



H3ABioNet



H3ABioNet

Pan African Bioinformatics Network for H3Africa

Introduction to Bioinformatics online course: IBT

Multiple Sequence Alignment

Lec1: Download-Install and navigate Jalview

By

Ahmed Mansour Alzohairy

Professor (Full) at Department of Genetics,
Zagazig University, Zagazig, Egypt



H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy



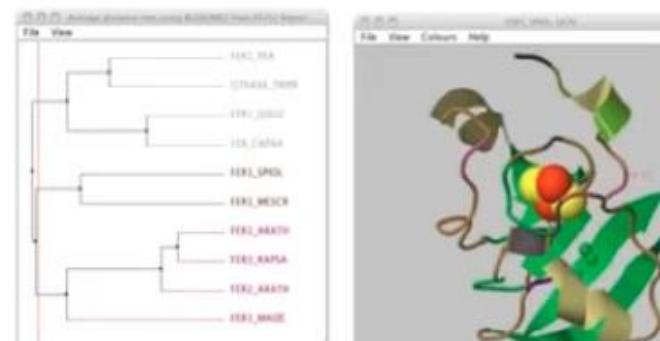
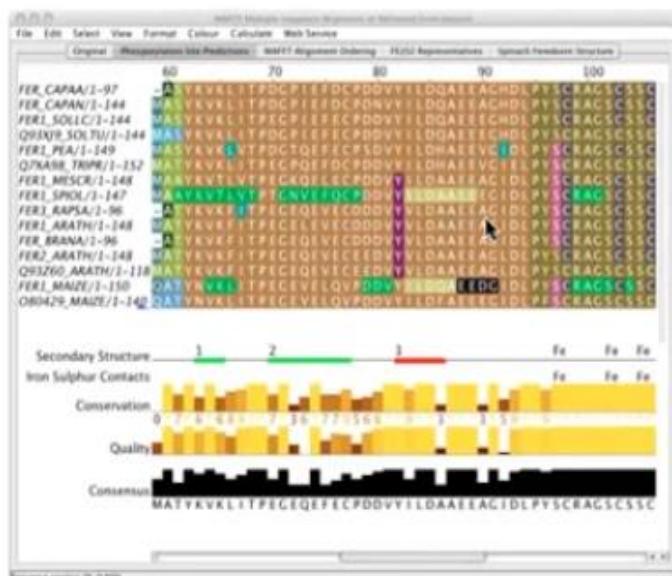
H3ABioNet



Standalone or
web based

alignment &
annotation,
tree, and
structure

Available at
www.jalview.org



The Barton Group
School of Life Sciences, University of Dundee, Dow Street, Dundee DD1 5EJ, Scotland, UK

