



# H3ABioNet

Pan African Bioinformatics Network for H3Africa

**Introduction to Bioinformatics online course: IBT**

## **Multiple Sequence Alignment**

### **Lec3: Navigation in Jalview**

By

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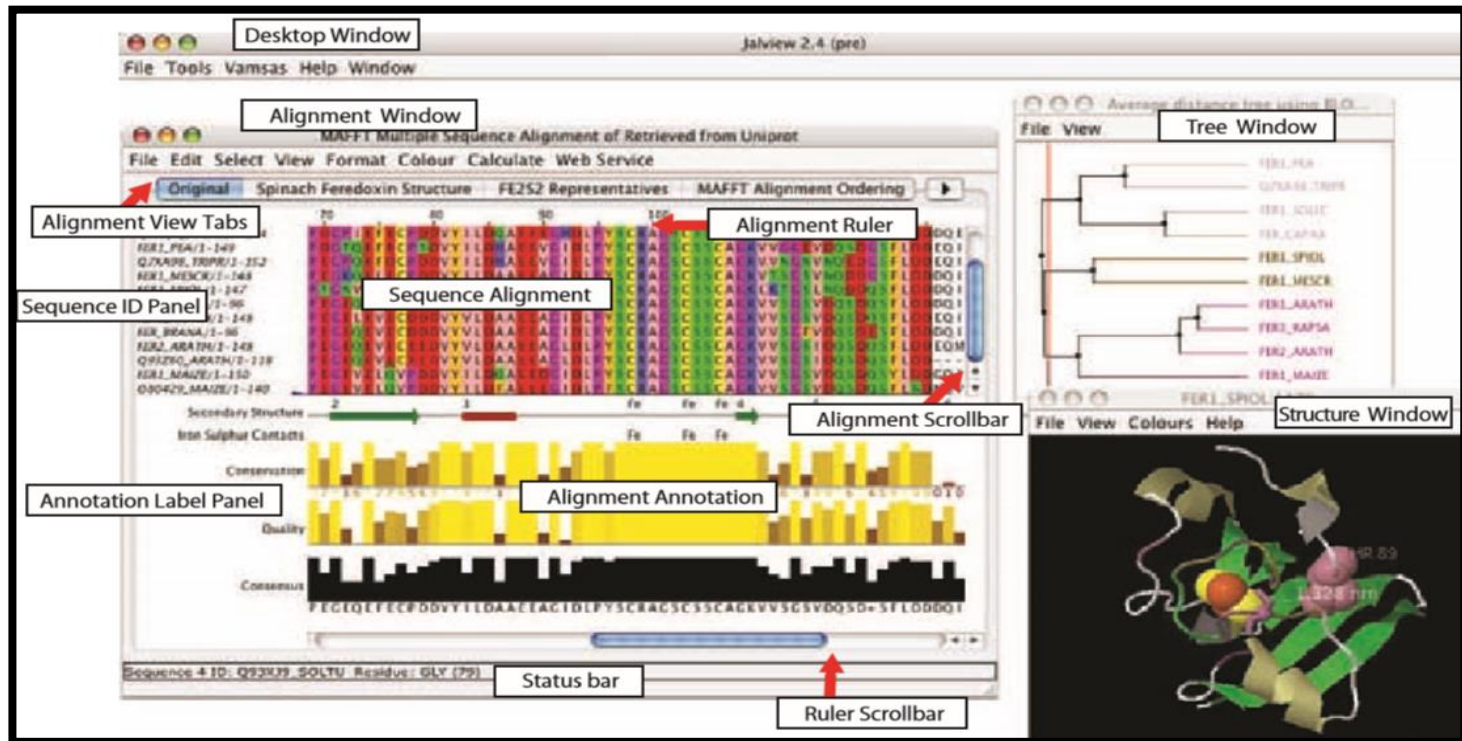


