

Protein Digestion, Peptide Mass and Peptide Fragmentation with MZCal: A User-Friendly Phone-Compatible Application

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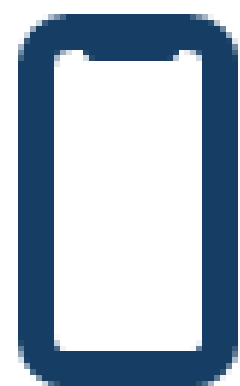
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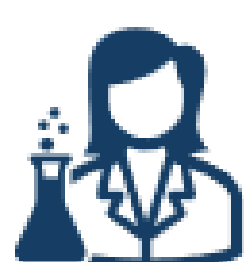
Teaching resource



Mobile-compatible web application



Supports iOS and Android



Optimised for lab settings

In Silico Digestion

Peptide Mass

*Dynamically Assign
Modifications*

*Physiochemical
Characteristics*

*Spectral Prediction
MS2PIP ^{Degroeve (2012)}*

Protein Digest

Peptides

Enter uniprot accession number

Accession number

P00924

Missed Cleavages

0

Minimum Length

5

Order by

☐ Start

☒ Mz

Carbamidomethylation

☒ True

☐ False

Protease

trypsin.strict

Submit

Download

Protein Digest

Peptides

Peptide Sequence

PEPTIDE

Cysteine Modification

C2NOH3

Fragmentation Options

Min Frag Mz

50

Max Frag Mz

2000

Fragment Charges to Display

☒ +1

☐ +2

☐ +3

☐ +4

☐ +5

☐ +6

☐ +7

☐ +8

☐ +9

☐ +10

☐ -1

☐ -2

☐ -3

☐ -4

☐ -5

☐ -6

Modifications

Summary

M/Z Values

Isotope Dist

Fragment Masses

MS2PIP

Insert the molecular formula (e.g. CH2) next to the appropriate amino acid. NOTE - ensure the amino acid sequence is correct prior to starting. Modifications to cysteine residues will be applied as well as those specified in the left hand pane (Cysteine Modification) in the result tabs.
Supported heavy isotopes: Ch = 13C; D = 2H; Nh = 15N. NOTE - heavy isotopes are NOT supported in the isotope distribution tab.

Add Modifications

Remove Modifications

NTerm

P1

E2

P3

T4

I5

D6

E7

CTerm

NTerm

P1

E2

P3

T4

I5

D6

E7

CTerm

AA	Add	Remove	Da
NTerm			0
P			0
E			0
P			0
T			0
I			0
D			0
E			0
CTerm			0

Download

TRY ME!

<https://harrywhitwell.shinyapps.io/MZCal/>



Publication

<https://doi.org/10.1016/j.jpro.2025.105456>