Source: Jaview Online Training Video

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



H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy

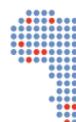


Source: Jaview Online Training Video

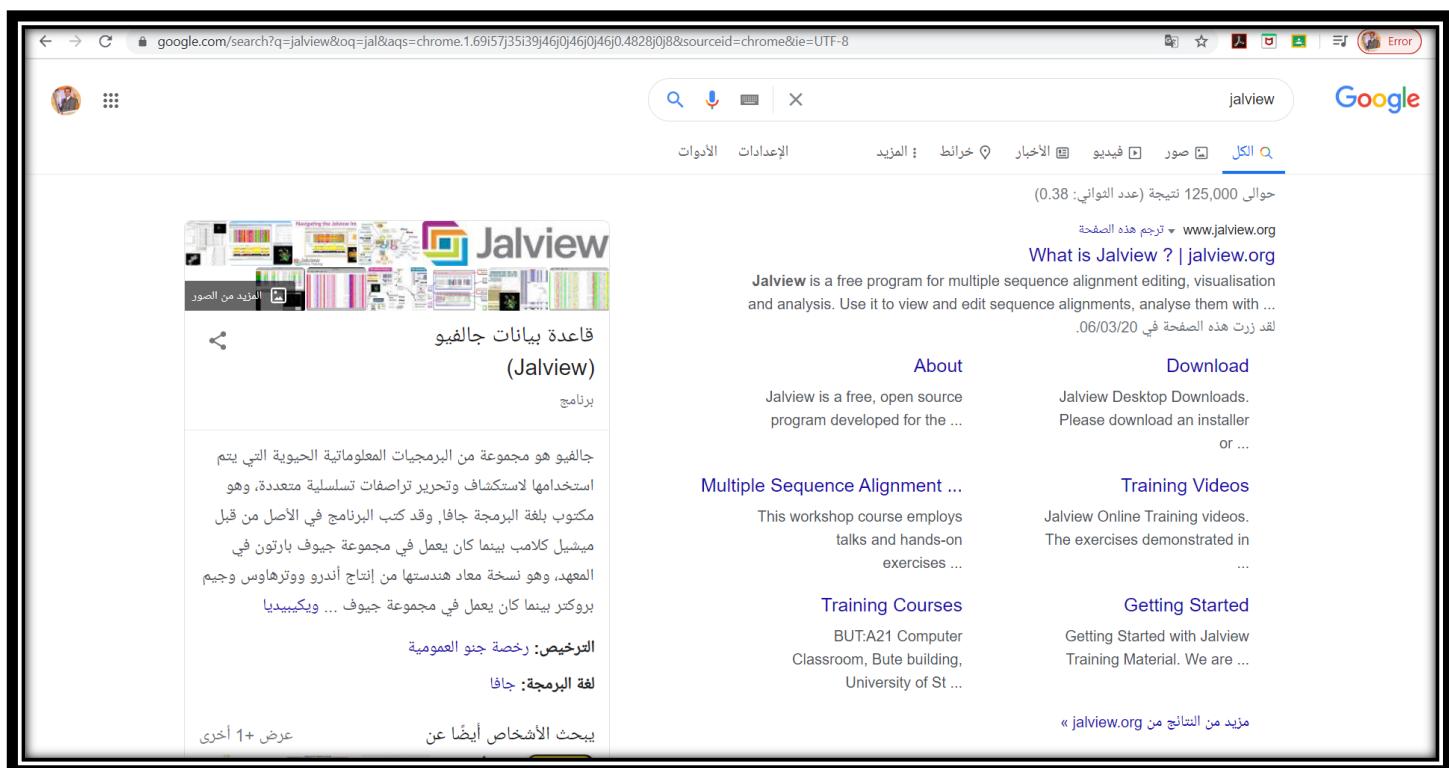
<https://www.jalview.org/>

Jalview History

- **Jalview** was initially developed in **1996** by Michele Clamp, James Cuff, Steve Searle and Geoff Barton at the ***University of Oxford*** and then the ***European Bioinformatics Institute***.
- Development of **Jalview 2** was made possible with eScience funding from the BBSRC8 in 2004, enabling Andrew Waterhouse and Jim Procter to re-engineer the original program to introduce contemporary developments in bioinformatics and take advantage of the latest web and Java technology.



- Jalview's development is now supported for a further 5 years from October **2009** by an award from the BBSRC's Tools and Resources fund.
- In **2010**, **2011**, and **2012**, Jalview benefitted from the Google Summer of Code, when Lauren Lui and Jan Engelhardt introduced new features for handling RNA alignments and secondary structure annotation, in collaboration with Yann Ponty



google.com/search?q=jalview&oq=jal&aqs=chrome.1.69i57j35i39j46j0j46j0j46j0.4828j0&sourceid=chrome&ie=UTF-8

الإعدادات الأدوات المزيد خرائط الأخبار فيديو صور الكل

حوالي 125,000 نتائج (عدد النواتي: 0.38)

ترجم هذه الصفحة www.jalview.org

What is Jalview ? | jalview.org

Jalview is a free program for multiple sequence alignment editing, visualisation and analysis. Use it to view and edit sequence alignments, analyse them with ...

لقد زرت هذه الصفحة في 06/03/20

About
Jalview is a free, open source program developed for the ...

Download
Jalview Desktop Downloads. Please download an installer or ...

Multiple Sequence Alignment ...
This workshop course employs talks and hands-on exercises ...

Training Videos
Jalview Online Training videos. The exercises demonstrated in ...

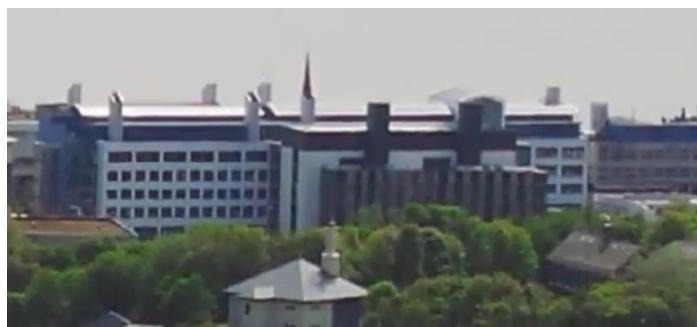
Training Courses
BUT:A21 Computer Classroom, Bute building, University of St ...

Getting Started
Getting Started with Jalview Training Material. We are ...

