# **NIST 17**

### What is this mass spectrum?



## Identify it with NIST 17, the world's most widely trusted mass spectral library!



#### NIST 17 contains *nearly a million mass spectra*:

306,000+ electron ionization (EI) spectra for 267,000+ compounds. 652,000+ tandem MS/MS spectra:

176,000+ ion trap spectra for 120,000+ ions of 14,000+ compounds 475,000+ collision cell spectra for 39,000+ ions of 14,000+ compounds

## NIST 17 also contains <u>search software</u> to match your spectra against spectral libraries.

Each spectrum has corresponding information, such as

- chemical formula, structure, and mass
- chemical names, synonyms, CAS#, InChiKey (PubChem)
- GC method and retention indices if applicable (72,000+ in EI library)



## Scientific Instrument Services, Inc.

www.sisweb.com/nist

### Mass Spectral Library & Search Software Version 2017

#### **Improvements since 2014**

- Increased coverage and quality in all libraries:
  - Nearly <u>3x increase in MS/MS</u> spectra.
  - 30,000+ new EI spectra
  - 16,000+ more compounds with GC & retention index citations
- Improved search software (v. 2.3)
  - New search methods and algorithms, such as our new "hybrid" search type for MS/MS and EI.
  - See back for details.

Upgrade discount for any previous version. Agilent format option.

Compatible with most mass spectral data systems, including Agilent ChemStation/ MassHunter, Thermo Xcalibur, Waters MassLynx, Shimadzu GC/MS Solutions, and others.

*Quality, broad coverage, and accessibility* — these are what the NIST MS Library is known for, a product of a three decade, comprehensive evaluation, where each spectrum is validated for correctness by a team of experienced mass spectrometrists.

Additional utilities bundled with NIST 17:

AMDIS - extracts noise-free component spectra from GC/MS data files and can library search them with NIST MS Search

*MS Interpreter -* assists in analysis and interpretation of mass spectra (New Version)

## **NIST Libraries & Search Software**

The included **NIST MS Search Software** allows browsing and searching the EI MS, MS/MS, and GC libraries.



The GC library contains 404,045 citations of retention indices (Kovats or Lee) RI and GC methods for 99,400 compounds (72,361 in the EI library) with structures, covering both polar and non-polar columns. When available, this data is displayed with the spectrum search results. RI values can now be displayed in the hit list and used for scoring.

The MS/MS library contains 652,475 tandem spectra from ion trap, qTOF, HCD, and tandem QQQ collision cell instruments, most acquired under electrospray. Spectra can be browsed by mass, formula, and energy from the MS/MS tab or library searched against your own spectra or search criteria. Details on experimental conditions on each library spectrum are displayed.



The **Mass Spectrum Interpreter** utility assists in the evaluation of mass spectra. You can examine neutral losses, isotope patterns and possible chemical formulas, along with computer-assisted chemical structure/spectra analysis.

AMDIS Chromatogram - Component Mode - CAR	RD5P.D - IC:\TEMP\CARD5P.D\DAT
File Analyze Mode View Library Optio	ns Window Help
<u>Run</u> Rescale Info	
Abundance 107334 15 targets (T), 263 co	mponents (*) TIC
100	
75-	
50 -	
25-	
	un Munchand Manual
Time: 11.28 12.38 13.49 14.60	15.70 16.81 17.92 19.02
Abundance [7.83%] [3227]	IC 10.4105
100	11.5687 · 2 2.6,10-Dodecatrien-1-ol, 3,7,
75	12.0045 12.7765 - 2 2,6,10-Dodecation-1-ol, 3,7,
50	13.0870 • Caffeine •
	09 Component: Match:
25	94 Punity = 33% Net = 34 A Weighted = 96
Time: 13108 13141	Model = TIC + Simple = 36 +
Abundance [247]   Scan 365 (13.084 min)	and Extracted spectrum (13.087 min)
	194
100-	
75 55 109	
50 28 82	
25- 0	207 242 263 284 313 342
m/z: 25 50 75 100 125 150 175	5 200 225 250 275 300 325

