For this demo, we will analyze explore proteomics data and run a database search.

Important: Proteomics tools may not run on Mac OS

Getting the data

1. **MaxQuant** can be downloaded from https://www.maxquant.org/.
2. Mass spectrometry data (.raw files) and protein database (.fasta) are at https://figshare.com/articles/dataset/Sample_mass_spectrometry_data_for_human_bottom-up_proteomics/24288913
    a. The data originally came from https://zenodo.org/record/4274987
    b. They are proteomics data of healthy human serum samples that were digested with Trypsin and analyzed on a Q-Exactive Plus mass spectrometer (Orbitrap mass analyzer).
3. **MZmine** tool for visualizing mass spectra can be downloaded from https://github.com/mzmine/mzmine3/releases/tag/v3.2.8 (select the _portable file if you don't want to install it)
4. A proteomics paper where we can learn to spot key protocol details: https://www.nature.com/articles/s41586-020-2402-x.

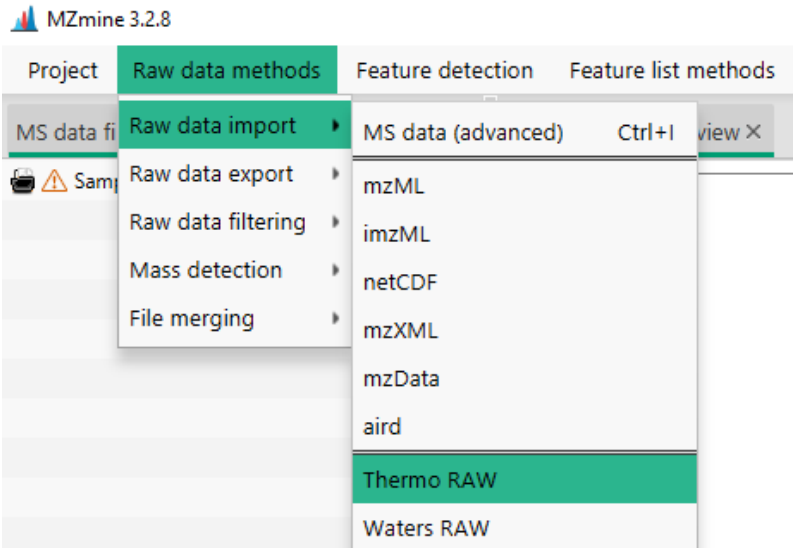
Setting up software

Just unzip **MaxQuant** and **MZmine** (if you selected the_portable version). When launching **MaxQuant**, if there is an error about **Microsoft .NET framework**, please follow the link to download and install .NET on your PC.