Source: Jaview Online Training Video

<https://www.jalview.org/>

# Navigation

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



Source: Jaview Online Training Video

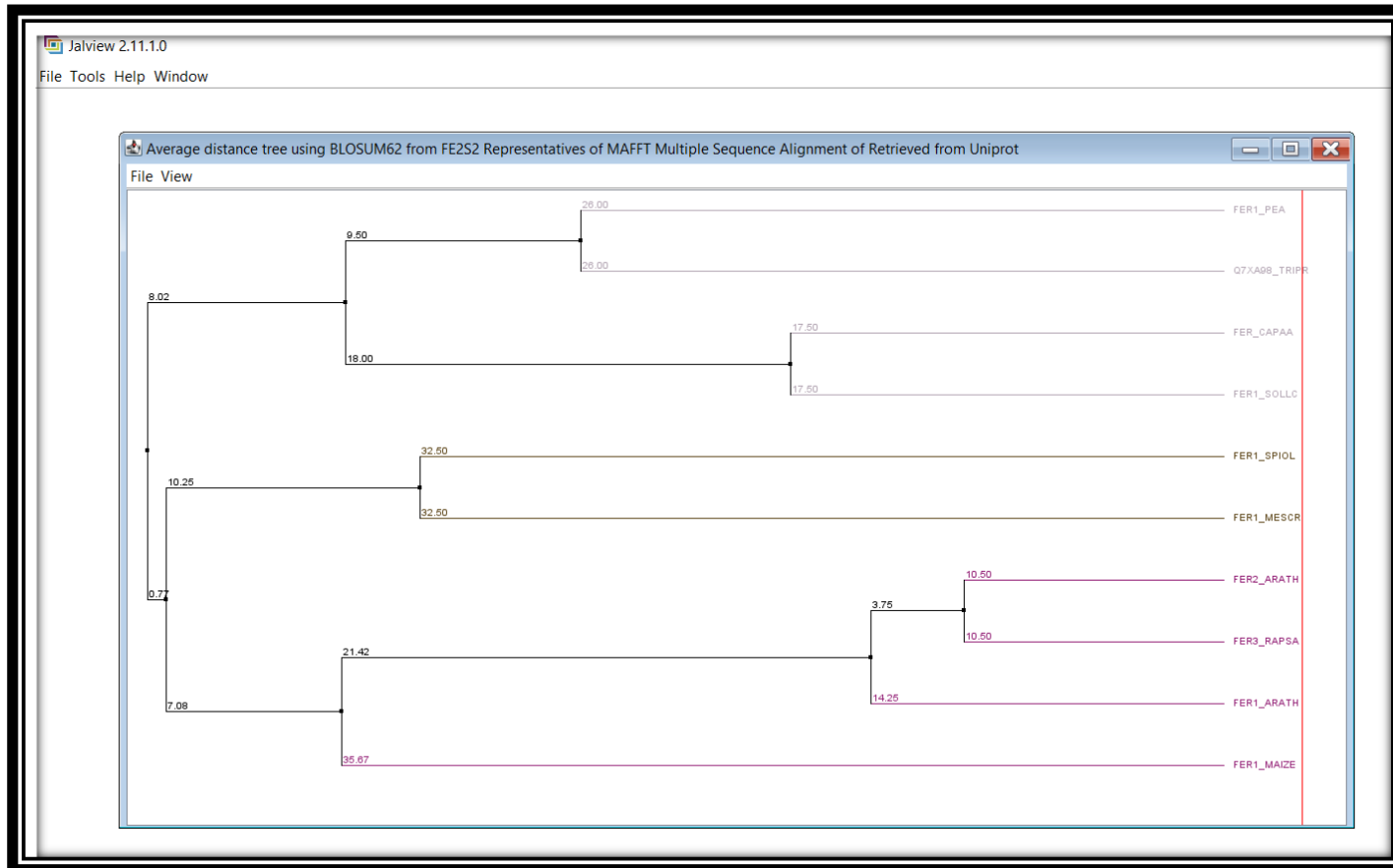
<https://www.jalview.org/>

# Alignment window

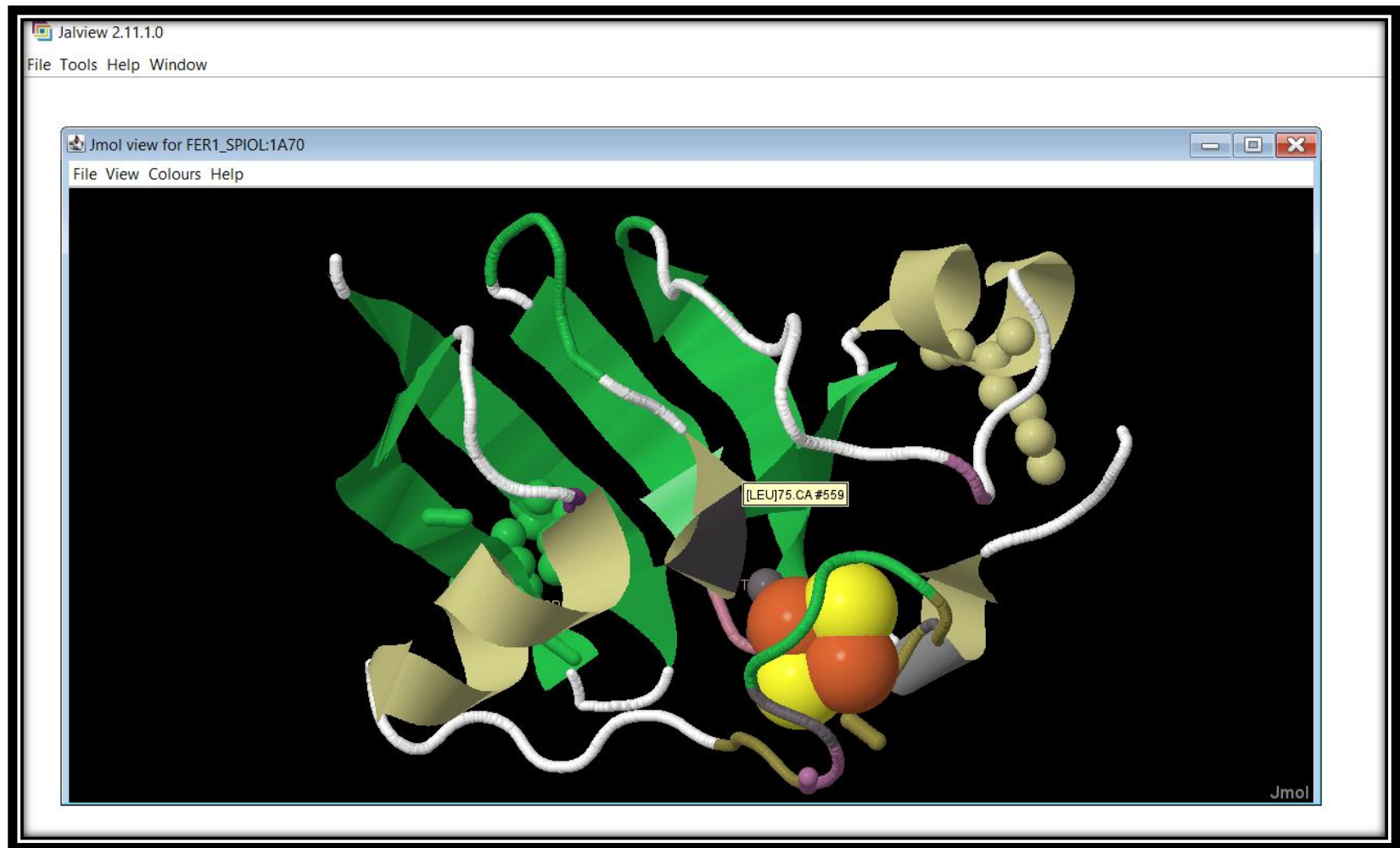
The alignment window is the primary window for editing and visualization, and can contain several independent views of the alignment being worked with.



# Tree window



# Struture window





# *Editing Modes*

Source: Jaview Online Training Video

<https://www.jalview.org/>

# Jalview has two navigation and editing modes:

- 1- ***Normal mode***, where editing and navigation is performed 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



# Navigation

Source: Jaview Online Training Video

<https://www.jalview.org/>

# *Navigation in Normal mode*

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



**Move to Sequence,  
Column or Residue**

Jalview 2.11.10

File Tools Help Window

MAFFT Multiple Sequence Alignment of Retrieved from Uniprot

File Edit Select View Annotations Format Colour Calculate Web Service

Original MAFFT Alignment Ordering FE2S2 Representatives Spinach Feredoxin Structure

10 20 30 40 50 60 70 80 90 100 110 120 130 140 150

FER\_CAPAA/1-97 ..... ASYKVKLITPDGPIEFDCPDVVYILDQAEAGHLPYSCRAGSCSSCAGKIAGGAVDQDGNFLDQDLLEGGWVLTCAVYPSDVTIETHKEAELVG.

FER\_CAPAN/1-144 MA.....SVSATMISTFMPKPAVTSL.KPIPNVGE..ALFGLKS.A..NGGKVTCMAASYKVKLITPDGPIEFDCPDVVYILDQAEAGHLPYSCRAGSCSSCAGKIAGGAVDQDGNFLDQDLLEGGWVLTCAVYPSDVTIETHKEAELVG.

FER1\_MESCR/1-148 MAAT...TAALSGATMSTAFAPK..TPMTAALPTNVGR..ALFGLKS.SASR.GRVTAMAAYKVLITVPEGKDELCDDVVYILDQAEAGHLPYSCRAGSCSSCAGKVTSGVNVQDQSGFLDQDQIKEGWVLTCAVYPTGDTVETHKEELTA.

Q93KJ9\_SOLTU/1-144 MA.....SISGMTISTFMRKPVVTSL.KAISNVGE..ALFGLKS.G..RNGRITCMASYKVKLITPDGPIEFDCPDVVYILDQAEAGHLPYSCRAGSCSSCAGKVTAGTVDDSDGKFLDQDQAEAGFVLTCAVYPKDVTIETHKEELTA.

FER1\_PEA/1-149 MATT...PALYGTAVSTFSLRTPMPMSV..TTTKAFSN..GFLGLKT.SLKRGLAVAMASYKVKLITPDGPIEFDCPDVVYILDQAEAGHLPYSCRAGSCSSCAGKVVGGVDDSDGKFLDQDQIEAGFVLTCAVYPTSDVVIETHKEEDLTA.

Q7XA98\_TRIPR/1-152 MATT...PALYGTAVSTFMRQPVPMVS..ATTTTKAFSGFGLKSVSTKRGLAVAMATYKVKLITPEGPDEFCDDVVYILDQAEAGHLPYSCRAGSCSSCAGKVVNGVNVQDQSGFLDQDQIEAGFVLTCAVYPTSDVTIETHKEELTA.

