PSI Recommendation

PSI Mass Spectrometry and Proteomics Informatics Working Groups

Status: DRAFT

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August 7, 2025

**mzPAF: Peak Annotation Format - Peptides**

Status of this document

This document provides information to the proteomics community about the mzPAF peak annotation format specification for fragment ion mass spectra. The current specification document is focused on peptides. Distribution is unlimited. This document was ratified via the HUPO Proteomics Standards Initiative (PSI) Document Process. Any alterations of this document MUST also follow the HUPO PSI Document Process.

Version: Draft 18 of Version 1.0

# Abstract

The Human Proteome Organization (HUPO) Proteomics Standards Initiative (PSI) defines community standards for data representation in proteomics to facilitate data comparison, exchange and verification. This document presents a specification for a fragment ion peak annotation format for mass spectra, focused on peptides. This provides for a standardized format for describing the origin of fragment ions to be used in spectral libraries, other formats that aim to describe fragment ions, and software tools that annotate fragment ions. Further detailed information, including any updates to this document, implementations, and examples, is available at <http://psidev.info/mzPAF/>.

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# Introduction

## Description of the need

As part of the PSI spectral library format mzSpecLib, it is possible to annotate individual peaks, as is already done in spectral libraries from the National Institute for Standards and Technology (NIST, <https://chemdata.nist.gov/dokuwiki/doku.php?id=peptidew:start>), SpectraST,1 and PeptideAtlas.2 However, there have been several different styles of annotations in the past (even from a single provider), and therefore this document describes a single common peak annotation format for peptides that is recommended for all peptide libraries and related applications for which peak annotations are desirable.

The specification is heavily based on the formatting used in the NIST MSP format and the SpectraST sptxt format. These precursor formats were quite similar, but not exactly the same, and were never fully documented. NIST MSP annotations have undergone small changes over the years. Those annotation formats are based on the original nomenclature proposals published by Roepstorff and Fohlman3, which was further refined by Biemann4. Participants from NIST and SpectraST have led the development of this standard.

This format, as currently described, is designed for linear peptides with “simple” modifications, i.e. those routinely identified by typical proteomics pipelines (with or without enrichment methods), and for fragmentation methods commonly used in proteomics such as collision-induced dissociation (CID), higher-energy C-trap dissociation (HCD), and electron-transfer dissociation (ETD). Although there are some provisions for annotating small molecules (e.g., contaminants in a predominantly peptide spectrum), as well as unusual fragments, it is expected that for other major classes of analytes (metabolites, glycans, lipids, glycopeptides, cross-linked peptides, etc.), alternative peak annotation formats should be defined, ideally compatible with this format.

Throughout this document, when referring to mzPAF, it will primarily be in the context of supporting peptides in proteomics.

The content of this specification is inspired in part by and addresses some of the wishes laid out by the journal article “Expanding the Use of Spectral Libraries in Proteomics”5 following extensive discussions at the Dagstuhl Seminar and at several PSI workshops.

## Requirements

The main requirements to be fulfilled for the peak annotation format are:

* It MUST be machine parsable as well as easily human readable.
* It MUST be compatible with existing PSI file formats (especially mzSpecLib), where it will be used.
* It MUST support the encoding of linear peptides with “simple” modifications, i.e. those routinely identified by typical proteomics pipelines, but not including glycans.
* It MUST support fragmentation methods commonly used in proteomics such as CID, HCD, and ETD.
* It MUST support all reasonably common peaks observed in fragment ion spectra.

# Notational Conventions

The key words “MUST”, “MUST NOT”, “REQUIRED”, “SHALL”, “SHALL NOT”, “SHOULD”, “SHOULD NOT”, “RECOMMENDED”, “MAY”, and “OPTIONAL” are to be interpreted as described in RFC 2119.6 In general, “MUST” means required, “SHOULD” means recommended, and “MAY” means optional.

# The Peak Annotation Format Definition

## The documentation

The document provides the full specification of the mzPAF peak annotation format. It is accompanied by several other products. All products in their most recent form are available at the HUPO-PSI website (<http://psidev.info/mzPAF/>) or at the GitHub version control repository (<https://github.com/HUPO-PSI/mzPAF>). Additional components that accompany this specification are:

* An extendable list of isobaric label ions in text and JSON formats
* An extendable list of neutral losses in text and JSON formats
* A set of exemplary annotated spectra that demonstrate the use of mzPAF

## Relationship to other specifications

The format specification described in this document is not being developed in isolation; it is designed to be complementary to, and thus used in conjunction with, other PSI standards. Current related specifications include the following:

1. *mzSpecLib, the PSI spectrum library format* (<http://psidev.info/mzSpecLib>). The PSI spectrum library format is designed as a standard mechanism for storing spectrum libraries. Individual peaks from mass spectra encoded in the libraries are annotated using this format.
2. *ProForma 2.X.* This PSI format containsrules on how to encode peptidoforms and molecular formulae7 (<https://psidev.info/proforma>).

# The Basic Form of the Peak Annotation Format

The mzPAF peak annotation format is composed of a string of characters. It is case sensitive. There is no limit in its maximum length. Line breaks MUST NOT be used. The character encoding is not enforced, but all characters shown in this specification are UTF-8 characters below 128 unless otherwise stated in this specification.

The basic format of each annotation is:

*annotation1/delta,annotation2/delta*,...

or

*annotation1/delta\*confidence,annotation2/delta\*confidence*,...

e.g.

b2-H2O/3.2ppm,b4-H2O^2/3.2ppm

where multiple possible explanations are separated with a comma. Deltas of (observed – theoretical) *m*/*z* values are prefixed with a slash (/). Scores MAY be provided for different annotations prefixed with an asterisk (\*), such as:

b2-H2O/3.2ppm\*0.75,b4-H2O^2/3.2ppm\*0.25

The sections below define each component of these annotations.

## Annotation of multiple analytes

It is common for there to be multiple analytes co-fragmented together to produce a spectrum, or there may be alternative interpretations of the spectrum. These can take the form of two or more separately described precursors, or just low-level contamination from background peptide ions, or other miscellaneous molecules. It is possible to define more than one analyte in the context of a single spectrum, and these MUST be assigned numbers 1, 2, etc. The number 1 is assumed to be the primary analyte, the one that the annotation writer recommends as first in a list of analytes. The number 0 is reserved as one or more unspecified contaminant molecules (see example below for common y1 ion observations for unidentified contaminant peptides).

For spectra that have multiple analytes associated with them, peak annotations MUST be prefixed with their analyte number as defined for the spectrum and an @ symbol. For such cases of multiple specified analytes, the prefix notation MUST be present on every ion to indicate to which analyte the annotation applies. If there is only one analyte defined, peak annotations SHOULD NOT be annotated with 1@. For example,

1@y12/0.13,2@b9-NH3/0.23

indicates that the peak may be either the y12 ion from analyte 1 or the b9-NH3 ion from analyte 2. As another example, most high signal-to-noise ratio HCD spectra of tryptic digests contain the y1 ions corresponding to both lysine and arginine. If analyte 1 is a peptide ending in R, it will be common to see:

0@y1{K}

0@y1{K}-NH3

which is the lysine y1 ion and the y1-NH3 ion corresponding to some unspecified (hence the number 0) contaminating peptide ion ending with a lysine. See section 4.4.3 for more information about specifying sequences for ion series fragments.

## Multiple annotations

Each peak may have multiple annotations separated by commas. These multiple annotations MAY represent AND or OR. There is no distinction between whether the annotation system intends that there are two contributors to a peak or whether they are mutually exclusive.

If there are several annotations, they SHOULD be ordered by decreasing likelihood (based on existing knowledge about fragmentation), e.g. a primary series ion should be listed before a rare neutral loss.

If a regular expression-based annotation parser designed for a single annotation is used, additional logic is required to handle multiple annotations. A procedure like the following SHOULD be applied:

* From the current position, attempt to pattern-match the longest possible regular expression and record it.
* If the next unmatched character is a comma, skip the comma and begin again, and repeat until done.
* If the regular expression goes to the end of the string, then parsing is complete.
* If the next unmatched character is not a comma, this is a parsing error.

See Appendix A for a Python-like pseudo code description of this procedure.

## Deviation of observed *m*/*z* from the theoretical *m*/*z* values

Each annotation SHOULD include an *m*/*z* delta (observed m/z - theoretical m/z), UNLESS the m/z values provided are all theoretical values, as in the case for a library of predicted spectra. The theoretical *m/z* is calculated from the sum of the atoms and charged particles comprising the ion reportedly explaining the annotated peak. A negative delta MUST be preceded by a minus sign. A non-negative delta MUST NOT be preceded by any sign. There are two possible units, either *m*/*z* units (Daltons per elementary charge) or parts per million (ppm). Any *m*/*z* deltas in parts per million MUST have the suffix “ppm” in lower case without a preceding space. *m*/*z* deltas in *m*/*z* units (Daltons divided by charge) MUST NOT have any suffix. Examples:

y1/-1.4ppm

y1/-0.0002

## Ion notation

Each annotation begins with an ion notation describing the putative peak origin. The ion notation has multiple components described as follows:

**[ion type]**(neutral loss)(isotope)(adduct type)(charge)

Of these five components, only the first (ion type) is always required. The others are optional. Each of these components is described in the following subsections. A complex example with all five components is:

y4-H2O+2i[M+H+Na]^2

Here, a peak from two isotopes above the monoisotope of a doubly charged protonated and sodiated y4 ion with a water loss is annotated.

