H3ABioNet

Bioinformatics Training Unit

H3ABioNet

Pan African Bioinformatics Network for H3Africa

Introduction to Bioinformatics online course: IBT

Multiple Sequence Alignment

Lec3: Navigation in Jalview

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Source: Jaview Online Training Video

https://www.jalview.org/

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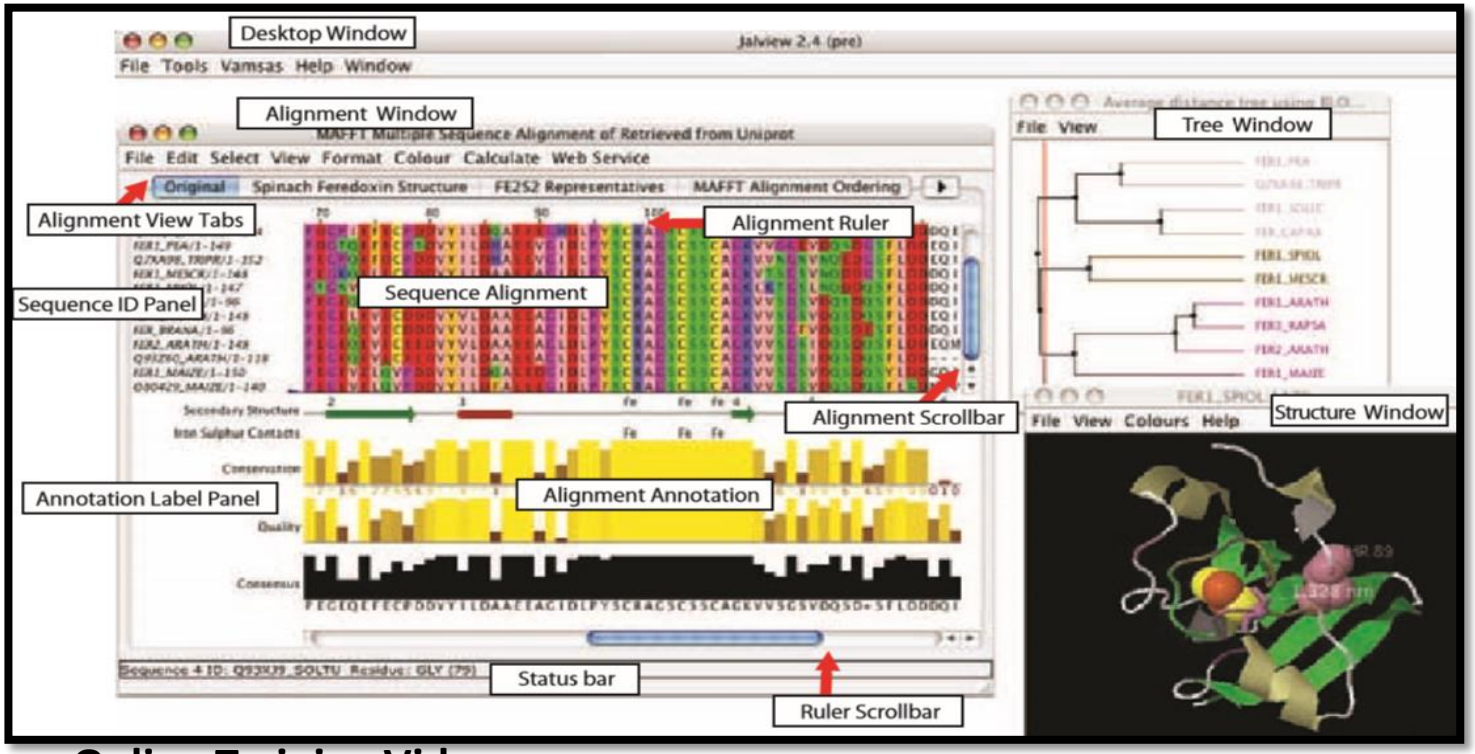
Navigation

The major features of the Jalview Desktop are illustrated in Figure.



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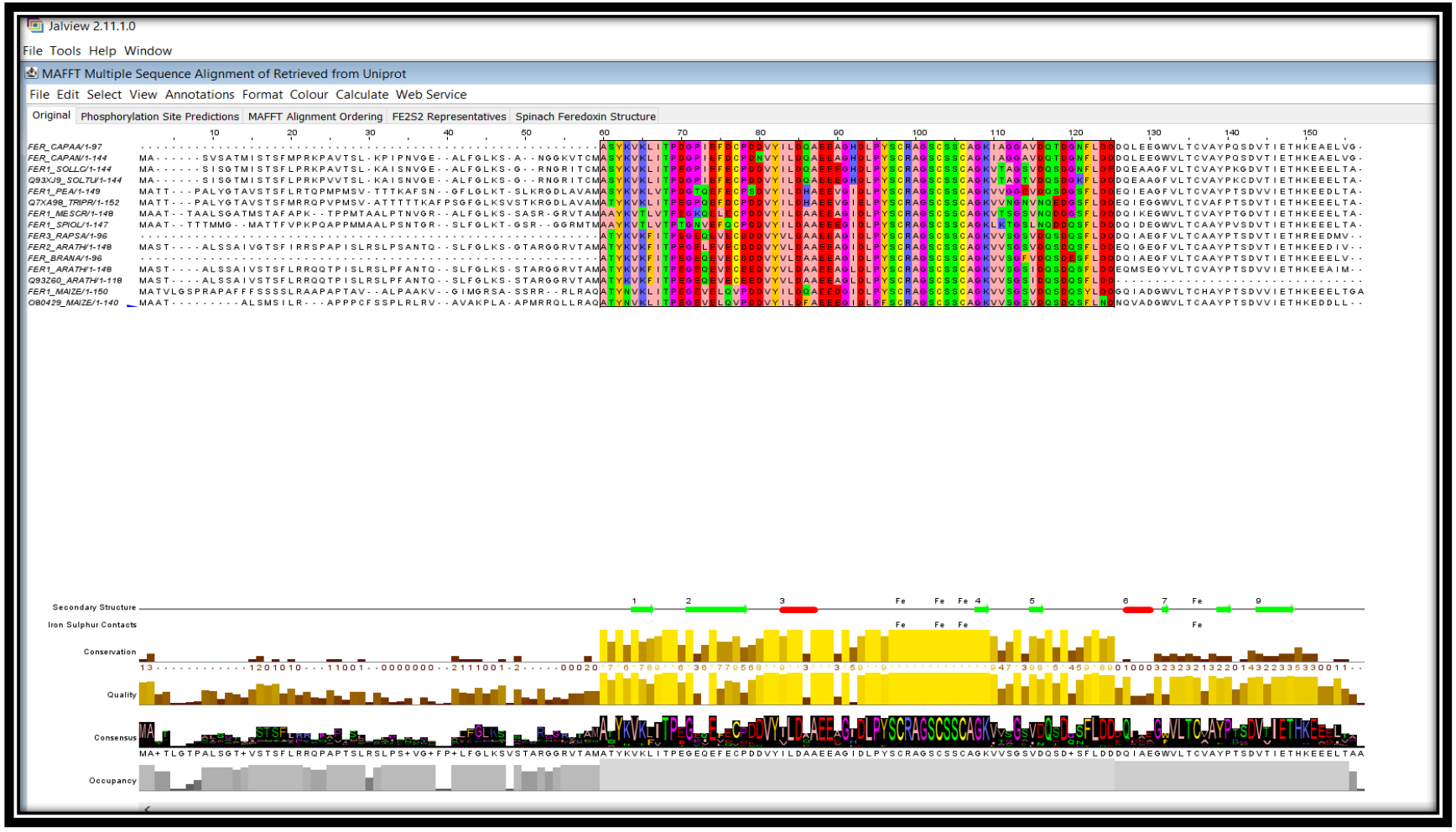
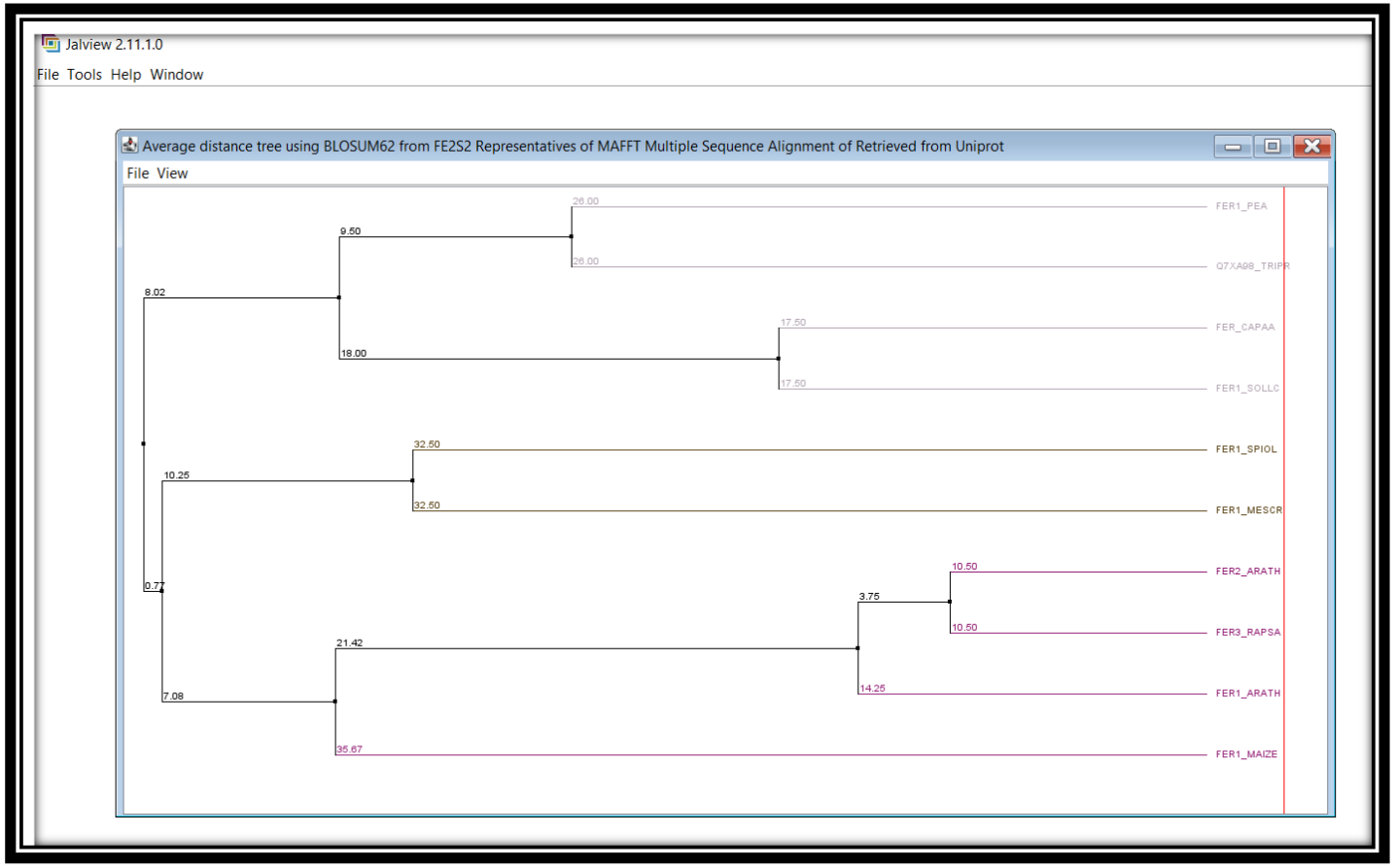
Alignment window

The alignment window is the primary window for editing and visualization, and can contain several independent views of the alignment being worked with.