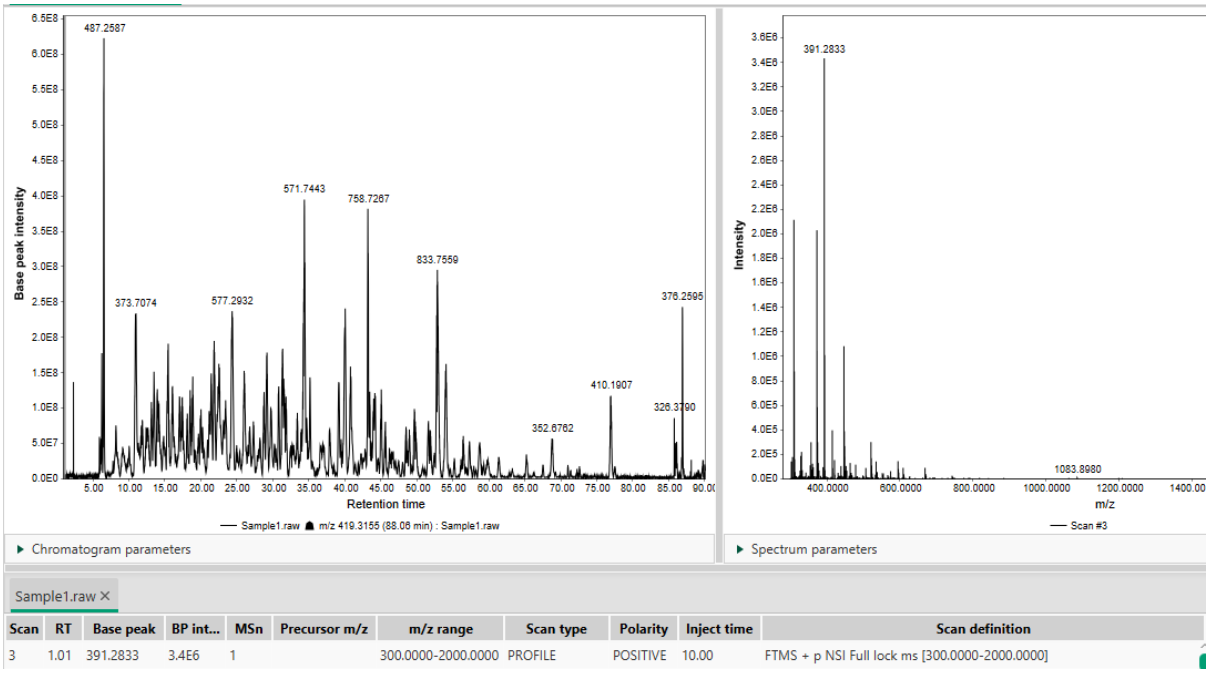
Running the demo

Section 1: MS data exploration

1. The .raw files came from Thermo Scientific's mass spectrometer machine. We can view the spectra in **MZmine** by specifying the import format as **Thermo RAW** as shown below.



2. Once imported, you will be shown the **Chromatogram** (left panel). This shows the most intense ions that eluded out from liquid chromatography into the mass spectrometer.

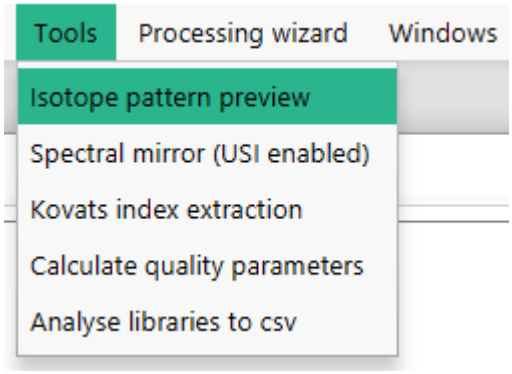


3. At the bottom, you will see the list of all spectra (sorted by scan number, or time). The **MSn** column tells us whether the spectrum is **MS1** (of intact peptides) or **MS2** (of fragmented peptides). **MS1** is like a survey of existing peptides while **MS2** provides signature ions that can be matched to protein/peptide databases.

