

FTMS Services

Itemized Fees (\$)

<p>Accurate mass measurement – external calibration (Positive-ion) <2ppm mass error</p> <p>Positive-ion ESI measurement, infusion of the sample, external standard calibration; mass accuracy better than 2 ppm</p>	<p>50.00 per sample 20.00 for generating elemental composition list</p>
<p>Accurate mass measurement – internal calibration (Positive-ion) <1ppm mass error</p> <p>Positive-ion ESI measurement, infusion of the sample, internal standard calibration with at least one std; mass accuracy better than 1 ppm</p>	<p>80.00 per sample 20.00 for generating elemental composition list</p>
<p>Accurate mass measurement – (Negative-ion) <2ppm mass error</p> <p>Negative-ion ESI measurement, infusion of the sample, external calibration; mass accuracy better than 2 ppm</p>	<p>Inquire</p>
<p>Peptide Sequencing with MS/MS and accurate mass Denovo Sequencing</p> <p>CID, ECD, or IRMPD fragmentation methods available with FTMS</p> <p>Samples introduced by infusion or nano-spray (pico-tip) (ESI) Samples can also be ionized by AP-MALDI Includes: Mascot™, PEAKS™, or DenovoX™ sequence search</p>	<p>50.00 per sample or peptide 20.00 for each additional peptide analyzed by MS/MS in the same sample 20.00 for each denovo sequence prediction using Mascot™ or PEAKS™ software</p>
<p>LC/MS and LC/MS/MS (Liquid Chromatography/ Mass Spectrometry) FTMS instrument</p> <p>Positive-ion ESI; sample introduction by nanoLC or microLC</p>	<p>110.00 per LC/MS run 15.00 per sample for Ziptip™ purification as required</p> <p><i>Discount rates apply for high number of samples and depending on gradient or isocratic LC runs</i></p>
<p>“Top-Down” Proteomics</p> <p>ECD fragmentation and sequencing of intact proteins</p>	<p>Inquire</p>
<p>Identification of Sulfur-containing peptides (i.e. cysteine or methionine)</p> <p>High resolution separation of heavy isotopes, e.g. ¹³C and ³⁴S isotopes; limited to peptides < 1000 MW</p>	<p>Inquire</p>
<p>Intact Protein MW Analysis</p> <p>ESI/FTMS analysis with sample introduction by infusion. Deconvolution of data using Xtract™ or ProMass™ software.</p>	<p>55.00 per sample with deconvolution 15.00 for samples requiring Ziptip™ purification 20.00 for sequence elucidation; searches to assign observed truncation, cut sites, or protein degradation products</p>

Custom Database Searching:	
Create a custom Mascot™ database For specific protein sequences not in the MSDB or NCBI databases	22.00 per protein sequence created for the custom database
Create a custom modification for Mascot™ searches For searching custom or non-standard modifications or derivatives	22.00 per custom modification created for searches
Special request/ additional modification searches with Mascot™ or additional database searches Other database search engines available on request (e.g. Sequest™, PEAKS™, Protein Prospector™, OMSSA). Each search includes up to three modifications and report of results	22.00 per search