### Ion types overview

The ion type component is required and describes the basic type of ion being described. Examples are b ions, y ions, immonium ions, unfragmented precursor ions, internal fragmentation ions, isobaric tag ions, etc. Each of these is described in the subsections below. As mentioned above, the specification is peptide centric. Although there is desire to support other kinds of molecules (e.g. small molecules, lipids, and glycans) in the future as well, an accepted nomenclature for specifying such ion types has not yet been decided. However, this specification offers limited support for such ion types through the use of chemical formulae, SMILES strings or a free-text name of the non-peptide molecule.

The following is a list of ion type prefixes, as described in detail in the subsections below:

|  |  |  |
| --- | --- | --- |
| Prefix | Code point | Description |
| ? | 63 | Unknown ion |
| a | 97 | Peptide a ion series |
| b | 98 | Peptide b ion series |
| c | 99 | Peptide c ion series |
| d | 100 | Peptide d ion series |
| v | 118 | Peptide v ion series |
| w | 119 | Peptide w ion series |
| x | 120 | Peptide x ion series |
| y | 121 | Peptide y ion series |
| z | 122 | Peptide z ion series |
| I | 73 | Immonium ion |
| m | 109 | Internal fragment (‘m’iddle) |
| \_ | 95 | Named compound (underscore) |
| p | 112 | Precursor ion |
| r | 114 | Reference molecule, such as a TMT or iTRAQ ion or Hex or Adenine |
| f | 102 | Chemical formula |
| s | 115 | SMILES string |

For most ion types, one or two ordinal numbers or additional characters follow the ion type prefix to complete the specification; see examples below.

The following prefixes are reserved for future extensions for custom annotation formats for other molecule types: G for glycan ion fragments; L for lipid ion fragments; X for cross-linked peptide fragments.

### Unknown ions

If a spectrum has been annotated and peak annotations are included for other peaks, those peaks that cannot be interpreted SHOULD be marked with ‘?’. The charge state and isotopic state MAY be specified after the ‘?’ if they can be determined (e.g. by charge deconvolution), such as:

?

?^3

?+2i^4

See the “Isotope” and “Charge State” sections below for more information on those components.

An unknown ion MAY be assigned a positive integer in order to annotate relationships with other unknown ions. In the following examples, one ion is designated as number 17 and then an isotope and neutral loss of this ion are annotated to indicate their proposed relationship to a primary unknown ion:

?17

?17+i/1.45ppm

?17-H2O/-0.87ppm

Unknown ion annotations MAY be preceded with an analyte identifier such as 0@ or 1@ or left unspecified. Writers MAY specify their preference if orthogonal information indicates whether an ion belongs to a specified analyte or a contaminant.

### Primary series ions

The primary fragmentation series ions include a, b, and c ions from the N terminus and x, y, and z ions from the C terminus. The ion types are followed by an ordinal to indicate how many residues from the terminus are included in the fragment. For example, a b2 ion indicates 2 residues from the N terminus.

The following table describes how the theoretical mass of each type of primary ion is calculated. The formulae as shown assume that the N and C termini are unmodified, and the adduct type is [M + zH]. Ʃ(AA) is the sum of masses of the neutral, modified amino acid residues (i.e. the structure -NH-CHR-CO- where R is the side-chain, for non-proline). (H+)z is the proton mass multiplied by the charge state.

|  |  |  |
| --- | --- | --- |
|  | Formula | Remarks |
| a | ∑(AA) – CO + (H+)z |  |
| b | ∑(AA) + (H+)z |  |
| c | ∑(AA) + NH3 + (H+)z | The “c-1” radical ion, which arises when the c ion loses a hydrogen to the z.+ ion, is also observed in ETD. This is denoted with a “neutral loss” of -H, e.g. “c12-H^2”. See “Neutral losses” section below. |
| d  (da)  (db) | ∑n-1(AA) + C2H3N + (H+)z | The d ion is partial loss of the side chain from an a ion, breaking at the second carbon atom. For Threonine and Isoleucine there are two possible d ions; these can be listed as ‘daN’ and ‘dbN’ where a is the heaviest of the two options. For Threonine da has an additional group of OH and db a group of CH3. Isoleucine da has an additional group of C2H5, and db a group of CH3. Valine is a special case; it has CH3 as additional mass. Glycine, alanine, and proline have no d ions. |
| v | ∑c-1(AA) + C2H2NO + (H+)z | The v ion is complete loss of the side chain of the y ion. |
| w  (wa)  (wb) | ∑c-1(AA) + C3H3O + (H+)z | The w ion is partial loss of the side chain from the z ion, breaking at the second carbon atom. For Threonine and Isoleucine there are two possible w ions; these can be listed as ‘waN’ and ‘wbN’ where a is the heaviest of the two options. For more details see the d ion. |
| x | ∑(AA) + CO – 2H + (H+)z |  |
| y | ∑(AA) + H2O + (H+)z |  |
| z | ∑(AA) + H2O – NH2 + (H+)z | This is also known as the z.+ radical ion, which is found in ETD spectra. This ion is heavier by one hydrogen atom than the non-radical “z ion” originally defined by Biemann (1990).4  In addition, the “z+1” ion, which arises when the z.+ abstracts a hydrogen atom from the c ion, is also observed in ETD. This is denoted with a “neutral gain” of +H, e.g. “z12+H^2”. See “Neutral losses” section below. |

For any peptide fragmentation annotations that do not come from the proposed peptide analyte(s) used to annotate other peaks in the same spectrum, the ion type and ordinal for any additional asserted interpretations MAY be indicated by following the peak annotation with a peptide sequence in curly braces, such as:

0@b2{LL}

0@y1{K}

0@b2{LC[Carbamidomethyl]}

0@b1{[Acetyl]-M}

0@y4{M[Oxidation]ACK}-CH4OS[M+H+Na]^2

The peptide sequence is defined using ProForma7. The sequence MUST be a ‘base-ProForma compliant’ sequence with the added rule that labile modifications MUST NOT be used.

The amino acid count of the peptide sequence SHOULD NOT be greater than the ion series ordinal. The amino acid count of the peptide sequence MUST NOT be less than the ion series ordinal. This notation can be useful for annotating identifiable low-mass ions from contaminants that are clearly not associated with a specified analyte, or for marking sequence tags identified by de novo sequencing algorithms.

### Internal fragment ions

Canonical internal fragments result from two amide bond cleavages – those forming b/y ions – of the peptide precursor ion. As such, they do not contain either terminus. An internal fragment is denoted by the ion type ‘m’ (for “middle”). To describe an internal fragment, specify a range n1:n2 where n1 is the ordinal (beginning with 1, counting from the N terminus) of the N-terminal amino acid residue of the fragment in the original peptide sequence, and n2 is the ordinal (beginning with 1, counting from the N terminus) of the C-terminal amino acid residue of the fragment in the original peptide sequence.

For example, for the peptide precursor ion MYPEPTIDEK/2, the 1+ internal fragment ion of PEPT (the 3rd to 6th amino acids in the original peptide sequence) should be denoted by:

m3:6

Internal fragments of only one residue SHOULD be encoded as immonium ions, not as internal fragments of length 1. Even though b ions have the same masses as internal fragments with n1 = 1, one MUST NOT denote any b ion as m1:n2. In cases where there is an N- or C-terminal mass modification that is lost, it MUST be encoded as a neutral loss as described below. For example, for the precursor [Carbamidomethyl]-MYPEPTIDEK/2, a fragment ion that is MYP without the N-terminal Carbamidomethyl should be denoted as:

b3-C2H3NO

or

b3-[Carbamidomethyl]

instead of:

m1:3

Other internal fragment ions are possible. For instance, one that results from the cleavage of the C-N bond (a b/y cleavage) on the N-terminal side and a C-C bond (an a/x cleavage) on the C-terminal side produces a “ya” ion. The “yb” and “ya” (-CO) internal fragments are commonly seen in HCD spectra. These are encoded as a neutral loss/gain (see section 4.5 on Neutral Loss (or gain) below) of the corresponding canonical internal fragment, e.g.

m3:6-CO

The resulting neutral loss or gain from any internal ion can be found in the table below.

|  |  |  |  |
| --- | --- | --- | --- |
| Backbone cleavage | x | y | z |
| a | No difference | -CO | -CHNO |
| b | +CO | No difference | -NH |
| c | +CHNO | +NH | No difference |

Following the primary ion series convention, singly-charged internal fragment ions are not labeled with a charge component, but multiply-charged internal fragments should be labeled with ^N at the end, where N is 2, 3, 4, etc.