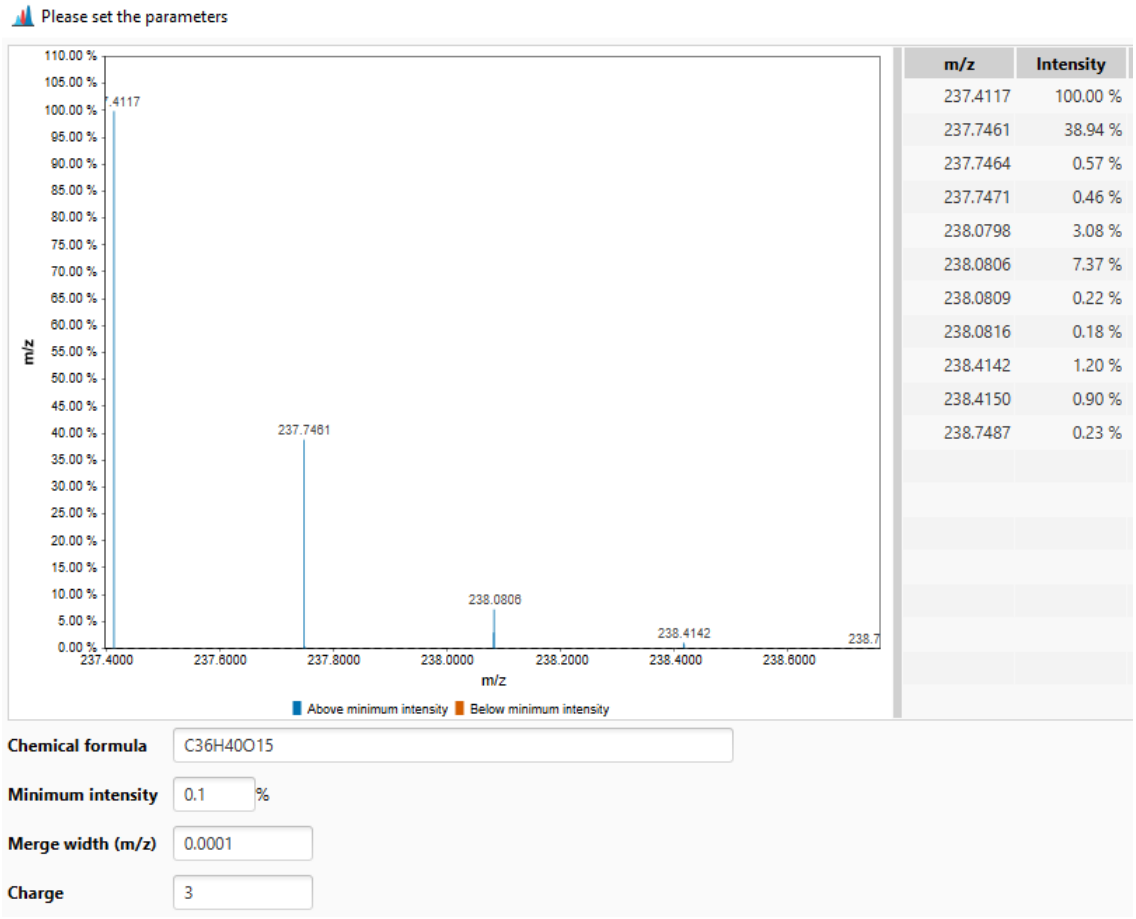
Sample1.raw ×

Scan	RT	Base peak	BP int...	MSn	Precursor m/z	m/z range	Scan type	Polarity	Inject time	Scan definition
1	1.00	391.2833	3.6E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
2	1.01	391.2833	4.0E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
3	1.01	391.2833	3.4E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
4	1.02	391.2832	3.8E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
5	1.02	310.0276	6.7E4	2	388.0055	80.6667-1210.0000	CENTROIDED	POSITIVE	80.00	FTMS + c NSI d Full ms2 388.0055@hcd25.00 [80.6667-1210.0000]
6	1.02	391.2834	3.9E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
7	1.03	391.2850	3.4E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
8	1.03	391.2833	3.7E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
9	1.04	391.2834	3.7E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
10	1.04	391.2834	3.9E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
11	1.05	391.2833	3.9E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
12	1.05	391.2834	3.6E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
13	1.06	391.2834	3.5E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
14	1.06	391.2833	3.9E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
15	1.07	391.2833	3.7E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
16	1.07	391.2835	5.2E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
17	1.08	391.2834	3.8E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]
18	1.08	97.0412	6.5E3	2	381.8745	53.3333-800.0000	CENTROIDED	POSITIVE	80.00	FTMS + c NSI d Full ms2 381.8745@hcd25.00 [53.3333-800.0000]
19	1.09	298.9213	2.4E4	2	376.8994	78.3333-1175.0000	CENTROIDED	POSITIVE	80.00	FTMS + c NSI d Full ms2 376.8994@hcd25.00 [78.3333-1175.0000]
20	1.09	391.2833	3.4E6	1		300.0000-2000.0000	PROFILE	POSITIVE	10.00	FTMS + p NSI Full lock ms [300.0000-2000.0000]

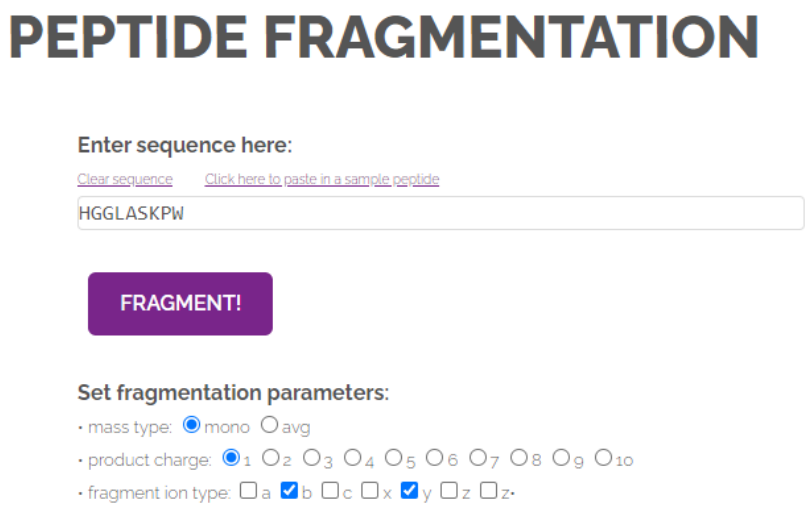
4. We can visualize isotopic envelope pattern using the tools shown below.