Tree window



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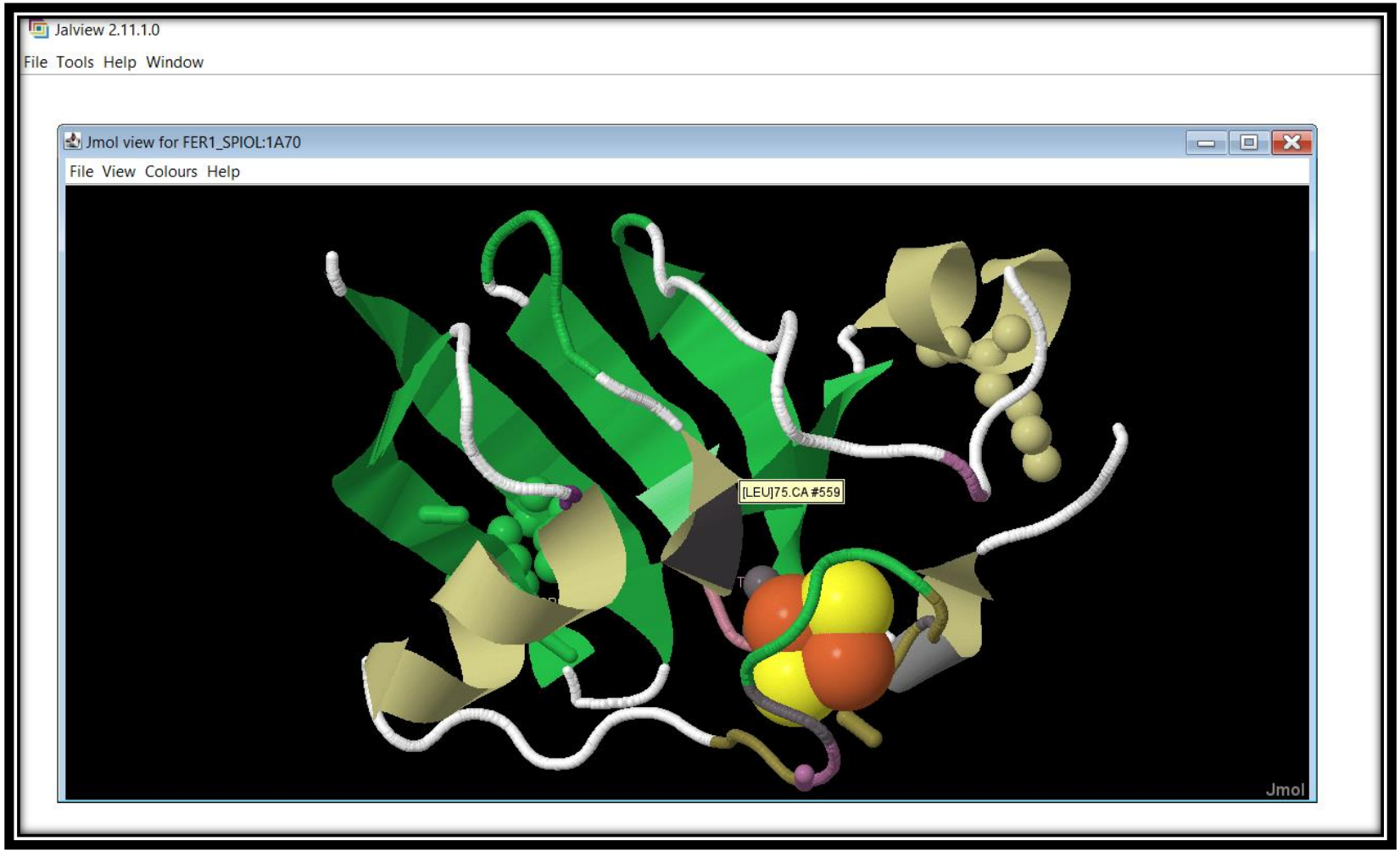
Struture window



Editing Modes

Source: Jaview Online Training Video
https://www.jalview.org/

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Jalview has two navigation and editing modes:

1- ***Normal mode***, where editing and navigation is per- formed using the mouse.

2- ***Cursor mode*** where editing and navigation are performed using the keyboard.

The ***F2 key*** is used to switch between these two modes

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Navigation

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https://www.jalview.org/

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Navigation in Normal mode

- Jalview always **starts up** in **Normal mode**, where the mouse is used to interact with the displayed alignment view.

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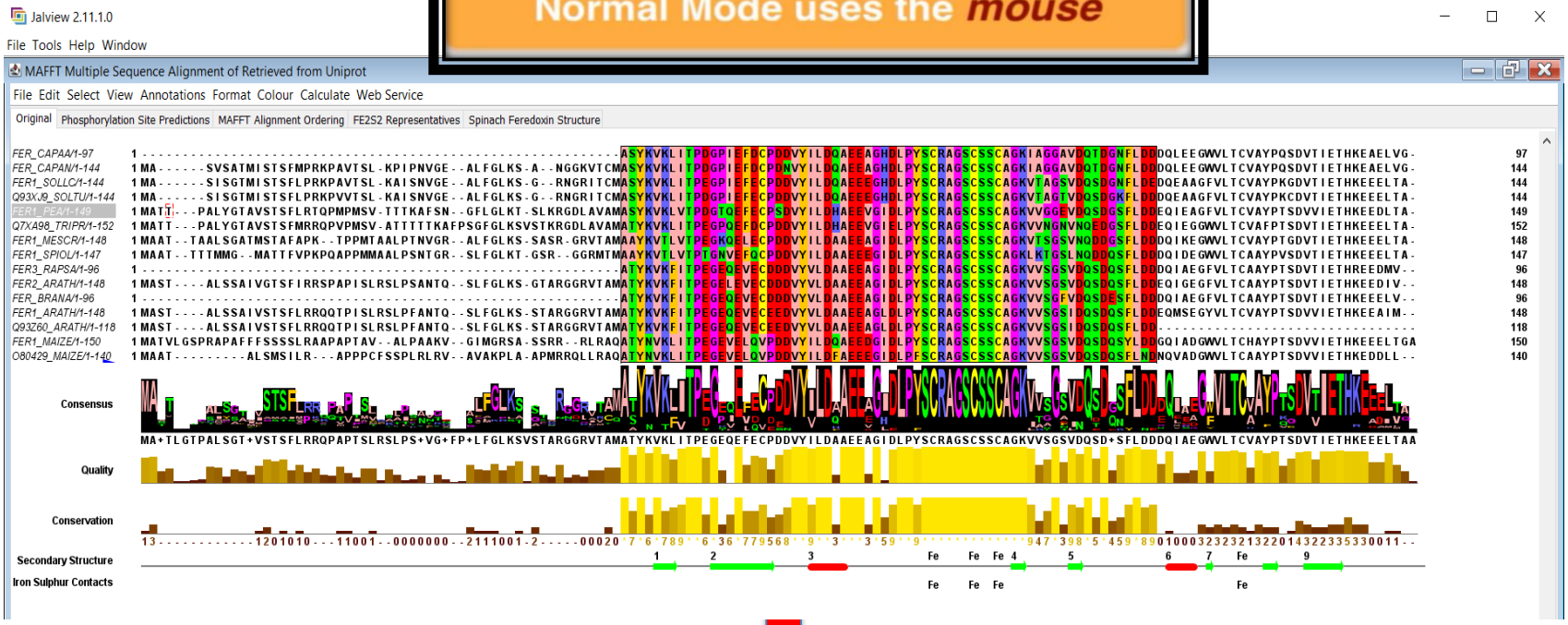
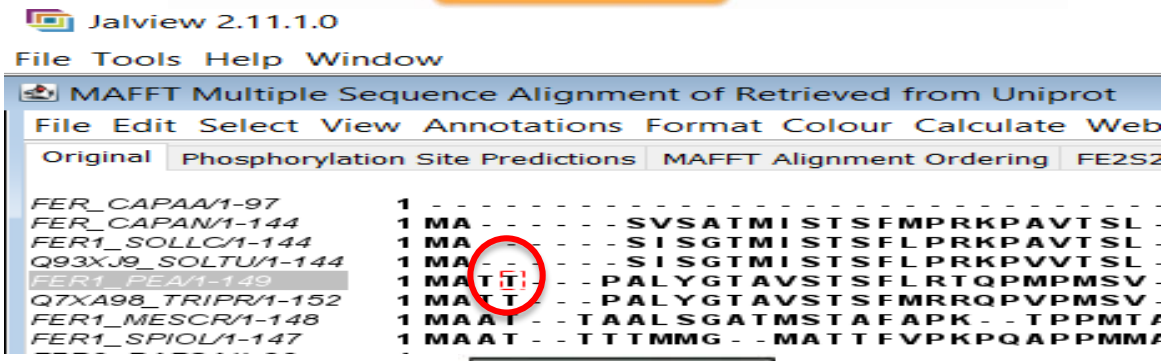
Normal Mode uses the *mouse*



