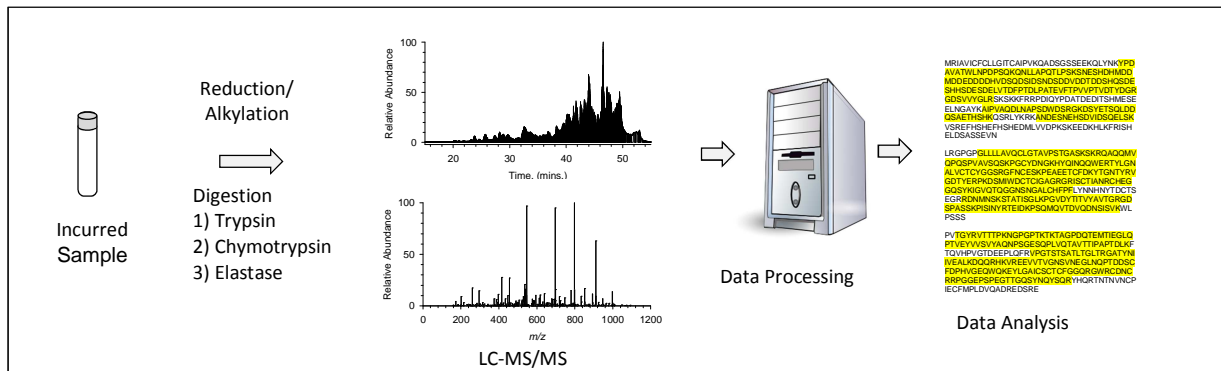


## Protein-works - Protein Mapping

MS Bioworks protein mapping service (MSB-03) enables the identification of the entire sequence of a protein by using three enzymes for digestion. This service is ideal for identifying regions of interest inaccessible to trypsin alone, confirming a primary sequence or finding truncations. The basic experimental workflow is presented below.



Our protein mapping service is compatible with *most* buffers and we recommend submitting at least 1µg of material, in gel or solution.

### Example: GST-MAPK3

GST-tagged MAPK3 was digested with trypsin, chymotrypsin and elastase. Each digest was analyzed by LC/MS/MS on an Orbitrap Velos Pro tandem mass spectrometer. The target protein was observed with 100% sequence coverage when the data from all three enzymes was combined:

GST-MAPK1 (100%), 69,796.2 Da

GST-MAPK1

638 unique peptides, 863 unique spectra, 1948 total spectra, 609/609 amino acids (100% coverage)

```

MSPILGYWKI  KGLVQPTRL  LEYLEEKYEE  HLYERDEGDK  WRNKKFELGL  EFPNLPYYID
GDVKLTQSM  IIRYIADKHN  MLGGCPKERA  EISMLEGAVL  DIRYGVSRIA  YSKDFETLKV
DFLSKLPEML  KMFEDRLCHK  TYLNGDHVTH  PDFMLYDALD  VVLYMDPMCL  DAFPKLVCFK
KRIEAIPIQID  KYLKSSKYIA  WPLQGWAQTF  GGGDHPPKSD  LVPRGSPGIP  MAAAAAQGGG
GGEPRRTIEGV  GPGVPGEVEM  VKGQPFVDVGP  RYTQLQYIGE  GAYGMVSSAY  DHVRKTRVAI
KKISPFEHQ  YCQRTLREIQ  ILLRFRHENV  IGIRDILRAS  TLEAMRDVYI  VQDLMETDLY
KLLKSQQLSN  DHICYFLYQI  LRGLKYIHSA  NVLHRDLKPS  NLLINTTCDL  KICDFGLARI
ADPEHDHTGF  LTEYVATRWY  RAPEIMLNSK  GYTKSIDIWS  VGCILAEMLS  NRPFIIPGKHY
LDQLNHLGI  LGSPSQEDLN  CIINMKARNY  LQSLPSKTKV  AWAKLFPKSD  SKALDLLDRM
LTFNPNKRIT  VEEALAHPYL  EQYYDPTDEP  VAEEPFTFAM  ELDDLPKERL  KELIFQETAR
FQPGVLEAP
    
```

MSB-03 can be ordered directly from our website at [www.msbioworks.com](http://www.msbioworks.com).

Service ID	Cost (\$)
MSB-03	800

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