[مزيد من النتائج من jalview.org](#)

Jalview
قاعدة بيانات غالفيو (Jalview) برنامج
جالفيو هو مجموعة من البرمجيات المعلوماتية الجوبية التي يتم استخدامها لاستكشاف وتحرير تراصفات تسلسلية متعددة، وهو مكتوب بلغة البرمجة جافا، وقد كتب البرنامج في الأصل من قبل ميشيل كلامب بينما كان يعمل في مجموعة جيوف بارتون في المعهد، وهو نسخة معاد هندستها من إنتاج أندرو ووترهاوس وجيم بروكتور بينما كان يعمل في مجموعة جيوف ... [ويكيبيديا](#)

الترخيص: [رخصة جنو العمومية](#)
لغة البرمجة: [جافا](#)
يبحث الأشخاص أيضاً عن [عرض +1 أخرى](#)



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



H3ABioNet



The screenshot shows the Jalview website running in a Firefox browser. The title bar reads "What is Jalview ? | jalview...." and the address bar shows "www.jalview.org". The main content area features the Jalview logo (a colorful square icon) and the text: "Jalview is a powerful, fully integrated and interactive method for visualising and analysing the structure and function of proteins and RNAs". Below this, it says: "This free, open source multiple sequence alignment program developed at the University of Dundee". On the left, there are two news items: "Jalview Lightning Talk" (Posted On: 16-05-2014) and "Jalview is on the move" (Posted On: 09-05-2014). On the right, there are links for "Launch Jalview Desktop" and "Launch Jalview Applet", along with a "Download" button. A sidebar on the right lists various services: Alignment Analysis, Protein Disorder, Multiple alignment, JalviewLite, ENA-Web, Bioinformatics Web Server, and others like PDB, RCSB, PDB-101, Proveai, Mola, and Proveai.

