

# Proteograph

Typst proteomics package

v0.2.0      September 10, 2025

<https://codeberg.org/olangella/proteograph>

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## ABSTRACT

**proteograph** is a package defining [Typst](#) functions dedicated to proteomics.

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## REFERENCE

### XIC (eXtracted Ion Chromatogram) plot

#### Example :

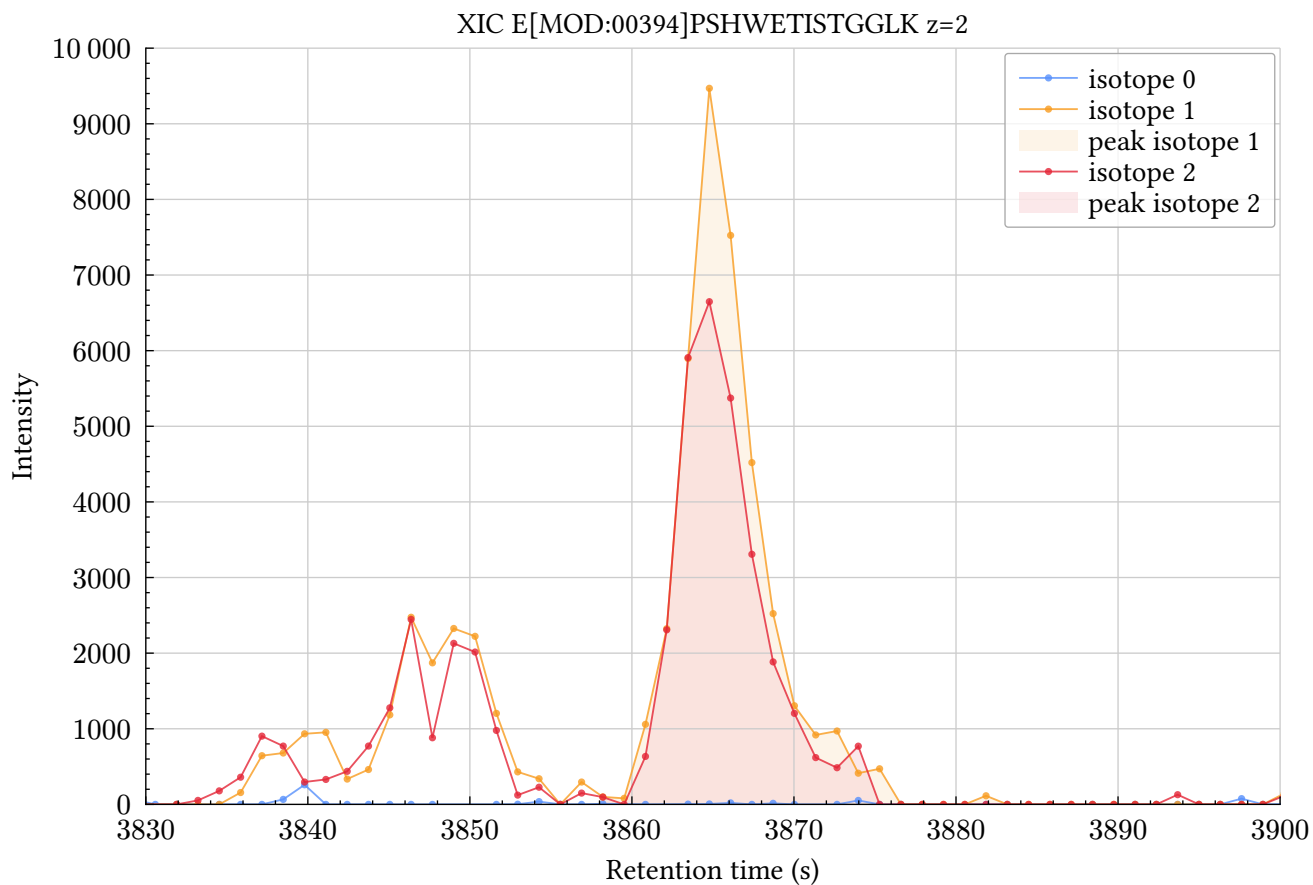
```
#import "@preview/tegraph:0.2.0": *

#let data_json = json("../examples/data/pepalb35.json")

#let xic0 = data_json.found_list_first_pass.first().xics.first().trace
#xic0.insert("title", "isotope 0")
#let xic1 = data_json.found_list_first_pass.first().xics.at(1).trace
#xic1.insert("title", "isotope 1")
#xic1.insert("peak-
begin", data_json.found_list_first_pass.first().xics.at(1).peak.rt.first())
#xic1.insert("peak-
end", data_json.found_list_first_pass.first().xics.at(1).peak.rt.last())
#let xic2 = data_json.found_list_first_pass.first().xics.at(2).trace
#xic2.insert("title", "isotope 2")
#xic2.insert("peak-
begin", data_json.found_list_first_pass.first().xics.at(2).peak.rt.first())
#xic2.insert("peak-
end", data_json.found_list_first_pass.first().xics.at(2).peak.rt.last())

#xic-plot(height: 10cm, title: "XIC E[MOD:00394]PSHWETISTGGLK z=2", rt-range: (3830,
3900), max-intensity: 10000, xic0, xic1, xic2)
```

## Result :



## XIC plot full documentation

- [xic-plot\(\)](#)

### xic-plot

Generates a XIC plot.

