the discovery of prosurvival and/or antiapoptotic factors, which can lead to identification of chemotherapeutic targets. Over 300 publications describing a wide variety of cell types and apoptotic inducers have reported the proteolysis of approximately 360 human proteins in apoptosis (Lüthi and Martin, 2007). Adding to this complexity, the nature of the apoptotic response varies widely in a cell-dependent and stimulus-dependent manner that cannot be easily predicted (Fulda et al., 2001; Stepczynska et al., 2001; Wiegand et al., 2001). Thus, combined data sets of caspase substrates from studies using varied inducers and cell types have limited use for understanding how a single inducer can cause apoptosis in a particular cell type.

We have developed an enzymatic approach for global profiling of proteolysis and sequencing of cleavage sites in complex mixtures that is based on positive selection of protein fragments containing unblocked α -amines, characteristically produced in proteolysis. This positive selection is enabled by use of an engineered peptide ligase termed subtiligase to selectively biotinylate unblocked protein α -amines with absolute selectivity over ϵ -amines of lysine side chains. We have used this method to sequence 333 cleavage sites in 292 different protein substrates targeted by caspase-like proteolysis in Jurkat cells after intrinsic induction of apoptosis with the classic chemotherapeutic etoposide. In profiling the proteolysis that is induced by a single

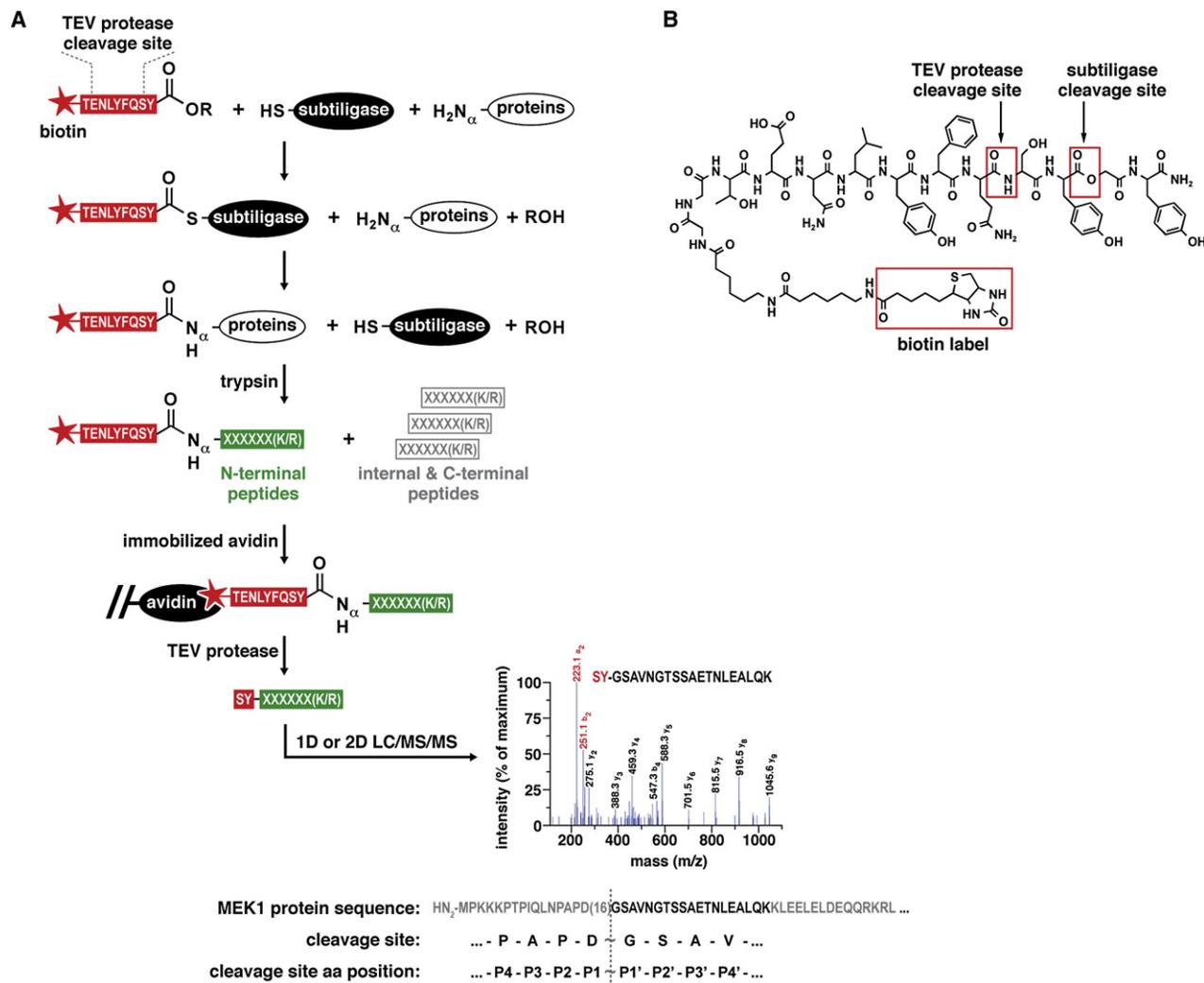


Figure 1. A Subtiligase-Based Method for Positive Selection of Peptides Corresponding to N Termini of Proteins from Complex Mixtures

(A) Workflow for biotinylation of protein N termini in complex mixtures using subtiligase and a biotinylated peptide ester that contains a TEV protease cleavage site, trypsinization of labeled proteins, capture of biotinylated N-terminal peptides with immobilized avidin, recovery of captured peptides with TEV protease, and analysis of N-terminal peptides by 1D or 2D LC/MS/MS for identification of corresponding proteins and cleavage sites. The representative MS/MS spectrum corresponds to semitryptic peptide GSAVNGTSSAETNLEALQK from MEK1 (MP2K1_HUMAN) and identifies a previously unknown caspase-like cleavage site at Asp 16. The a_2 and b_2 ions at m/z 223 and 251 are characteristic hallmarks of a ligated, SY-bearing, N-terminal peptide.

