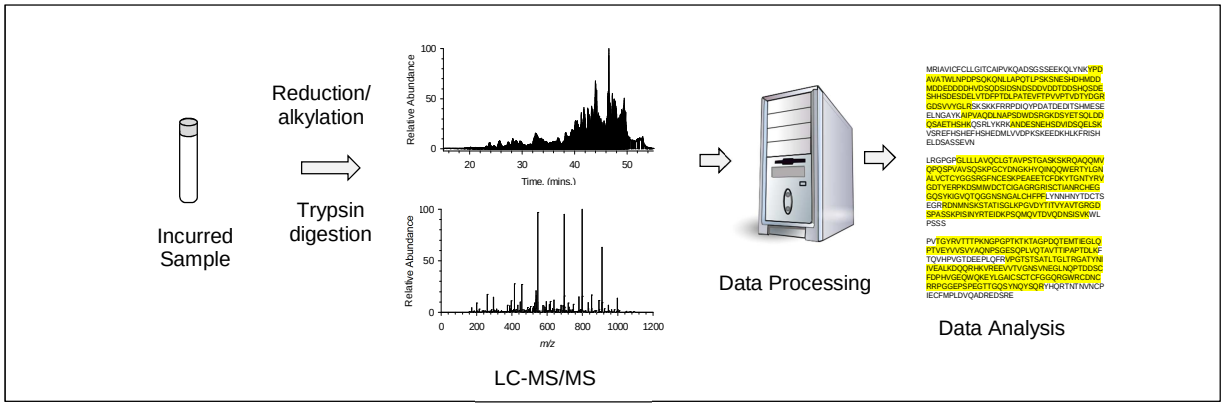
MS Bioworks
Protein Mass Spectrometry Services

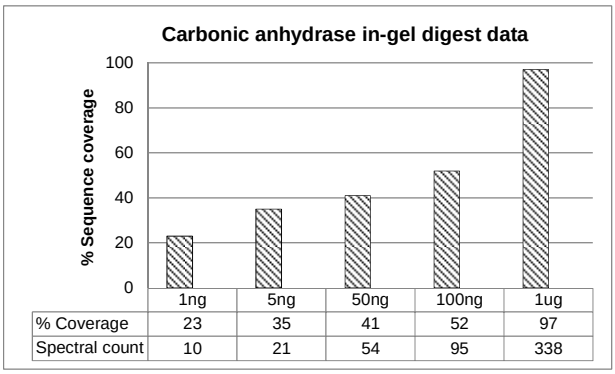
PROTEIN-WORKS

Protein-works - Protein Identification

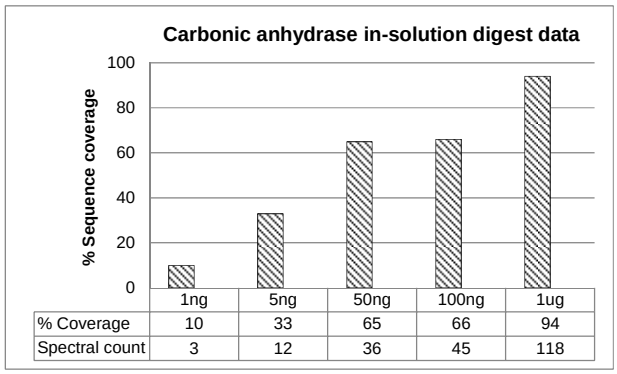
MS Bioworks protein identification services can be used to identify a protein in gel (MSB-01) or in solution (MSB-02). The basic experimental workflow for our protein identification service is presented below.



Samples are digested using sequencing grade trypsin (Promega), analyzed by nanoscale LC-MS/MS on a LTQ Orbitrap Velos mass spectrometer. Data are searched and protein identified using Mascot (Matrix Science) and processed via the Scaffold software (Proteome Software). We provide a report summarizing the proteins identified in a sample and a summary file to allow independent data interrogation. Examples of sequence coverage from varying amounts of submitted proteins are presented in the charts below.



	1ng	5ng	50ng	100ng	1ug
% Coverage	23	35	41	52	97
Spectral count	10	21	54	95	338



	1ng	5ng	50ng	100ng	1ug
% Coverage	10	33	65	66	94
Spectral count	3	12	36	45	118

Service ID	Cost ($)
MSB-01	250
MSB-02	450

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