FER1\_SPIOL/1-147 MAAT...TTTMMG..MATTVPKPDAPPMAALPSNTGR..SLFGLKT.GSR..GGRMTMAAYKVLITVPEGKDELCDDVVYILDQAEAGHLPYSCRAGSCSSCAGKLTGSLNQDQSGFLDQDQIDEGWVLTCAVYPTSDVTIETHKEELTA.

FER3\_RAPSA/1-96 ..... ATYKVKFITPEGEDEVECDVVYLDQAEAGHLPYSCRAGSCSSCAGKVVSGVDDSDGKFLDQDQIAEGFVLTCAVYPTSDVTIETHKEEDMV..

FER2\_ARATH/1-148 MAST...ALSSAIVGTSFIRRPAPISLRSPLFANTQ..SLFGLKS.GTAGGRVTAMATYKVKFITPEGEDEVECDVVYLDQAEAGHLPYSCRAGSCSSCAGKVVSGVDDSDGKFLDQDQIAEGFVLTCAVYPTSDVTIETHKEEDIV..

FER\_BRANA/1-96 ..... ATYKVKFITPEGEDEVECDVVYLDQAEAGHLPYSCRAGSCSSCAGKVVSGVDDSDGKFLDQDQIAEGFVLTCAVYPTSDVTIETHKEELV..

FER1\_ARATH/1-148 MAST...ALSSAIVSTFLLRQQTPISLRSLPFANTQ..SLFGLKS.STARGGRVTAMATYKVKFITPEGEDEVECDVVYLDQAEAGHLPYSCRAGSCSSCAGKVVSGVDDSDGKFLDQDQIEQMSGVVLTCAVYPTSDVVIETHKEEAIM..

Q93Z60\_ARATH/1-118 MAST...ALSSAIVSTFLLRQQTPISLRSLPFANTQ..SLFGLKS.STARGGRVTAMATYKVKFITPEGEDEVECDVVYLDQAEAGHLPYSCRAGSCSSCAGKVVSGVDDSDGKFLDQDQIEQMSGVVLTCAVYPTSDVVIETHKEEAIM..

FER1\_MAIZE/1-150 MATVLGSPRAPAFFSSSLRAAPATAV..ALPAKV..GIMGRSA.SSRR..RLRAQATYKVKLITPEGEDEVECDVVYLDQAEAGHLPYSCRAGSCSSCAGKVVSGVDDSDGKFLDQDQIADGWVLTCHAYPTSDVVIETHKEELTGA.

Q80429\_MAIZE/1-140 MAAT.....ALSMSILR..APPCFSSPLRLRV..AVAKPLA.APMRRQLLRQAATYKVKLITPEGEDEVECDVVYLDQAEAGHLPYSCRAGSCSSCAGKVVSGVDDSDGKFLDQDQINQVADGWVLTCAVYPTSDVVIETHKEDLL..

FER1\_SOLLC/1-144 MA.....SISGMTISTFMRKPAVTSL.KAISNVGE..ALFGLKS.G..RNGRITCMASYKVKLITPDGPIEFDCPDVVYILDQAEAGHLPYSCRAGSCSSCAGKVTAGTVDDSDGKFLDQDQAEAGFVLTCAVYPKDVTIETHKEELTA.

Move to Sequence Row: click on sequence in ID panel



Jalview 2.11.1.0

File Tools Help Window

MAFFT Multiple Sequence Alignment of Retrieved from iprot

File Edit Select View Annotations Format Colour Calculate Web Service

Original MAFFT Alignment Ordering FE2S2 Representatives Spinach Feredoxin Structure

10 20 30 40 50 60 70 80 90 100 110 120 130

FER1\_MAIZE/1-150 MATVLGSPRAPAFFSSSSLRAPAPTAV--ALPAAKV--GIMGRSA-SSRR--RLRAQATYVVKLITPEGEVELEQVDDVYILDQAEEDGIDLPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDGQIADGWVLTCHAY

FER\_CAPAA/1-97 .....ASYKVKLITPDGPIEFDCDDVYILDQAEBAAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGDFLDDQDLEEGWVLTCAVAY

FER1\_MESCR/1-148 MAAT--TAALSGATMSTAFAPK--TPPMTAALPTNVGR--ALFGLKS-SASR-GRVTAMAAVKVTLVTPGKOELECPDDVYILDQAEBAAGIDLPYSCRAGSCSSCAGKVTSGSVNDDGSDFLDDQDIKEGWVLTCAVAY

FER3\_RAPSA/1-96 .....ATYKVKFITPEGEQVEECDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDQDIAEGFVLTCAAY

FER2\_ARATH/1-148 MAST...ALSSAIVGTSFIRRPAPISLRSLPSANTQ--SLFGLKS-GTARGGRVTAMATYKVKFITPEGELEVEECDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDQDIKEGFVLTCAAY

FER\_CAPAN/1-144 MA.....SVSATMISTSFMPKPAVTSLKPIPNVGE--ALFGLKS-A--NGGKVTCMASYKVKLITPDGPIEFDCDDVYILDQAEBAAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGDFLDDQDLEEGWVLTCAVAY

Q93XJ9\_SOLTU/1-144 MA.....SISGTMISTSFPRKPVVTSLKAINVGE--ALFGLKS-G--RNGRITCMASYKVKLITPDGPIEFDCDDVYILDQAEBAAGHDLPYSCRAGSCSSCAGKVTAGTVDQSDGKFLDDQDEAAGFVLTCAVAY

FER1\_PEA/1-149 MATT...PALYGTAVSTSLRTPMPMSV-ITTKAFSN--GFLGLKT-SLKRGLD LAVAMASYKVKLITPDGTOEFECDDVYILDQAEBAAGHDLPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDQDIKEGFVLTCAVAY

Q7XA98\_TRIPR/1-152 MATT...PALYGTAVSTSFMRQPVPMSV-ATTTTTKAPPSGFLKSVSTKRGDLAVAMATYKVKLITPEGPQEFDCDDVYILDQAEBAAGHDLPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDQDIKEGFVLTCAVAY

FER1\_SPIO/1-147 MAAT...TTTTMMG--MATTFVPKQAPPMMAALPSNTGR--SLFGLKT-GSR--GGRMTMAAYKVTLVTPGTVNVEFCDDVYILDQAEBAAGHDLPYSCRAGSCSSCAGKVTAGTVDQSDGKFLDDQDEAAGFVLTCAVAY

FER\_BRANA/1-96 .....ATYKVKFITPEGEQVEECDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDQDIAEGFVLTCAAY

FER1\_ARATH/1-148 MAST...ALSSAIVSTSLRQQTPISLRSLPFANTQ--SLFGLKS-STARGGRVTAMATYKVKFITPEGEQVEECDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDQEQMSEGVLTCAVAY

Q93260\_ARATH/1-118 MAST...ALSSAIVSTSLRQQTPISLRSLPFANTQ--SLFGLKS-STARGGRVTAMATYKVKFITPEGEQVEECDDVYVLDAAEEAGIDLPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDQEQMSEGVLTCAVAY

OB0429\_MAIZE/1-140 MAAT...ALSMSILR...APPPCFSSPLRLRV--AVAKPLA-APMRRQLLRAQATYVVKLITPEGELEQVDDVYILDQAEBAAGHDLFPYSCRAGSCSSCAGKVVSGSDQSDQSFLDDQDQVADGWVLTCAVAY

FER1\_SOLLG/1-144 MA.....SISGTMISTSFPRKPAVTSLKAINVGE--ALFGLKS-G--RNGRITCMASYKVKLITPEGPQEFDCDDVYILDQAEBAAGHDLPYSCRAGSCSSCAGKVTAGTVDQSDGKFLDDQDEAAGFVLTCAVAY

Move to column: click on column in ruler



Jalview 2.11.1.0

File Tools Help Window

MAFFT Multiple Sequence Alignment of Retrieved from Uniprot

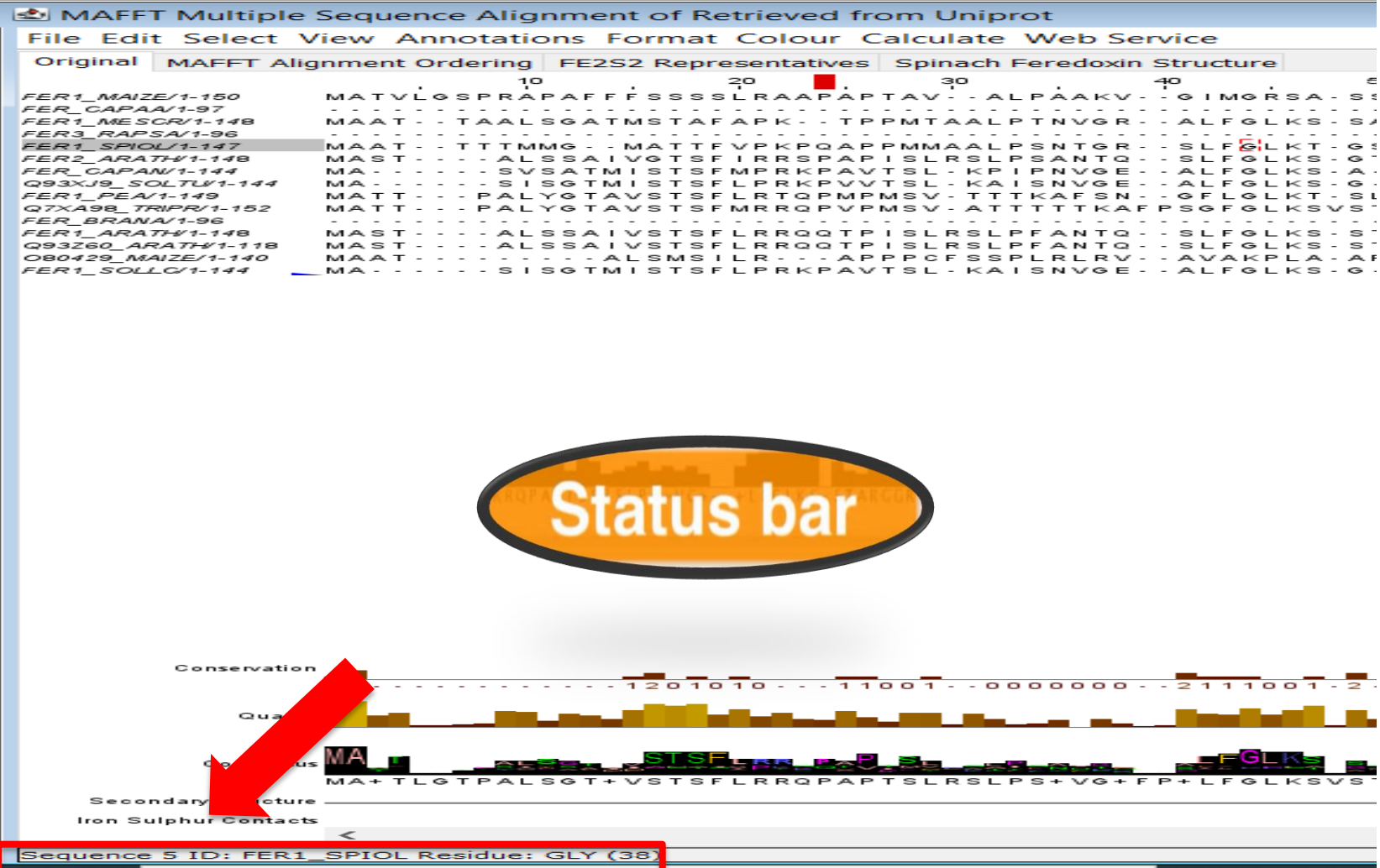
File Edit Select View Annotations Format Colour Calculate Web Service

Original	MAFFT Alignment	Ordering	FE2S2 Representatives	Spinach Ferredoxin Structure
FER1_MAIZE/1-150	MATVLGSPRAPAFF	SSSSSLRAAPAPTAV	ALPAAKV	GIMGRSA
FER_CAPAA/1-97	.....	.....	.....	.....
FER1_MESCR/1-148	MAAT	TAALSGATMSTAFAPK	TIP	PPMTAALPTNVGR
FER3_RAPSA/1-96	.....	.....	.....	.....
FER1_SPIOL/1-147	MAAT	TTTMMG	MATTFVPKPQAPP	MMALPSNTGR
FER2_ARATH/1-148	MAST	ALSSAIVGTSF	IRRSPAPISL	RLSPSANTQ
FER_CAPAN/1-144	MA	SVSATMISTSF	MPRKPAVTSL	KPIPNVGE
Q93XJ9_SOLTU/1-144	MA	SISGTMISTSF	LPRKPVVTS	LKAISNVGE
FER1_PEA/1-149	MATT	PALYGTA	VSTFSLRTQ	PMPSVTTTKAF
Q7XA98_TRIPR/1-152	MATT	PALYGTA	VSTFMRQP	VPMPSVATTTT
FER_BRANA/1-96	.....	.....	.....	.....
FER1_ARATH/1-148	MAST	ALSSAIVST	SFLRRQQTPI	SLRSLPFANTQ
Q93Z60_ARATH/1-118	MAST	ALSSAIVST	SFLRRQQTPI	SLRSLPFANTQ
O80429_MAIZE/1-140	MAAT	ALSMSILR	APPPCFSS	PLRLRVAVAKPLA
FER1_SOLLG/1-144	MA	SISGTMISTSF	LPRKPAVTSL	LKAISNVGE

Move to residue **click on residue**

Jalview 2.11.1.0

File Tools Help Window



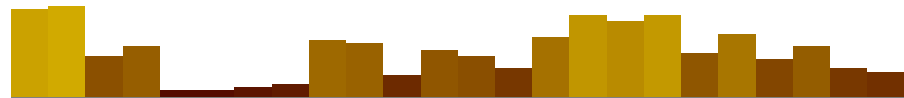
Status bar

# Status bar

Conservation



Quality

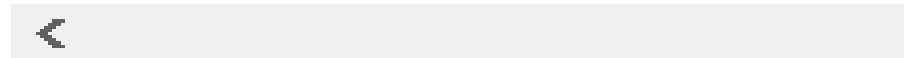


Consensus



Secondary Structure

Iron Sulphur contacts



Sequence 5 ID: FER1\_SPIOL Residue: GLY (38)