(B) Structure of the biotinylated peptide glycolate ester used in the proteomic workflow.

agent in a single cell line, this work reveals the vastness of caspase-like proteolysis that takes place during apoptosis, sheds light on determinants of specificity for this activity in a cellular context, and demonstrates the utility of a powerful degradomic technology to study proteolysis in biological samples.

RESULTS

A Degradomic Technology for Positive Selection of Protease Substrates

Direct and selective labeling of protein α -amines or α -carboxylates is a powerful approach for profiling proteolysis in complex mixtures since it permits direct identification of cleavage sites in protein substrates. Approximately 80% of mammalian pro-

teins are known to be N-terminally acetylated (Brown and Roberts, 1976). Thus, greater signal over background can be achieved through N-terminal instead of C-terminal labeling. However, such labeling must still be extremely selective for α -amines over lysine ϵ -amines, which are approximately 25 times more abundant in an average protein. To achieve this selectivity, we have adopted an enzymological approach that makes use of the rationally designed protein ligase subtiligase. This engineered enzyme exhibits absolute selectivity for modification of α -amines (Abrahmsén et al., 1991; Chang et al., 1994).

We have developed a proteomic method utilizing subtiligase that enables capture and sequencing of N-terminal peptides found in complex biochemical mixtures (Figure 1A). Proteins in biological samples are N-terminally biotinylated by treatment

with subtiligase and a peptide glycolate ester substrate specially tailored to our proteomic workflow (Figure 1B). Biotinylated samples are exhaustively digested with trypsin, and N-terminal peptides are captured with avidin affinity media. The peptide ester substrate contains a tobacco etch virus (TEV) protease cleavage site to permit facile recovery of captured peptides. An important aspect of our workflow is that recovered peptides retain an N-terminal SY-dipeptide modification, providing a key hallmark to distinguish labeled peptides from contaminating unlabeled peptides with tandem mass spectrometry (LC/MS/MS). In standard protease nomenclature, substrates are cleaved between the P1 (N-terminal) and P1' (C-terminal) residues, with P_n and P_n' residues increasing in count by one in both directions away from the scissile bond (Schechter and Berger, 1968). Thus, the P_n' residues of a cleavage site correspond to N-terminal residues of the labeled peptide identified, whereas the P_n residues of a cleavage site can be inferred from the protein sequence preceding the identified peptide.

As a validation of this method, we analyzed endogenous N termini in nonapoptotic Jurkat cells in two small-scale experiments using one-dimensional reversed-phase (1D) LC/MS/MS and two large-scale experiments using two-dimensional strong cation exchange/reversed-phase (2D) LC/MS/MS (summarized in Tables S1 and S2 available online). Comparison of data obtained in both types of experiments is informative since 1D LC/MS/MS typically results in identification of abundant N termini, whereas the increased proteomic coverage afforded by 2D LC/MS/MS results in additional identification of lower-abundance N termini. Of the combined 131 unique N termini identified in small-scale experiments, 72% are either annotated in Swiss-Prot as native protein N termini or correspond to cleavages within the first 50 residues of proteins, as would be expected for N-terminal signal or transit peptide processing (Figure S1A). The remaining 28% correspond to cleavages outside of the first 50 residues, arising from additional processing or constitutive protein degradation. In support of this notion, 51% of the combined 661 unique N termini identified in large-scale experiments correspond to cleavages outside of the first 50 residues (Figure S1A). The increased frequency of such N termini in large-scale experiments is consistent with the expected lower abundance for products of constitutive protein degradation.

Degradomic Analysis of Apoptotic Jurkat Cells

For analysis of apoptosis in Jurkat cells, we conducted several small-scale (1D) and large-scale (2D) LC/MS/MS experiments (representatives are summarized in Tables S3 and S4) with cells treated with the topoisomerase II poison etoposide. The experiments with untreated cells described above serve as respective controls for the small- and large-scale experiments with apoptotic cells, in which a combined 244 and 733 unique N termini, respectively, were identified. Combined data sets of all N-terminal peptides identified in untreated and apoptotic Jurkat cells, respectively, are included as supplemental data (Tables S5 and S6). Caspases are known to exhibit strict substrate specificity for aspartate at P1, and for glycine > serine > alanine at P1' (Schilling and Overall, 2008; Stennicke et al., 2000). In small-scale experiments, 43% of N termini identified in apoptotic cells were derived from P1 aspartate cleavages, in contrast to less

than 1% in untreated cells (Figure 2A). In large-scale experiments, 43% of N termini identified in apoptotic cells were derived from P1 aspartate cleavages, in contrast to 3% in untreated cells (Figure 2B). An increased frequency of glycine at the first position of N termini is also observed in apoptotic cells relative to untreated cells at both experimental scales (Figures 2A and 2B). The N termini uniquely identified in apoptotic Jurkat cells are thus consistent with induction of caspase-like activity.

Of the 3% P1 aspartate N termini detected in large-scale experiments with untreated cells (Figure 2B), 55% correspond to reported caspase substrates (Lüthi and Martin, 2007). Thus, it is likely that these originate from the small number of apoptotic cells typically present in untreated cultures. The detection of 3% P1 aspartate N termini in large-scale experiments with untreated cells and less than 1% in small-scale experiments is consistent with the low abundance of such N termini in cultures of normal cells. Additionally, if one considers that N termini annotated in Swiss-Prot are representative of native N termini in healthy cells, it is notable that less than 1% are derived from proteolytic processing after an aspartate residue (Figure S2). In apoptotic samples, we find that the increased frequency of N termini located beyond the first 50 residues is solely attributable to P1 aspartate cleavages (Figures S1B and S1C). Thus, the vast majority of proteolysis we observe in apoptosis is attributable to caspases or proteases with caspase-like substrate specificity.