#### Parameters

```
xic-plot(  
  width: length relative ,  
  height: length relative ,  
  rt-range: auto array ,  
  max-intensity: none float ,  
  title: content ,  
  ..xic-item: dictionary  
) -> content
```

**width**   `length` or `relative`

The width of the diagram. This can be

- A `length` ; in this case, it defines just the width of the data area, excluding axes, labels, title etc.
- A `ratio` or `relative` where the ratio part is relative to the width of the parent that the diagram is placed in. This is not allowed if the parent has an unbounded width, e.g., a page with `width: auto` .

Default: `15cm`

**height**   `length` or `relative`

The height of the diagram. This can be

- A `length` ; in this case, it defines just the height of the data area, excluding axes, labels, title etc.
- A `ratio` or `relative` where the ratio part is relative to the height of the parent that the diagram is placed in. This is not allowed if the parent has an unbounded height, e.g., a page with `height: auto` .

Default: `10cm`

**rt-range**   `auto` or `array`

Data limits along the x-axis (retention time in seconds). Expects auto or a tuple (min, max) where min and max may individually be auto

Default: `auto`

**max-intensity**   `none` or `float`

Maximum intensity to display. **Optional.**

Example: `30000`

Default: `none`

**title**   `content`

Graph title

Default: `none`

**..xic-item**     dictionary

dictionary containing XIC data

```
1  /// XIC dictionary structure typc
2  #let xic_item = (
3    /// Array of retention times values
4    "x": (),
5    /// Array of intensity values
6    "y": (),
7    /// Title for this XIC
8    "title": "title for this XIC"
9    /// Detected peak retention time start. *Optional*.
10   "peak-begin": 3500,
11   /// Detected peak retention time end. *Optional*.
12   "peak-end": 3500,
13 )
```

## Retention time alignment

The alignment of retention times between MS runs done with MassChroQ3 are represented as follow in the JSON output

*MS run alignment data*

```
{
  "corrections": {
    "msrun1": {
      "aligned": [],
      "ms2_delta_rt": {
        "x": [],
        "y": []
      },
      "ms2_mean": [],
      "ms2_median": [],
      "original": []
    },
    "msrun2": {
      "aligned": [],
      "ms2_delta_rt": {
        "x": [],
        "y": []
      },
      "ms2_mean": [],
      "ms2_median": [],
      "original": []
    },
    "msrun3": {
      "aligned": [],
      "ms2_delta_rt": {
        "x": [],
        "y": []
      },
      "ms2_mean": [],
      "ms2_median": [],
      "original": []
    },
    "msrun_ref": "msrun4"
  }
}
```

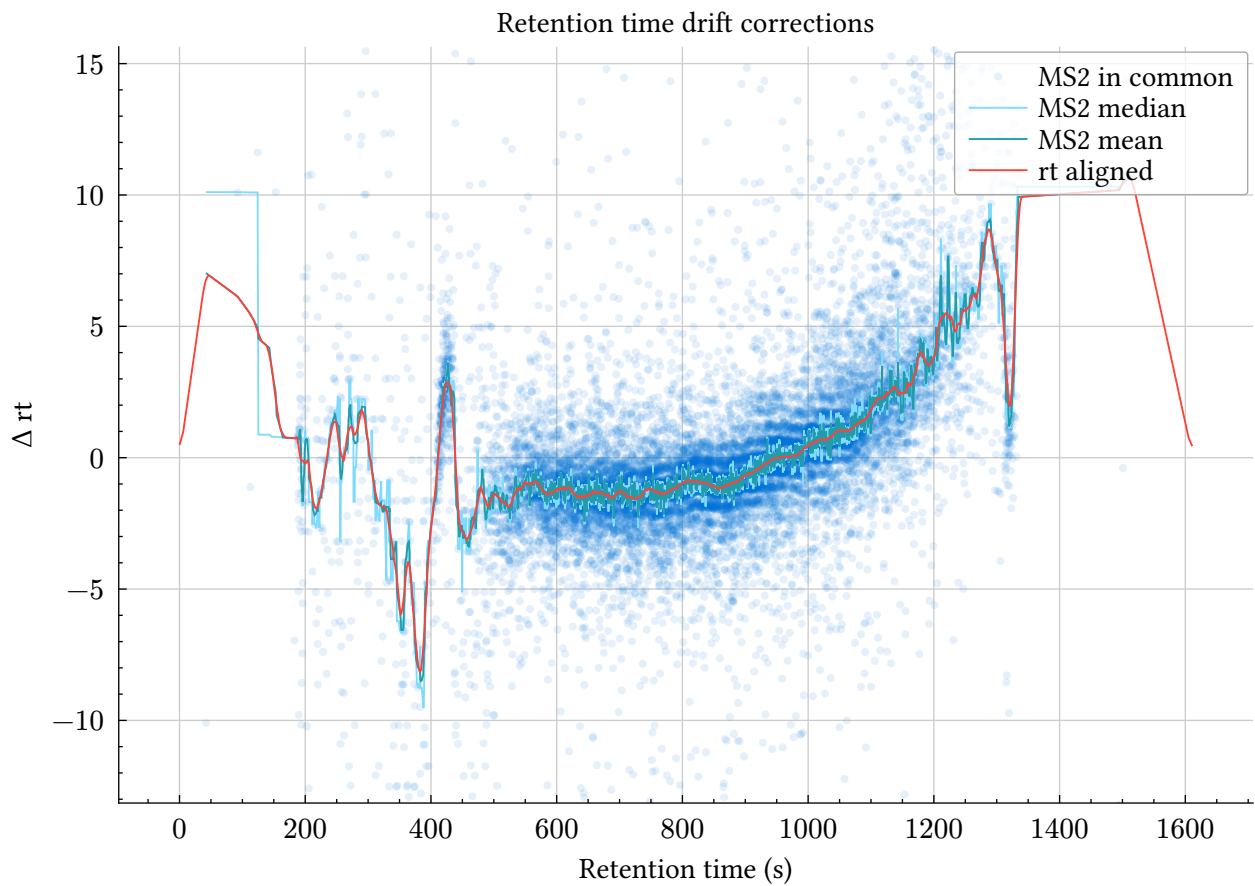
### Example :

```
#import "@preview/teproteograph:0.2.0": *

#let rt_align = json("../examples/data/one_alignment.json")
#rtalign-plot(title: "Retention time drift corrections", ylim: auto,
  ms2-delta-rt: rt_align.ms2_delta_rt,
  aligned: rt_align.aligned,
  ms2-mean: rt_align.ms2_mean,
  ms2-median: rt_align.ms2_median,
```

```
original: rt_align.original)
```