A doubly charged “ya” internal fragment with a water loss would be written

m3:6-CO-H2O^2

In case there are multiple instances of the same combination of residues (with differing order) of the internal fragment ion in the sequence of the precursor, all MAY be specified, and MAY be ordered from most likely to least likely. For example, for a precursor of MYPEPTIDEK/2, m3:4 is far more likely than m4:5, although they have the same mass and both might be produced. In this case one MAY annotate the peak as

m3:4/1.1ppm,m4:5/1.1ppm

On the other hand, if the multiple possible internal fragments are identical in sequence, only the annotation with the smallest ordinals SHOULD be used. For example, for the precursor GGAAAAAAK/2, the internal fragment ion of AAA SHOULD only be annotated as:

m3:5

since m3:5, m4:6, m5:7 and m6:8 are all equivalent.

### Immonium ions

An internal fragment with just a single amino acid formed by a b/y cleavage on the N-terminal side and an a/x cleavage on the C-terminal side is called an immonium ion (forming an “ya” internal fragment that is equivalent to the residue mass minus CO). Immonium ions are denoted by capital ‘I’, followed by the one-letter amino acid abbreviation. For example, the common tyrosine immonium and histidine immonium ions are denoted by:

IY

IH

There are other related ions from a single amino acid residue that are sometimes referred to as “immonium ions.” These MUST be annotated as a neutral loss/gain of the corresponding true immonium ion (see section 4.5 on Neutral Loss below). For example, the leucine immonium ion can lose a CH2, which is written as:

IL-CH2

Some immonium ions are derived from residues that already have a mass modification attached. In this case the modification can be specified as either the Unimod entry name in square brackets or a monoisotopic mass following the residue letter. If multiple modifications are present on the amino acid these MUST be encoded using a single mass modification. For example, common immonium ions from carbamidomethylated cysteine and phosphorylated tyrosine are:

IC[Carbamidomethyl]

IY[Phospho]

IC[+58.005]

Neutral losses may be added to these as usual.

### Intact precursor ions

The intact, unfragmented, precursor ion, as well as its neutral losses, can often be found in the tandem mass spectrum in CID. For an MS3 spectrum, the precursor is the MS2 fragment ion selected for fragmentation for MS3. The precursor is denoted by the ion type ‘p’. For example, the intact 2+ precursor ion is denoted by:

p^2

As with all peak annotations, the omission of an adduct type specification (see Section 4.8) implies that 2 protons are added to the neutral precursor to yield the 2+ charge. For another example, the phosphate neutral loss of a 2+ precursor ion, which is often an intense peak in CID spectra of peptides containing a phosphorylated serine is given by:

p-H3PO4^2

Note that the charge state needs to be included explicitly, even though it is implied by the precursor charge state. This is needed to distinguish charge-reduced precursor ions, which are common in ETD spectra. For instance, in the ETD spectrum of a 4+ precursor ion, one might find the 4+ unfragmented precursor ion (p^4), a charge-reduced 3+ unfragmented precursor ion (p+H^3) after the capture of an electron, a charge-reduced 2+ unfragmented precursor ion (p+2H^2) after the capture of two electrons, and a charge-reduced 1+ unfragmented precursor ion (p+3H) after the capture of three electrons. ETD spectra can also have charge-reduced precursors due to lost protons (not always addition of electrons), so that would be denoted as fewer added hydrogens, e.g. p^2 for the loss of two protons from a 4+ precursor. The possible intact precursor ions from a 4+ precursor are:

Annotation Adduct type Description

p^4 [M+4H]4+ original 4+ precursor with four additional protons

p+H^3 [M+4H]3+ capture of one electron

p^3 [M+3H]3+ loss of one proton

p+2H^2 [M+4H]2+ capture of two electrons

p^2 [M+2H]2+ loss of two protons

p+H^2 [M+3H]2+ capture of one electron, loss of one proton

p+3H [M+4H]+ capture of three electrons

p+2H [M+3H]+ capture of two electrons, loss of one proton

p+H [M+2H]+ capture of one electron, loss of two protons

p [M+H]+ loss of three protons

To summarize, to distinguish the possible charge-reduced precursor ions, one attaches a “neutral gain” of hydrogens to the ion type whenever the number of protons is different from what one would expect from a purely protonated adduct at that charge state. As with the regular fragment ion types (b, y, etc.), a 1+ precursor MUST NOT get a charge suffix (i.e, use p instead of p^1).

WARNING: This is a different convention than used by the NIST MSP format where the original charged precursor did not get the charge suffix and all other charge states, including 1+, did.

### Reference ions

Peptide MS2 spectra can contain a substantial number of non-peptidic fragment ions, and many of them are well known. In MS2-based labeled quantification strategies employing an isobaric tag, such as iTRAQ and TMT, fragment ions of the tags are used for quantification. The isobaric tag is typically attached to the N terminus or to the side-chain amino group of certain residues, and the cleavage of the tag releases the reporter ion. Typical examples of this are TMT and iTRAQ reporter ions, and other isobaric labeling reagent derived ions. In addition to isobaric tags, some peptide PTMs may also be labile, resulting in fragments corresponding to the protonated modification group which can be useful as a diagnostic marker for the PTM. Other reference ions derived from monosaccharides and nucleotides are often seen in peptide MS2 spectra.

Reference ions are prefixed with the letter ‘r’ with the name following in square brackets. The name MAY be a Unimod entry name, or defined in the version-controlled JSON document in GitHub that may be updated as the field advances. The version-controlled JSON document in GitHub MUST be given priority over Unimod when there are entries with the same name. There is also a human-readable markdown version autogenerated from the JSON. The markdown version is viewable here:

<https://github.com/HUPO-PSI/mzPAF/blob/main/specification/reference_data/reference_molecules.md>

and the software-parsable JSON version is available here:

Viewable:

<https://github.com/HUPO-PSI/mzPAF/blob/main/specification/reference_data/reference_molecules.json>

Raw:

<https://raw.githubusercontent.com/HUPO-PSI/mzPAF/main/specification/reference_data/reference_molecules.json>

The current version of this list is provided as Appendix B of this document, but the above URLs should be checked for updates.

When appearing as independent ions, reference ions are prefixed with the letter ‘r’ with the name following in square brackets in order to provide a reliable handle for software parsers such as:

r[TMT127N]

r[iTRAQ114]

r[TMT6plex]

r[Hex]

r[Adenosine]

These names MAY contain paired “[“ and “]” characters. They are assumed to be protonated (as are other ions in the specification) (and thus heavier than the neutral mass by a proton and singly charged) unless followed by an adduct component that specifies some other charge-bearing moiety (e.g. [M+Na]). For example, the Unimod entry name of HexNAc(2) specifies a mass modification of 406.1587 Da. The corresponding 1+ protonated reference ion (e.g., the oxonium ion of GlcNAc-GlcNAc) denoted r[HexNAc(2)], has a mass of 407.1660 Da.

### 

### Named compounds

If a fragment ion does not fit into the previous categories, yet is more easily understood by a name rather than a chemical formula or a SMILES string, it MAY be specified as a compound name. Such a name MUST be prefixed with an underscore (\_) followed by a string enclosed in curly braces ({}). The string within curly braces does not need to be software-interpretable. It may be followed by neutral loss, isotope, adduct type, and charge information in the usual manner. As an example,

0@\_{Urocanic Acid}

attributes the annotated peak as coming from a singly charged urocanic acid molecule (uncharged would not be detected, and doubly charged MUST be postfixed with ^2, etc.). The string after the underscore and enclosed in curly braces should be as informative and concise as possible. The string MUST imply the neutral molecule to which charge is then added. It is not obligatory that tools supporting this format are able to understand a peak annotation of 0@\_{Urocanic Acid}+HPO3^2 as the 2+ ion of some molecule monophosphate and display it to a user, but a more formal specification MAY be developed in the future. Tools MAY encode a list of known named compounds to annotate, but this is not required. Readers of this notation MUST simply understand that it is some named compound ion, but are not obligated to understand more than that.

### Chemical Formulas

Chemical formulas for identified peaks may be encoded if they are non-peptidic in origin. This may be useful for contamination peaks or for small molecule spectra where the small molecule is a named analyte. Chemical formulas MUST be prefixed by ‘f’, enclosed in curly braces, and follow the formatting described below in the neutral loss subsection.

The chemical formula enclosed in the curly braces is understood to represent all the nuclei in the charged molecule. For example, if the compound is singly charged with a proton, there will be an extra H in the formula over what would be the neutral molecule. Adduct information MAY be specified as described in section 4.8 to denote the charged atoms; however, it does NOT add mass to the molecular formula. In the first line of the example below, C13H9 corresponds directly to all nuclei present in the ion and theoretical *m/z* is computed as the mass of C13H9 minus the mass of one electron (since it has a charge of 1+) to yield the *m/z* of 165.069988, and it may be assumed that one of the H atoms is a proton.

