

## ASCII MS Spectrum File format (\*.spectrum)

The ASCII MS Spectrum File format (\*.spectrum) is fully compatible to the NIST mass spectra file format and has the following specifications:

Each row of the file is introduced by a special case-insensitive keyword, which is immediately followed by a colon, separating the key from the corresponding value(s). Spaces or other characters between the keyword and the colon are not allowed. Some keywords can be abbreviated; the optional part is listed in parentheses in the table below.

The order of the keywords is irrelevant, but the first one must be the *Name* keyword and the last one must be the *Num Peaks* keyword. Other keywords are optional, but may appear only once (except for the *Synonym* keyword).

**Note:** Some keywords accept only predefined arguments, which are listed in braces.

<b>Keyword</b>	<b>Description</b>
<i>Name</i>	This entry is required, only ASCII characters between ' ' (ASCII no. 32) and '~' (ASCII no. 126) are allowed, see table II a below. For Greek characters see table II b below.
<i>CAS</i>	The chemical abstracts registry number (with or without '-').
<i>NIST</i>	The database entry number of NIST libraries.
<i>UN</i>	The four-digit <i>United Nations</i> number of the compound.
<i>MW</i>	The molecular weight in the sense of a nominal mass (an integer number).
<i>Form(ula)</i>	The chemical formula.
<i>Syn(onym)</i>	A synonym for the compound. This entry can appear multiply.
<i>Com(ment)</i>	Any comment.
<i>Struc(ture)</i>	The hex decimally coded structure information of an MDL <sup>®</sup> MOL file, continuously written in the same line. Each single byte value is a two-digit number, where each digit must be a hexadecimal number (0..9,A..F,a..f). <i>Example: The first five bytes of some arbitrary MDL MOL file with the molecule name H2O in the first line should start with Structure: 48324F0D0A...</i>
<i>Cont(ributor)</i>	Contributor, recommended as "Name, Organization".
<i>InstType</i>	Type of instrument. Recognized symbols are: { <b>IT, TQ, Q, TOF, ICR, FTMS, ESI-TOF</b> }.
<i>InstName</i>	Any description for the instrument.
<i>IoniMethod</i>	Method of ionization. Recognized symbols are: { <b>EI, CI, APCI, ESI, nano-ESI, TS, MALDI, CAESIUM, APMALDI, APPI</b> }.
<i>IonPol(arity)</i>	Ion polarity. The following symbols are recognized: { <b>neg</b> or <b>0</b> for negative, <b>pos</b> or <b>1</b> for positive, <b>-1</b> for undefined polarity, <b>both</b> or <b>2</b> for both polarities}.
<i>MSMS(Stage)</i>	An integer number $n$ describing the MS <sup><math>n</math></sup> stage.
<i>Prelon</i>	A comma-separated list of precursor ions in $m/z$ (floating-point numbers). Although not obligatory, it is recommended to provide a list of $n-1$ precursor ions, if the MSMS stage was specified to be of order $n$ .
<i>ProdIon</i>	A floating-point number describing the product ion in $m/z$ .
<i>TrapDrive</i>	A floating-point number describing the trap drive value of the <i>esquire</i> instruments.
<i>Skim1</i>	A floating-point number describing the skim 1 value of the <i>esquire</i> instruments.
<i>FragAmpI</i>	A floating-point number describing the fragmentation amplitude value in $V$ .
<i>IsolWidth</i>	A floating-point number describing the isolation width value in $m/z$ .
<i>TargetGas</i>	Any identifier for the target gas.
<i>TargetGasPres(sure)</i>	A floating-point number describing the target gas pressure in $hPa$ .
<i>ReagentIon</i>	Any identifier for the reagent ion.
<i>ReagentGasPres(sure)</i>	A floating-point number describing the reagent gas pressure in $hPa$ .
<i>ColEnergy</i>	A floating-point number describing the collision energy in $eV$ .
<i>PeakWidth</i>	A floating-point number describing the original mass spectral peak width of the raw spectrum in $m/z$ .
<i>Refl(ector)</i>	Integer number describing the reflector mode as linear { <b>0</b> } or reflector { <b>1</b> }.
<i>PSD</i>	Integer number describing whether the spectrum is a post source decay spectrum

	{0, 1}.
<i>ChargeDeconvolved</i>	Integer number denoting whether the spectrum has been charge deconvoluted into the singly charged state {0, 1}.
<b>Date</b>	Date and time of the analysis given as a local time in the ISO 8601 format: <i>YYYY-MM-DD [T   ] HH:MM:SS [+ -] hh:mm</i> <i>Each item is presented as an integer value, hh:mm corresponds to the time offset between local time and the Coordinated Universal Time (UTC), such that UTC = local time - hh:mm</i>
<i>Column</i>	Any description of the chromatographic column.
<i>RetTime</i>	A floating-point number describing the retention time of the spectrum in analysis in seconds.
<i>SSID</i>	Unique software system ID of the analysis (Bruker-specific).
<i>AnalID</i>	Unique ID of the analysis (Bruker-specific).
<i>AnalName</i>	Any descriptive identifier of the analysis.
<i>Mass(Range)</i>	Two comma-separated floating-point numbers describing the lowest and the highest mass values of the MS measurement range.
<i>Num(Peaks)</i>	This item is obligatory and must be the last one of the list. The format is as follows: An integer number of peaks followed by pairs of mass (floating-point) and intensity (floating-point) values delimited by characters of the set "\n,;:")([]{}".

#### List of ASCII symbols allowed in the *Name* field:

SPACE	!	"	#	\$	%	&	'	(	)
*	+	,	-	.	/	0-9	:	;	<
=	>	?	@	A-Z	[	\	]	^	_
`	a-z	{		}	~				

Greek characters in the *Name* and *Synonym* fields can be embedded by placing their English transcription between dots:

.alpha.	.beta.	.gamma.	.delta.	.epsilon.	.zeta.
.eta.	.theta.	.iota.	.kappa.	.lambda.	.mu.
.nu.	.xi.	.omicron.	.pi.	.rho.	.sigma.
.tau.	.upsilon.	.phi.	.chi.	.psi.	.omega.