Among the total 1099 SY-labeled peptides identified in etoposide-treated Jurkat cells, 418 follow aspartate in corresponding protein sequences (Tables S4 and S6). These peptides correspond to 333 P1 aspartate N termini and caspase-like cleavage sites (identified cleavage sites are listed in Table S7). In turn, these cleavage sites map to 282 unique substrates and ten additional others that cannot be distinguished from homologs containing the same identified N terminus (identified substrates are listed in Table S8). The average overlap between data sets obtained in separate experiments is 55% at the peptide level and 58% at the protein level (Figures S3A and S3B). Similar overlap levels (~67%) have been previously observed for replicate analyses of complex mixtures of peptides with LC/MS/MS (Elias et al., 2005). We have verified 16 of the proteins identified as caspase substrates in our studies to be cleaved during apoptosis, using immunoblotting (representative examples are included as Figure S4A). We have also determined that the proteolysis of a representative set of substrates is blocked by the broad-spectrum caspase inhibitor Z-VAD(OMe)-fmk, consistent with this proteolysis being caspase dependent (Figure S4B).

The most frequent residues at the P4, P3, P2, and P1' positions of the caspase-like cleavage sites identified in apoptotic Jurkat cells are aspartate, glutamate, valine, and glycine, respectively (Figure 3A). Thus, an averaged composite of these cleavage sites indicates that the most common caspase activity in apoptotic cells exhibits a specificity that is most similar to the substrate specificity of executioner caspases-3 and -7, as determined with peptide substrates (Figure 3B) (Thornberry et al., 1997). However, there are significant differences between the cellular cleavage sites and the in vitro specificity profiles. Notably, the canonical DEVD cleavage site motif is found in less than 1% of the caspase-like cleavage sites observed in apoptotic Jurkat cells, and the broader DXXD motif is still only found in

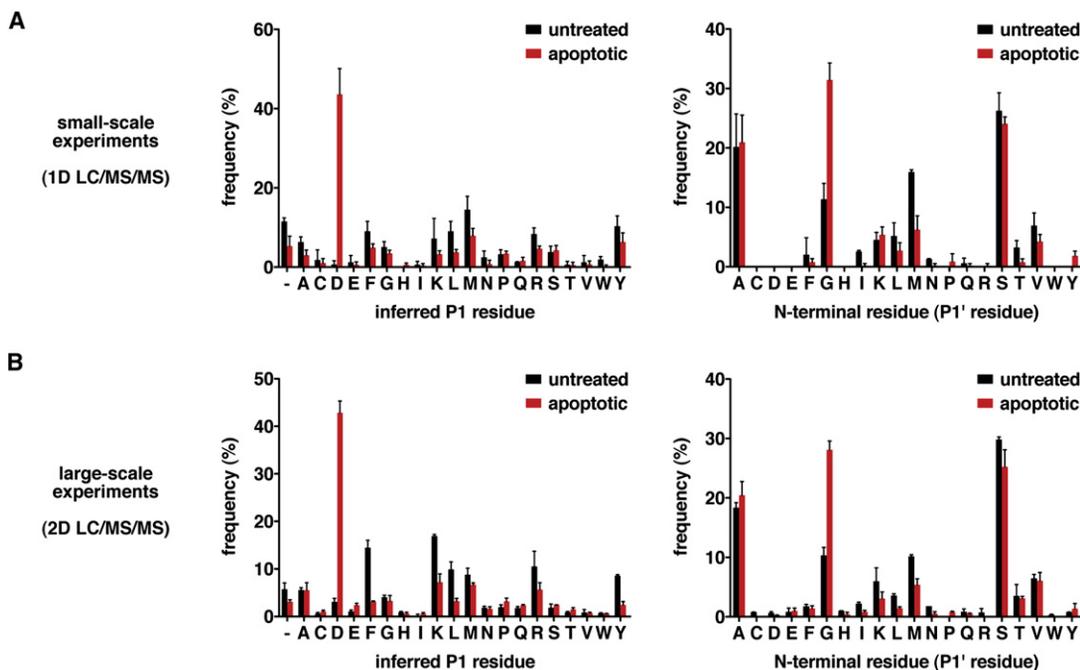


Figure 2. N Termini Derived from Caspase-like Proteolytic Processing Are a Hallmark of Apoptotic Cells

(A) Frequencies of P1 and P1' amino acid residues corresponding to nonhomologous N termini identified in small-scale 1D LC/MS/MS experiments with untreated and apoptotic Jurkat cells. Data are represented as mean \pm SD ($n = 2$ for untreated, and $n = 4$ for apoptotic).
 (B) Frequencies of P1 and P1' amino acid residues corresponding to nonhomologous N termini identified in large-scale 2D LC/MS/MS experiments with untreated and apoptotic Jurkat cells. Data are represented as mean \pm SD ($n = 2$ for untreated, and $n = 3$ for apoptotic).
 “-” indicates lack of a putative P1 residue in cases where the P1' residue is an initiator methionine.

22% of the identified cleavage sites (Figure 3D). A distinct difference in the composite cellular profile is the high frequency of serine and threonine residues at P4, P3, and P2, which is not observed in vitro for any of the caspases (Figure S5). Interestingly, a composite of all reported human caspase cleavage sites and human orthologs of reported rodent caspase cleavage sites

(Lüthi and Martin, 2007) is very similar to the Jurkat cellular profile reported here (Figure 3C).