Normal Mode



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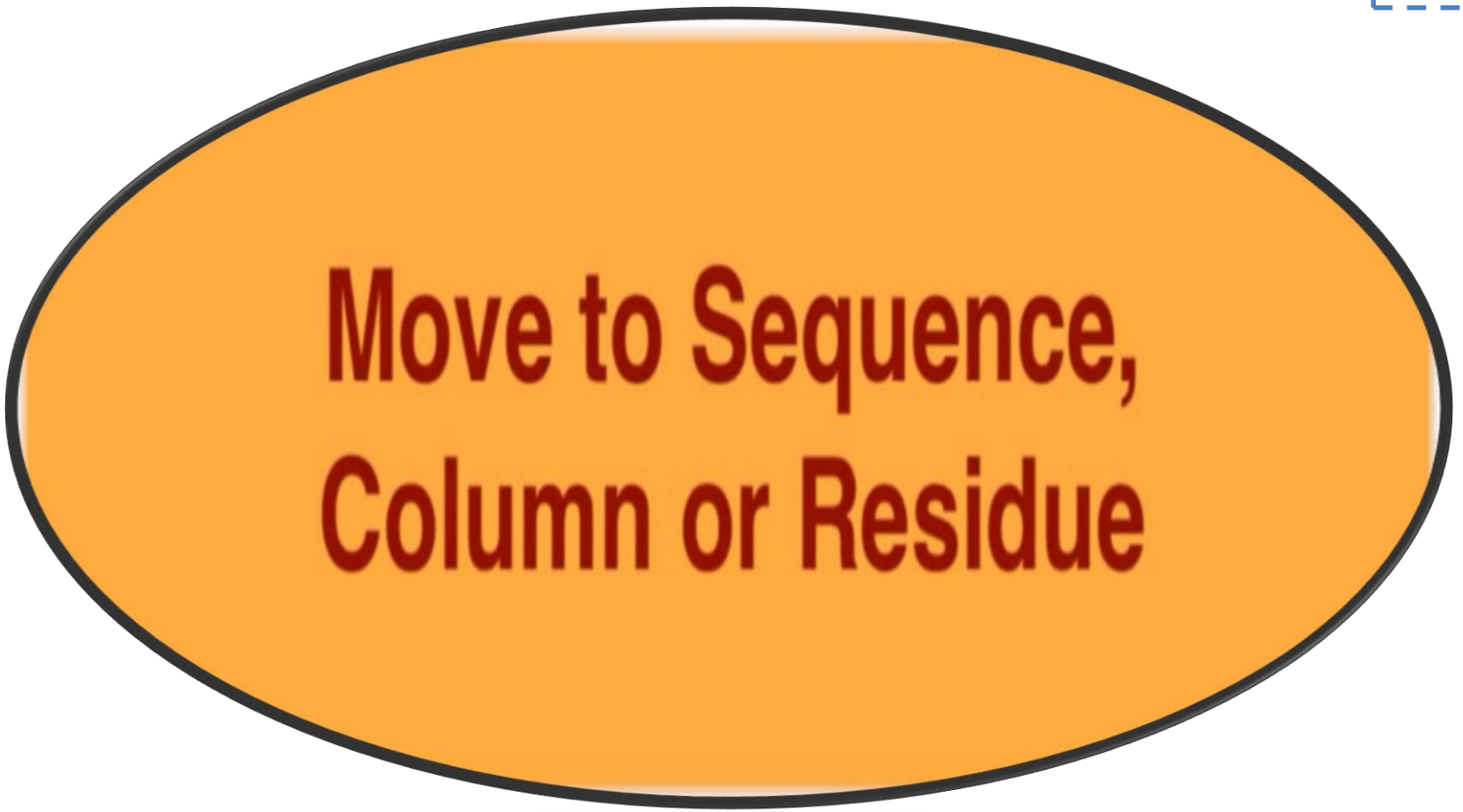

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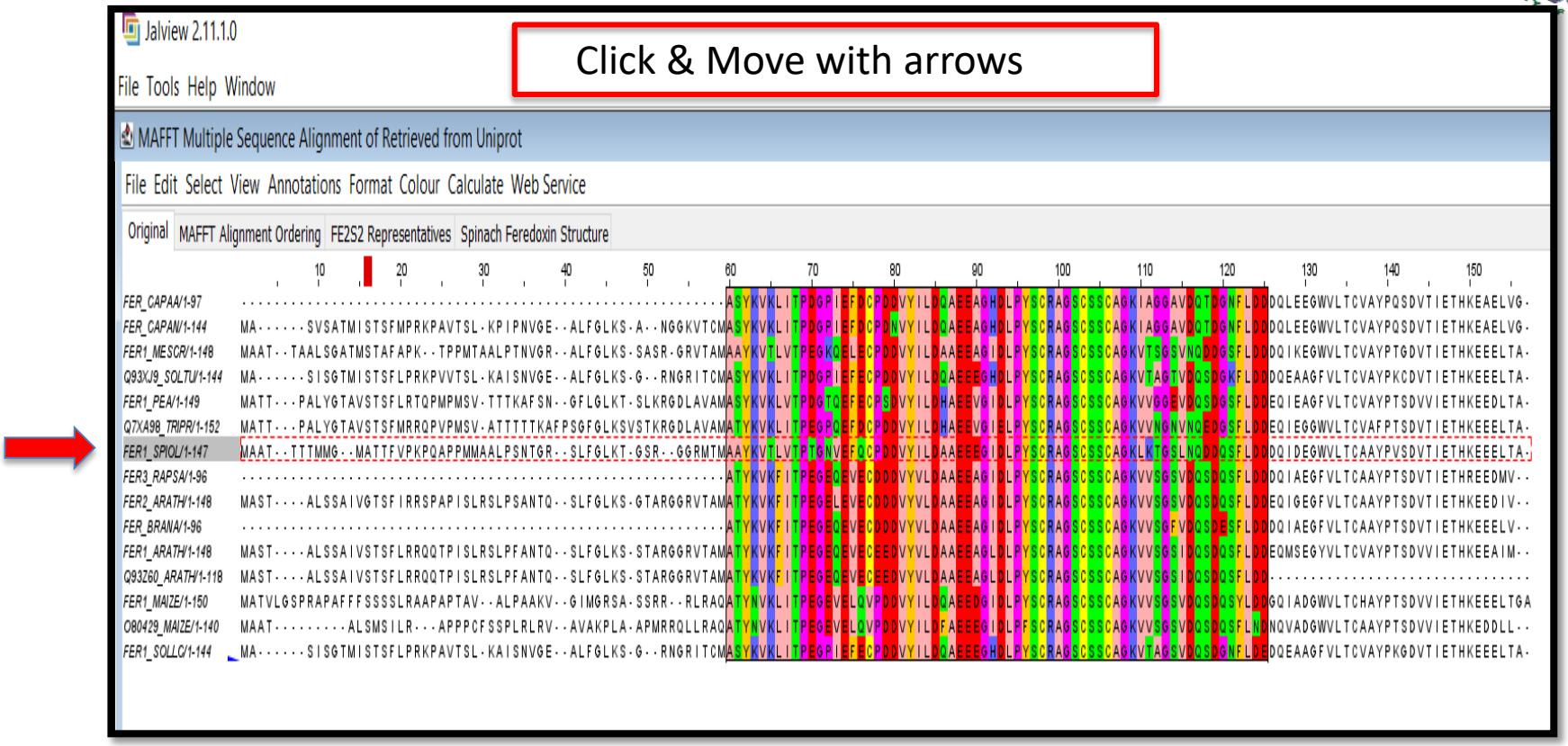

Move to Sequence Row: click on sequence in ID panel

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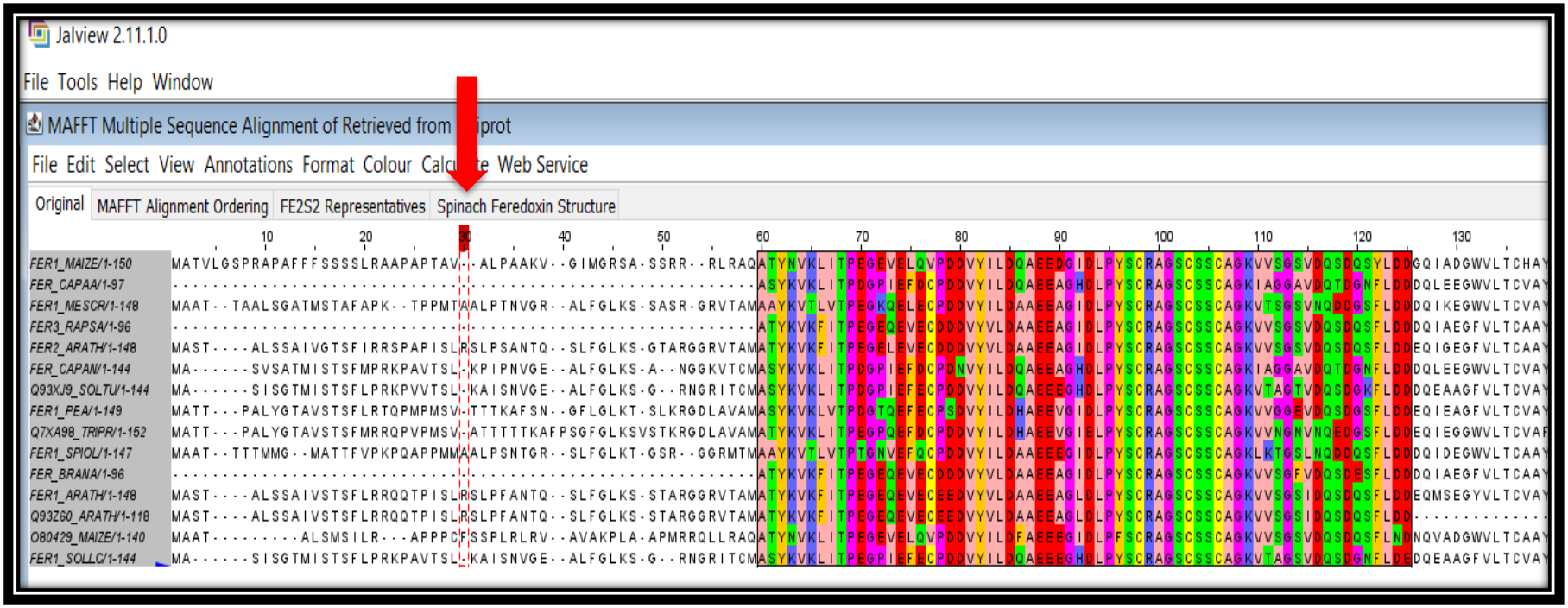

