

NIST MS Search with The NISTmAb Mass Spectral Library

This free product is for searching and browsing the NISTmAb peptide fragmentation library (MS/MS).

It includes:

- o NIST MASS SPECTRAL SEARCH PROGRAM Version 2.0g for use with Microsoft(R) Windows(TM)
- o The NISTmAb Mass Spectral Library (1/12/2018, HCD).

System requirements:

This MS search program is a 32-bit Unicode application and thus requires Windows NT 4.0, 2000, XP, Vista, or Windows 7. MS Search is compatible with MGF, DTA, and PKL formats, all common to proteomics workflows.

Instructions:

1. To install, run the program "NISTmAb_Mass_Spectral_Library.exe" and then follow instructions.
2. To run, execute "nistms.exe" for searching and browsing the NISTmAb peptide fragmentation library.
3. To search peptide spectra, go to "names" option at the bottom as