These observations suggest that caspase substrate specificity determined with peptide substrates has limited value as a predictor of physiological caspase cleavage sites. To investigate the predictive value of a large set of known physiological caspase

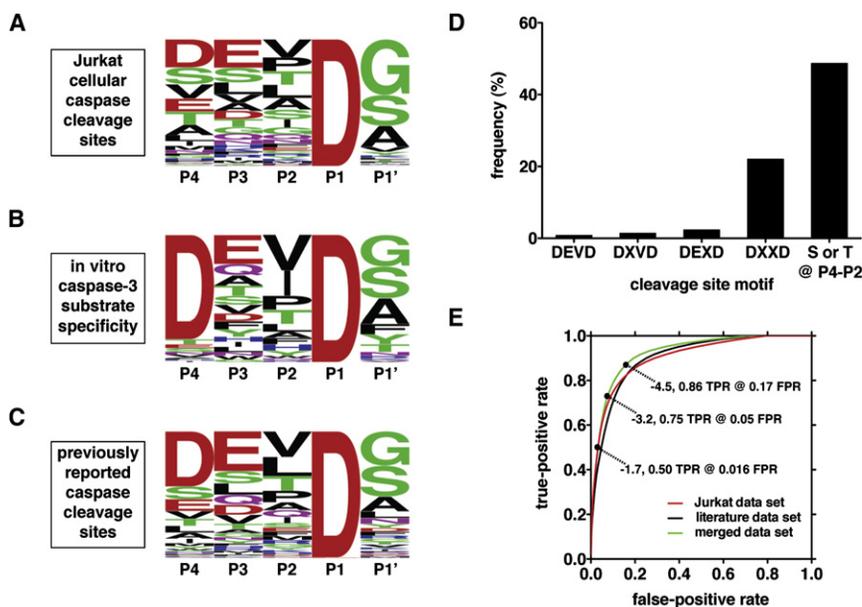


Figure 3. Substrate Specificity of the Caspase-like Proteolytic Activity Induced in Apoptotic Cells

(A) Sequence logo representation (Crooks et al., 2004) of the frequency of amino acid residues in the caspase-like cleavage sites identified in apoptotic cells.
 (B) Sequence logo representation of the in vitro substrate specificity of caspase-3 (Stennicke et al., 2000; Thornberry et al., 1997).
 (C) Sequence logo representation of the frequency of amino acid residues in previously reported caspase cleavage sites.
 (D) Frequency of P4-P1 motifs in the caspase-like cleavage sites identified in apoptotic Jurkat cells.
 (E) ROC curves for predictive HMMs constructed from three different cleavage site training sets (Jurkat, literature, and merged). Three representative HMM score threshold values for the merged data set are indicated (TPR, true-positive rate; FPR, false-positive rate).

frequently cleave protein substrates at loops relative to the octapeptide reference control described above (Figure 4B). Surprisingly, proteolysis at α -helical regions is not uncommon. Binning of cleavage sites into secondary structure motifs reveals that although an all-loop motif is the most common secondary structure motif, the second most common one is an all-helix motif (Figure 4C). The finding that some cleavages occur at solvent inaccessible and α -helical regions likely reflects structural dynamics of these regions. Structural examples of cleavages identified in our studies are included as supplemental data (Figure S6).

Analysis of the location of cleavage sites in caspase substrates annotated in the Pfam database (Finn et al., 2006) indicates that 46% of them are located within an annotated functional domain, 38% are located between annotated domains, and 16% are located at protein termini, either before the first annotated domain or after the last (Figure 4D). This distribution is relatively similar to the distribution of a reference control of all octapeptide sequences in the human Swiss-Prot database containing an aspartate residue at the fourth position. Thus, caspases do not exhibit a strong preference for cleavage of substrates either inside or outside functional domains. Caspase cleavage sites are also evenly distributed over the length of protein substrates (data not shown).

Analysis of Protein-Protein Interactions between Caspase Substrates

Upon inspection of the entire data set of caspase substrates, we noted a number of instances where multiple proteins along a single biochemical pathway, or in a single protein complex, are targeted by caspases. For a more systematic analysis of this property, we utilized data from three different protein interaction databases (HPRD, IntAct, and MINT) to create a network of caspase substrate protein interactors (Chatr-aryamontri et al., 2007; Kerrien et al., 2007; Mishra et al., 2006). This network is made up solely of the substrates identified in our studies, reported human caspase substrates, and human orthologs of reported rodent caspase substrates (Lüthi and Martin, 2007) but excludes the caspases themselves (binary interactions constituting this network are listed in Table S9). A total of 415 interactors and 1253 interactions were found among the merged human caspase substrate data set of 602 proteins, for an average of 2.1 intra-data set interactions per caspase substrate. Ten data sets of 602 randomly chosen proteins from the protein interaction databases had an average of 0.2 intra-data set interactions per protein. This indicates a 10-fold enrichment in protein interactions between caspase substrates relative to randomly interacting proteins (Figure 5A) (a detailed description of this analysis is found in the Supplemental Experimental Procedures).

To determine which biological processes are preferentially targeted by caspases during apoptosis, we used the BiNGO (Maere et al., 2005) plugin of Cytoscape (Shannon et al., 2003) to find GO biological process terms that are overrepresented relative to the complete human GO annotation. We then focused on the 132 terms in the three deepest levels of the GO hierarchy to find the ten most overrepresented GO terms and the substrates annotated to those terms. This analysis yielded subnetworks of substrates involved in regulation of transcription, transcription from RNA polymerase II promoter, DNA repair, antiapoptosis, induc-

tion of apoptosis, apoptotic mitochondrial changes, regulation of translational initiation, DNA unwinding during replication, endocytosis, and cell division (Figures 5B–5K). The regulation of transcription GO term yielded the densest subnetwork, with 188 edges among 93 nodes (Figure 5B). In sharp contrast to the other nine GO terms, the cell division GO term barely yielded a network at all, with only two edges among 20 nodes (Figure 5K).

The N-CoR/SMRT Complex Is a Target of Caspase Proteolysis during Apoptosis

To analyze whether multiple cleavages along a pathway or in a complex occur at physiologically relevant rates, we focused on the portion of the regulation of transcription subnetwork representing N-CoR/SMRT transcriptional corepressor complex components and interactors (Figures 6A and 6B). This complex is involved in the recruitment of histone deacetylase activity to chromatin, which leads to chromatin condensation and transcriptional repression. Our studies identified N-CoR/SMRT complex resident components N-CoR and TBLR1 (Karagianni and Wong, 2007), as well as additional N-CoR/SMRT complex interactors HDAC7 (Fischle et al., 2001), MINT/SHARP/SPEN (Shi et al., 2001), and RBBP7/RbAp46 (Takezawa et al., 2007) as caspase substrates (MS/MS spectra of N-terminal peptides corresponding to cleavage sites in these proteins are included as Figures S7–S14). We probed for cleavage of these proteins during etoposide-induced apoptosis in Jurkat cells by immunoblot in order to qualitatively determine extent of proteolysis in each case.