An example from MassBank <https://massbank.eu/MassBank/RecordDisplay.jsp?id=SM858102> adapted for this format is as follows:

165.0698 104629.2 f{C13H9}/-0.55ppm

167.0730 479334.8 f{C12H9N}/0.06ppm

179.0726 82567.1 f{C13H9N}/-2.01ppm

180.0808 27526884.0 f{C13H10N}/-0.11ppm

181.0886 783300.1 f{C13H11N}/-0.09ppm

182.0965 6583053.0 f{C13H12N}/0.26ppm

192.0808 189835.2 f{C14H10N}/0.19ppm

193.0887 66613.2 f{C14H11N}/0.45ppm

208.0757 1080071.1 f{C14H10NO}/0.03ppm

Other suffixes such as for isotope and charge state, as described elsewhere in this document, may be used following the chemical formulae, e.g.:

f{C16H22O}+i^3

Stable isotopes can be encoded as in ProForma 2.X by prefixing the atom with its isotopic number in square brackets. This notation MUST only be used for stably labeled molecules. Any peak that is isotopically related to another annotated peak MUST use the isotope notation as written in section 4.6. Thus, the following is only permitted if it is known that this is a stable isotope label:

f{C15[13C1]H22O}^3

The ProForma 2.X specification7 (<https://psidev.info/proforma>) provides further rules on how to encode molecular formulas regarding white space and recommended element ordering.

### SMILES strings for chemical compounds

Chemical compounds may also be expressed using SMILES notation (<https://en.wikipedia.org/wiki/Simplified_molecular-input_line-entry_system>). SMILES strings MUST be prefixed by ‘s’ and enclosed in curly braces. For example:

s{CN=C=O}[M+H]/-0.55ppm

s{COc(c1)cccc1C#N}[M+H+Na]^2/1.29ppm

Since the structure of the adduct ion is often unclear, the SMILES string MUST NOT include the charge-bearing moieties (H+, Na+, etc.) which may be attached at unspecified sites. Therefore, the SMILES string MUST correspond to the neutral molecule, and the charge-bearing moieties should be specified by the adduct notation as described in Section 4.8.

In the example above s{CN=C=O}[M+H] should be interpreted as the neutral molecule methyl isocyanate H3C-N=C=O with an additional proton attached to it at an unspecified location, to yield a 1+ charge (a charge state of 1+ is assumed for all peak annotations unless specified with a ^c suffix). This also means that the mass of the ion should be calculated from the neutral mass of methyl isocyanate plus that of a proton. Likewise, s{COc(c1)cccc1C#N}[M+H+Na]^2 denotes an adduct ion of 2+ charge state, in which the neutral molecule of COc(c1)cccc1C#N (3-methoxybenzonitrile) is attached to one proton and one Na+ ion at some unspecified sites.

Note that while the SMILES format allows for the specification of charged nuclei, it only supports this use case where the molecular structure is fully known. Although sometimes it is possible to place the charge-bearing moiety at an exact location with high confidence, in order to avoid confusion about how the mass should be calculated, the SMILES string MUST encode neutral molecules only. The charge state and the charge-bearing moiety(-ies) MUST be encoded in the adduct notation following the SMILES string, as described in Section 4.8. In addition, if SMILES strings are used, the [M+nH] suffix MUST always be included even if the adduct is only protonated (unlike for peptides for which protonated adducts are assumed if omitted).

For the purpose of mass calculation, it is assumed that what follows the M in the adduct notation are ions which should confer the correct charge state, i.e., [M+Na] means the addition of a 1+ sodium ion, not a sodium atom, whereas [M+HCOO] means the addition of formate HCOO-, not the neutral radical of HCOO. It should be noted that sometimes the adduct notation is used in the literature to also specify neutral loss/gain to the neutral analyte, in addition to the charge-bearing moiety(-ies). Since mzPAF already provides for a mechanism to specify neutral loss/gain (Section 4.5), it is recommended that what follows the M in the adduct notation SHOULD only include charge-bearing ions, and neutral loss/gain SHOULD NOT be included in the adduct notation. For example, s{OCCCC=OOH}-H2O[M+H] is preferred over s{OCCCC=OOH}[M-H2O+H] to denote 4-hydroxybutyric acid with a water loss (with exact structure unknown), charged with an additional proton.

If the ion is generated by the gain/loss of electrons only, then the adduct notations of [M+/-ne] MUST be used. For example, [M-e] stands for the 1+ ion generated when the neutral molecule specified by the SMILES string loses an electron. [M+2e] stands for the 2- ion generated when two electrons are added to the neutral molecule. The shorthand of [M+] to mean [M-e] MUST NOT be used.

In this version of the specification, only SMILES is supported as opposed to InChI, because SMILES is more human readable. If both SMILES strings and chemical formulas are provided, they MAY be equivalents or alternatives.

## Neutral losses

The neutral loss (or gain) component MAY be denoted as a string of 0 to n loss (or gain) components, described by their molecular formula. Most losses are negative and preceded by a minus sign. However, neutral gains may be signified with a plus sign. Double (and triple and up) losses SHOULD be preceded by an integer indicating the number (e.g., -2H2O signifies a double water loss). Single losses MUST NOT have a preceding 1.

Reference group names in square brackets, which can either be defined in the version-controlled JSON document as described in Section 4.4.7 or a Unimod entry name, MAY also be used as a neutral loss. Common use cases of reference group neutral losses are the losses of glycan groups in the fragmentation of glycopeptides, and of the quantitation tag in the fragmentation of TMT- or iTRAQ-labeled peptides. Here, the lost mass is equal to the neutral mass of the reference group, e.g.:

p-[Hex]

which denotes the precursor ion with a neutral loss of about 162 Da (C6H10O5, corresponding to the “Hex” modification in Unimod).

The following are a table of common neutral losses/gains. If the neutral loss/gain in question is listed below, they SHOULD be followed as a matter of convention (e.g., do not write an ammonia loss (NH3) as H3N). If the neutral loss/gain in question is not listed, one may prescribe new ones as chemical formulae as described in section 4.4.9. This table is not complete, and other losses are possible.

|  |  |  |  |
| --- | --- | --- | --- |
| Neutral loss/ gain group | Common name | Exact mass (monoisotopic) | Remark |
| H | Hydrogen | 1.007825 | e.g., for specifying hydrogen transfer from c to z ions in ETD |
| NH3 | Ammonia | 17.026549 | From amine groups |
| H2O | Water | 18.010565 | From -OH and -COOH groups |
| CO | Carbon monoxide | 27.994915 | For backbone fragments, use “a” instead of “b-CO”. But for internal fragments, use “mx:y-CO”. Also seen as a neutral loss from formylated serine or threonine. |
| CO2 | Carbon dioxide | 43.989829 | From -COOH groups |
| HCONH2 | Formamide | 45.021464 | From -CONH2 groups |
| HCOOH | Formic acid | 46.005479 | From -COOH groups |
| CH4OS | Methanesulfenic acid | 63.998301 | From oxidized methionine |
| SO3 | Sulfur trioxide | 79.956818 | From sulfotyrosine |
| HPO3 | Metaphosphoric acid | 79.966331 | From phosphotyrosine and sometimes from phosphoserine and phosphothreonine |
| C2H5NOS | Mercaptoacetamide | 91.009195 | From carbamidomethyl cysteine |
| C2H4O2S | Mercaptoacetic acid | 91.993211 | From carboxymethyl cysteine |
| H3PO4 | Phosphoric acid | 97.976896 | From phosphoserine and phosphothreonine |
| [reference group ]  Note: The square bracket is mandatory for non-chemical formulae. |  | (variable) | See the reference ions section above. The reference group name inside the square bracket can either be a Unimod entry name, or defined in the aforementioned version-controlled JSON document. |

Such neutral gains and losses may be strung together as in these examples:

y2+CO-H2O

y2-H2O-NH3

p-[Hex]

p-[TMT6plex]-2H2O-HPO3

p-2[iTRAQ115]

p-[iTRAQ116]-CO-H2O-HPO3

If there are multiple neutral gains/losses, alphanumeric order SHOULD be followed, e.g. y2-H2O-NH3 rather than y2-NH3-H2O. Annotations such as y2-H2O-NH3 and y2-NH3-H2O are considered identical, and SHOULD NOT be listed as multiple plausible annotations.

Special care should be taken in supporting isotopes in the neutral losses. There are two major tricky cases. Isotopes could exist as a single element of the loss in which case it is very similar to a named reference molecule. The other case is when isotopes and adduct ions, as described in section 4.7, are mixed. In this case the adduct type will always start with ‘M+’ which makes it possible to distinguish these cases.

y2-[2H1]-NH3

y5-H2[18O1][M+Na]

## 

## Isotopes

The isotope component is optional. If the monoisotopic ion is being described, then there MUST NOT be any isotope component. However, if another isotope is being described, then isotope notation MUST be used. For generic isotopes, the component MUST be “+ni” or “-ni” where n is the isotope number above or below the monoisotope; however, an n of 1 SHOULD be suppressed, following the precedent from the NIST MSP format. Examples are: +i, +2i, +3i, -i, -2i, etc.

This notation does not differentiate among isotopes of different constituent atoms of the fragment (C, H, N). The theoretical mass of the generic isotope ‘+i’ is taken to be the difference between 13C and 12C (1.003355 Da) greater than that of the monoisotope ion.

