

The Human SRM Atlas: A compendium of quantitative mass spectrometry assays for all accessible human proteins

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Targeted proteomics utilizing selected reaction monitoring (SRM) has become an important new technique for the unambiguous detection and quantification of specific sets of proteins in complex samples. The technique depends on the a priori determination of the peptides that optimally represent the targeted proteins and their variants, and relies on precursor-to-fragment ion transitions that uniquely identify the targeted peptides in sample mixtures. The targeted peptides and their optimal transition sets constitute definitive and generally applicable proteomic assays for the detection of the targeted proteins in any sample with direct applicability to clinical based assays.

The SRMAtlas is a publicly accessible web-based resource for the selection of SRM assays to conduct targeted proteomics. SRMAtlas supports the selection of both optimized peptides and their transitions for each targeted protein. We have recently developed the complete Human SRMAtlas, an assay library of over 170,000 SRM assays for all human proteins to account for the entire mass spectrometry accessible 20,333 predicted human protein-coding ORF's (99.9%). For the development of the SRM assays we used a high-throughput approach based on the synthesis of equimolar synthetic computationally selected proteotypic peptides for each human protein coding ORF and over 11,000 isoforms and SNP's. The synthetic peptides were employed as reference compounds to generate the corresponding fragment ion spectra and to extract the SRM assay coordinates. The SRMAtlas set of libraries are publicly available via the SRMAtlas website developed at ISB (<http://www.srmatlas.org/>).