N-CoR, TBLR1, HDAC7, and SHARP were all fully cleaved at rates similar to those observed for hallmark substrates procaspase-3 and DFF45 (Figures 6C and 6D). This proteolysis also tracked reasonably well with the time course for DNA fragmentation. In contrast, only partial proteolysis of RBBP7 was observed, suggesting it to be a possible bystander substrate (Figure 6D). Although not detected in our proteomic studies, we predicted the N-CoR homolog SMRT (Karagianni and Wong, 2007) to also be a caspase substrate on the basis of high sequence similarity to N-CoR cleavage sites. Indeed, SMRT was fully cleaved during etoposide-induced apoptosis in Jurkat cells (Figure 6E). The previously identified caspase substrate HDAC3 (Escaffit et al., 2007), another N-CoR/SMRT complex component (Karagianni and Wong, 2007), was also fully cleaved. Organization of functional domains in these proteins indicates that proteolytic processing at the cleavage sites identified in our studies likely results in inactivation of protein function by virtue of separating functional domains from one another (Figure 7).

DISCUSSION

One of the most striking findings of this study is that caspase substrates as a whole tend to physically interact with one or more other caspase substrates, either in protein complexes or networks. We interpret this as an indication that caspases target a limited set of biological pathways to elicit programmed cell death, as opposed to indiscriminately targeting the entire cellular proteome. These data also suggest that caspases target protein complexes that are hubs for cell viability in essential processes such as transcription and that targeting of multiple components

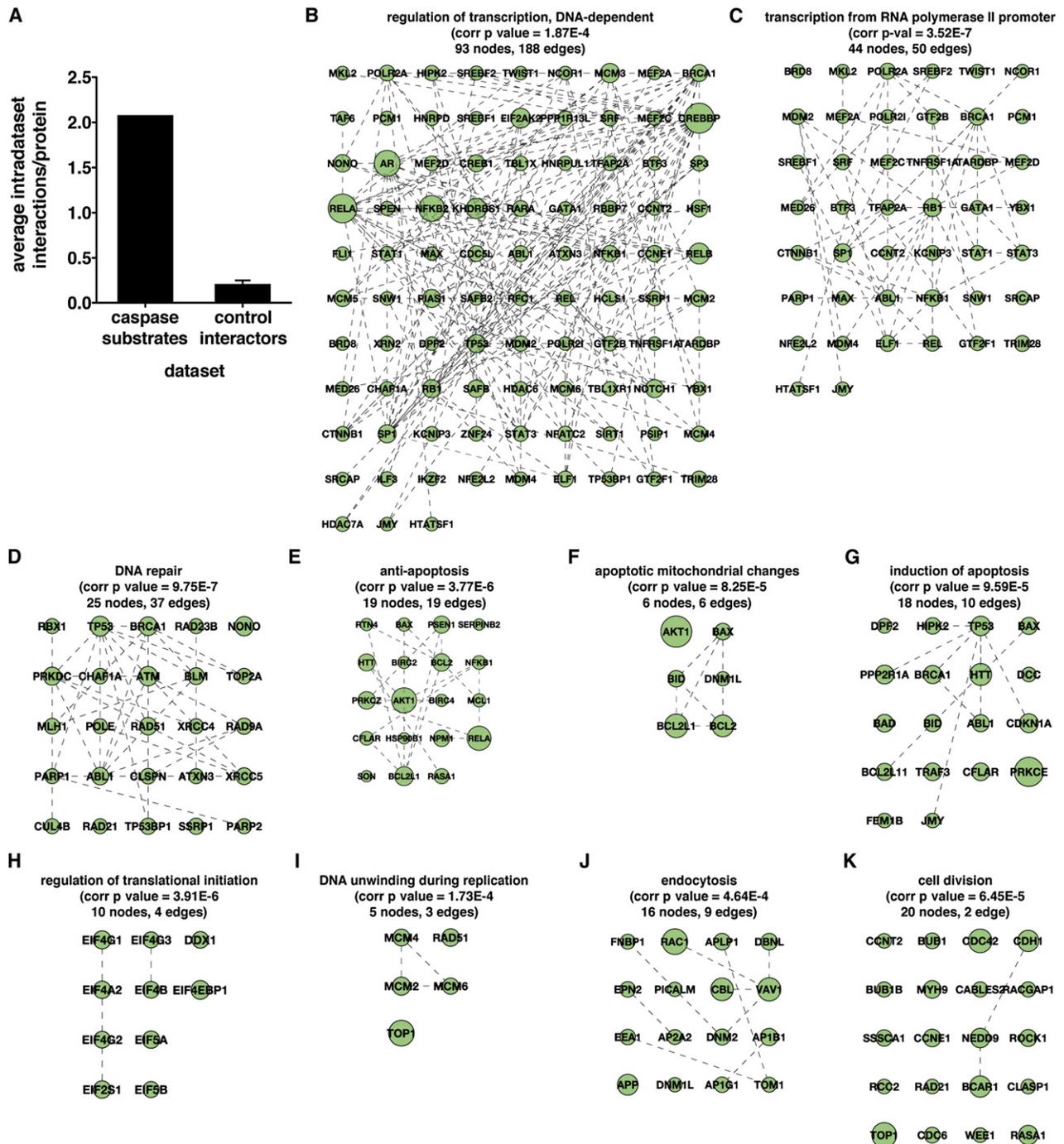


Figure 5. Network Analysis of Protein Interactions between Caspase Substrates

This analysis was applied to the substrates identified in this work and previously reported caspase substrates (Lüthi and Martin, 2007). (A) Enrichment in protein-protein interactions between the 602 total caspase substrates relative to an equally sized reference control set of protein interactors randomly selected from protein interaction databases. Data for the control set are represented as mean \pm SD (n = 10). (B–K) Caspase substrate protein interaction subnetworks encompassing substrates annotated to overrepresented GO biological process terms relative to the entire human GO annotation. Substrates are labeled with gene symbols. Corrected p values, number of nodes, and number of edges are indicated in each case.