Isotope peaks derived from isotopes of specific atoms MAY be specified with the form ‘+niZE’ where Z is the number of nucleons and E is the element, e.g. ‘+i13C’ or ‘+3i15N’. For the complex cases with multiple isotopes from different elements these MAY be listed sequentially, eg ‘+6i13C+2i15N’. Because a generic isotope ‘+i’ mass is assumed to be the difference between 13C and 12C, the following expressions are identical in their theoretical mass, but the first indicates that there is no evidence to describe the isotope solely to carbon 13:

+i

+i13C

The following are distinct, however:

+i

+i15N

If a nucleon identity is specified, it MUST include the number of nucleons; the following is NOT valid:

+iN

For large molecules, the number of possible isotopologues expands combinatorially, and with sufficient resolving power, a peak could be assigned to be a specific combination of them, such as an isotopologue which contains two carbon 13 atoms and one nitrogen 15 atom:

+2i13C+i15N

As higher order combinations are considered, it becomes increasingly difficult to distinguish between isotopomers. Writers SHOULD NOT specify alternative isotopomers if there is ambiguity unless absolutely necessary.

If an annotated peak is thought to be an unresolved blend of multiple isotopomers, not just 13C, it MAY be annotated with an A (average) after the i.

+iA

+2iA

Such blending can be seen in orbitrap spectra at commonly-used resolving powers, as summarized in Figure 1.

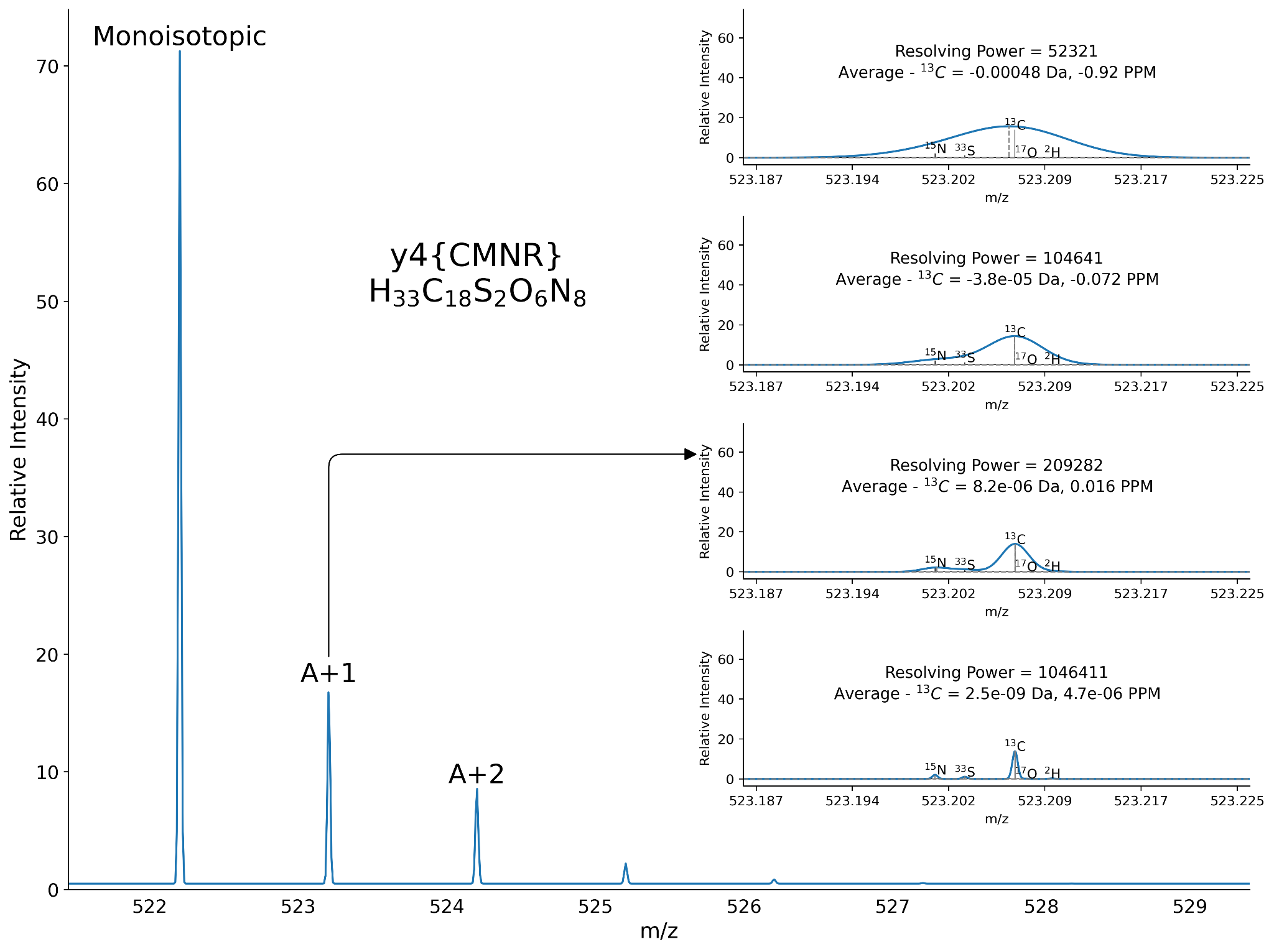


Figure 1. Summary of the common isotope fine structure situation for a molecule containing C, H, N, O, and S. At resolving power 1000000, the fine structure is resolved, but at the more common resolving power = 50000, the isotopes are blended, but the centroid is shifted by 0.92 ppm from the theoretical 13C - 12C delta by isotopes of other atoms, primarily 15N.

## Adduct Type

The adduct type component is optional. Typical conditions for peptide ionization for proteomics generates protonated cations [M+H], [M+2H], etc, which are implied if the adduct type component is omitted. When the adduct type is omitted, the number of added protons is taken to be equal to the charge state, which is specified with the ^ notation as described in the following section. However, under some conditions other charged atoms convey the charge, such as the sodiated peptide ion. If the fragment ion is anything except a purely protonated adduct, it MUST be specified in the form [M+nA] or [M-nA] where M is the neutral fragment being annotated, A is the atom/molecule added to the neutral fragment to form the ion using the molecular formula notation from section 4.4.9, and n is the number of specified atoms/molecules added. If n is 1 it SHOULD be left out. If more than one kind of atom/molecule is added, it will be specified by [M+n1A+n2B…], etc. Some examples are:

[M+Na] denotes a sodiated adduct ion

[M+NH4] denotes an ammonium adduct ion

[M+2Na] denotes an adduct ion with two sodium atoms (which MUST be followed by ^2 to specify the charge state, see below under “Charge State”)

[M+2H+Na] denotes an adduct ion with two hydrogen atoms and one sodium atom (which MUST be followed by ^3 to specify the charge state, see below under “Charge State”)

If there are multiple types of atoms/molecules, alphabetical order SHOULD be followed, e.g. [M+2H+Na] rather than [M+Na+2H].

A useful reference for adducts may be found at the web page: <https://fiehnlab.ucdavis.edu/staff/kind/Metabolomics/MS-Adduct-Calculator/>. Note that at the time of this writing, the concept of mass and *m/z* are conflated at this web page. Table columns that are labeled “mass” are actually “m/z”.

Complete Examples:

A sodiated y4 singly charged ion is written:

y4[M+Na]

A doubly charged y5 ion with one charge from Na+ and one from a proton and a water loss:

y5-H2O[M+H+Na]^2

A specific isotope in a charge is written:

y6[M+[2H2]]^2

y5[M+[15N1]H4]

IMPORTANT NOTE: In this context, the M represents the annotated neutral fragment, NOT the precursor or some other parent analyte. In the above example, M represents a neutral y5-H2O. Therefore, it is not valid to specify 2M to indicate that the primary analyte has formed a dimer, or similar.

## Charge state

If the charge is 1+ (most common), this component MUST be suppressed. If the charge is not 1+, then the charge MUST be provided as ^n where n is the charge number (without a + symbol). Examples are ^2, ^3, etc.

Charge 0 MUST NOT be used. If the charge state is not known, the peak annotation SHOULD be marked as ‘?’.

For spectra acquired in the negative ion mode, the spectrum identification should be a negative precursor ion. In this case, the charge state is interpreted to be negative n. The charge state component in the peak annotation MUST NOT include the minus sign.

WARNING: This is a different rule than implemented in the NIST MSP format, where the precursor p does not carry a charge component if it is the fully charged unfragmented precursor, but does include a charge if it is a charge-reduced precursor, even a charge 1+. For example, in NIST MSP, a singly charged charge-reduced precursor is p^1 and the doubly charged original precursor is just p. The NIST MSP convention MUST NOT be used in this standard.

## Multiple peaks associated with the same fragment ion

As a general rule, a specific peak annotation SHOULD be placed on one peak only (the most likely one), even if multiple peaks might be within some tolerance around the theoretical fragment ion m/z, to avoid excessive cluttering. However, this format allows for placing the same peak annotation on multiple peaks, which may be useful in some cases, according to the following guideline.

