

Search engine for proteome mapping

ProteoMetrics, based in Canada, has developed quality software tools that anticipate the needs of high-throughput protein mass spectrometry. SonarMS/MS is a fast MS/MS search engine that incorporates a robust quality control method. It can search DNA from the genome directly, as well as translated protein sequences, allowing for detection of exons, alternate splice sites and novel genes.

SonarMS/MS identifies proteins using MS/MS information from digest peptides. It has been designed specifically for the needs of protein identification automation, using breakthrough concepts and designs that make protein identification easier and more reliable. Apart from being faster, the results obtained need not be reviewed by hand, which is necessary for most other commercially available search routines. Furthermore, instead of searching one mass spectrum at a time through a sequence database and finding peptides that match the spectrum, SonarMS/MS takes a protein/EST/chromosome segment and looks at a compilation of mass spectra and identifies evidence for that particular sequence. (Website: <http://www.bioresearchonline.com>)