in each complex is required for a full commitment to apoptosis. In this regard, it is notable that active caspases are dimeric, which is rare for proteases. A dimer is well equipped for semiprocessive

activity consistent with targeting multiple components of protein complexes. Another reported example of targeted proteolysis of a protein complex is the cleavage of SET, HMG-2, and

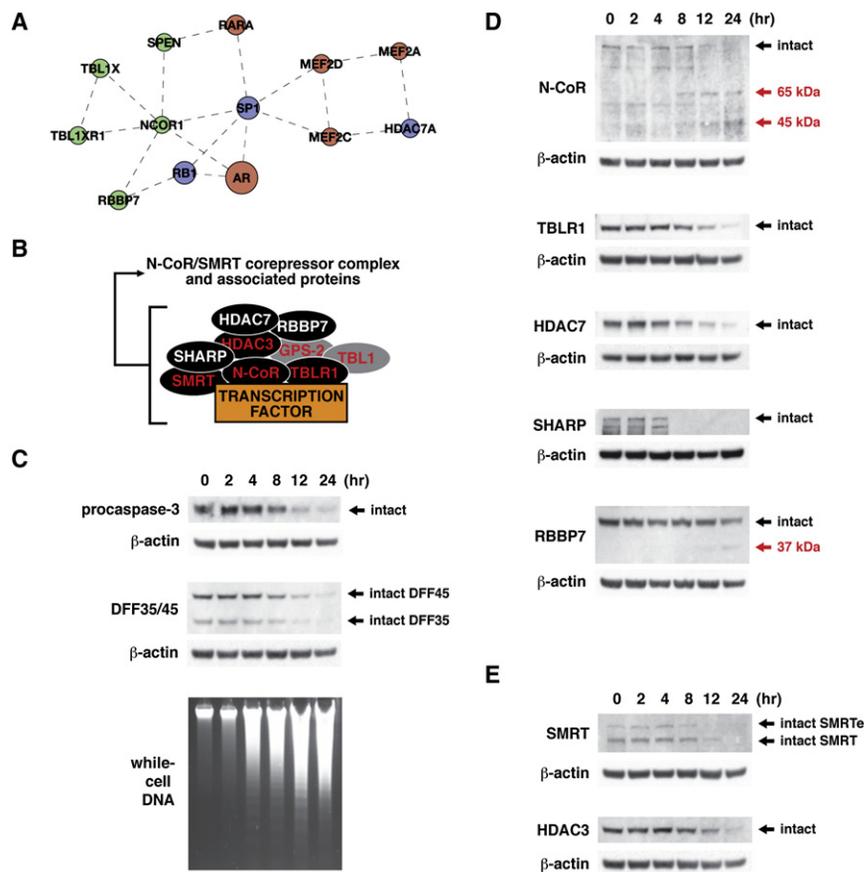


Figure 6. Analysis of Proteolysis of N-CoR/SMRT Corepressor Complex Components during Apoptosis in Jurkat Cells after Treatment with 50 μ M Etoposide

(A) Caspase substrate protein interaction subnetwork encompassing components of the N-CoR/SMRT corepressor complex (N-CoR, SPEN, TBLR1, RBBP7, and HDAC7), and transcription factors such as retinoic acid receptor, androgen receptor, and SP1 (green, from this work; red, from literature; and blue, in both data sets).

(B) Schematic representation of N-CoR/SMRT corepressor complex resident components and visiting interactors (red label, resident component; white label, visiting interactor; and black fill, target of proteolysis in apoptosis).

(C) Time courses for the proteolysis of procaspase-3 and DFF35/45 and for oligonucleosomal DNA fragmentation.

(D) Full cleavage of N-CoR, HDAC7, SHARP, and TBLR1, and partial cleavage of RBBP7.

(E) Full cleavage of SMRT and of HDAC-3, a previously identified caspase substrate.

Black arrows indicate full-length proteins. Red arrows indicate expected cleavage products for cleavage at the sites identified in our studies (cleavage products were not detected in all cases).

Ape1, three components of the SET complex, by the cytotoxic lymphocyte protease granzyme A (Lieberman and Fan, 2003). Interestingly, granzyme A is also dimeric.

The discovery that several components of the N-CoR/SMRT transcriptional corepressor complex are targets of caspase proteolysis presents a remarkable example of multiple cleavages in a single protein complex or pathway during apoptosis. Six proteins that are part of, or interact with, the N-CoR/SMRT complex are fully cleaved during etoposide-induced apoptosis in Jurkat cells, including the corepressors N-CoR and SMRT themselves. This finding was made possible by our large-scale discovery-oriented proteomic approach, as opposed to a more typical focused hypothesis-driven approach. Inactivation of the N-CoR/SMRT complex during apoptosis may achieve a result similar to the effect of HDAC inhibitors, with decreased histone deacetylation leading to opening of chromatin and transcriptional upregulation of proapoptotic genes (Bolden et al., 2006). Interestingly, HDAC 7 has recently been implicated as a physiological substrate of caspase-8, with its proteolytic inactivation leading to upregulation of Nur77 (Scott et al., 2008).

Our studies indicate that a change in function of proteins targeted by caspases during apoptosis must be rationalized by one or occasionally a few cuts per protein. We have found that caspase cleavages occur inside functional domains and between functional domains at approximately equal frequencies. In either case, relatively stable products must be produced after cleavage of the substrates since we detected them. Stability of

these products is also consistent with the relatively strict P1' glycine, serine, and alanine specificity we observe for the cellular caspase-like activity, which creates fragments conforming to the N-end rule (Varshavsky, 1992). In addition to functional disruption of the substrate protein, such cleavages may result in products that function as dominant negatives. For example, in the case of the N-CoR and SMRT corepressors, the C-terminal cleavage products contain the CoRNR boxes known to interact with nuclear receptors (Hu and Lazar, 1999). These proteolysis products could thus inhibit interaction between N-CoR/SMRT and nuclear receptors.