## Result :



## Retention time alignment full documentation

- [rtalign-plot\(\)](#)

### rtalign-plot

retention time delta plot between MS runs plot.

#### Parameters

```
rtalign-plot(  
  width: length relative,  
  height: length relative,  
  xlim: auto array,  
  ylim: auto array,  
  title,  
  original,  
  aligned,  
  ms2-delta-rt,  
  ms2-mean,  
  ms2-median  
) -> content
```

**width**   `length` or `relative`

The width of the diagram. This can be

- A `length` ; in this case, it defines just the width of the data area, excluding axes, labels, title etc.
- A `ratio` or `relative` where the ratio part is relative to the width of the parent that the diagram is placed in. This is not allowed if the parent has an unbounded width, e.g., a page with `width: auto` .

Default: `15cm`

**height**   `length` or `relative`

The height of the diagram. This can be

- A `length` ; in this case, it defines just the height of the data area, excluding axes, labels, title etc.
- A `ratio` or `relative` where the ratio part is relative to the height of the parent that the diagram is placed in. This is not allowed if the parent has an unbounded height, e.g., a page with `height: auto` .

Default: `10cm`

**xlim**   `auto` or `array`

Data limits along the x-axis (retention time in seconds). Expects `auto` or a tuple (min, max) where min and max may individually be `auto`

Default: `auto`

**ylim**   `auto` or `array`

Data limits along the y-axis (retention time delta in seconds). Expects `auto` or a tuple (min, max) where min and max may individually be `auto`

Default: `auto`



## MS2 spectra

### Simple MS2 spectra

The spectra is a dictionary containing 2 arrays of floats : mz and intensity

*spectra dictionary*

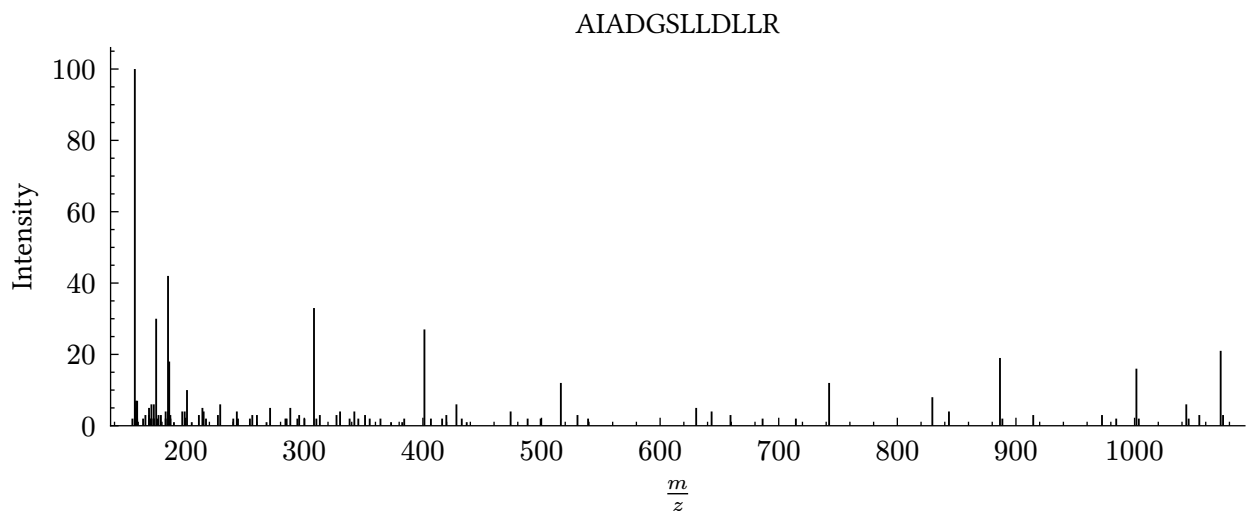
```
{
  "intensity": [
    2,
    2,
    100,
    5,
    7,
    2
  ],
  "mz": [
    155.081,
    157.097,
    157.133,
    158.092,
    158.137,
    159.076
  ]
}
```