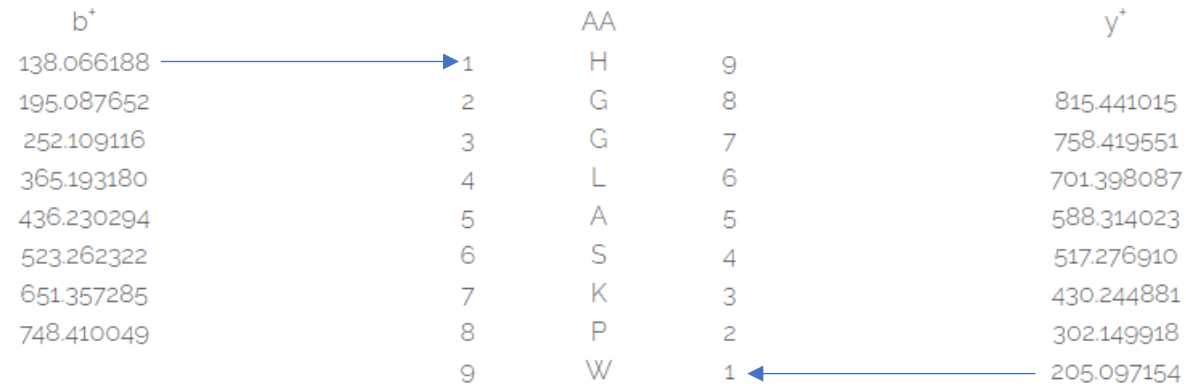
5. Given a chemical formula, $C_xH_yN_zO_w$, we can compute the expected abundance of all isotopes of this molecule based on the frequencies of naturally occurring C^{13}, C^{14}, N^{15}, and O^{18}.



6. To visualize the process of peptide fragmentation, we use an online tool https://proteomicsresource.washington.edu/cgi-bin/fragment.cgi. Let's input a peptide **HGGLASKPW**.

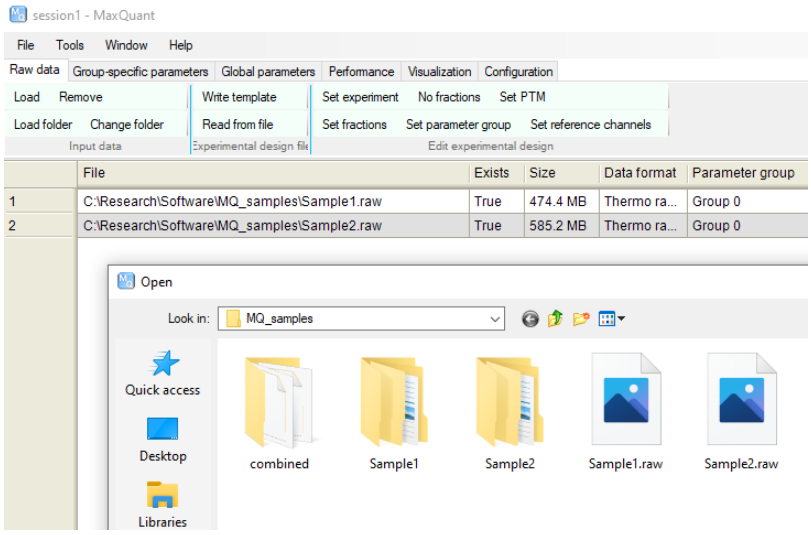


7. The tool will show all b- and y-ions that could be produced from this peptide. The default setting is to show the monoisotopic masses (without extra neutron) and to the show the masses at charge state of +1.
    a. b-1 ion (from the N-terminus) consists of only a Histidine. Histidine's molecular weight is 137.06. The weight shown is Histidine with an addition of a proton = 138.066.
        i. b-ions at +1 charge = 1 + total amino acid molecular weight
    b. y-1 ion (from the C-terminus) consists of only a Tryptophan. Tryptophan 's molecular weight is 186.08. The weight shown is Tryptophan with an addition of H_2O + proton = 205.097.
        i. y-ions at +1 charge = 19 + total amino acid molecular weight
    c. The mass difference between adjacent ions is equal to amino acid mass
        i. Glycine's weight is 57.02 = 195.088 – 138.066 = 252.109 – 195.088