The peak annotation string, the format of which is described above, will still be placed on the most likely peak. Any other peaks that are regarded as possibly belonging to the same fragment ion MAY be assigned the same peak annotation string prefixed with an ampersand (&) before the analyte identifier (if one is provided), with the m/z deviation changed accordingly. For example:

677.298 69 &1@y7/-0.002

677.299 572 &y7/-0.001

677.300 5681 y7/0.000\*0.95

677.301 1320 &y7/0.001

677.302 240 &y7/0.002

677.303 34 b6-H2O/-0.005,&y7/0.003

This can be used as the mechanism to annotate multiple peaks belonging to one fragment ion in profile-mode data. It can also be used if there is more than one centroided peak within the tolerance of the annotation and it is unclear which peak might best correspond to the ion annotation. However, the present format does not mandate such kind of peak annotations.

## Confidence estimates for the annotations

Annotations MAY be annotated at the end with a confidence estimate by placing an asterisk followed by a number that MUST be between 0.0 and 1.0, inclusive, with 1.0 being the highest confidence. This signifies the confidence or probability that the offered annotation is correct. This example:

y12-H2O^2/7.4ppm\*0.70

indicates that the offered annotation is only judged to be 70% likely by the interpreting software (perhaps based on a model of mass deltas). To allow for the use of other confidence measures with more precise statistical definitions, a proper CV term of such a metric can be defined as a child of MS:1003274 “peak annotation confidence metric”, and specified in the spectrum metadata.

If there is no peak annotation confidence metric specified, this number SHOULD be interpreted as the probability of the peak being this annotation (in the Bayesian sense that the probability indicates a degree of belief, which may be subjective). If multiple annotations are offered, the one with the highest confidence SHOULD come first. If multiple annotations are present, they SHOULD all have a confidence estimate or none should. If there are multiple annotations with confidence scores, the confidence scores MUST sum to a number equal to or less than 1.0. The difference between the sum and 1.0 MAY be interpreted to mean that the confidence that the true source of the peak is something else not listed. The following:

y12/3.4ppm\*0.85,b9-NH3/5.2ppm\*0.05

would signify that the first annotation is judged to be 85% likely and the second 5% likely, with the balance of 10% reserved for some other origin not listed.

# Object Model

All the above data elements MAY be encoded in the following object model in memory or some other data serialization format such as JSON. The formal JSON Schema definition is available at <https://github.com/HUPO-PSI/mzPAF/blob/main/specification/annotation-schema.json>.

## Definition

* **analyte\_reference**: Label of analyte to which this annotation belongs. Default: null.
  + **One of**
    - *integer*
    - *null*
* **molecule\_description** *(object, required)*: Description of the molecule or molecule fragment that this peak is annotated with.
  + **One of**
    - : Refer to [*#/definitions/peptide*](about:blank).
    - : Refer to [*#/definitions/internal*](about:blank).
    - : Refer to [*#/definitions/precursor*](about:blank).
    - : Refer to [*#/definitions/immonium*](about:blank).
    - : Refer to [*#/definitions/reference*](about:blank).
    - : Refer to [*#/definitions/named\_compound*](about:blank).
    - : Refer to [*#/definitions/formula*](about:blank).
    - : Refer to [*#/definitions/smiles*](about:blank).
    - : Refer to [*#/definitions/unannotated*](about:blank).
* **neutral\_losses** *(array)*: Any additional gains or losses of chemical groups defined by formula or by name; multiple may be specified. Default: [].
  + **Items** *(string)*
* **isotope**: An isotopic peak offset from the monoisotopic peak. Default: [].
  + **Any of**
    - *integer*
    - *array*
      * **Items**
        + **Any of**

*integer*

: Refer to [*#/definitions/isotope\_specification*](about:blank).

* **adducts** *(array)*: The charge carrier(s) for the given annotation. Default: [].
  + **Items** *(string)*
* **charge** *(integer)*: The charge state of the ion generating this peak; this value is unsigned. Minimum: 1. Default: 1.
* **mass\_error**: Error between observed and theoretical mass. Default: null.
  + **One of**
    - *null*
    - : Refer to [*#/definitions/mass\_error*](about:blank).
* **confidence**: Number defining confidence in peak annotation. Default: null.
  + **One of**
    - *number*
    - *null* ## Definitions
* **series\_label** *(string)*: Type of ion being described, specifies the required molecule description keys. Must be one of: ["peptide", "internal", "precursor", "immonium", "reference", "named\_compound", "formula", "smiles", "unannotated"].
* **mass\_error** *(object)*: Error between observed and theoretical mass.
  + **value** *(number, required)*: Mass error value.
  + **unit** *(string, required)*: Mass error unit. Must be one of: ["ppm", "Da"]. Default: "Da".
* **peptide** *(object)*: Canonical peptide fragment ion. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["peptide"]. Refer to [*#/definitions/series\_label*](about:blank).
  + **series** *(string, required)*: The peptide ion series this ion belongs to. Must be one of: ["b", "y", "a", "x", "c", "z", "d", "v", "w", "da", "db", "wa", "wb"].
  + **position** *(integer, required)*: The position from the appropriate terminal along the peptide this ion was fragmented at (starting with 1). Minimum: 1.
  + **sequence**: A ProForma 2.0 formatted peptidoform sequence describing the ion, which may be useful for contaminants or de novo sequencing.
    - **One of**
      * *string*
      * *null*
* **internal** *(object)*: Internal fragment ion. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["internal"]. Refer to [*#/definitions/series\_label*](about:blank).
  + **start\_position** *(integer, required)*: N-terminal amino acid residue of the fragment in the original peptide sequence (beginning with 1, counting from the N-terminus). Minimum: 1.
  + **end\_position** *(integer, required)*: C-terminal amino acid residue of the fragment in the original peptide sequence (beginning with 1, counting from the N-terminus). Minimum: 1.
  + **sequence**: A ProForma 2.0 formatted peptidoform sequence describing the ion, which may be useful for contaminants or de novo sequencing.
    - **One of**
      * *string*
      * *null*
* **precursor** *(object)*: Precursor ion. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["precursor"]. Refer to [*#/definitions/series\_label*](about:blank).
* **immonium** *(object)*: Immonium ion. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["immonium"]. Refer to [*#/definitions/series\_label*](about:blank).
  + **amino\_acid** *(string, required)*: One-letter code of the amino acid represented by this immonium ion. Length must be equal to 1.
  + **modification** *(string)*: An optional modification that may be attached to this immonium ion.
* **reference** *(object)*: Reference ion. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["reference"]. Refer to [*#/definitions/series\_label*](about:blank).
  + **reference** *(string, required)*: The name of a reference molecule or ion defined in a registry.
* **named\_compound** *(object)*: named compound ion. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["named\_compound"]. Refer to [*#/definitions/series\_label*](about:blank).
  + **compound\_name** *(string, required)*: The name of the named compound ion being marked.
* **formula** *(object)*: Ion described by chemical formula. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["formula"]. Refer to [*#/definitions/series\_label*](about:blank).
  + **formula** *(string, required)*: The elemental formula of the ion being marked.
* **smiles** *(object)*: Ion described by SMILES molecular structure. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["smiles"]. Refer to [*#/definitions/series\_label*](about:blank).
  + **smiles** *(string, required)*: The SMILES definition of the ion being marked.
* **unannotated** *(object)*: Unannotated ion. Cannot contain additional properties.
  + **series\_label**: Must be one of: ["unannotated"]. Refer to [*#/definitions/series\_label*](about:blank).
  + **unannotated\_label** *([‘string’, ‘null’], required)*: A user-specified numeral label for an unannotated peak.
* **isotope\_specification** *(object)*: A defined isotopic variant of another peak. Cannot contain additional properties.
  + **isotope** *(integer, required)*: The number of times this isotope occurs in the chemical composition of the ion.
  + **variant**
    - **One of**
      * : Refer to [*#/definitions/element\_isotopic\_variant*](about:blank).
      * : Refer to [*#/definitions/average\_isotopic\_variant*](about:blank).
      * *null*
* **element\_isotopic\_variant** *(object)*
  + **nucleon\_count** *(integer, required)*: The number of nucleons this isotope differs in with respect to the monoisotopic isotopologue.
  + **element** *(string, required)*: The name of element the isotopologue comes from.
* **average\_isotopic\_variant** *(object)*: Cannot contain additional properties.
  + **averaged** *(boolean, required)*: Whether or not the isotopic peak is defined as the “average” isotopomer of the known chemical composition.

## Examples

1@y7-H2O+i^2[M+NH4]/-0.2ppm\*0.5

{

"adducts": [

"NH4"

],

"analyte\_reference": "1",

"charge": 2,

"confidence": 0.5,

"isotope": 1,

"mass\_error": {

"unit": "ppm",

"value": -0.2

},

"molecule\_description": {

"position": 7,

"series": "y",

"series\_label": "peptide"

},

"neutral\_losses": [

"-H2O"

]

}

m5:8-H2O/14.4ppm

{

"neutral\_loss": ["-H2O"],

"isotope": 0,

"adduct":[],

"charge": 1,

"analyte\_reference": 1,

"mass\_error": {

"value": 14.4,

"unit": "ppm"

},

"confidence": null,

"molecule\_description": {

"series\_label": "internal",

"start\_position": 5,

"end\_position": 8

}

}

p/-1.7ppm

{

"neutral\_loss":[],

"isotope": 0,

"adduct":[],

"charge": 1,

"analyte\_reference": 1,

"mass\_error": {

"value": -1.7,

"unit": "ppm"

},

"confidence": null,

"molecule\_description": {

"series\_label": "precursor"

}

}

# Regular Expressions and grammars

mzPAF annotations may be parsed by a regular expression or by a grammar, as described below.