### Example :

```
#import "@preview/tegraph:0.2.0": *

#let complete_psm = json("../examples/data/complete_psm.json")
#ms2spectra-plot(height: 5cm, title: "AIADGSLLDLLR", spectra: complete_psm.spectra)
```

### Result :



### MS2 spectra with ion annotations

This example shows an MS2 spectra with ion series annotation

The ion annotations are described in a dictionary :

*ion-series dictionary*

```
{
  "a": [
    {
      "charge": 1,
      "intensity": 100,
      "mz": 157.133,
      "mzth": 157.13353961189497,
      "size": 2
    }
  ],
  "b": [
    {
      "charge": 1,
      "intensity": 42,
      "mz": 185.128,
      "mzth": 185.12845423145498,
      "size": 2
    },
    {
      "charge": 1,
      "intensity": 3,
      "mz": 256.165,
      "mzth": 256.16556801702,
      "size": 3
    }
  ]
}
```

The first key is the ion series name as follow :

y, b, yp, ystar, y\*, yO, x, bstar, b\*, bO, a, astar, aO, c, z, bp

and any ion can be described by :

- [ion-description\(\)](#)

## ion-description

Ion description

### Parameters

```
ion-description(
  "charge": integer,
  "intensity": float,
  "mz": float,
  "mzth": float,
  "size": integer
)
```

**"charge"** integer

Ion charge

Default: 1

**"intensity"** float

Ion intensity

Default: none

**"mz"** float

Ion experimental mass on charge ratio

Default: none

**"mzth"** float

Ion theoretical mass on charge ratio. **Optional.**

Default: none

**"size"** integer

Ion size : number of residues for this fragment

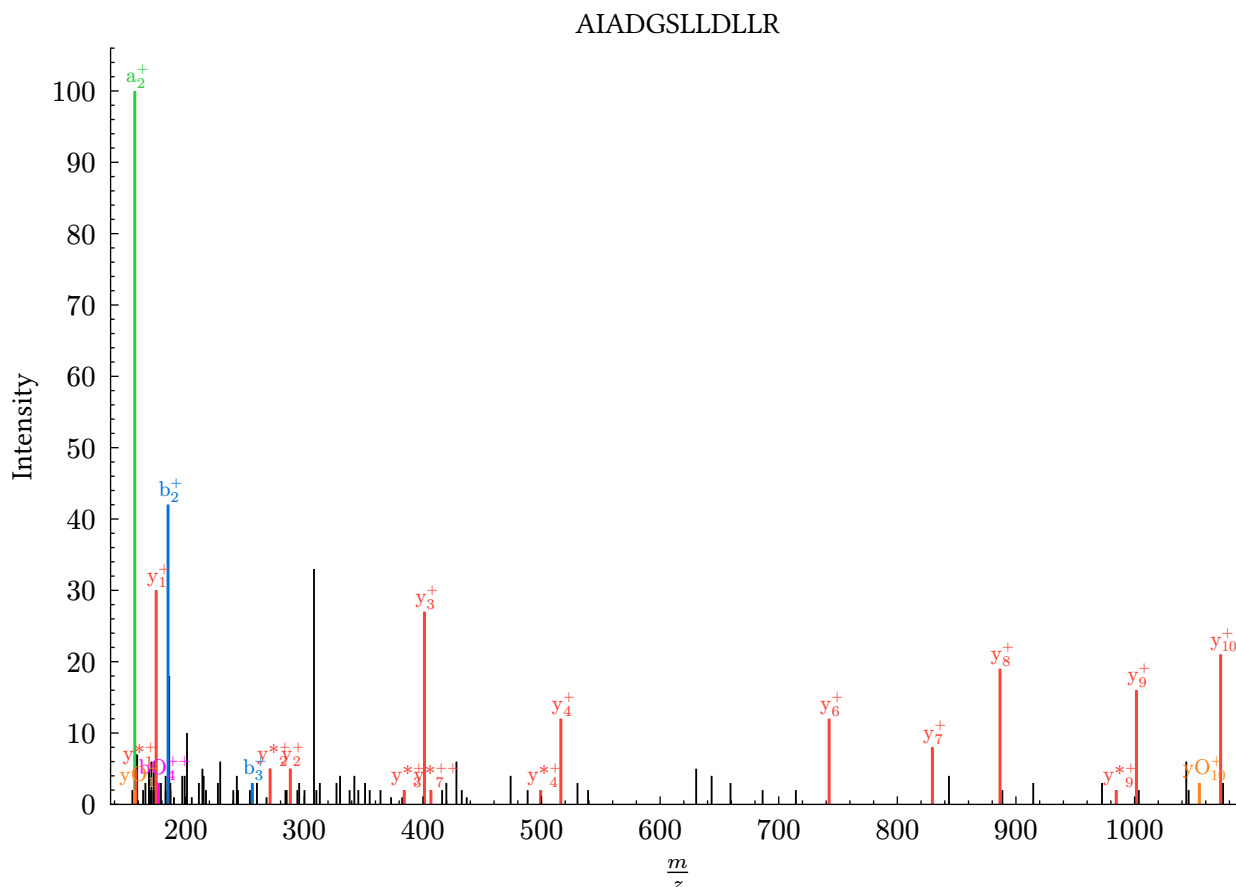
Default: 1

### Example :

```
#import "@preview/tegraph:0.2.0": *

#let complete_psm = json("../examples/data/complete_psm.json")
#ms2spectra-plot(title: "AIADGSLLDLLR", spectra: complete_psm.spectra, ion-series:
complete_psm.ion-series)
```