Move to column: click on column in ruler

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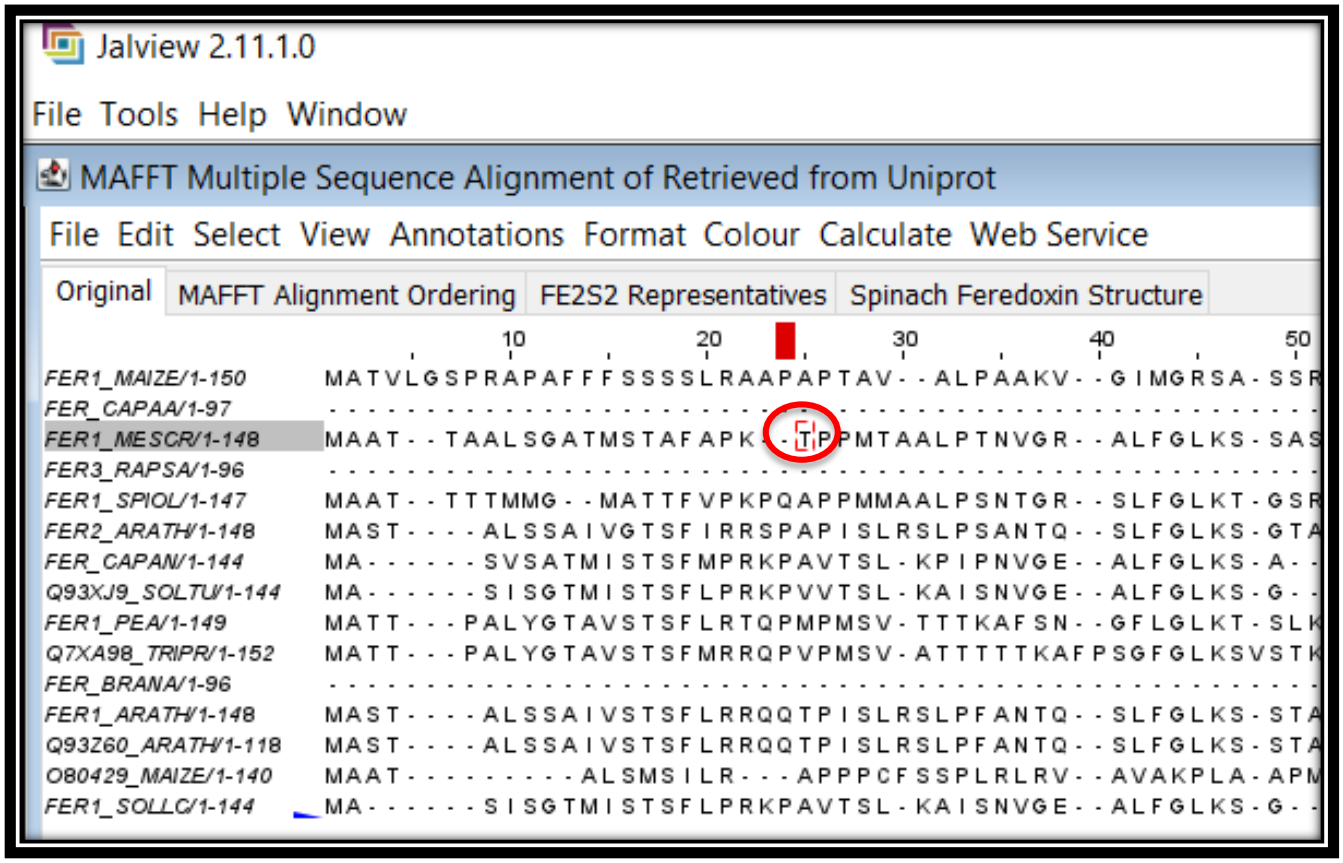

Move to residue click on residue

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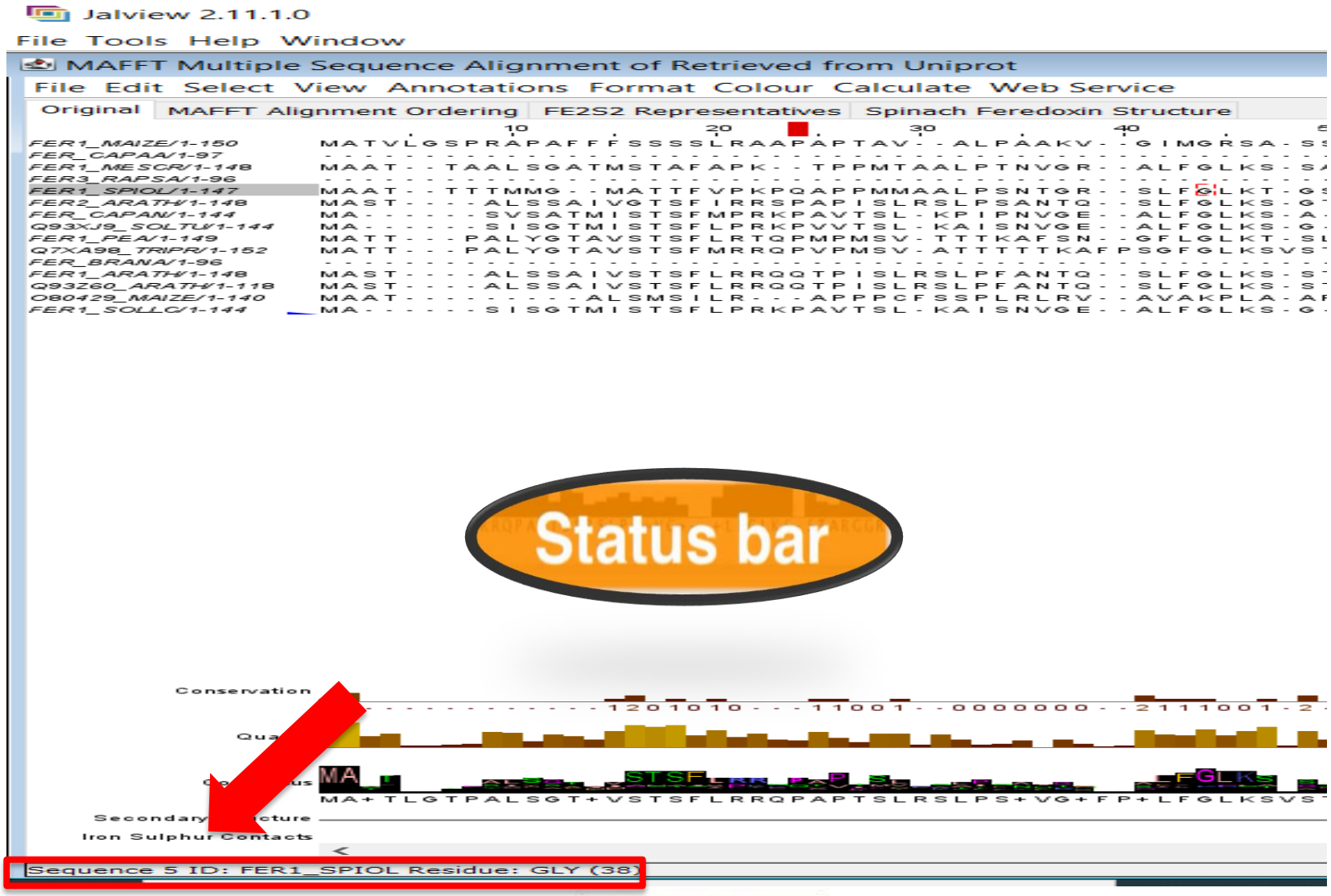

Status bar

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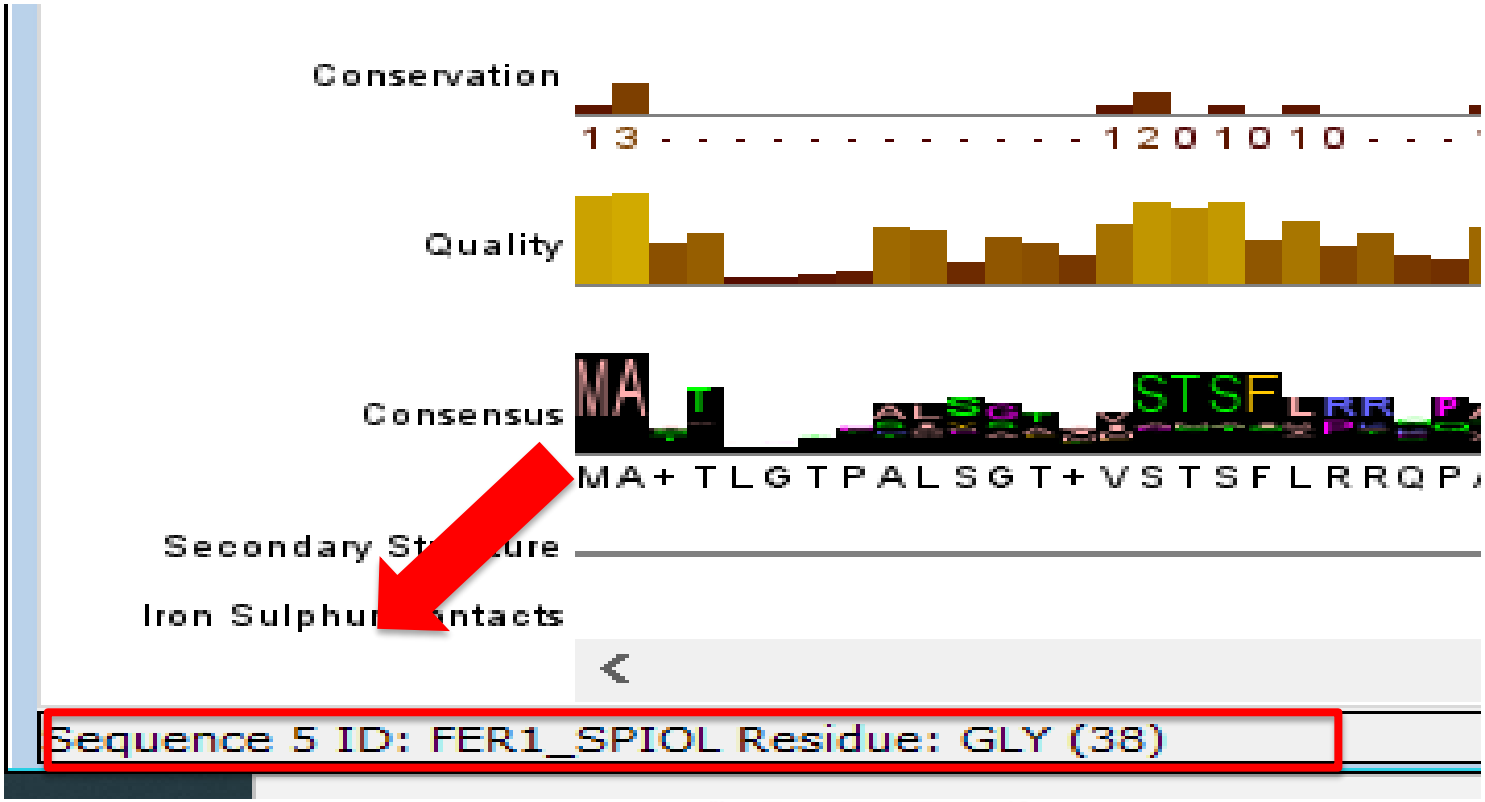
Status bar



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- You can move about the alignment by clicking and dragging the ruler scroll bar to move horizontally, or by clicking and dragging the alignment scroll bar to the right of the alignment to move vertically.

