* For “Q3 charge”, use

[Term]

id: MS:1000041

name: charge state

def: "The charge state of the ion, single or multiple and positive or negatively charged." [PSI:MS]

synonym: "z" EXACT []

xref: value-type:xsd\:int "The allowed value-type for this CV term."

is\_a: MS:1000455 ! ion selection attribute

* For “Q3 area”, use

[Term]

id: MS:1001858

name: XIC area

def: "Area of the extracted ion chromatogram (e.g. of a transition in SRM)." [PSI:PI]

xref: value-type:xsd\:double "The allowed value-type for this CV term."

is\_a: MS:1001805 ! quantification datatype

* For “Q3 normalized area”, use

[Term]

id: MS:1001859

name: normalized XIC area

def: "Normalized area of the extracted ion chromatogram (e.g. of a transition in SRM)." [PSI:PI]

xref: value-type:xsd\:double "The allowed value-type for this CV term."

is\_a: MS:1001805 ! quantification datatype

* For “Q3 m/z” or “product ion m/z”, use

[Term]

id: MS:1000827

name: isolation window target m/z

def: "The primary or reference m/z about which the isolation window is defined." [PSI:MS]

xref: value-type:xsd\:float "The allowed value-type for this CV term."

is\_a: MS:1000792 ! isolation window attribute

relationship: has\_units MS:1000040 ! m/z

* For “Q3 peak rank”, use

[Term]

id: MS:1000926

name: product interpretation rank

def: "The integer rank given an interpretation of an observed product ion. For example, if y8 is selected as the most likely interpretation of a peak, then it is assigned a rank of 1." [PSI:MS]

xref: value-type:xsd\:positiveInteger "The allowed value-type for this CV term."

is\_a: MS:1001221 ! fragmentation information

[Term]

id: MS:100XXXX

name: product retention time

def: "The centre of the retention time window of a product ion in SRM run" [PSI:PI]

xref: value-type:xsd\:double "The allowed value-type for this CV term."

is\_a: MS:1000894 ! retention time

[Term]

id: MS:100XXXX

name: Anubis

def: "Anubis software for selected reaction monitoring data. http://quantitativeproteomics.org/anubis" [PSI:PI]

is\_a: MS:1000871 ! SRM software

is\_a: MS:1001139 ! quantitation software name

[Term]

id: MS:100XXXX

name: TraML file

def: "The PSI TraML format - http://www.psidev.info/traml" [PSI:MS]

is\_a: MS:1000560 ! mass spectrometer file format

[Term]

id: MS:100XXXX

name: total XIC area

def: "Summed area of all the extracted ion chromatogram for the peptide (e.g. of all the transitions in SRM " [PSI:PI]

xref: value-type:xsd\:double "The allowed value-type for this CV term."

is\_a: MS:1001805 ! quantification datatype

[Term]

id: MS:100XXXX

name: product background

def: "The background area for the quantified transition." [PSI:PI]

xref: value-type:xsd\:double "The allowed value-type for this CV term."

is\_a: MS:1001805 ! quantification datatype

[Term]

id: MS:100XXXX

name: Q3 peak height

def: "The peak height of the quantified product ion" [PSI:PI]

xref: value-type:xsd\:double "The allowed value-type for this CV term."

is\_a: MS:1001805 ! quantification datatype

Also should rules on these:

<CvTerm termAccession="MS:1001221" useTerm="false" termName="fragmentation information" isRepeatable="true" allowChildren="true" cvIdentifierRef="MS"/>

<CvTerm termAccession="MS:1000903" useTerm="true" termName="product ion series ordinal" isRepeatable="false" allowChildren="false" cvIdentifierRef="MS"/>