Source: Jaview Online Training Video

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



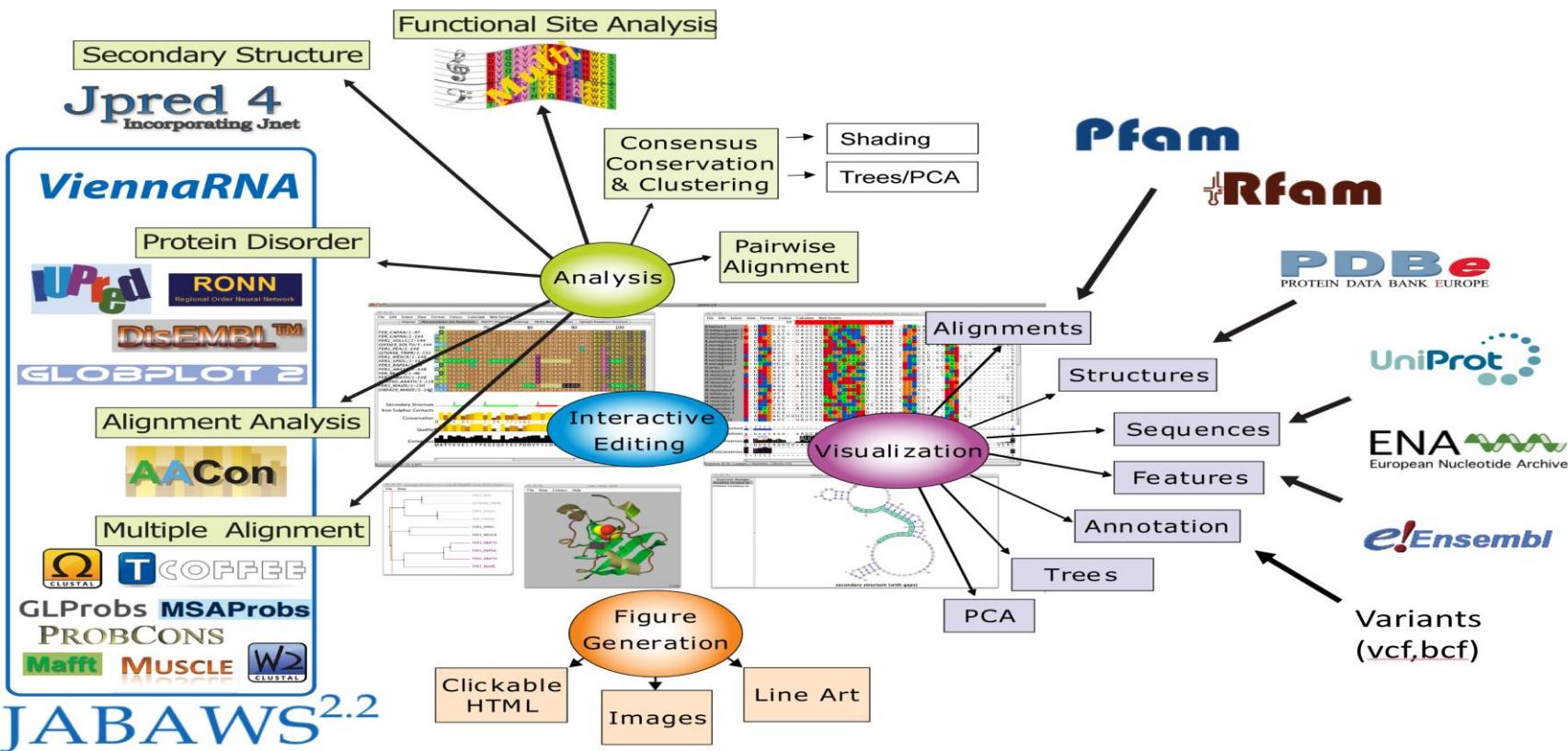
H3ABioNet

Pan African Bioinformatics Network for H3Africa



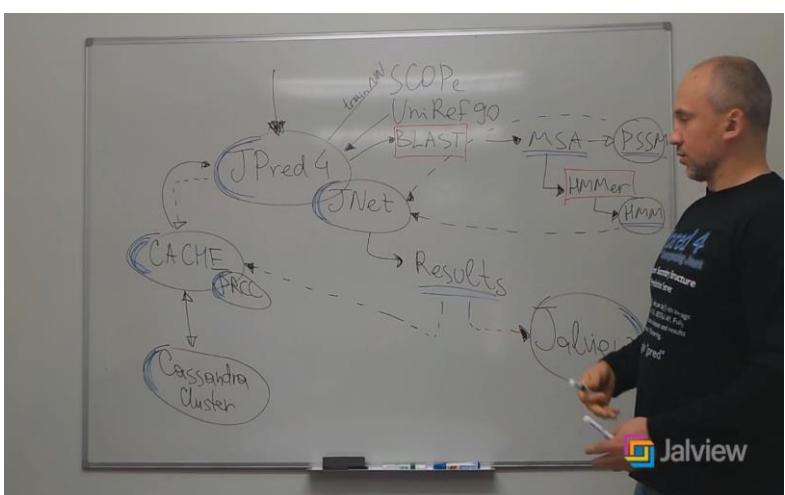
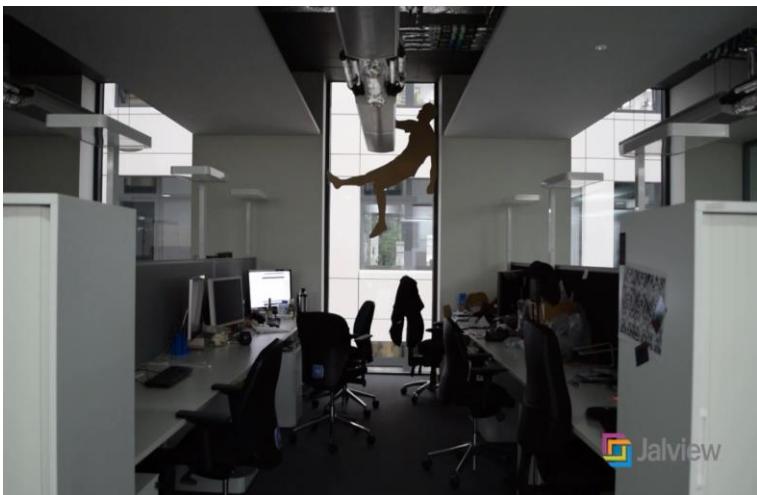
Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment| Prof. Ahmed M. Alzohairy

Multifunction



Source: Jaview Online Training Video

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



Source: Jaview Online Training Video

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

Jalview's main features:

- > integrated multiple window interface
- > sequence visualization, editing and annotation
- > **multiple sequence alignment**
- > consensus, conservation and clustering analysis
- > 2^o structure prediction plus protein disorder prediction
- > functional site analysis
- > phylogenetic tree and principle component analysis
- > 3D structure visualization with Jmol
- > accessing data from databases repositories
- > figure generation

Source: Jalview Online Training Video

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



H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy



Launching Jalview on your computer online training

Source: Jalview Online Training Video

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



H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy



H3ABioNet



the.0.35i39j69i57j46j0j46j0j46j0.7279j0j8&sourceid=chrome&ie=UTF-8

Search bar: jalview

Google search results:

- حوالي 135,000 نتائج (عدد النتائج: 0.39)
- ترجم هذه الصفحة www.jalview.org
- What is Jalview ? | jalview.org
- Jalview is a free program for multiple sequence alignment editing, visualisation and analysis. Use it to view and edit sequence alignments, analyse them with ...
- لقد زرت هذه الصفحة في 06/03/20
- About
- Jalview is a free, open source program developed for the ...
- Download
- Jalview Desktop Downloads. Please download an installer or ...
- Training Courses
- BUT:A21 Computer Classroom, Bute building, University of St ...
- Training Videos
- Jalview Online Training videos. The exercises demonstrated in ...
- Links
- The following links are to projects which are actively using new ...
- Getting Started
- Getting Started with Jalview Training Material. We are ...
- « jalview.org من مزيد من النتائج
- فيديوهات
- ImageJ
- أداة تقصي التراث المورثي...
- مايكرو...
- ويندوز
- كلوستال
- يبحث الأشخاص أيضاً عن
- التعليقات
- Jalview Online Training: Colouring Sequences and Alignments
- Jalview Online Training: Colouring proteins residues in an alignment using Jalview
- Jalview Online Training: Multiple Sequence Alignment and Analysis with Jalview



H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment| Prof. Ahmed M. Alzohairy



H3ABioNet





Jalview

- [Home](#)
- [About](#)
- [Help](#)
- [Community](#)
- [Development](#)
- [Training](#)
- [JalviewJS](#)
- [Schools](#)
- [Download](#)

Latest News

Jalview's 1st online training workshop was a great success! [Trained](#) On: 07-05-2020

[View News Archive](#)

[View Jalview courses >>>](#)

Tweets by @Jalview

Jalview.org (@Jalview) · May 25, 2020
JABAWS Services have been suspended until further notice. Normal services will be resumed within the hour!

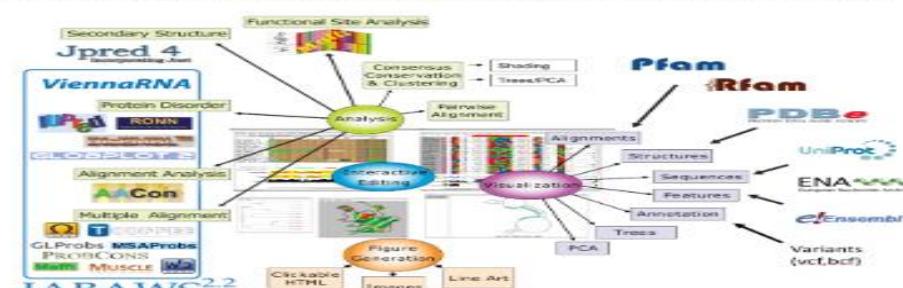
Jalview.org (@Jalview) · May 24, 2020
JABAWS services have been suspended until further notice. Normal services will be resumed within the hour!

[Subscribe to RSS Feed](#)

Looking for the 'Launch Jalview' buttons?

You need to download an [installer](#) to run Jalview 2.11. You can still use webstart to access old versions of Jalview in the [version archive](#).

Jalview is a free program for multiple sequence alignment, editing, visualisation and analysis. Use it to view and edit sequence alignments, analyse them with phylogenetic trees and principal components analysis (PCA) plots and explore molecular structures with annotation.



Jalview runs built-in DNA, RNA and protein sequence and structure visualisation and analysis capabilities. It uses [JPanel](#) to parse 3D structures and [J3DNA](#) to display RNA secondary structures. The Jalview Desktop can also connect with database and analysis services, and provides a graphical interface to the alignment and analysis services provided by the [JABAWS Bioinformatics Analysis Web Services](#) framework.

Finding out more

The [About](#) section provides more information. The Jalview Desktop App installs on most operating systems, and is available via the [Download](#) page, along with links to compiled jars and source code. An alpha release of the web based JalviewJS app is also available via the [Jalview JS](#) link. The web based version of Jalview is the same Jalview Java program, but compiled into JavaScript with [Java2Script](#) and [Swing](#) (with thanks to [Guy Holloway](#) of St. Olaf College, USA).

Availability

Jalview is an open source project released under the [LGPL](#). The development is coordinated by [Jen Prickett](#) and [Graeme Hartley](#) in the [Computational Biology Group](#) at the University of Leicester, [Institute of Life Sciences](#), with support from the [Biosciences and Computer Science Research Councils](#) and the [Wellcome Trust](#).

ELIXIR-UK Resource

 Jalview is a proud member of [ELIXIR](#) – the European-wide project providing high-quality and sustainable infrastructures for biological research. Following a strict selection procedure, Jalview has been identified as a Tier 1 resource by [ELIXIR-UK](#) (Protein Structure and Function).