## Result :



## MS2 spectra zoom (mz\_range and intensity)

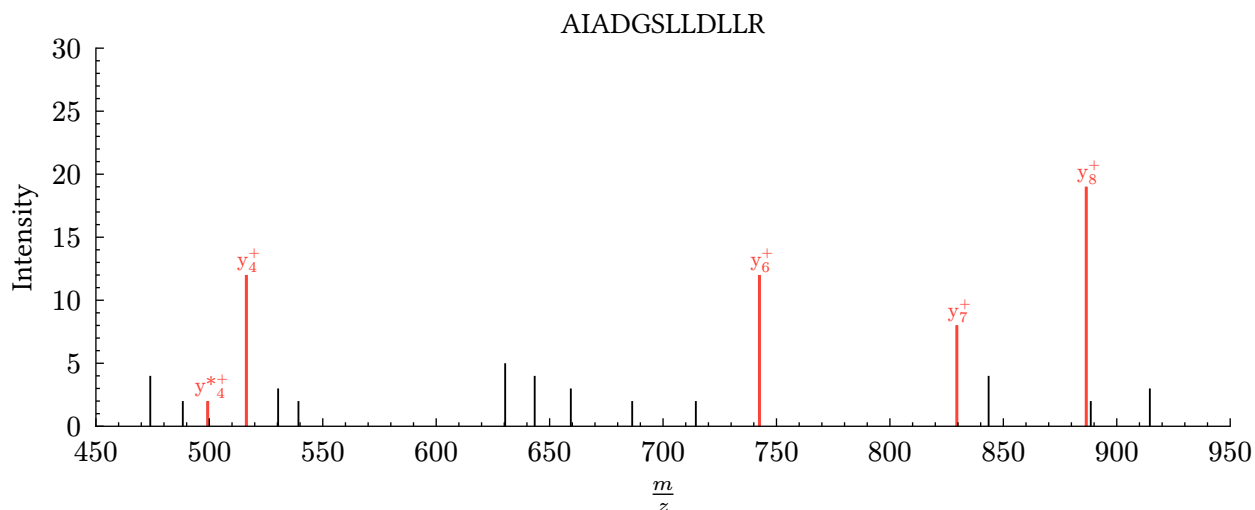
This example shows an MS2 spectra zoomed on a specific m/z range and maximum intensity.

## Example :

```
#import "@preview/teotograph:0.2.0": *

#let complete_psm = json("../examples/data/complete_psm.json")
#ms2spectra-plot(width: 15cm, height: 5cm, title: "AIADGSLLDLLR", spectra:
complete_psm.spectra, ion-series: complete_psm.ion-series, mz-range: (450, 950), max-
intensity: 30)
```

## Result :



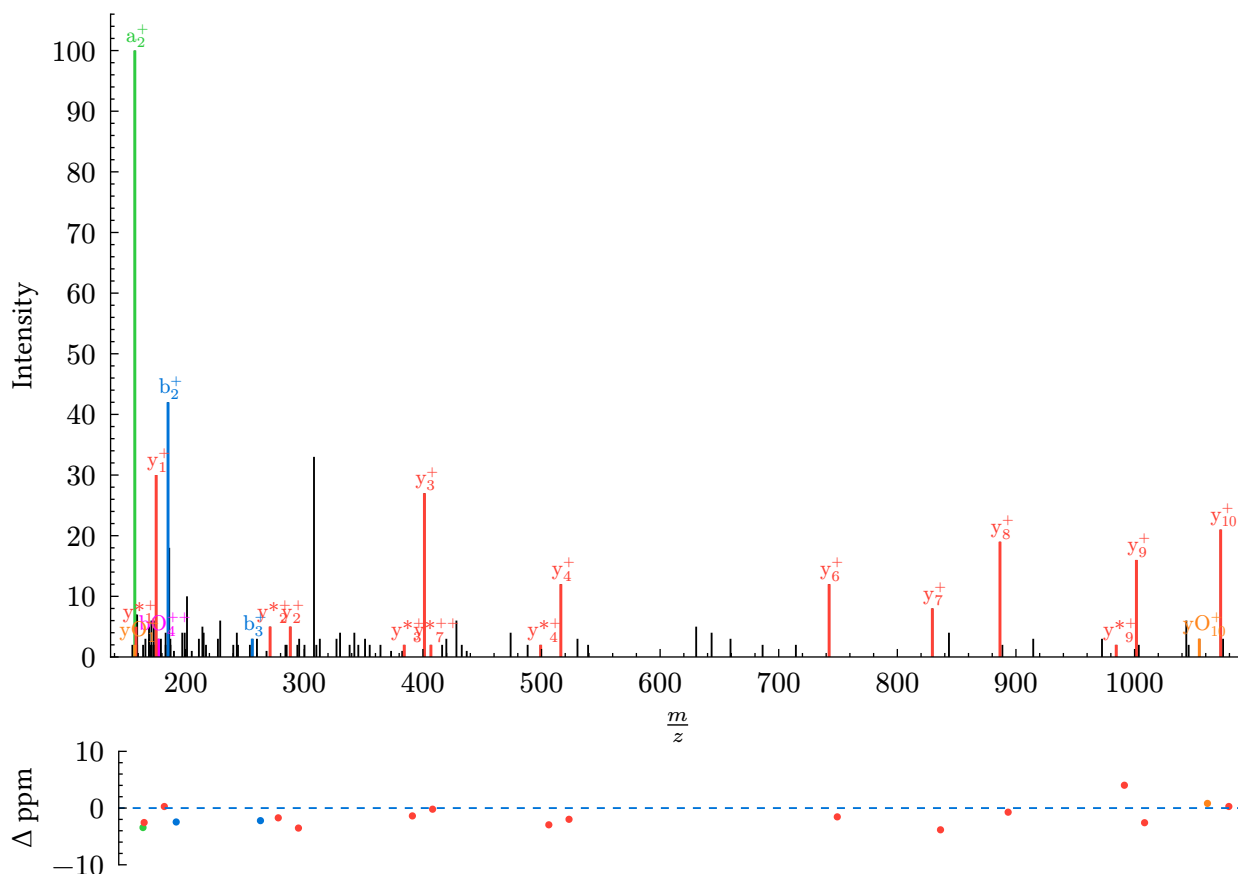
## MS2 spectra with ion annotations and MS2 fragments mass delta