By globally identifying caspase-like cleavage sites in the proteome of apoptotic cells, this work presents a large-scale substrate specificity profile of caspase processing of endogenous proteins in intact cells. Importantly, this profile is influenced not only by the primary structure of cleavage sites but also by solvent accessibility, secondary and higher order protein structure, and possibly posttranslational modifications of substrates (Tózsér et al., 2003). Our finding that caspases often target proteins in complexes underscores the value of studying determinants of proteolysis under physiologically relevant conditions. The caspase-like cleavage sites identified in apoptotic Jurkat cells likely result from the action of several members of the caspase family of proteases. Although the aggregate substrate specificity of the observed caspase-like activity is most similar to the known specificity of executioner caspases, *in vitro* studies of caspases using peptides do not fully account for the observed cellular specificity (Schilling and Overall, 2008; Stennicke et al., 2000; Thornberry et al., 1997). Peptide-centric approaches are

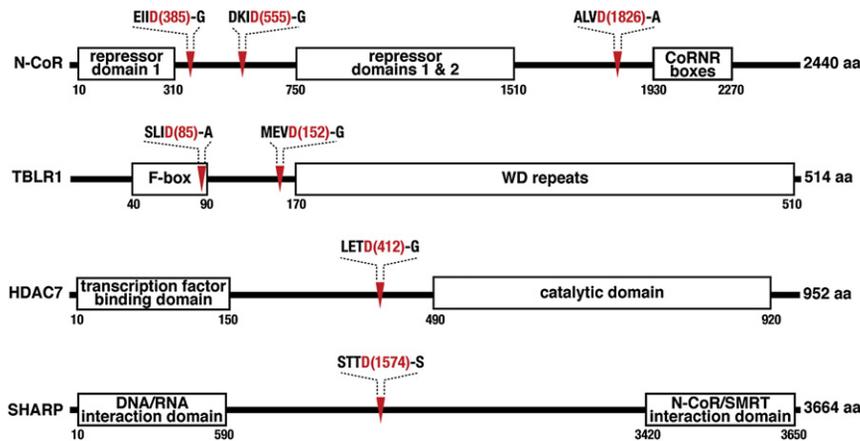


Figure 7. Caspases Cleave Resident N-CoR/SMRT Complex Components and Visiting Interactors at Regions Leading to Separation of Functional Domains

Functional domain organization and candidate caspase cleavage sites in SMRT and TBL1 are similar to those indicated for the respective homologs, N-CoR and TBL1R.

best suited for determination of optimal protease substrate specificity, invaluable in development of sensitive synthetic substrates or potent inhibitors. In contrast, a protein-centric method such as the one presented here is best suited for characterization of endogenous proteolysis in biological samples.

This work indicates that the widely used primary structural determinants of caspase *in vitro* substrate specificity are insufficient to predict physiological caspase cleavage sites. However, the cellular cleavage sites we have identified significantly expand a data set that can be used to train algorithms for predicting cleavage sites. Indeed, a proof of principle is provided by an accurate prediction of caspase cleavage sites by our preliminary HMMs. In addition to demonstrating that caspase cleavage sites are most commonly found in solvent accessible loop regions, as shown for other proteases (Hubbard et al., 1991), our analysis also indicates that a number of cleavage sites appear in partially solvent inaccessible regions and α helices. This information could also be incorporated into predictive algorithms. Finally, based on our protein interaction analysis, predictive algorithms may also benefit from scoring that considers physical interactions of candidate substrates with other caspase substrates.

Common approaches for the study of proteolysis in complex mixtures employ gel electrophoresis and mass spectrometry for analysis of proteins in cells, typically identifying tens of protein substrates at a time (Machuy et al., 2005). These approaches do not usually identify specific cleavage sites. In contrast, modern proteomic methods using positive enrichment of phosphorylated, glycosylated, or ubiquitinated polypeptides can lead to the identification of hundreds or thousands of posttranslationally modified sites on proteins (Collins et al., 2007; Peng et al., 2003; Vosseller et al., 2006). However, selective capture of the products of proteolysis is not facile. Gevaert et al. and McDonald et al. have reported methods for negative selection of N-terminal peptides, while Timmer et al. have reported an approach for positive selection of N-terminal peptides (Gevaert et al., 2003; McDonald et al., 2005; Timmer et al., 2007). These chemical approaches require two consecutive and quasiorthogonal derivatization steps, the first to block lysine ϵ -amines and the second to label terminal α -amines. We believe the success of our method is based on the advantage of achieving great selectivity for α -amines in a single labeling step through use of the enzyme subtiligase.

whether peptidic or not, precludes complete sampling (Elias et al., 2005). The number of caspase substrates we have identified is thus likely smaller than the total number of caspase substrates in apoptotic Jurkat cells. We identified 50 of approximately 361 previously reported human caspase substrates and 50 of approximately 307 previously reported human caspase cleavage sites (Figures S3C–S3E) (Lüthi and Martin, 2007). Incomplete proteomic sampling of caspase substrates in our studies is likely an important contributor to the modest overlap between the substrates we have identified and those previously reported.

In addition to incomplete sampling, three additional factors can contribute to the modest overlap with previously reported substrates. First, only cleavage sites corresponding to N-terminal semitryptic peptides 7 to 40 residues in length (without the additional SY dipeptide label) are generally identified in our studies. With collision-induced dissociation (CID), fragmentation of peptides below this range generally does not provide enough information for unambiguous matching to databases, and most peptides above this range do not fragment efficiently. Approximately half of the 307 previously reported human caspase cleavage sites result in N-terminal semitryptic peptides that fall outside this range and would not be identified with our current method (Figure S15). Second, each analytical method, whether global or focused, will have its own associated biases and limitations. For example, a limitation of the subtiligase labeling method is that the enzyme cannot access protein N termini that are buried or occluded. Third, we employed a single apoptotic inducer in a single cell line, using a single analysis method, whereas the previously reported set of substrates comes from a multitude of studies using varied inducers, cell types, and methods.