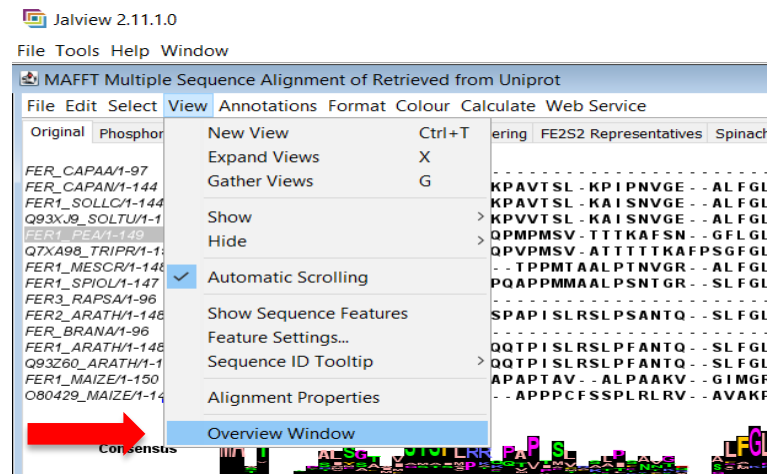
- You can move about the alignment by clicking and **dragging the ruler scroll bar** to move **horizontally**, or by clicking and dragging the alignment scroll bar to the right of the alignment to **move vertically**.

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



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.







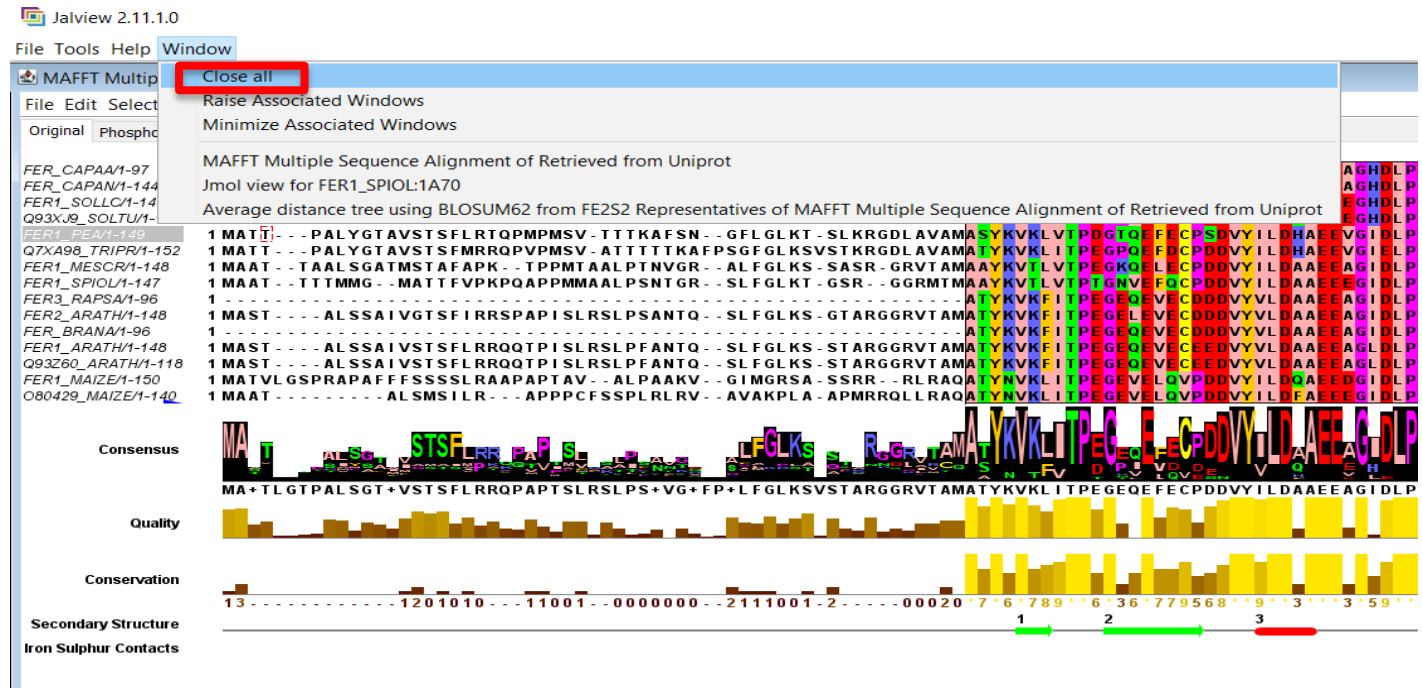
- **The red box** in the overview window shows the **current view** in the alignment window.
- A percent identity histogram is plotted below the alignment overview.
- Shaded parts indicate rows and columns of the alignment that are **hidden** (in this case, a single row at the bottom of the alignment).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

# 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 !**



# Cursor Mode

**F2 key  
for PC**

**F2 key (+ Fn)  
for Mac**

Source: Jaview Online Training Video

<https://www.jalview.org/>

Cursor Mode uses the *keyboard*



Cursor Mode

	Original	Phosphorylation Site
		10
FER1_ARATH/1-148	MAST - - - - A L S S A I V G T S F	
FER1_MAIZE/1-150	MATV L G S P R A P A F F F S S S S	
FER1_MESCR/1-148	MAAT - - T A A L S G A T M S T A F	
FER1_PEA/1-149	MATT - - - P A L Y G T A V S T S F	
FER1_SOLLC/1-144	MA - - - - - S I S G T M I S T S F	

Move to sequence: type sequence row, followed by S

Type: 7S

File Edit Select View Format Colour Calculate Web Service

Original Phosphorylation Site Predictions MAFFT Alignment

	10	20	30	40	50
FER_CAPAA/67-97	-----				
FER_CAPAN/1-78	MA-----SVSATMISTSFMPRKPAVTS L-KP I PNVGE--ALFGLKS-A--NGG				
FER1_SOLLC/1-78	MA-----SISGTMISTSF LPRKPAVTS L-KAISNVGE--ALFGLKS-G--RNG				
Q93XJ9_SOLTU/1-78	MA-----SISGTMISTSF LPRKPVVTS L-KAISNVGE--ALFGLKS-G--RNG				
FER1_PEA/1-83	MATT---PALYGTAVSTSF LRTQPMPSV-TTTKAFSN--GFLGLKT-SLKRGD				
Q7XA98_TRIPR/1-86	MATT---PALYGTAVSTSF MRRQVPMSV-ATTTTTKAFP SGFGLKSVSTKRGD				
FER1_MESCR/1-82	MAAT--TAALSGATMSTAFAPK--TPPMTAALPTNVGR--ALFGLKS-SASR-G				
FER1_SPIOL/1-81	MAAT--TTTMMG--MATT FVPKPQAPP MMAALP SNTGR--SLFGLKT-GSR--G				
FER3_RAPSA/67-96	-----				
FER1_ARATH/1-82	MAST---ALSSAIVGTSF IRRSPAP I SLRSLP SANTQ--SLFGLKS-GTARGG				
FER_BRANA/67-96	-----				
FER2_ARATH/1-82	MAST---ALSSAIVSTSF LRRQQTPI SLRSLP FANTQ--SLFGLKS-STARGG				
Q93Z60_ARATH/1-52	MAST---ALSSAIVSTSF LRRQQTPI SLRSLP FANTQ--SLFGLKS-STARGG				
FER1_MAIZE/1-84	MATVLGSPRAPAFF FSSSS LRAAPAPTAV--ALPAAKV--GIMGRSA-SSRR--				
O80429_MAIZE/1-74	MAAT-----ALSMSILR--APPPCFSSPLRLRV--AVAKPLA-APMRRQ				