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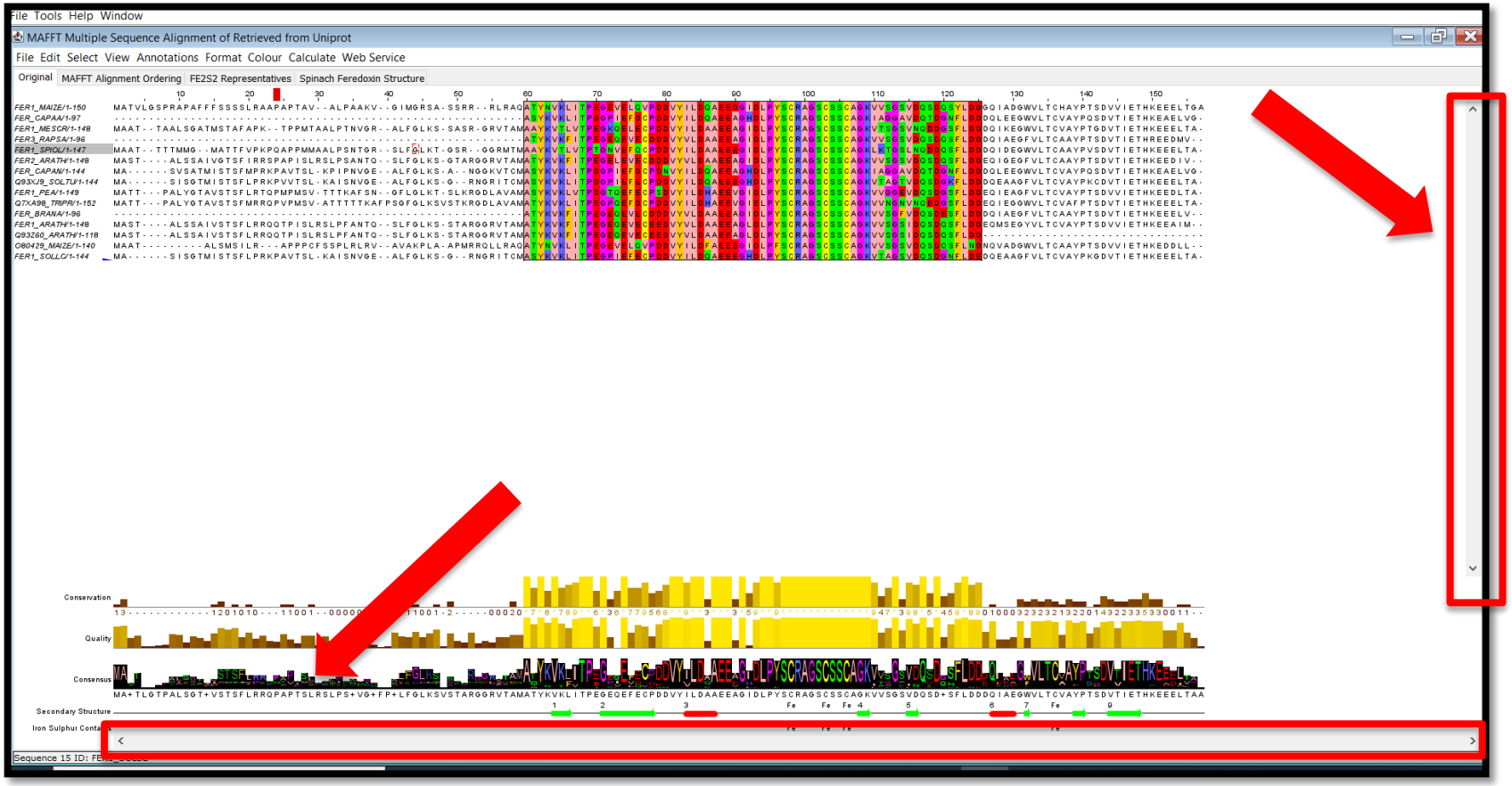
- If all the rows or columns in the alignment are displayed, the scroll bars will not be visible.



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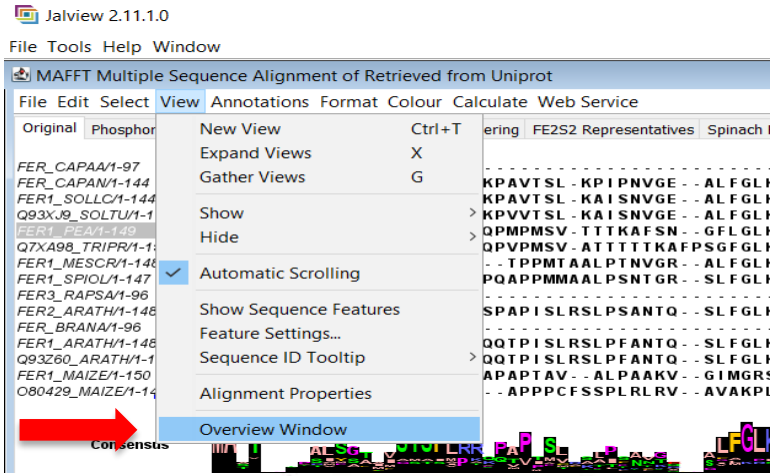
Each alignment view shown in the alignment window presents a window onto the visible regions of the alignment. This means that with anything more than a few residues or sequences, alignments can become difficult to visualize on the screen because only a small area can be shown at a time. It can help, especially when examining a large alignment, to have an overview of the whole alignment.

Select View ⇒ Overview Window

from the Alignment window menu bar.



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- **The red box in the overview window shows the current view in the alignment window.**
- **A percent identity histogram is plotted below the alignment overview.**
- **Shaded parts indicate rows and columns of the alignment that are hidden (in this case, a single row at the bottom of the alignment).**
- **you can navigate around the alignment by dragging the red box.**

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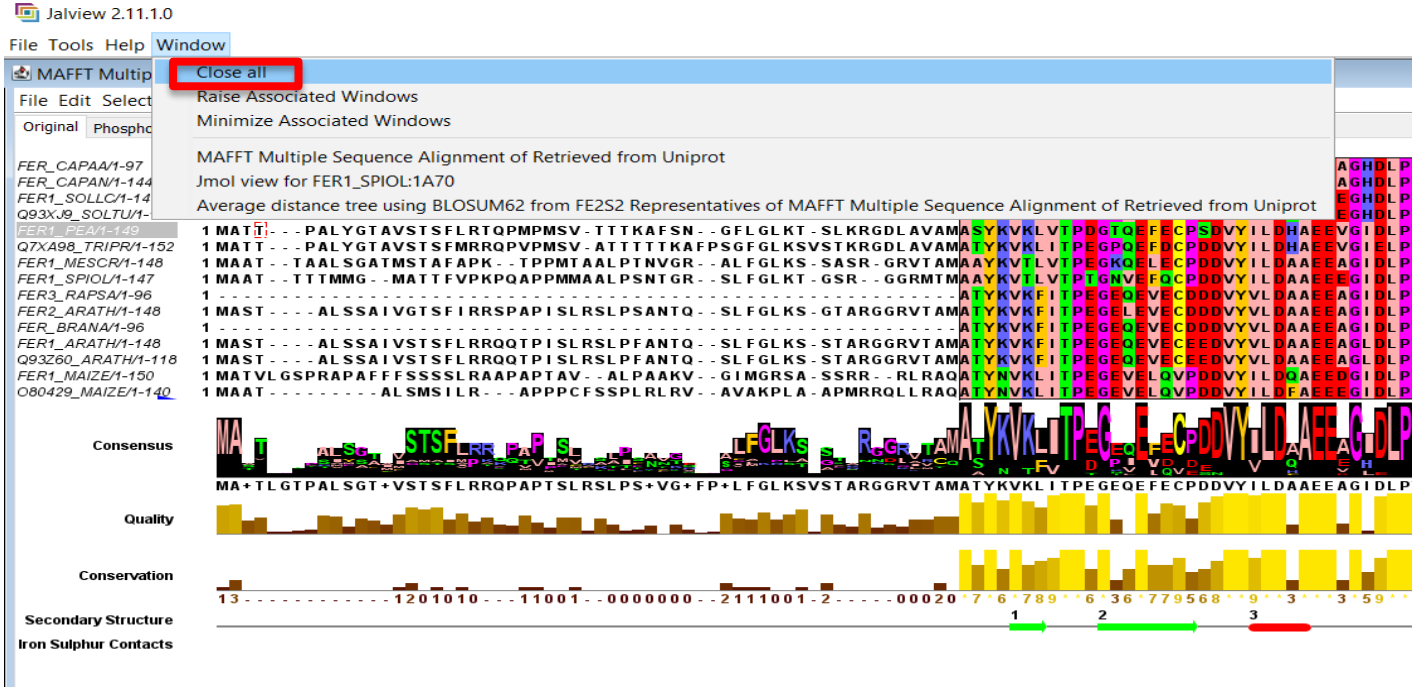
Close windows

Alignment and analysis windows are closed by clicking on the usual 'close' icon (indicated **by arrows on Mac OS X). If you want to close all the alignments and analysis windows at once, then use the**

Window ⇒ Close All

Warning: make sure you have saved your work because this cannot be undone !