This example shows an MS2 spectra with ion series annotation

## Example :

```
#import "@preview/teotegraph:0.2.0": *  
  
#let complete_psm = json("../examples/data/complete_psm.json")  
#ms2spectra-plot(width: 15cm, height: 10cm, spectra: complete_psm.spectra, ion-series:  
complete_psm.ion-series, delta-fragments: true)
```

**Result :**



## MS2 spectra with ion annotations and highlighted mass delta between peaks

The space between two peaks can be highlighted and manually annotated using an array defined as follow

*Highlight space between peaks array*

```
[
{
    "ion": "y",
    "mz": [401.287, 516.313],
    "level": 1,
    "label": "D"
},
{
    "ion": "y",
    "mz": [742.481, 829.511],
    "level": 1,
    "label": "S"
},
{
    "ion": "y",
    "mz": [829.511, 886.535],
    "level": 1,
    "label": "G"
},
{
```

```

    "ion": "y",
    "mz": [886.535,1001.56],
    "level": 1,
    "label": "D"
  }
]

```

### Example :

```
#import "@preview/proteograph:0.2.0": *
```

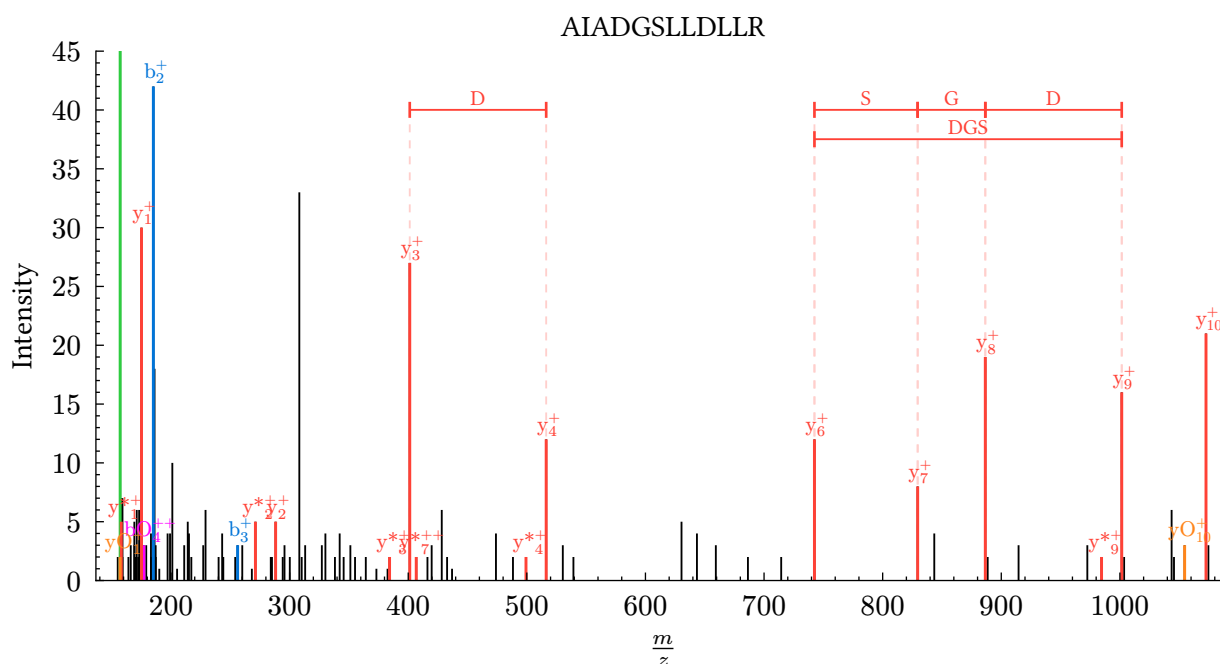
```

#let delta_arr = (
  (
    "ion": "y",
    "mz": (401.287,516.313),
    "level": 1,
    "label": "D"
  ),
  (
    "ion": "y",
    "mz": (742.481,829.511),
    "level": 1,
    "label": "S"
  ),
  (
    "ion": "y",
    "mz": (829.511,886.535),
    "level": 1,
    "label": "G"
  ),
  (
    "ion": "y",
    "mz": (886.535,1001.56),
    "level": 1,
    "label": "D"
  ),
  (
    "ion": "y",
    "mz": (742.481,1001.56),
    "level": 2,
    "label": "DGS"
  )
)

#let complete_psm = json("../examples/data/complete_psm.json")
#ms2spectra-plot(width: 15cm, height: 7cm, max-intensity: 45, title: "AIADGSLLDLLR",
spectra: complete_psm.spectra, ion-series: complete_psm.ion-series, delta: delta_arr)