If you use Jalview in your work, please cite this publication:

Watkinson, A.M., Prickett, J.S., Martin, D.M.A., Clamp, M., and Barton, G. J. (2009). Jalview Version 2: A multiple sequence alignment editor and analysis workbench. *Bioinformatics* 25(11): 1424-1425. doi: 10.1093/bioinformatics/btp233



Published under CC BY-SA



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment| Prof. Ahmed M. Alzohairy

Jalview Desktop Downloads

Please download an installer or archive for your platform from the links below. Once installed, the Jalview application will keep itself up to date.



[Windows x64 Installer](#)



[View all platforms](#)

To see what's new, view the [Jalview 2.11.10 Release Notes](#).

If you need the source, then please download the [Jalview 2.11.10 Source Tarball](#).

Running a specific version of Jalview

If you need to install a specific version and have an existing Java installation then we recommend downloading the Jalview Executable Jar (see table above). The [Version Archive](#) provides links to builds for earlier versions. Alternatively, up to date versions of Jalview designed for command line use are also available via conda and homebrew.

Install via Conda

A Jalview conda package is also available (tested on OSX and Linux) thanks to the great folk over at [BioConda](#)

Anaconda Cloud 2.11.1.0 | Last updated 18 May 2020 | Platforms linux-64,noarch,osx-64 | downloads 13k total

To install via conda, first download [Miniconda](#) for your platform.

Then: open a terminal and type:

```
conda config --add channels defaults  
conda config --add channels bioconda  
conda config --add channels conda-forge  
conda install jalview
```

Thanks to [ej_technologies](#) for granting a free install4j license to the Jalview Open Source Project. Jalview's installers were built with the [install4j multi-platform installer builder](#) and [gradle](#).



Source: Jaview Online Training

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



H3ABioNet



Jalview Desktop Downloads

Please download an installer or archive for your platform from the links below. Once installed, the Jalview application will keep itself up to date.

	Mac OSX Disk Image
	Windows x64 Installer 
	Linux shell installer (x64)
	Linux shell installer (any)
	Unix .tar.gz file archive (any)
	Jalview executable .jar file

To see what's new, view the [Jalview 2.11.1.0 Release Notes](#).

If you need the source, then please download the [Jalview 2.11.1.0 Source Tarball](#).

Running a specific version of Jalview

If you need to install a specific version and have an existing Java installation then we recommend downloading the Jalview Executable Jar (see table above). The [Version Archive](#) provides links to builds for earlier versions. Alternatively, up to date versions of Jalview designed for command line use are also available via [conda](#) and [homebrew](#).

Install via Conda

A Jalview conda package is also available (tested on OSX and Linux) thanks to the great folk over at [BioConda](#).

To install via conda, first download [Miniconda](#) for your platform.

Then: open a terminal and type:

```
conda config --add channels defaults
conda config --add channels bioconda
conda config --add channels conda-forge
conda install jalview
```

Thanks to [ej-technologies](#) for granting a free install4j license to the Jalview Open Source Project. Jalview's installers were built with the [install4j multi-platform installer builder](#) and [gradle](#).



Published under CC SA v3

If you use Jalview in your work, please cite this publication:

Waterhouse, A.M., Procter, J.B., Martin, D.M.A., Clamp, M. and Barton, G. J. (2009) "Jalview Version 2 - a multiple sequence alignment editor and analysis workbench" Bioinformatics 25 (9) 1189-1191 doi:10.1093/bioinformatics/btp033



Authenticity questions?

Jalview Desktop Downloads

Please download an installer or archive for your platform from the links below. Once installed, the Jalview application will keep itself up to date.

	Mac OSX Disk Image
	Windows x64 Installer
	Linux shell installer (x64)
	Linux shell installer (any)
	Unix .tar.gz file archive (any)
	Jalview executable .jar file

To see what's new, view the [Jalview 2.11.10 Release Notes](#).

If you need the source, then please download the [Jalview 2.11.10 Source Tarball](#).

Running a specific version of Jalview

If you need to install a specific version and have an existing Java installation then we recommend downloading the Jalview Executable Jar (see table above). The [Version Archive](#) provides links to builds for earlier versions. Alternatively, up to date versions of Jalview designed for command line use are also available via [conda](#) and [homebrew](#).

Install via Conda

A Jalview conda package is also available (tested on OSX and Linux) thanks to the great folk over at [Bioconda](#).

To install via conda, first download [Miniconda](#) for your platform.

Then: open a terminal and type:

```
conda config --add channels defaults
conda config --add channels bioconda
conda config --add channels conda-forge
conda install jalview
```

The launching process may vary between different browsers



If you use Jalview in your work, please cite this publication:

Waterhouse, A.M., Procter, J.B., Martin, D.M.A., Clamp, M. and Barton, G. J. (2009) "Jalview Version 2 - a multiple sequence alignment editor and analysis workbench" Bioinformatics 25 (8) 1169-1171 doi: 10.1093/bioinformatics/btp053



 This type of file can harm your computer. Do you want to keep Jalview-2_11_1_0....exe anyway?

