Readme.txt file for the Human Serum Albumin Library of Tryptic Peptides

This library is provided in both a ASCII text format (.msp file) as well as in a Windows user interface software package. The software package is a general one use developed at NIST for browsing and searching various types of mass spectral libraries.

To use the user interface HSA digest library, first download the .zip file and then unzip using standard software. Then, activate the Setup.exe program when will then begin the installation. You will be asked where the program should be installed. You may accept the default location or select a new folder.

After intallation, run the NISTMS.exe program from the folder selected for installation. To browse the library, select the 'Name' tab at the bottom. Spectra will be presented in alphabetical (by sequence) order. Entries in the box on the upper left will bring up the peptides whose first characters match the entered sequence (this is an 'incremental' search).

Details of the spectrum format found in both the .msp and user interface program can be found in the file NIST_peplib_6_14.doc that is in the folder containing the NIST.exe program. Note that the HSA library is in a folder within that base folder.

Operation of the user interface program is described in the .pdf file Ver20Man.pdf in the base folder. You may also use the help system within the program.

You can adjust the display with a right click and then selecting 'Properties'. You can even search the library by selecting a spectrum with a mouse on the windown, right clicking and then selecting library search.