## Regular expression for mzPAF

The compact ion notation may be encoded via the following regular expressions:

ECMAScript Regex

^(?<is\_auxiliary>&)?(?:(?<analyte\_reference>\d+)@)?(?:(?:(?<series>(?:da|db|wa|wb)|[axbyczdwv]\.?)(?<ordinal>\d+)(?:\{(?<sequence\_ordinal>.+)\})?)|(?<series\_internal>[m](?<internal\_start>\d+):(?<internal\_end>\d+)(?:\{(?<sequence\_internal>.+)\})?)|(?<precursor>p)|(:?I(?<immonium>[A-Z])(?:\[(?<immonium\_modification>(?:[^\]]+))\])?)|(?<reference>r(?:(?:\[(?<reference\_label>[^\]]+)\])))|(?:f\{(?<formula>[A-Za-z0-9\[\]]+)\})|(?:\_\{(?<named\_compound>[^\{\}\s,\/]+)\})|(?:s\{(?<smiles>[^\}]+)\})|(?:(?<unannotated>\?)(?<unannotated\_label>\d+)?))(?<neutral\_losses>(?:[+-]\d\*(?:(?:(?:(?:\[[0-9]+[A-Z][A-Za-z0-9]\*\])|(?:[A-Z][A-Za-z0-9]\*))+)|(?:\[(?:(?:[A-Za-z0-9:\.]+)(?:\[(?:[A-Za-z0-9\.:\-\ ]+)\])?)\])))+)?(?<isotope>(?:([+-]\d\*)i(:?\d+(:?[A-Z][a-z]\*))?)\*)?(?:\[(?<adducts>M(:?[+-]\d\*[A-Z][A-Za-z0-9]\*)+)\])?(?:\^(?<charge>[+-]?\d+))?(?:\/(?<mass\_error>[+-]?\d+(?:\.\d+)?)(?<mass\_error\_unit>ppm)?)?(?:\\*(?<confidence>\d\*(?:\.\d+)?))?

Python SRE in verbose mode

^(?P<is\_auxiliary>&)?

(?:(?P<analyte\_reference>\d+)@)?

(?:(?:(?P<series>(?:da|db|wa|wb)|[axbyczdwv]\.?)(?P<ordinal>\d+)(?:\{(?P<sequence\_ordinal>.+)\})?)|

(?P<series\_internal>[m](?P<internal\_start>\d+):(?P<internal\_end>\d+)(?:\{(?P<sequence\_internal>.+)\})?)|

(?P<precursor>p)|

(:?I(?P<immonium>[A-Z])(?:\[(?P<immonium\_modification>(?:[^\]]+))\])?)|

(?P<reference>r(?:

(?:\[

(?P<reference\_label>[^\]]+)

\])

))|

(?:f\{(?P<formula>[A-Za-z0-9\[\]]+)\})|

(?:\_\{

(?P<named\_compound>[^\{\}\s,/]+)

\})|

(?:s\{(?P<smiles>[^\}]+)\})|

(?:(?P<unannotated>\?)(?P<unannotated\_label>\d+)?)

)

(?P<neutral\_losses>(?:[+-]\d\*

(?:(?:(?:(?:\[[0-9]+[A-Z][A-Za-z0-9]\*\])|(?:[A-Z][A-Za-z0-9]\*))+)|

(?:\[

(?:

(?:[A-Za-z0-9:\.]+)(?:\[(?:[A-Za-z0-9\.:\-\ ]+)\])?

)

\])

)

)+)?

(?P<isotope>

(?:[+-]\d\*)i(?:(?:\d+)(?:[A-Z][a-z]?)|(?:A))?

)?

(?:\[(?P<adducts>M(:?[+-]\d\*(?:\[\d+\])?[A-Z][A-Za-z0-9]\*)+)\])?

(?:\^(?P<charge>[+-]?\d+))?

(?:/(?P<mass\_error>[+-]?\d+(?:\.\d+)?)(?P<mass\_error\_unit>ppm)?)?

(?:\\*(?P<confidence>\d\*(?:\.\d+)?))?

The isotope component may be further decomposed as follows:

Written as a regular expression:

(?<isotope\_expression>(?<sign>[+-])(?<nucleon\_count>[0-9]\*)i(?<nucleon\_identity>[0-9]+[A-Z][a-z]\*)?)\*

Written in EBNF:

isotopic\_peak\_annotation := <isotopic\_expression> | <isotopic\_expression>, <isotopic\_peak\_annotation> ;

isotopic\_expression := <sign>, <nucleon\_count>, "i", [ <nucleon\_identity> ];

sign := "+" | "-" ;

nucleon\_count := <digit>\*;

nucleon\_identity := <digit>\*, <element>;

digit := "0" | "1" | "2" | "3" | "4" | "5" | "6" | "7" | "8" | "9" ;

element := ?IUPAC element symbols?

## Formal Grammar for mzPAF

In addition to the regular expression, we provide two alternative presentations of the peptide peak annotation format to either aid understanding or guide implementation.

Parsing state machine diagrams:

<https://github.com/HUPO-PSI/mzPAF/blob/main/specification/grammars/grammar.md>

Grammar:

<https://github.com/HUPO-PSI/mzPAF/blob/main/specification/grammars/annotation.lark>

# 

# Pending Issues - Future developments

There are several use cases that are NOT currently supported in the current version of the specification. These complications are left open and will ideally be addressed in future versions, after the community has gained more experience with the common cases. The objective here is to document those cases appropriately and, in some cases, to propose some possible solutions for representing the information in future versions of mzPAF.

## Side-chain fragments and other fragment ions

This format currently does not allow for the specification of side-chain fragments (which are important for glycopeptides, for example) and other fragments (unless they are simple chemical formulas). It also does not have a mechanism to denote fragments of cross-linked peptides. Moreover, in the case of metabolites/small molecules, there is no notion of a backbone and the fragment will need to be specified by a chemical formula.

To accommodate these other kinds of molecules, separate peak annotation formats will need to be defined, similar to this document. We anticipate that in the future, a number of peak annotation formats will be defined and put into use.

Without a separate peak annotation format, the prefix ‘\_’ (see “External Fragment Ions” above) can be used to denote any fragment not covered by this format. Software tools supporting this format can choose to ignore such peak annotations, or merely display them to the user as-is.

* 1. Specifying the backbone cleavages for internal ions

Internal fragments can be formed from all combinations of backbone cleavage. The current specification defaults to ‘yb’ and specifies that any other backbone cleavage should be written as the corresponding neutral loss or gain from this reference point. Extending the specification to allow to directly specify which backbones led to the internal ion could be done, this would enhance the clarity for internal fragments annotations that are not formed by ‘yb’. Some syntax suggestions were to append the backbone cleavage directly after the’ m’ tag ‘mxa3:6’, ‘mzc3:6’, another way would be to specify the backbone on the position ‘mx3:a6’, ‘mz3:c6’. If support for this notation the ‘m3:6’ could be left in as meaning ’yb’.

# Appendix A. Parsing multiple annotations strategy

If the provided regular expression-based annotation parser is used, additional logic is required to handle multiple annotations. A procedure like the following pseudo code SHOULD be applied:

def unpack\_match(match):

...

def match\_pattern(text):

...

def parse\_annotation\_string(text):

i = 0

annotations = []

n = len(text)

while i < n:

match = match\_pattern(text[i:])

if not match:

raise Exception(f"{text[i:]} does not match annotation pattern!")

annot = unpack\_match(match)

i\_end = match.end()

if i\_end < n:

if text[i\_end] == ',':

i\_end += 1

else:

raise Exception(f"Unparsed content following annotations " +

"starting at {i\_end}")

i = i\_end

annotations.append(annot)

return annotations

# Appendix B. Reference molecules

The most up-to-date list of reference molecules can be found here:

<https://github.com/HUPO-PSI/mzPAF/blob/main/specification/reference_data/reference_molecules.md>

and a JSON serialization with m/z and other information is available here:

Viewable:

<https://github.com/HUPO-PSI/mzPAF/blob/main/specification/reference_data/reference_molecules.json>

Raw:

<https://raw.githubusercontent.com/HUPO-PSI/mzPAF/main/specification/reference_data/reference_molecules.json>

