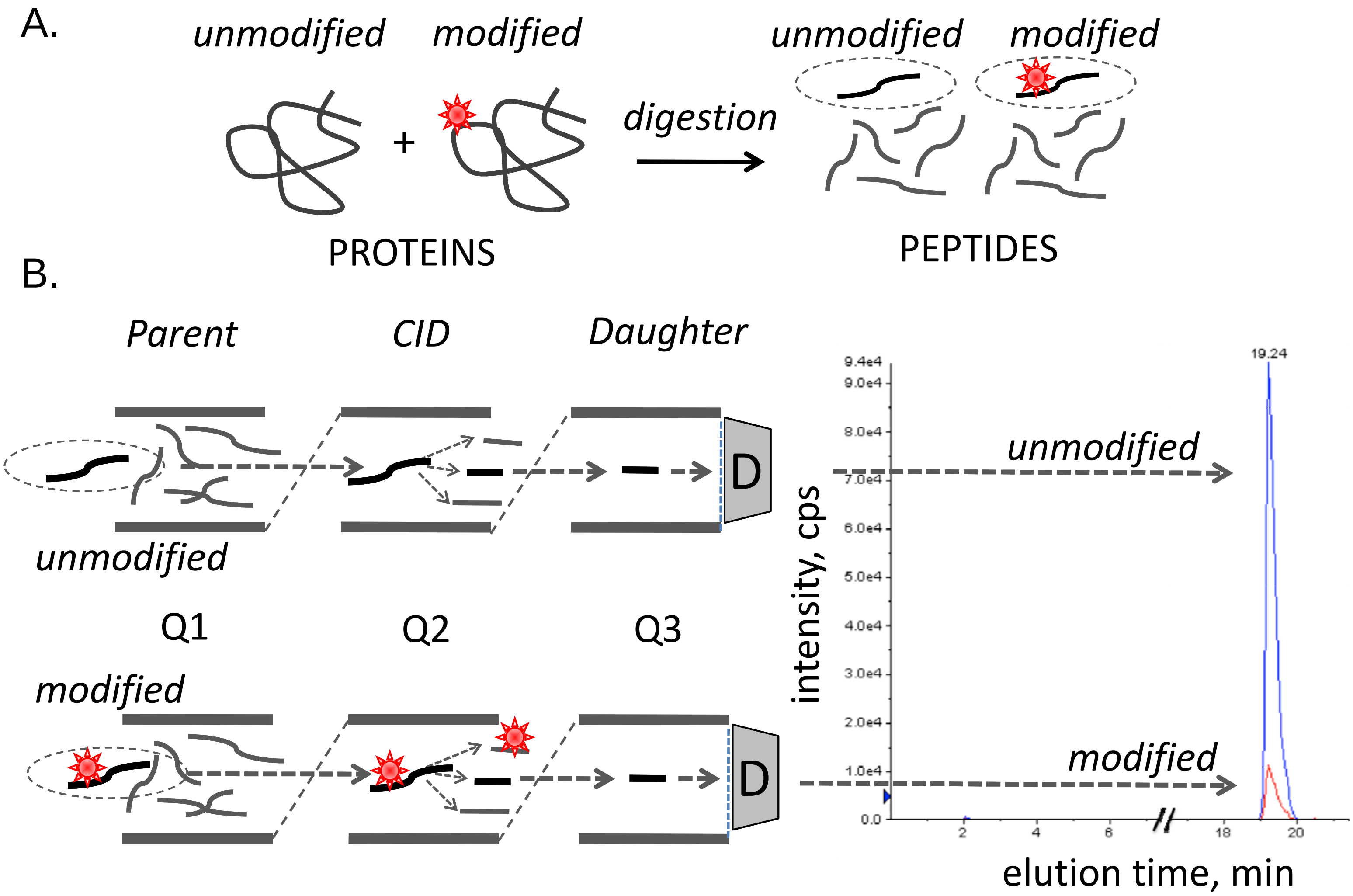

Online Figure I.MRM quantification of modified and unmodified peptides by triple Q MS. (A) Initial digestion of proteins into peptides. (B) The peptide mixture is injected in the triple quadrupole MS, where the quadrupole Q1 is used to select a specific peptide (parent). The parent ion is fragmented in the Q2 and transition (daughter) ions are monitored in the Q3. Relative quantification is obtained by comparing the spectral count from different transitions. Normally, five to six pairs (parent and daughter) for each peptide are monitored in order to achieve a reliable quantification. D: detector.

Online Table I: See separate excel spreadsheet

Online Table II: See separate excel spreadsheet

Online Table III: Selected protein databases

Database	Features	link
NCBI	• Merging annotations from GenBank, RefSeq, TPA, SwissProt, PIR, PRF and PDB • The most comprehensive resource of protein sequences (ref Martens L. Methods Mol Biol. 2009) • Heterogenic in sequence reliability, annotation, and peptide sequence redundancy (ref Martens L. Methods Mol Biol. 2009) • Limited additional biological information • Curated by the National Center for Biotechnology Information (NCBI) at the National Institutes of Health (NIH)	ncbi.nlm.nih.gov/protein
Uniprot Protein knowledgebase (UniprotKB)	• Including both manually (Swiss-Prot) and automatically annotated (TrEMBL) entries • Currently containing more than 519 300 curated entries • No particular focus regarding species or PTMs • Extensive additional biological information • Curated by UniProt comprising the European Bioinformatics Institute (EBI), the Swiss Institute of Bioinformatics (SIB) and the Protein Information Resource (PIR)	www.uniprot.org
The human protein reference database (Hprd)	• Manually curated • Currently comprising more than 93 700 PTMs • Restricted to the human proteome • Curated by The Pandey lab and the Institute of Bioinformatics at Johns Hopkins University.	www.hprd.org
PhosphositePlus®	• Manually curated • Currently containing more than 71 400 curated entries on phosphorylation sites • Major focus on phosphorylation sites in mouse and human • Including non published PTMs from Cell Signaling Technology (CTS) • Curated by CTS	www.phosphosite.org