```

**Result :**



## MS2 spectra full documentation

- ms2spectra-plot()

## ms2spectra-plot

Generates an annotated MS2 spectra plot.

## Parameters

```
ms2spectra-plot(  
  width: length relative,  
  height: length relative,  
  title: str content,  
  mz-range: none array,  
  max-intensity: none float,  
  spectra: none dictionary,  
  ion-series,  
  delta,  
  delta-fragments: bool  
) -> content
```

**width**   length   or   relative

The width of the diagram. This can be

- A `length` ; in this case, it defines just the width of the data area, excluding axes, labels, title etc.
- A `ratio` or `relative` where the ratio part is relative to the width of the parent that the diagram is placed in. This is not allowed if the parent has an unbounded width, e.g., a page with `width: auto`.

Default: 15cm



**height** `length` or `relative`

The height of the diagram. This can be

- A `length` ; in this case, it defines just the height of the data area, excluding axes, labels, title etc.
- A `ratio` or `relative` where the ratio part is relative to the height of the parent that the diagram is placed in. This is not allowed if the parent has an unbounded height, e.g., a page with `height: auto` .

Default: `10cm`

**title** `str` or `content`

Shows the plot title. **Optional.**

Default: `none`

**mz-range** `none` or `array`

m/z range to display. **Optional.**

Example: `(450, 950)`

Default: `none`

**max-intensity** `none` or `float`

maximum intensity to display. **Optional.**

Example: `30000`

Default: `none`

**spectra** `none` or `dictionary`

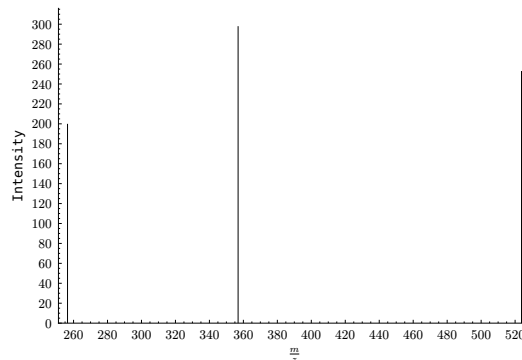
Mass spectra values. **Optional.**

a dictionary with the keys `mz` (array of mass to charge ratios) and `intensity` (array of intensities) with the same length for each array

(e.g., `spectra: (mz: (256.45, 356.89, 523.78), intensity: (200, 298, 253))`)

```
1 #import "@preview/  
  proteograph:0.2.0": *  
2 #set text(size: 12pt)  
  #ms2spectra-plot( spectra: (mz:  
3 (256.45, 356.89, 523.78), intensity:  
  (200, 298, 253)))
```

typ



Default: `none`

**delta-fragments** `bool`

Whether to clip the matched ion mass delta to the plot. **Optional.**

Default: `false`

## Protein sequence

### Example :

```
#import "@preview/teograp:0.2.0": *
```

```
#protein-sequence(line-length: 60,
```

```
"MASTKAPGPGEKHHSIDAQLRQLVPGKVSEDDKLEIYDALLVDRFLNQLDLHGPSLREFVQECYEVSADYEGKGDITKLGLGAKLTGLAPADAILV
```

### Result :

```
0  MASTKAPGPGEKHHSIDAQLRQLVPGKVSEDDKLEIYDALLVDRFLNQLDLHGPSLREF
60  VQECYEVSADYEGKGDITKLGLGAKLTGLAPADAILVASSILHMLNLANLAEEVQIAHR
120 RRNSKLKKGFADEGSATTESDIEETLKRVLSEVGKSPPEVFEALKNQTVDLVFTAHTQ
180 SARRSLLQKNARIRNCLTQLNAKDITDDDKQELDEALQREIQAAFRTDEIRRAQPTPQDE
240 MRYGMSYIHETVWKGVPKFLRRVDTALKNIGINERLPYNVSLIRFSSWMGGDRDGNPRVT
300 PEVTRDVCLLARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSKVTKYIE
360 FWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSIEEFLEPLELCY
420 KSLCDCGDKAIADGSLLDLLRQVFTFGLSLVKLDIRQESERHTDVIDAITTHLGIGSYRE
480 WPEDKRQEWLLSELRGKRPLLPDLPQTDEIADVIGAFHVLAELPPDSFGPYIISMATAP
540 SDVLAVELLQRECGVRQPLPVVPLFERLADLQSAPASVERLFSVDWYMDRIKQKQVMVG
600 YSDSGKDAGRLSAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGPHTLAISQP
660 PDTINGSIRVTVQGEVIEFCFGEEHLCFQTLQRFTAATLEHGMHPPVSPKPEWRKLMDM
720 AVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSRPAKRRPGGGITTLRAIPWIFS
780 WTQTRFHLPVWLGVAFAFKFAIDKDVRNFQVLKEMYNEWPFVRVTLDLLEMVFAKGDPI
840 AGLYDELLVAEELKPFQKLRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITT
900 LNVFQAYTLKRIRDPNFKVTPQPPLSKEFADENKPAGLVKLNPASEYPPGLEDTLILTMK
960 GIAAGMQNTGA
```