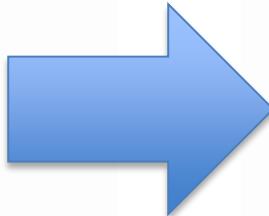
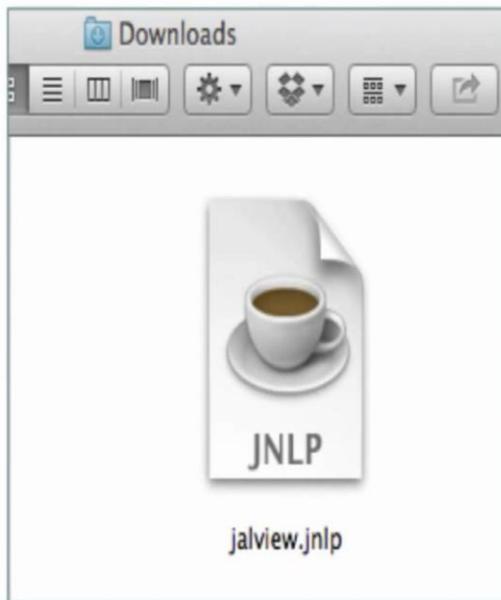
Keep

Discard



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment| Prof. Ahmed M. Alzohairy

JNLP file in the Downloads folder

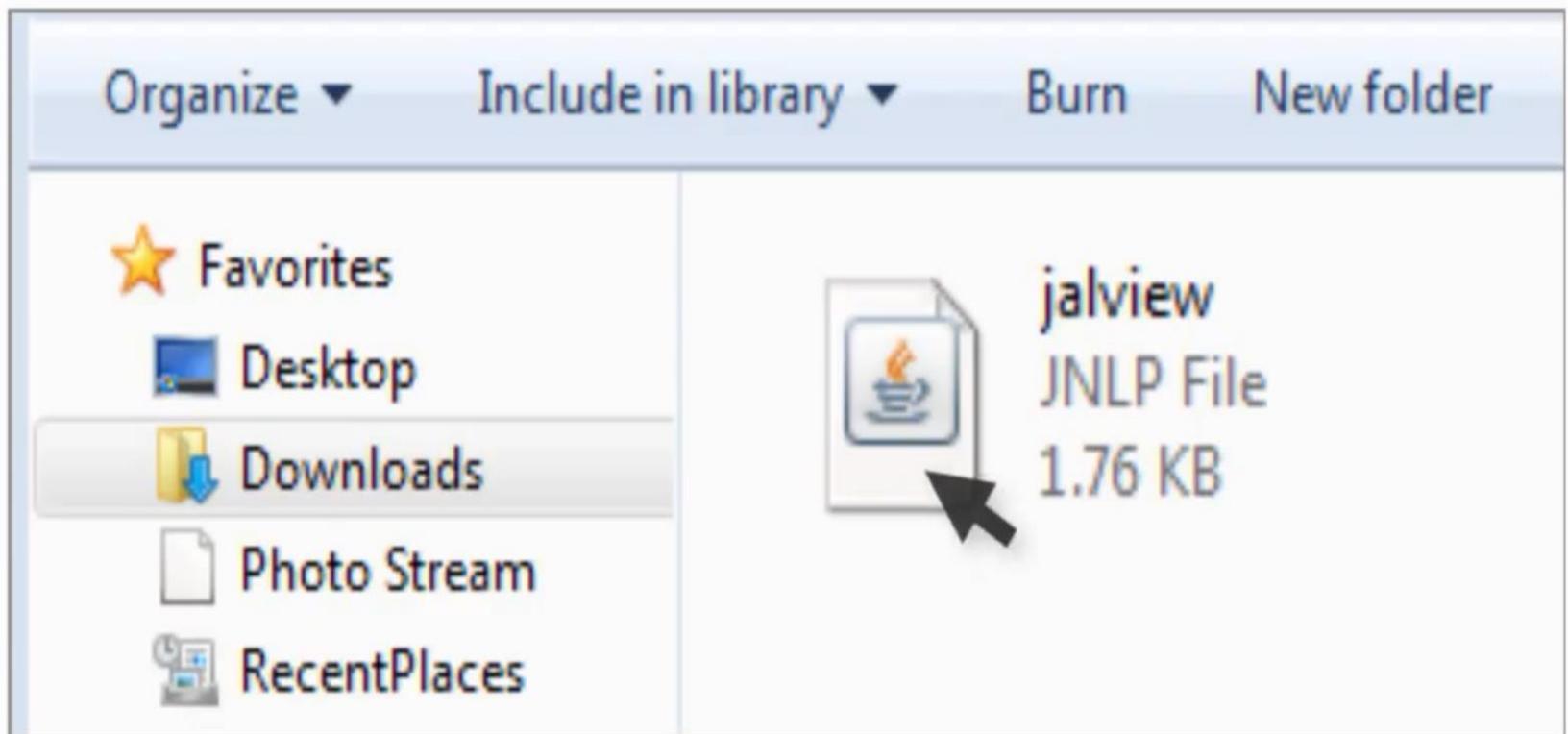


to start Jalview on your computer