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Cursor Mode

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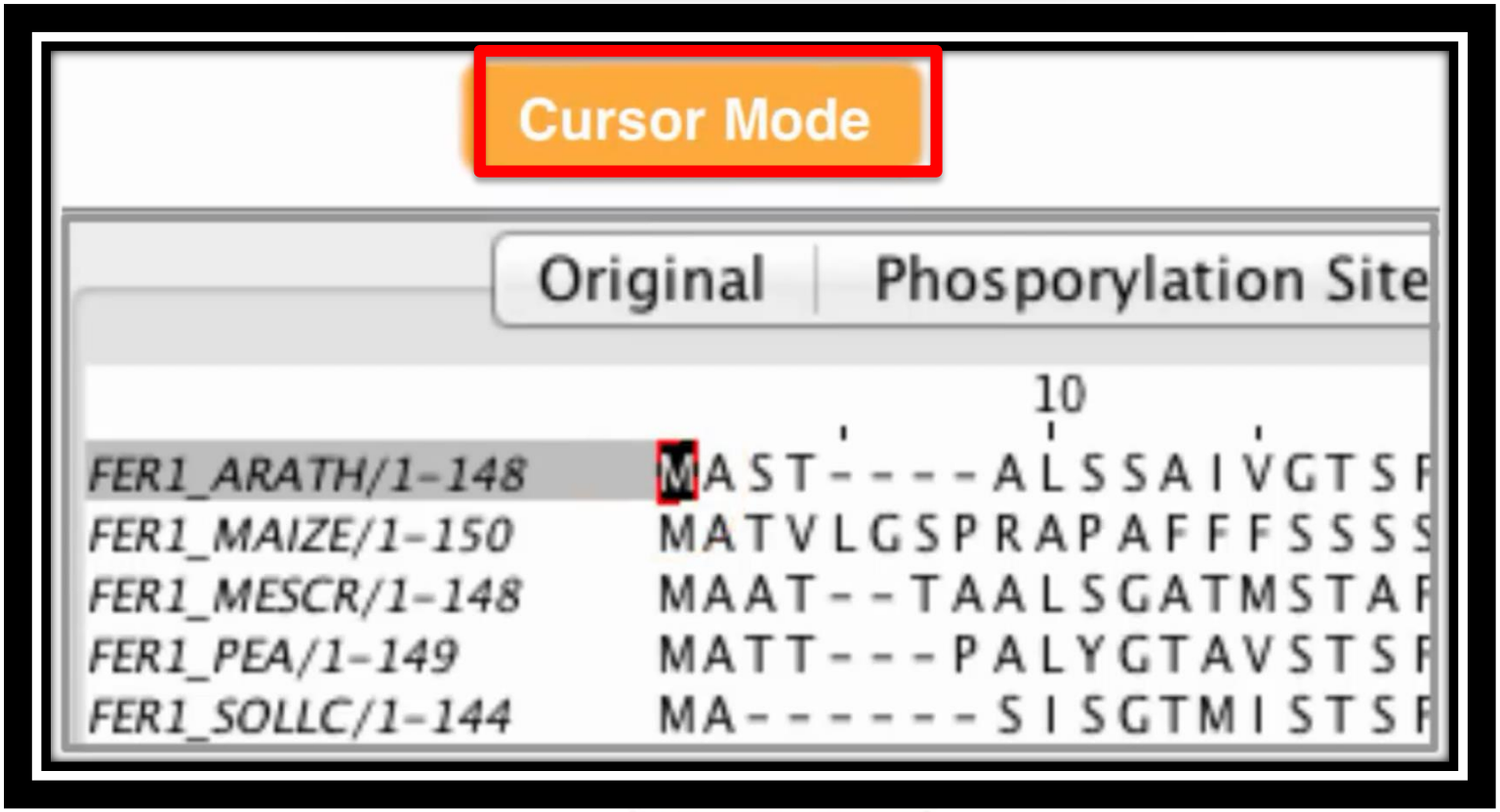
Source: Jaview Online Training Video

https://www.jalview.org/

Cursor Mode uses the *keyboard*



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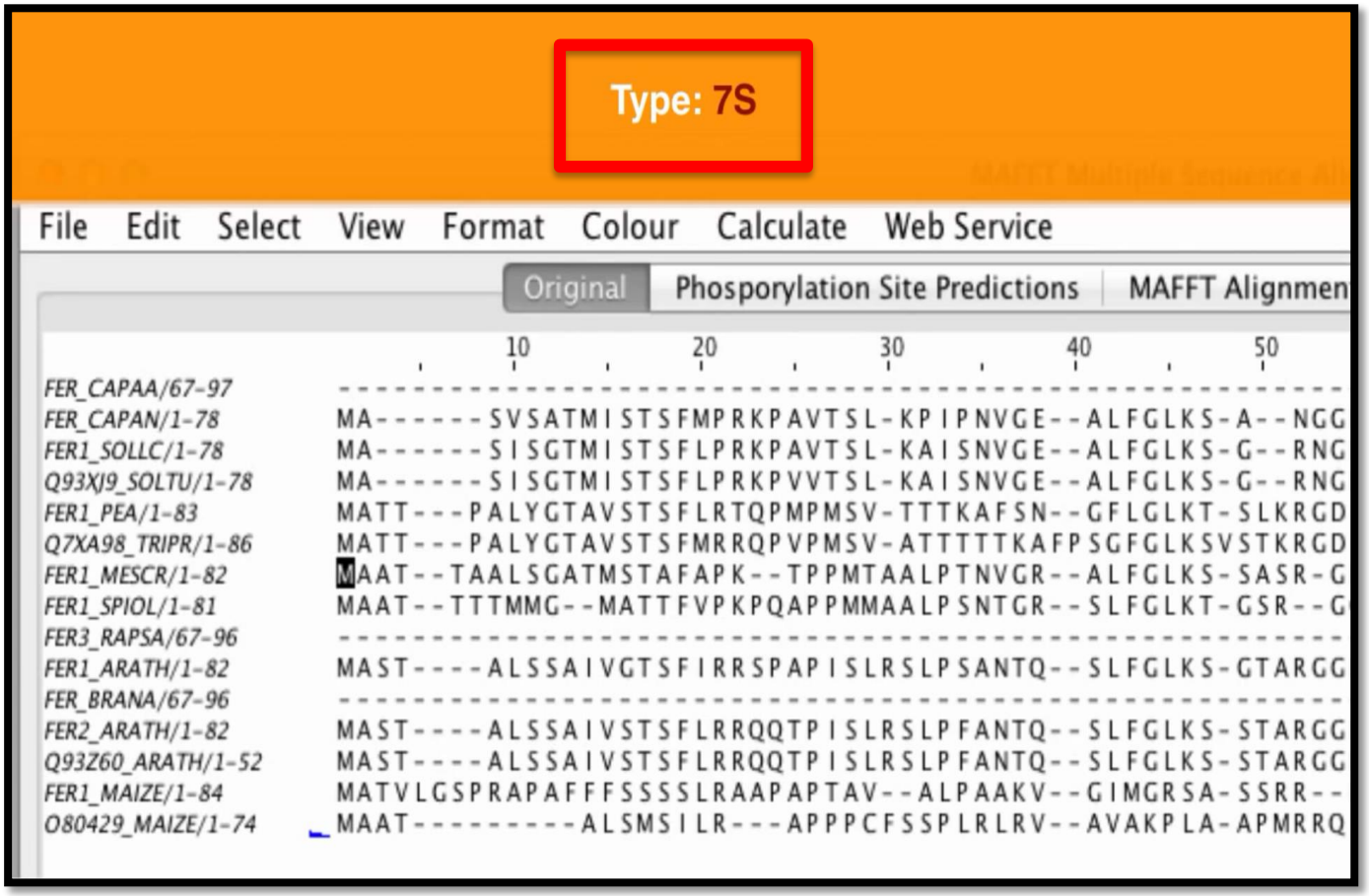
Move to sequence: type sequence row, followed by S



Source: Jaview Online Training Video
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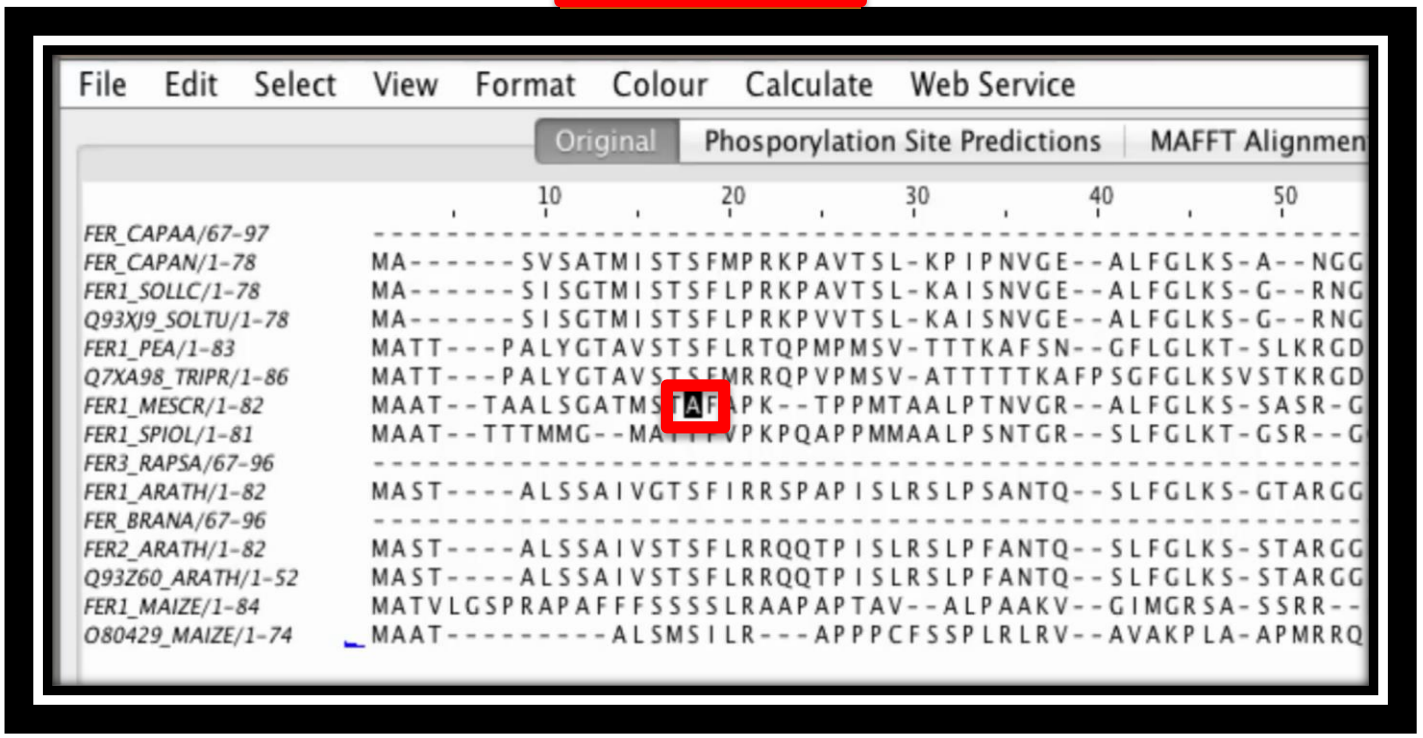
Move to column: type column number, followed by C