Although the data set of substrates we have identified is not comprehensive, it doubles the number of known cleavage sites in human targets of caspase-like proteolysis in apoptosis. The study of apoptotic pathways has important ramifications for identification of pathways that are critical for cellular homeostasis, and for development of potential anticancer therapeutics. A number of caspase targets are active or established drug targets for treating cancer, including topoisomerase II, Bcl-2, Hdm2, MEK1, and Akt, to name a few. Thus, it is possible that the list of substrates we have identified includes new candidate chemotherapeutic targets. The products of caspase proteolysis may

also serve as useful biomarkers for assessment of chemotherapeutic efficacy, as demonstrated in the case of cytokeratin-18 for breast cancer (Olofsson et al., 2007). Along with MS-based quantitation, the technology we describe should enable global analysis of the apoptotic phenotype as a function of time, cellular context, and type of induction. Finally, the technology should also be broadly applicable for global sequencing of proteolytic cleavage sites in other biological settings.

EXPERIMENTAL PROCEDURES

Preparation of Subtiligase and Peptide Ester Substrate

Subtiligase was recombinantly expressed in *B. subtilis* and purified essentially as previously described (Abrahmsén et al., 1991). The biotinylated peptide glycolate ester was synthesized by solid-phase peptide synthesis as described for other subtiligase substrates (Braisted et al., 1997).

Cell Culture, Induction of Apoptosis, and Cell Lysate Preparation

Jurkat clone E6-1 (ATCC) cells at a density of 1×10^6 cells/ml were treated with etoposide (50 μ M) for 0 or 12 hr prior to being harvested. Detergent lysates were prepared at a typical concentration of 2×10^8 cells/ml (approximately 20 mg/ml) with buffered 1.0% Triton X-100 in the presence of protease inhibitors.

Sample Biotinylation, Denaturation, Reduction, Alkylation, and Gel Filtration

Cell lysates were biotinylated by treatment with subtiligase (1 μ M), biotinylated peptide ester substrate (1 mM), and DTT (2 mM). Ligation reactions were typically left to proceed at room temperature for 60 min. Samples were then denatured, reduced, alkylated, and subjected to gel filtration for removal of hydrolyzed peptide ester substrate.

Trypsinization and Recovery of Biotinylated Peptides

Filtered samples were subjected to solution digestion with sequencing grade modified trypsin (Promega). Biotinylated N-terminal peptides were captured from trypsinized samples with NeutrAvidin agarose (Pierce). Captured peptides were recovered by treatment of agarose resin with recombinant TEV protease (1 μ M).

LC/MS/MS

N-terminal peptide samples were analyzed by one-dimensional reversed-phase LC/MS/MS or two-dimensional strong cation exchange/reversed-phase LC/MS/MS. In the latter case, samples were fractionated by offline strong cation exchange chromatography with a 60 min gradient on a 2.1 \times 200 mm PolySULFOETHYL Aspartamide column at a flow rate of 0.3 ml/min. Reversed-phase chromatography of unfractionated or fractionated samples was carried out with a 60 min gradient on a 75 μ m \times 15 cm C₁₈ column at a flow rate of 350 nl/min. The capillary column was coupled to a QSTAR Pulsar, QSTAR XL, or QSTAR Elite mass spectrometer (Applied Biosystems). For each acquired MS spectrum, either the single or the two most intense multiply charged peaks were selected for generation of CID spectra. A dynamic exclusion window of 3 min was applied. CID spectra not included as supplemental data will be made available upon request.

Interpretation of MS/MS Spectra

Data were analyzed with Analyst QS software, and MS/MS centroid peak lists were generated with the Mascot.dll script. Data were searched against the Swiss-Prot human database (March 2008 release) with Protein Prospector 5.0 (University of California, San Francisco). Peptide tolerances in MS and MS/MS modes were 100 ppm and 300 ppm, respectively. The digest protease specified was trypsin, allowing for two missed cleavages and nonspecific cleavage at N termini. An N-terminal SY modification and cysteine carbamidomethylation were specified as a fixed modifications, and methionine oxidation was specified as a variable modification. Peptides with scores ≥ 22 and expectation values ≤ 0.05 were considered positively identified. False-discovery rates for peptide identifications were estimated with a target-decoy strategy.

Bioinformatics

Cleavage site prediction was performed with HMMer version 2.3.2 (Eddy, 1998). The training and testing substrate sets were obtained by a jackknife procedure from data for the cleavage sites identified in our work and those previously reported in the literature (Lüthi and Martin, 2007). Solvent accessible surface area and secondary structure analysis of cleavage sites was carried out on a set of experimentally determined structures from the Protein Data Bank (Berman et al., 2002) and "good quality" comparative models from ModBase (Pieper et al., 2006). Domain analysis was performed with domain assignments from the Pfam database, (Finn et al., 2006). Protein-protein interaction analysis was carried out with data from the HPRD (Mishra et al., 2006), IntAct (Kerrien et al., 2007), and MINT (Chatr-aryamontri et al., 2007) databases.

DNA Fragmentation

Fragmentation of whole cell DNA was analyzed by agarose gel electrophoresis with the Apoptotic DNA Ladder Kit (Roche).

Immunoblotting

Jurkat cells at a density of 1×10^6 cells/ml were treated with etoposide (50 μ M) for 0, 2, 4, 8, 12, and 24 hr prior to being harvested. Whole-cell lysates were prepared at a concentration of 2×10^7 cells/ml with buffered 1.0% SDS in the presence of protease inhibitors and sonication. Lysates were normalized to a protein concentration of approximately 2 mg/ml prior to analysis by SDS-PAGE and western blot. Utilized antibodies are listed in the Supplemental Experimental Procedures.

SUPPLEMENTAL DATA

Supplemental Data include Supplemental Experimental Procedures, nine tables, and fifteen figures and can be found with this article online at <http://www.cell.com/cgi/content/full/134/5/866/DC1/>.

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