## Protein sequence documentation

- [protein-sequence\(\)](#)

### protein-sequence

Display a protein sequence in a block with amino acid numbering

#### Parameters

```
protein-sequence(  
  line-length,  
  protein  
) -> content
```

#### line-length

The maximum length of amino acid to display in a line. **Optional**.

Default: 50

#### protein

Amino acid sequence (one letter code) of the protein to display

## Protein diagram

This figure is based on the [fletcher](#) package features.

### Example :

```
#import "@preview/teotopology:0.2.0": *

#let tint(c) = (stroke: c, fill: rgb(..c.components().slice(0,3), 5%), inset: 1pt)

#protein-diag(line-length: 60,
"MASTKAPGPGGEKHHSIDAQLRQLVPGKVSDDKLEIYDALLVDRFLNILQDLHGPSLREFVQECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILV
(pos: (1,5), style: tint(green)),
(pos: (12,17), style: tint(teal)),
(pos: (75,177), style: tint(red)),
)
```

### Result :

```
MASTKAPGPGGEKHHSIDAQLRQLVPGKVSDDKLEIYDALLVDRFLNILQDLHGPSLREF
VQECYEVSADYEGKGDTTKLGELGAKLTGLAPADAILVASSILHMLNLANLAEVQIAHR
RRNSKLLKGGFADEGSATTESDIEETLKRLVSEVGKSPPEVFEALKNOTVDLVFTAHPTQ
SARRSLLQKNARIRNCLTQLNAKDITDDDKQELDEALQREIQAAFRTDEIRRAQPTPQDE
MRYGMSYIHETVWKGVPKFLRRVDTALKNIGINERLPYNVSLIRFSSWMGGDRDGNPRVT
PEVTRDVCLLARMMAANLYIDQIEELMFELSMWRCNDELRVRAEELHSSSGSKVTKYYIE
FWKQIPPNEPYRVILGHVRDKLYNTRERARHLLASGVSEISAESSFTSIEEFLEPLELCY
KSLCDCGDKAIADGSLDLLRQVFTFGLSLVKLDIRQESERHTDVIDAITTHLGIGSYRE
WPEDKRQEWLLSELRGKRPLLPDLPQTDEIADVIGAFHVLAELPPDSFGPYIISMATAP
SDVLAVELLQRECGVRQPLPVVPLFERLADLQSAPASVERLFSVDWYMDRIKQKQVMVG
YSDSGKDAGRLSAAWQLYRAQEEMAQVAKRYGVKLTLFHGRGGTVGRGGPHTLAILSQP
PDTINGSIRVTVQGEVIEFCFGEELHLCFQTLQRFTAATLEHGMHPPVSPKPEWRKLMDEM
AVVATEEYRSVVVKEARFVEYFRSATPETEYGRMNIGSRPAKRRPGGGITTTLRAIPWIFS
WTQTRFHLPVWLGVGAFAFKFAIDKDVRNFQVLKEMYNEWPFVRVTLDLLEMVFAKGDPI
AGLYDELLVAEELKPFQKQLRDKYVETQQLLLQIAGHKDILEGDPFLKQGLVLRNPYITT
LNVFQAYTLKRIRDPNFKVTPQPPLSKEFADENKPAGLVKLNPASEYPPGLEDTLILTMK
GIAAGMQNTGA
```

## Protein diagram documentation

- [protein-diag\(\)](#)

### protein-diag

Display a protein sequence in a block with amino acid numbering

#### Parameters

```
protein-diag(
  line-length: int,
  boxes: array,
  protein: str,
  ..box: dictionary
) -> content
```

**line-length** `int`

The maximum length of amino acid to display in a line. **Optional**.

Default: `50`

**boxes** `array`

Array of boxes to draw in the protein sequence **Optional**.

This can be used to visualize the position of one or more peptides

example for 3 peptides :

```
((pos: (1,5), style: tint(green)),(pos: (12,17), style: tint(teal)),(pos: (75,177), style: tint(red)))
```

Default: `()`

**protein** `str`

Amino acid sequence (one letter code) of the protein to display

**..box** `dictionary`

box item to draw in the protein sequence **Optional**.

This can be used to visualize the position of one or more peptides

example :

```
(pos: (1,5), style: tint(green))
```

```
1 #import "@preview/
2 #proteograph:0.2.0": *
3 "MASTKAPGPGGEKHHSIDAQLRQLV",
4 (pos: (1,5), style: (stroke: red,
5 inset: 1pt)),
6 (pos: (12,17), style: (stroke: teal,
7 inset: 3pt))
8 )
```



MASTKAPGPGGEKHHSIDAQLRQLV