Type: 18C



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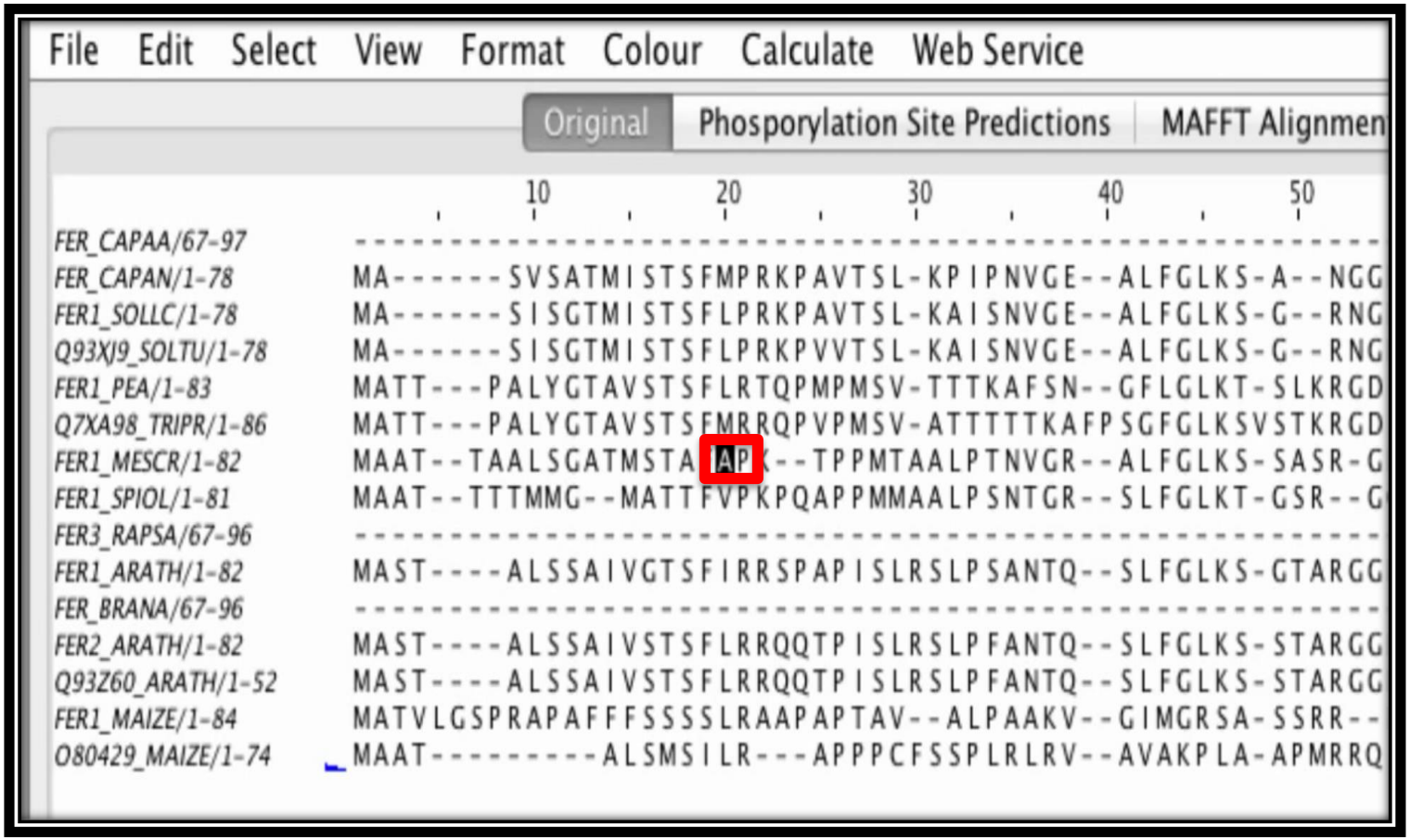
Type: 18P



Source: Jaview Online Training Video
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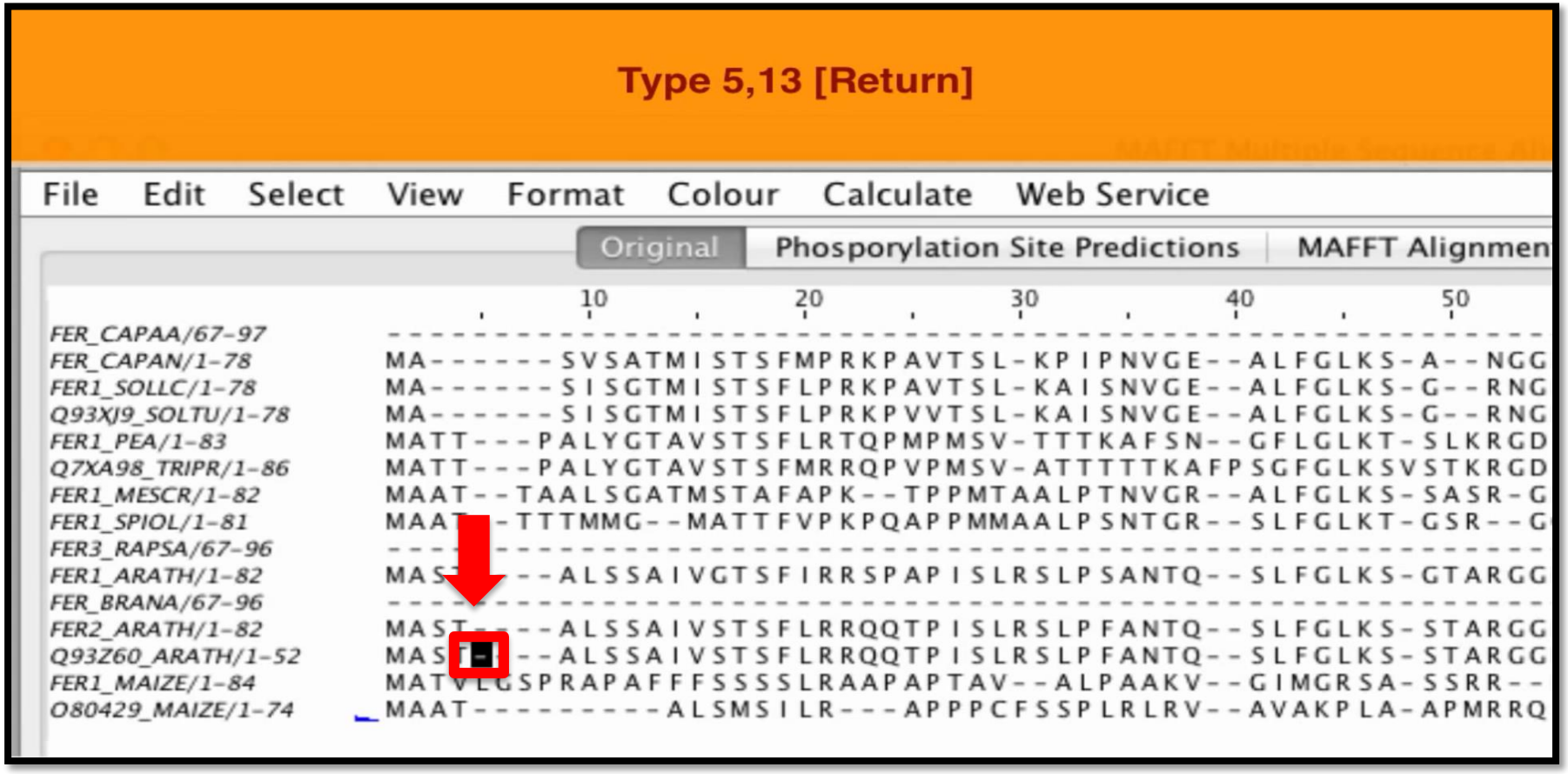
Move to column and row location: type column and row number



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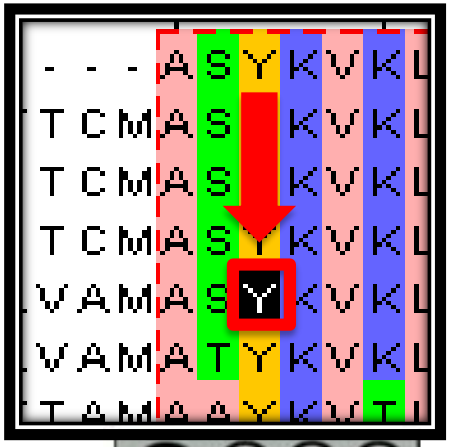
Navigation in Cursor mode

- **Cursor mode navigation enables the experienced user to quickly and precisely navigate, select and edit parts of an alignment.**
- **On pressing F2 to enter cursor mode the position of the cursor is indicated by a black background and white text.**
- **The cursor can be placed using the mouse or moved by pressing the arrow keys (↑, ↓, ←, →).**



Rapid movement to specific positions is accomplished as listed below:

◦ ***Jump to Sequence n***: Type a number n then press **[S]** to move to sequence **(row)** n

◦ ***Jump to Column n***: Type a number n then press **[C]** to move to **column** n in the alignment.

◦ ***Jump to Residue n***: Type a number n then press **[P]** to move to **residue number** n in the current sequence.

◦ ***Jump to column m row n***: Type the **column number m**, a comma, the **row number n** and press **[RETURN].**

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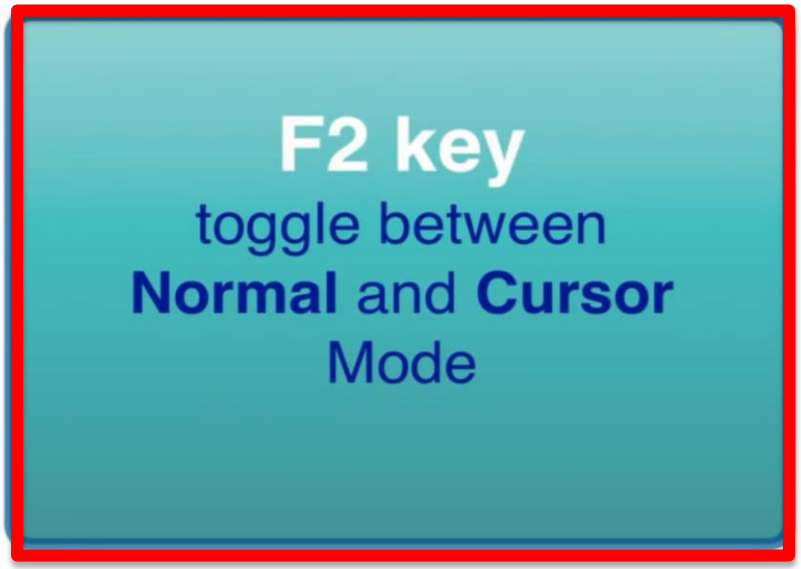

Source: Jaview Online Training Video
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Find Sequences