For the convenience of reading this specification, the state of this file as of version 1.0 of the specification is provided below, although the URLs above should be checked for updates:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Name | Label type | Molecule type | Chemical formula | Ion m/z | Neutral mass |
| TMT126 | TMT | reporter | C8N1H15 | 126.128 |  |
| TMT127N | TMT | reporter | C8[15N1]H15 | 127.125 |  |
| TMT127C | TMT | reporter | C7[13C1]N1H15 | 127.131 |  |
| TMT128N | TMT | reporter | C7[13C1][15N1]H15 | 128.128 |  |
| TMT128C | TMT | reporter | C6[13C2]N1H15 | 128.134 |  |
| TMT129N | TMT | reporter | C6[13C2][15N1]H15 | 129.131 |  |
| TMT129C | TMT | reporter | C5[13C3]N1H15 | 129.138 |  |
| TMT130N | TMT | reporter | C5[13C3][15N1]H15 | 130.135 |  |
| TMT130C | TMT | reporter | C4[13C4]N1H15 | 130.141 |  |
| TMT131N | TMT | reporter | C4[13C4][15N1]H15 | 131.138 |  |
| TMT131C | TMT | reporter | C3[13C5]N1H15 | 131.144 |  |
| TMT132N | TMT | reporter | C3[13C5][15N1]H15 | 132.142 |  |
| TMT132C | TMT | reporter | C2[13C6]N1H15 | 122.148 |  |
| TMT133N | TMT | reporter | C2[13C6][15N1]H15 | 133.145 |  |
| TMT133C | TMT | reporter | C1[13C7]N1H15 | 133.151 |  |
| TMT134N | TMT | reporter | C1[13C7][15N1]H15 | 134.148 |  |
| TMT134C | TMT | reporter | [13C8]N1H15 | 134.155 |  |
| TMT135N | TMT | reporter | [13C8][15N1]H15 | 135.152 |  |
| TMTzero | TMTzero | reporter+balance | C12H20N2O2 | 225.16 | 224.152 |
| TMTpro\_zero | TMTpro\_zero | reporter+balance | C15H25N3O3 | 296.197 | 295.19 |
| TMT2plex | TMT2plex | reporter+balance | C11[13C1]H20N2O2 | 226.163 | 225.156 |
| TMT6plex | TMT6plex | reporter+balance | C8[13C5]H20N1[15N1]O2 | 230.17 | 229.163 |
| TMTpro | TMTpro | reporter+balance | C8[13C7]H25[15N2]N1O3 | 305.214 | 304.207 |
| iTRAQ113 | iTRAQ | reporter | C6N2H12 | 113.108 |  |
| iTRAQ114 | iTRAQ | reporter | C5[13C1]N2H12 | 114.111 |  |
| iTRAQ115 | iTRAQ | reporter | C5[13C1]N1[15N1]H12 | 115.108 |  |
| iTRAQ116 | iTRAQ | reporter | C4[13C2]N1[15N1]H12 | 116.112 |  |
| iTRAQ117 | iTRAQ | reporter | C3[13C3]N1[15N1]H12 | 117.115 |  |
| iTRAQ118 | iTRAQ | reporter | C3[13C3][15N2]H12 | 118.112 |  |
| iTRAQ119 | iTRAQ | reporter | C2[13C4][15N2]H12 | 119.115 |  |
| iTRAQ121 | iTRAQ | reporter | [13C6][15N2]H12 | 121.122 |  |
| iTRAQ4plex | iTRAQ4plex | reporter+balance | C4[13C3]N1[15N1]O1H12 | 145.109 | 144.102 |
| iTRAQ8plex | iTRAQ8plex | reporter+balance | C7[13C7]N3[15N1]O3H24 | 305.213 | 304.205 |
| TMT126-ETD | TMT | reporter | C7N1H15 | 114.128 |  |
| TMT127N-ETD | TMT | reporter | C7[15N1]H15 | 115.125 |  |
| TMT127C-ETD | TMT | reporter | C6[13C1]N1H15 | 114.128 |  |
| TMT128N-ETD | TMT | reporter | C6[13C1][15N1]H15 | 115.125 |  |
| TMT128C-ETD | TMT | reporter | C5[13C2]N1H15 | 116.134 |  |
| TMT129N-ETD | TMT | reporter | C5[13C2][15N1]H15 | 117.131 |  |
| TMT129C-ETD | TMT | reporter | C4[13C3]N1H15 | 116.134 |  |
| TMT130N-ETD | TMT | reporter | C4[13C3][15N1]H15 | 117.131 |  |
| TMT130C-ETD | TMT | reporter | C3[13C4]N1H15 | 118.141 |  |
| TMT131N-ETD | TMT | reporter | C3[13C4][15N1]H15 | 119.138 |  |
| TMT131C-ETD | TMT | reporter | C2[13C5]N1H15 | 118.141 |  |
| sidechain\_A |  | sidechain | C1H3 |  | 15.0235 |
| sidechain\_C |  | sidechain | C1H3S1 |  | 46.9955 |
| sidechain\_D |  | sidechain | C2H2O2 |  | 58.0055 |
| sidechain\_E |  | sidechain | C3H4O2 |  | 72.0211 |
| sidechain\_F |  | sidechain | C7H7 |  | 91.0548 |
| sidechain\_G |  | sidechain | H1 |  | 1.00782 |
| sidechain\_H |  | sidechain | C4H5N2 |  | 81.0453 |
| sidechain\_I |  | sidechain | C4H9 |  | 57.0704 |
| sidechain\_J |  | sidechain | C4H9 |  | 57.0704 |
| sidechain\_K |  | sidechain | C4H10N1 |  | 72.0813 |
| sidechain\_L |  | sidechain | C4H9 |  | 57.0704 |
| sidechain\_M |  | sidechain | C3H7S1 |  | 75.0268 |
| sidechain\_N |  | sidechain | C2H4N1O1 |  | 58.0293 |
| sidechain\_O |  | sidechain | C9H17N2O1 |  | 169.134 |
| sidechain\_Q |  | sidechain | C3H6N1O1 |  | 72.0449 |
| sidechain\_R |  | sidechain | C4H10N3 |  | 100.087 |
| sidechain\_S |  | sidechain | C1H3O1 |  | 31.0184 |
| sidechain\_T |  | sidechain | C2H5O1 |  | 45.034 |
| sidechain\_U |  | sidechain | C1H3Se1 |  | 94.94 |
| sidechain\_V |  | sidechain | C3H7 |  | 43.0548 |
| sidechain\_W |  | sidechain | C9H8N1 |  | 130.066 |
| sidechain\_Y |  | sidechain | C7H7O1 |  | 107.05 |
| Cytosine |  | nucleobase | C4H5N3O | 112.0505 |  |
| Adenine |  | nucleobase | C5H5N5 | 136.0618 |  |
| Guanine |  | nucleobase | C5H5N5O | 152.0567 |  |
| Uracil |  | nucleobase | C4H4N2O2 | 113.0346 |  |
| Thymine |  | nucleobase | C5H6N2O2 | 127.0502 |  |

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# Glossary

All non-standard terms are already defined in detail in section 3.

# References

1. Lam H, Deutsch EW, Eddes JS, Eng JK, Stein SE, Aebersold R. Building consensus spectral libraries for peptide identification in proteomics. Nat Methods. 2008 Oct;5(10):873–875. PMCID: PMC2637392

2. Desiere F, Deutsch EW, King NL, Nesvizhskii AI, Mallick P, Eng J, Chen S, Eddes J, Loevenich SN, Aebersold R. The PeptideAtlas project. Nucleic Acids Res. 2006 Jan 1;34(Database issue):D655-658. PMCID: PMC1347403

3. Roepstorff P, Fohlman J. Proposal for a common nomenclature for sequence ions in mass spectra of peptides. Biomed Mass Spectrom. 1984 Nov;11(11):601. PMID: 6525415

4. Biemann K. Appendix 5. Nomenclature for peptide fragment ions (positive ions). Methods Enzymol. 1990;193:886–887. PMID: 2074849

5. Deutsch EW, Perez-Riverol Y, Chalkley RJ, Wilhelm M, Tate S, Sachsenberg T, Walzer M, Käll L, Delanghe B, Böcker S, Schymanski EL, Wilmes P, Dorfer V, Kuster B, Volders PJ, Jehmlich N, Vissers JPC, Wolan DW, Wang AY, Mendoza L, Shofstahl J, Dowsey AW, Griss J, Salek RM, Neumann S, Binz PA, Lam H, Vizcaíno JA, Bandeira N, Röst H. Expanding the Use of Spectral Libraries in Proteomics. J Proteome Res. 2018 07;17(12):4051–4060. PMCID: PMC6443480

6. Bradner S. RFC2119: Key words for use in RFCs to Indicate Requirement Levels (https://tools.ietf.org/html/rfc2119) [Internet]. 1997. Available from: https://tools.ietf.org/html/rfc2119

7. LeDuc RD, Deutsch EW, Binz PA, Fellers RT, Cesnik AJ, Klein JA, Van Den Bossche T, Gabriels R, Yalavarthi A, Perez-Riverol Y, Carver J, Bittremieux W, Kawano S, Pullman B, Bandeira N, Kelleher NL, Thomas PM, Vizcaíno JA. Proteomics Standards Initiative’s ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. J Proteome Res. 2022 Apr 1;21(4):1189–1195. PMCID: PMC7612572