MS/MS Library		#spectra	#ions	#compounds
small molecules,	ion trap	163,532	114,925	12,992
di- and tri-peptides	collision cell	411,294	34,517	12,728
commercial peptides	ion trap	13,062	6,422	1,828
	collision cell	77,182	5,637	1,814
total		652,475	123,881	



The NIST AMDIS utility integrates with NIST MS Search for

- *GC/MS deconvolution:* Preprocesses GC/MS or LC/MS data files, automatically reconstructing spectra from complex mixtures. Selected compounds can then be sent to the NIST MS Search software for library searching.
- *Chemical Identification:* Can also act as a "black box" chemical identifier, displaying all chemical identifications that meet a user-selectable degree of confidence. Identification can be aided by internal standards and retention times.

## New in NIST 17

#### All libraries have undergone substantial enhancements in the 2017 release.

- EI MS Library: 30,000+ new EI spectra. Expands coverage of metabolites and designer drugs, as well as the application of new computer-assisted evaluation methods for removal of low quality spectra.
- MS/MS Library: Nearly 3x increase in the MS/MS library. Spectra include metabolites, peptides (biologically active peptides and all di-peptides and tryptic tri-peptides), contaminants, metabolites, lipids and more.

Version	#EI Spectra	#MS/MS Spectra	#GC RI	Software
2017	306,622	652,475	404,045	v.2.3
2014	276,248	234,284	387,463	v.2.2
2012		121,586		
2011	243,893	95,409	349,757	v.2.0g
2008	220,460	14,802	224,038	v.2.0f
2005	190,825	5,191	121,112	v.2.0d
2002	179,948	0	0	v.2.0a

Library Search Options

Use Constraints

Search MS/MS Libraries Automation Limits Constraints

Clear All

Selected:1

• GC RI Library: 16,000+ more compounds have GC data method and retention indexes.

#### **Updated software** - some major new features include

#### MS/MS Searching

 New HiRes MS/MS Hybrid search type uses the logic of normal searching and the logic of neutral loss searching to find many more similar compounds in the hit list (requires a precursor mass).

Library Search Options

Hybrid

Spectrum Search Type O Identity 
Similarity

Search MS/MS Libraries Automation Limits Constraints RI (GC)

V Nom. Mass

- AnyPeak search: New accurate mass peak and loss types.
- MS/MS Precursor m/z search
- · Precursor type constraint to restrict results to specific precursor types, exclude isotopic precursors, and display MS3 and higher spectra in addition to MS2.
- Spectrum polarity filter
- EI MS Seaching
  - New EI Hybrid Search (Similarity / Hybrid) type uses both the logic of normal searching plus the logic of neutral loss searching. Same algorithm as MS/MS Hybrid search with unit charges and nominal MW instead of precursor m/z.
  - Presearch for EI Similarity/Neutral Loss search. Eliminates restrictions on the maximum loss considered.
- All Searching
  - An 'InChIKey' presearch for all library spectrum searches. Finds all spectra which have the same first InChIKey segment as the search spectrum, and compares them to the search spectrum.
  - Improved algorithms for scoring high mass accuracy searches that account for sparse spectra.
  - User interface enhancements.
  - New version of MS Interpreter software.
- · See "What's New" on our web page for additional details.



#### Visit http://www.sisweb.com/nist for more details, to contact us, or to order online.

Part No.	Description
941010	NIST 17 Library & Search Program, Standard Version
941010UG	NIST 17 Library & Search Program, Standard Version (Upgrade)
941010HP	NIST 17 Library & Search Program, Agilent Format Version
941010HPUG	NIST 17 Library & Search Program, Agilent Format Version (Upgrade)
941010MF	NIST 17 Library & Search Program, Multiformat/Shimadzu Version
941010MFUG	NIST 17 Library & Search Program, Multiformat/Shimadzu Version (Upgrade)
941010GC	NIST 17 Library & Search Program, GC RI Only
941010MSMS	NIST 17 Library & Search Program. MS/MS Only

Upgrade discount available for users of any previous version of NIST MS.



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