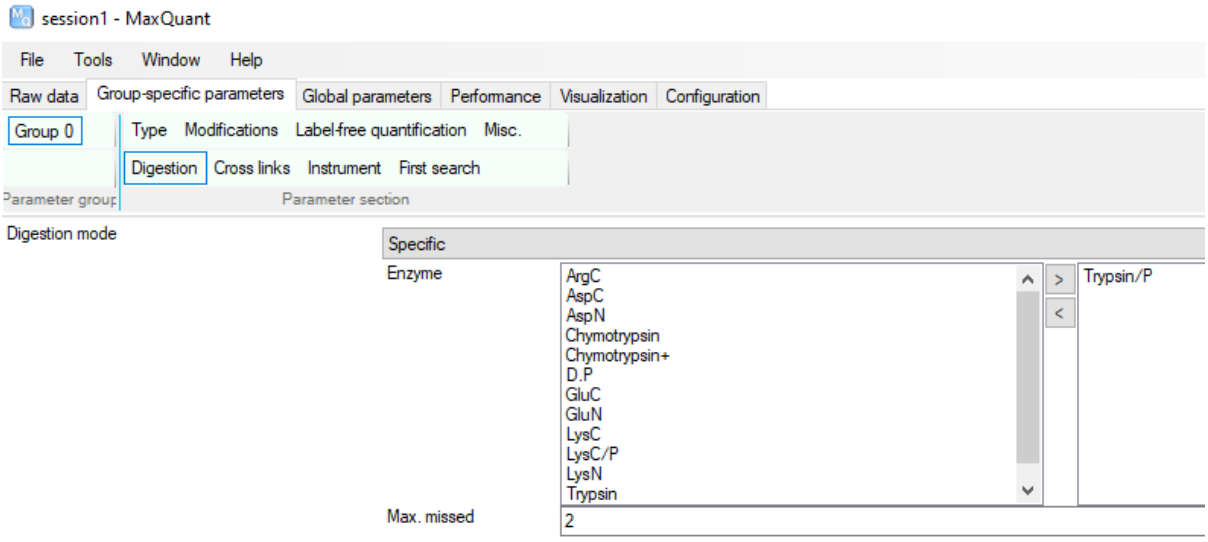


Section 2: Protein/peptide search with MaxQuant

1. Load individual .raw file or a folder containing multiple .raw files using the **Load** and **Load folder** buttons.



2. Next, let us explore the vast settings in **MaxQuant** (we will do this in class). Proteomics analysis is highly specific to the experimental conditions and mass spectrometer setups. So, if you want to re-analyze public data, you need to understand the entire protocol.



3. We can also add new post translational modification or chemical modification to be included in the protein/peptide search. This functionality is in the **Configuration** tab.

session1 - MaxQuant

File Tools Window Help

Raw data | Group-specific parameters | Global parameters | Performance | Visualization | Configuration

Modifications | Proteases | Crosslinks — Data type

Add | Duplicate | Move down | Discard changes | Remove | Move up | Save changes — Table actions

Modify table — Actions

	Name	Description	Composition	Position
1	Acetyl (K)	Acetylation	C(2) H(2) O	Not C-term
2	Acetyl (Protein N-term)	Acetylation of the protein N-terminus	C(2) H(2) O	Protein N-term
3	Carbamidomethyl (C)	Iodoacetamide derivative	C(2) H(3) N O	Anywhere
4	Oxidation (M)	Oxidation	O	Anywhere
5	Phospho (STY)	Phosphorylation	H O(3) P	Anywhere
6	GlyGly (K)	Ubiquitination residue	H(6) C(4) N(2) O(2)	Anywhere
7	RGG (K)	Ubiquitination residue (chymotrypsin)	H(18) C(10) N(6) O(3)	Anywhere
8	Methyl (KR)	Methylation	C H(2)	Anywhere
9	Dimethyl (KR)	di-Methylation	H(4) C(2)	Anywhere
10	Trimethyl (K)	tri-Methylation	C(3) H(6)	Anywhere
11	Pro5	Proline-13C5	Cx(5) C(-5)	Anywhere
12	Pro6	Proline-13C515N1	Cx(5) Nx C(-5) N(-1)	Anywhere