Source: Jaview Online Training Video

<https://www.jalview.org/>



H3ABioNet

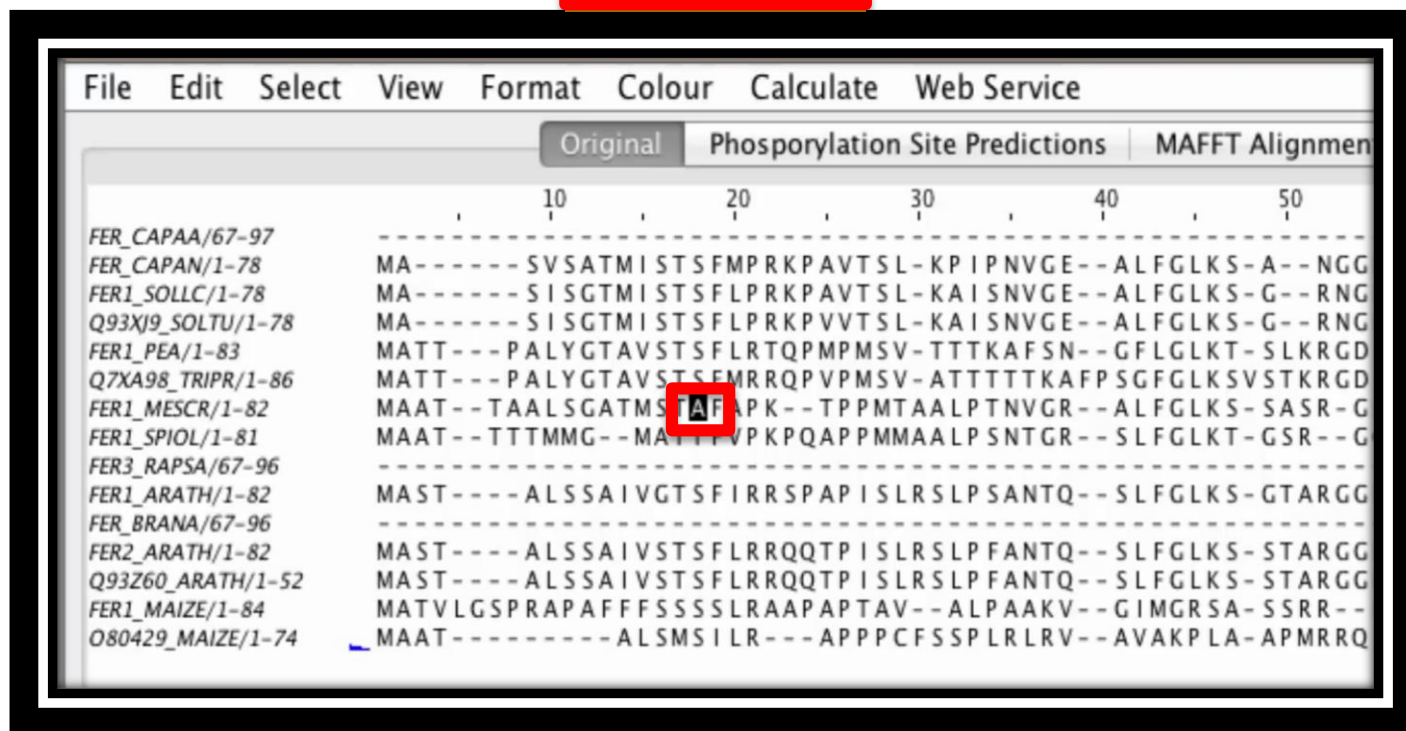
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Move to column: type column number, followed by C

Type: 18C



File Edit Select View Format Colour Calculate Web Service

Original Phosphorylation Site Predictions MAFFT Alignment

10 20 30 40 50

FER\_CAPAA/67-97  
FER\_CAPAN/1-78  
FER1\_SOLLC/1-78  
Q93XJ9\_SOLTU/1-78  
FER1\_PEA/1-83  
Q7XA98\_TRIPR/1-86  
FER1\_MESCR/1-82  
FER1\_SPIOL/1-81  
FER3\_RAPSA/67-96  
FER1\_ARATH/1-82  
FER\_BRANA/67-96  
FER2\_ARATH/1-82  
Q93Z60\_ARATH/1-52  
FER1\_MAIZE/1-84  
O80429\_MAIZE/1-74