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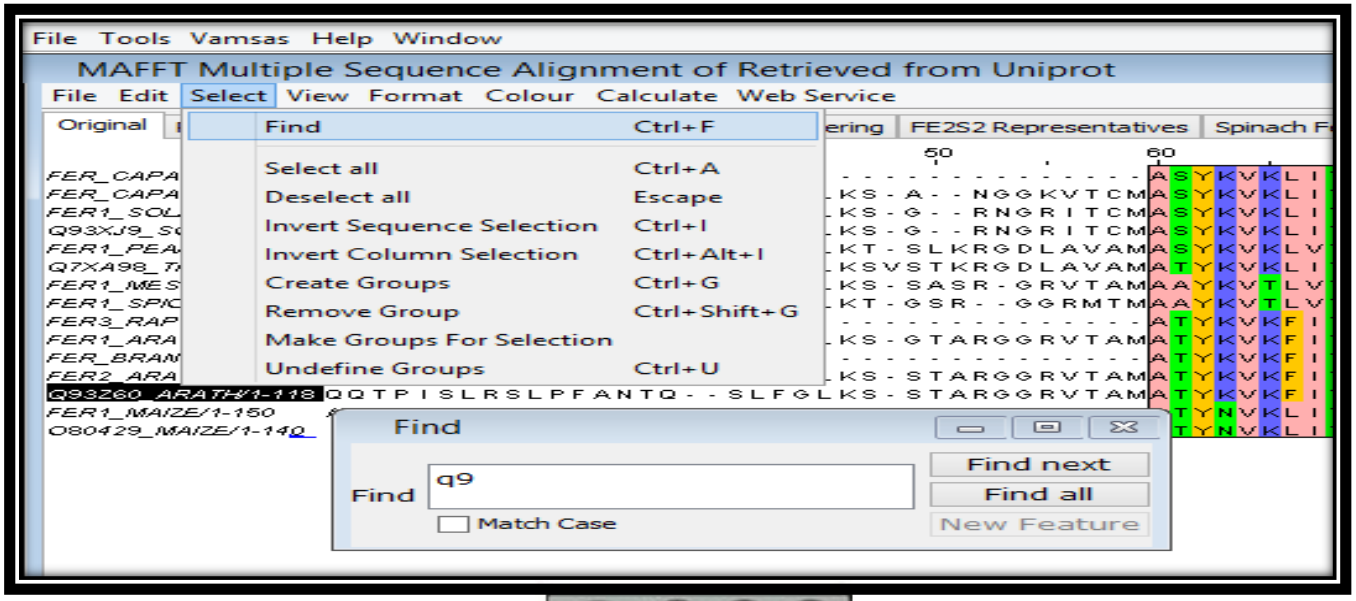
The Find Dialog Box

A further option for navigation is to use the

Select ⇒ Find... function.

- **This opens a dialog box** into which can be entered regular expressions for searching sequences and sequence IDs, or sequence numbers.
- **Hitting the [Find next]** button will highlight **the first (or next) occurrence** of that pattern in the sequence ID panel or the alignment, and will adjust the view in order t display the highlighted region.

•



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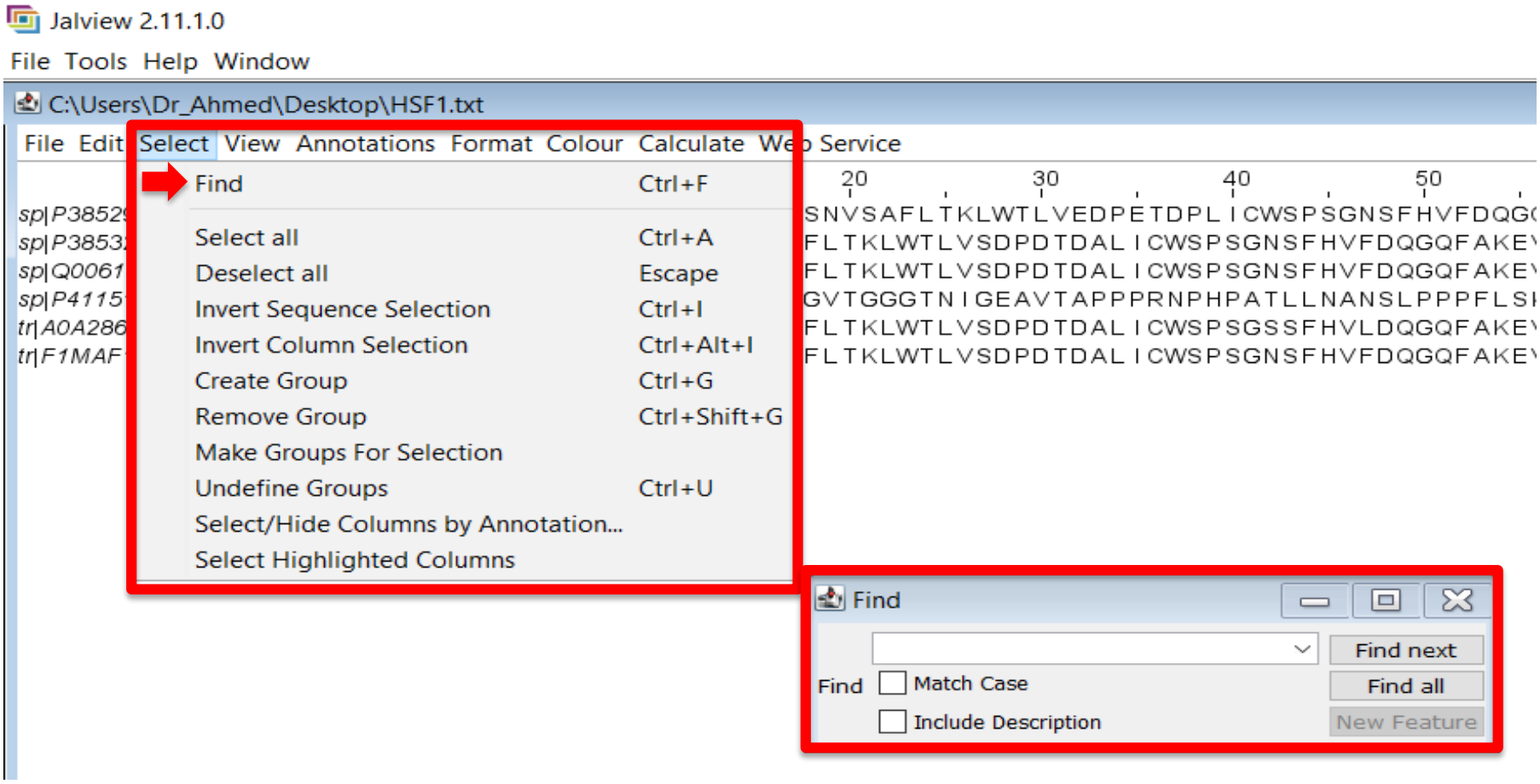

Source: Jaview Online Training Video
https://www.jalview.org/

Locate sequence group: use Select >> Find

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Jalview 2.11.1.0
File Tools Help Window
C:\Users\Dr_Ahmed\Desktop\HSF1.txt
File Edit Select View Annotations Format Colour Calculate Web Service
sp|P38529|HSF1_CHICK/1-491 281 PSASPSGSLDERSSPVVRIKEEPPSPSRSPKENEPSYTAAAGNSTEQPQPQEKCLSVACLDKNELNDHLDTIDSNLDNLQTMLSTHGFSVDTTALLDLFSPSMTVTI
sp|P38532|HSF1_MOUSE/1-525 281 GRSIDERPLSSSTLVRVKQEPPSPPHSPRVLEASPGRPSSMDTPLSPTAFIDSILRESEPTPAASNTAPMDTTGAQAPALPTPSTPEKCLSVACLDKNELSDHLDAM
sp|Q00613|HSF1_HUMAN/1-529 281 GGSIDERPLSSSPLVRVKEEPPSPPQSPRVEEASPGRPSSVDTLLSPTALIDSILRESEPAPASVTALTDARGHTDTEGRPPSPPPTSTPEKCLSVACLDKNELSDHI
sp|P41151|HFA1A_ARATH/1-495 281 SHSLEASDGQIVKYQPLRNDSMMWNMMKTDDKYPFLDGFSSPNQVSGVTLQEVLPITSGQSQAYASVPSGQPLSYLPSTSTSLPDTIMPETSQIPQLTRESINDFPTI
tr|A0A286ZSP4|A0A286ZSP4_PIG/1-590 281 GGSVDEERPLSGSPLVRVKEEPPSPPRSPDAEAAGPGHPSSIVETPLSPTALIDSILRESEPAPTASATLLPDTGGHPPSPLPTSAPEKCLSVACLDKTELSDHLDAI
tr|F1MAF1|F1MAF1_RAT/1-525 281 GRSIDERPLSSSTLVRVKEEPPSPPHSPRVLEASPGRPASMDTPLSPTAFIDSILRESEPTPAASNTAPMDTTGAQAPAPPAPSTPEKCLSVACLDKNELSDHLDAM
Conservation
Quality
Consensus
G+SIDERPLSSS+LVRVKEEPPSPP+SPRVLEASPGRPSS+DTPLSPTA+IDSILRESEPTPAASNTA++DTTGAQAPA+PTP++PEKCLS+ACL++N++SDHLD++
sp|P38529|HSF1_CHICK/1-491 421 ADTGKQLVHYTAQPLPEVDS
sp|P38532|HSF1_MOUSE/1-525 421 PDMSLPDLDSSLASIQELLS
sp|Q00613|HSF1_HUMAN/1-529 421 SVTVPDMSLPDLDSSLASIQ
sp|P41151|HFA1A_ARATH/1-495 421 PEDPEIDELMSNFEFLEEYM
tr|A0A286ZSP4|A0A286ZSP4_PIG/1-590 421 VPDMNLPDLDSSLASVRRQA
tr|F1MAF1|F1MAF1_RAT/1-525 421 PDMSLPDLDSSLASIQELLS
Find
AAG
Find next
Find
Match Case
Find all
Include Description
New Feature
6 subsequence matches found.
OK
Conservation

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Exercise : Navigation
"To try on your own time"

1- Reload the example file by accessing the Desktop's
File ⇒ Input Alignment ⇒ From URL dialog and clicking on the down arrow to retrieve the example file URL stored in its history (http://www.jalview.org/examples/exampleFile_2_7.jar)

2- Scroll around the alignment using the alignment (vertical) and ruler (horizontal) scroll bars.
3- Find and open the Overview Window. Move around the alignment by clicking and dragging the red box in the overview window.
4 Look at the status bar as you move the mouse over the alignment. It should indicate information about the sequence and residue under the cursor.

5- Press [F2] to enter Cursor mode. Use the arrow keys to move the cursor around the alignment.
- **Move to sequence 7 by pressing 7S.**
- **Move to column 18 by pressing 18C .**
- **Move to residue 18 by pressing 18P.**
- **Move to sequence 5, column 13 by typing 13, 5 [RETURN]**

Note that these can be two different positions if gaps are inserted into the sequence.

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4th Module How to Build a Multiple Sequence Alignment?
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