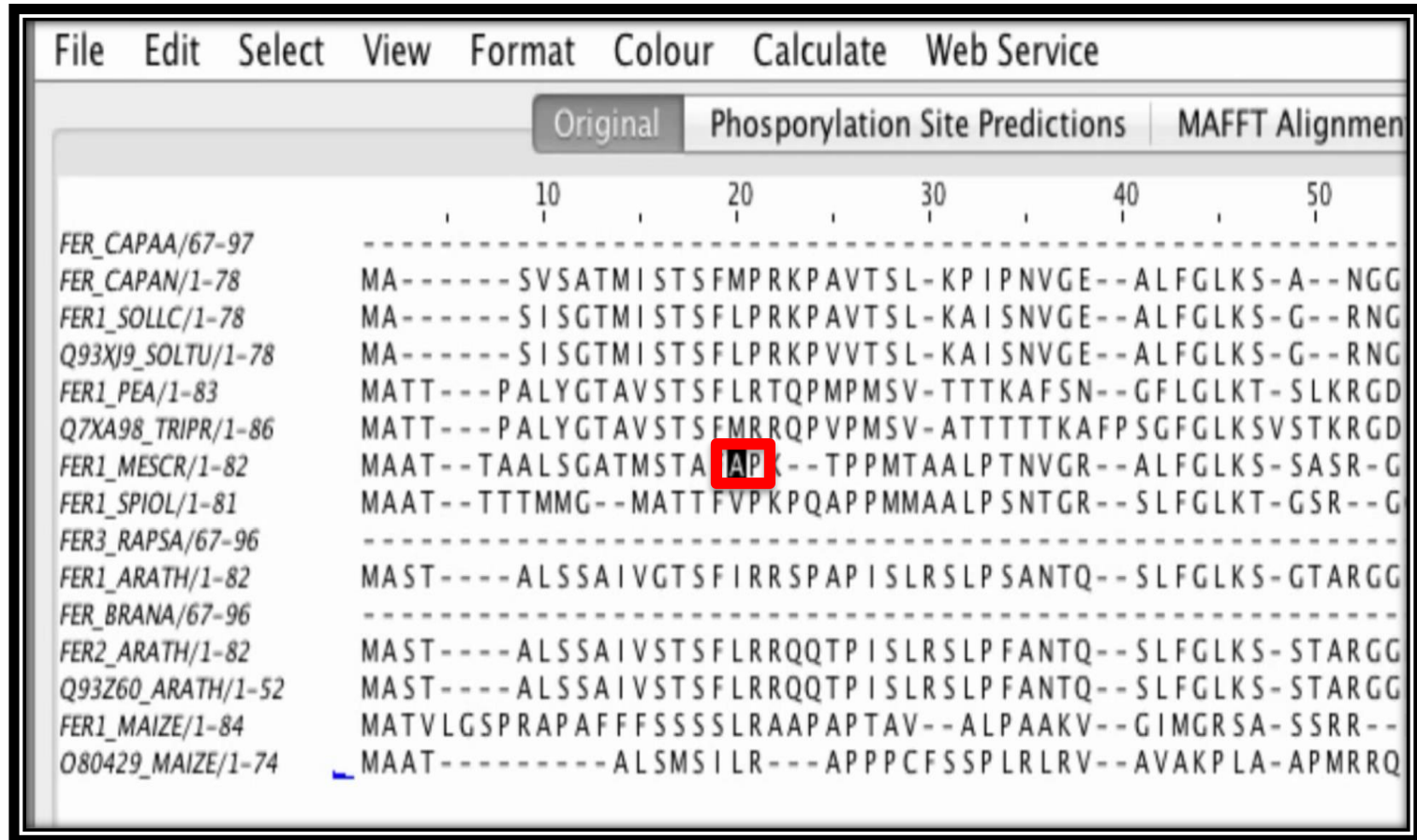
MA-----SVSATMISTSFMPRKPAVTS L-KPIPNVGE--ALFGLKS-A--NGG  
MA-----SISGTMISTSF LPRKPAVTS L-KAISNVGE--ALFGLKS-G--RNG  
MA-----SISGTMISTSF LPRKPVVTS L-KAISNVGE--ALFGLKS-G--RNG  
MATT--P ALYGTAVSTSF LRTQPMPSV-TTTKAFSN--GFLGLKT-SLKRGD  
MATT--P ALYGTAVSTSEMRQPVPMSV-ATTTT KAFP SGFGLKSVSTKRGD  
MAAT--TAALSGATMS TAFAPK--TPMTAALPTNVGR--ALFGLKS-SASR-G  
MAAT--TTTMMG--MATTPVPKPQAPP MMAALP SNTGR--SLFGLKT-GSR--G  
-----  
MAST----ALSSAIVGTSFIRRS PAPI SLRSLP SANTQ--SLFGLKS-GTARGG  
-----  
MAST----ALSSAIVSTSF LRRQQTPI SLRSLP FANTQ--SLFGLKS-STARGG  
MAST----ALSSAIVSTSF LRRQQTPI SLRSLP FANTQ--SLFGLKS-STARGG  
MATVLGSPRAPAFF FSSSS LRAAPAPTAV--ALPAKV--GIMGRSA-SSRR--  
MAAT-----ALSMSILR--APPCFSSPLRLRV--AVAKPLA-APMRRQ

Source: Jaview Online Training Video

<https://www.jalview.org/>



Type: 18P



Source: Jaview Online Training Video

<https://www.jalview.org/>



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Move to column and row location: type column and row number

Type 5,13 [Return]

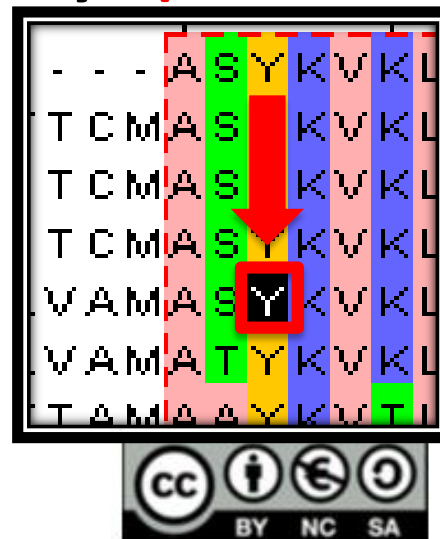
File Edit Select View Format Colour Calculate Web Service

Original Phosphorylation Site Predictions MAFFT Alignment

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FER_CAPAA/67-97	MA-----SVSATMI	STSFMPRKPAV	TSLS-KPIPNVGE--	ALFGLKS-A--	NGG
FER_CAPAN/1-78	MA-----SISGTM	ISTSFILPRKPAV	TSLS-KAISNVGE--	ALFGLKS-G--	RNG
FER1_SOLLC/1-78	MA-----SISGTM	ISTSFILPRKPV	TSLS-KAISNVGE--	ALFGLKS-G--	RNG
Q93XJ9_SOLTU/1-78	MATT---PALYGTA	VSTSFILRTQPM	MSV-TTTKAFSN--	GFLGLKT-SL	KRGD
FER1_PEA/1-83	MATT---PALYGTA	VSTSFIMRRQP	VPMSV-ATTTT	TKAFP SGFGLK	SVSTKRGD
Q7XA98_TRIPR/1-86	MAAT--TAALSGAT	MSTAFAPK--TP	PMTAALPTNVGR--	ALFGLKS-SASR	-G
FER1_MESCR/1-82	MAAT--TTTMMG--	MATTFVPK	PQAPPMMAALP	SNTGR--SLFGLKT	-GSR--G
FER1_SPIOL/1-81	MAST--ALSSAIV	GTSTFIRRS	PAPISLRS	SLP SANTQ--SLFGLKS	-GTARGG
FER3_RAPSA/67-96	MAST--ALSSAIV	STSTFLRR	QQTPISLRS	SLP FANTQ--SLFGLKS	-STARGG
FER1_ARATH/1-82	MAST--ALSSAIV	STSTFLRR	QQTPISLRS	SLP FANTQ--SLFGLKS	-STARGG
FER2_ARATH/1-82	MATVLS	SPRAPAFFFS	SSSLRAAP	APTAV--ALPAKV--	GIMGRSA-SSRR--
Q93Z60_ARATH/1-52	MAAT-----ALS	MSILR--APP	PCFSSPLRLRV--	AVAKPLA-APMRRQ	
FER1_MAIZE/1-84					
O80429_MAIZE/1-74					

# 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]**.



**F2 key**  
toggle between  
**Normal** and **Cursor**  
Mode

For **Mac**  
**Fn key plus F2**  
may be required  
to toggle between  
**Normal** and **Cursor** Mode

Source: Jaview Online Training Video

<https://www.jalview.org/>



# Find Sequences

Locate sequence group: use **Select >> Find**

Source: Jaview Online Training Video

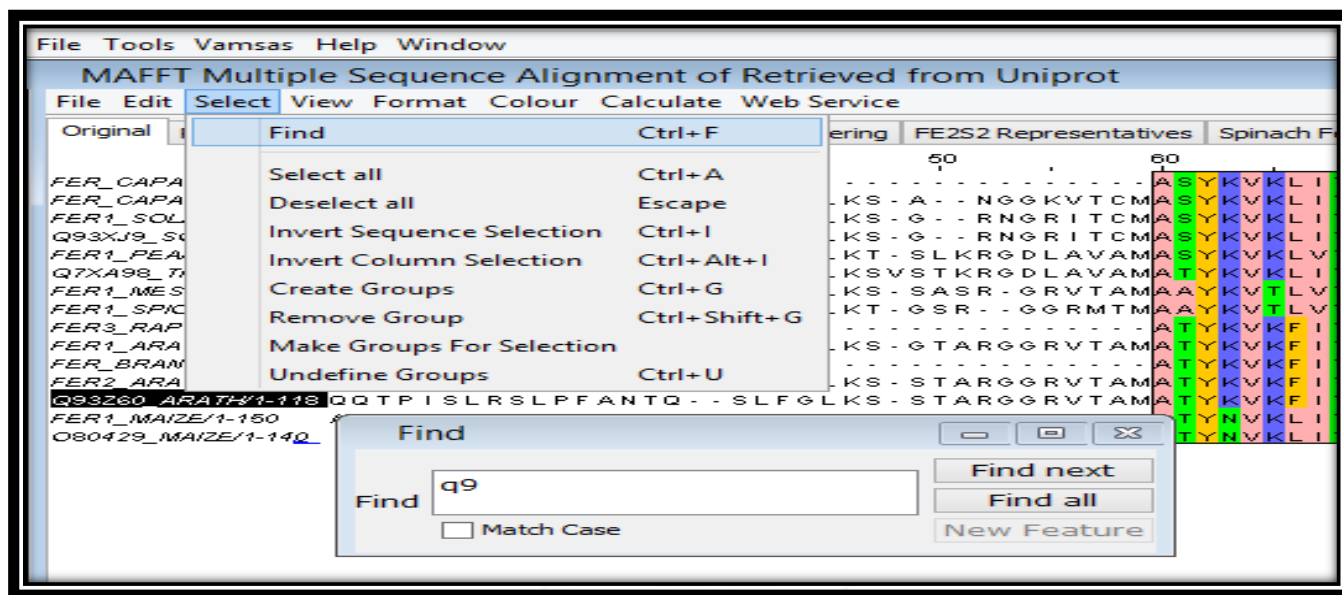
<https://www.jalview.org/>

## 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 to display the highlighted region.



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

- Find Ctrl+F
- Select all Ctrl+A
- Deselect all Escape
- Invert Sequence Selection Ctrl+I
- Invert Column Selection Ctrl+Alt+I
- Create Group Ctrl+G
- Remove Group Ctrl+Shift+G
- Make Groups For Selection
- Undefine Groups Ctrl+U
- Select/Hide Columns by Annotation...
- Select Highlighted Columns

sp|P38529|... SNVSAFLTKLWTLVEDPÉTDPLICWSPSGNSFHVFDQGG...  
 sp|P38530|... FLTKLWTLVSDPD TDALICWSPSGNSFHVFDQGGQFAKE...  
 sp|Q0061|... FLTKLWTLVSDPD TDALICWSPSGNSFHVFDQGGQFAKE...  
 sp|P4115|... GVTGGGTNIGEA VTAPPPRNPH PATLLNANSLPPPFLSI...  
 tr|A0A286|... FLTKLWTLVSDPD TDALICWSPSGSSFHVLDQGGQFAKE...  
 tr|F1MAF|... FLTKLWTLVSDPD TDALICWSPSGNSFHVFDQGGQFAKE...

Find

Find ☐ Match Case ☐ Include Description

Find next  
Find all  
New Feature

Locate sequence group: use **Select >> Find**

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

Jalview 2.11.1.0

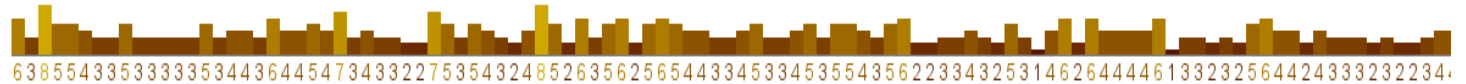
File Tools Help Window

C:\Users\Dr\_Ahmed\Desktop\HSF1.txt

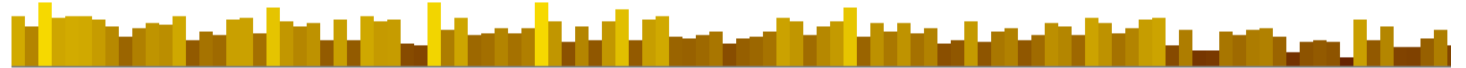
File Edit Select View Annotations Format Colour Calculate Web Service

sp P38529 HSF1_CHICK/1-491	281 PSASPSGSLDERSSPVVR I KEEPPSPSRSPKENEPSVTAAGNSTEQPQPQEKCLSVACLDKNELNDHLDT IDSNLDNLQTMLSTHGFSVDTTALLDLFSPSMTVTI
sp P38532 HSF1_MOUSE/1-525	281 GRSIDERPLSSSTLVRVKQEPSPPHSPRVLEASGRPSMDTPLSPTAF ID SILRESEPTAASNTAPMDTTGAQAPALPTSTPEKCLSVACLDKNELSDHLDAMI
sp Q00613 HSF1_HUMAN/1-529	281 GGSIDERPLSSSPLVRVKEPPSPQSPRVEEASGRPSVDLTLLSPTAL ID SILRESEPPASVTALTDARGHTDEGRPPSPPTSTPEKCLSVACLDKNELSDHI
sp P41151 HFA1A_ARATH/1-495	281 SHSLEASDGQ I VKYQPLRNDMMWNMMKTDDKYPFLDGFSSPNQVSGVTLQEVLP I TSGSQAYASVP SGQPLSYLPSTSTSLPDT IMPETSQ I PQLTRES I NDFPTI
tr A0A286ZSP4 A0A286ZSP4_PIG/1-590	281 GGSVDEERPLSGSPLVRVKEPPSPRSPAEAGPGHPSS I VETPLSPTAL ID SILRESEPTASATLLPDTGGHPPSPLPTSAPKCLSVACLDKTELSDHLDAI
tr F1MAF1 F1MAF1_RAT/1-525	281 GRSIDERPLSSSTLVRVKEPPSPPHSPRVLEASGRPASMDTPLSPTAF ID SILRESEPTAASNTAPMDTTGAQAPAPPAPSTPEKCLSVACLDKNELSDHLDAMI

Conservation



Quality



Consensus

G+S I D E R P L S S S + L V R V K E P P S P P + S P R V L E A S G R P S S + D T P L S P T A + I D S I L R E S E P T P A A S N T A + + D T T G A Q A P A + P T P + + P E K C L S + A C L + + N + + S D H L D + + I

sp P38529 HSF1_CHICK/1-491	421 ADTGKQLVHYTAQLELVDS
sp P38532 HSF1_MOUSE/1-525	421 PDMSLPDLSSSLASIQELLS
sp Q00613 HSF1_HUMAN/1-529	421 SVTVPDMSLPDLSSSLASIQ
sp P41151 HFA1A_ARATH/1-495	421 PEDPEIDELMSNFEELEYM
tr A0A286ZSP4 A0A286ZSP4_PIG/1-590	421 VPDMNLPDLSSSLASVRRQA
tr F1MAF1 F1MAF1_RAT/1-525	421 PDMSLPDLSSSLASIQELLS

Find

AAG

Find next

Find all

Find

Match Case

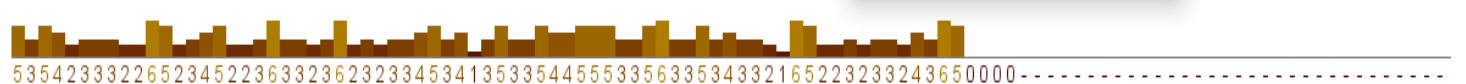
Include Description

New Feature

6 subsequence matches found.

OK

Conservation



## 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](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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