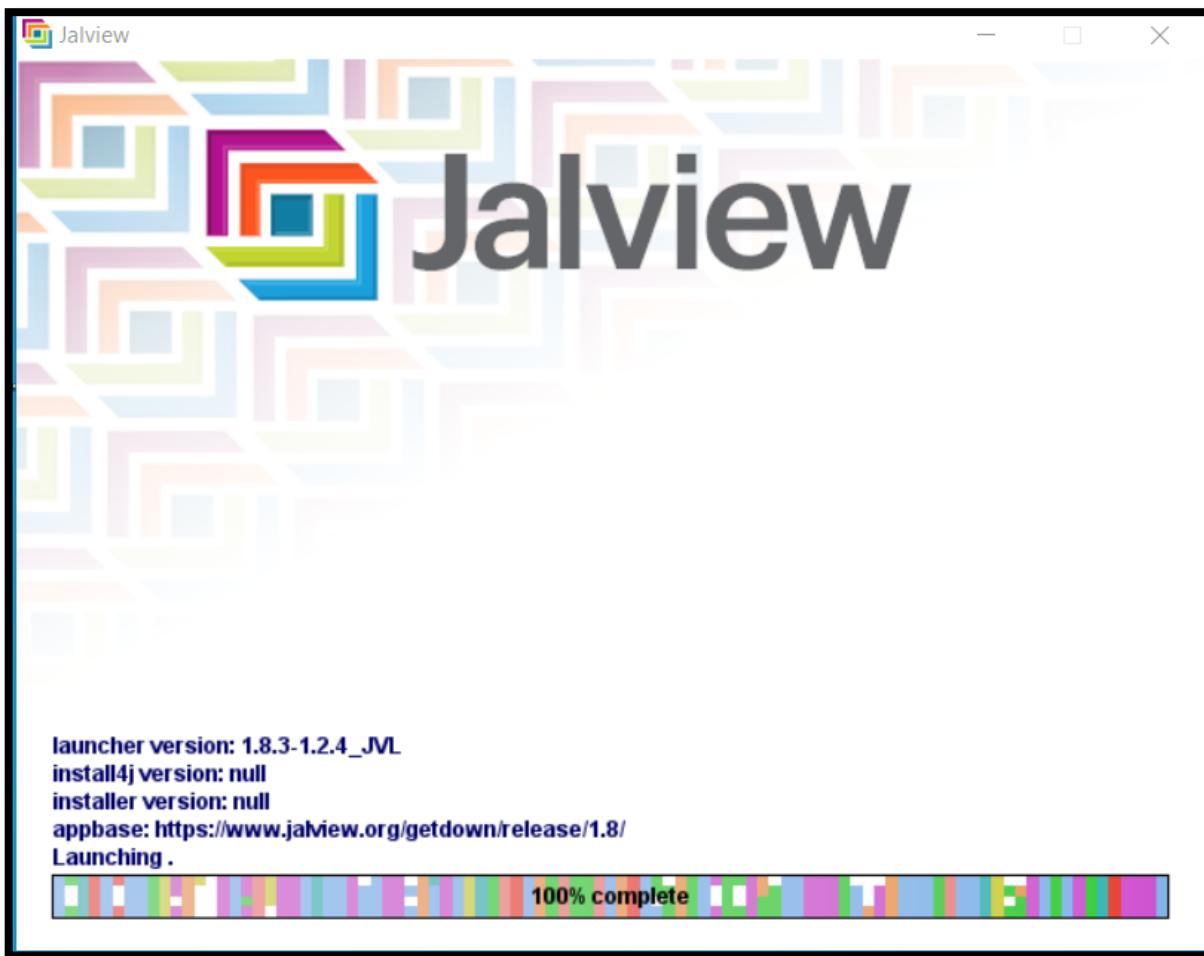
Source: Jalview Online Training Video

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



Source: Jaview Online Training Video

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



Source: Jaview Online Training Video

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

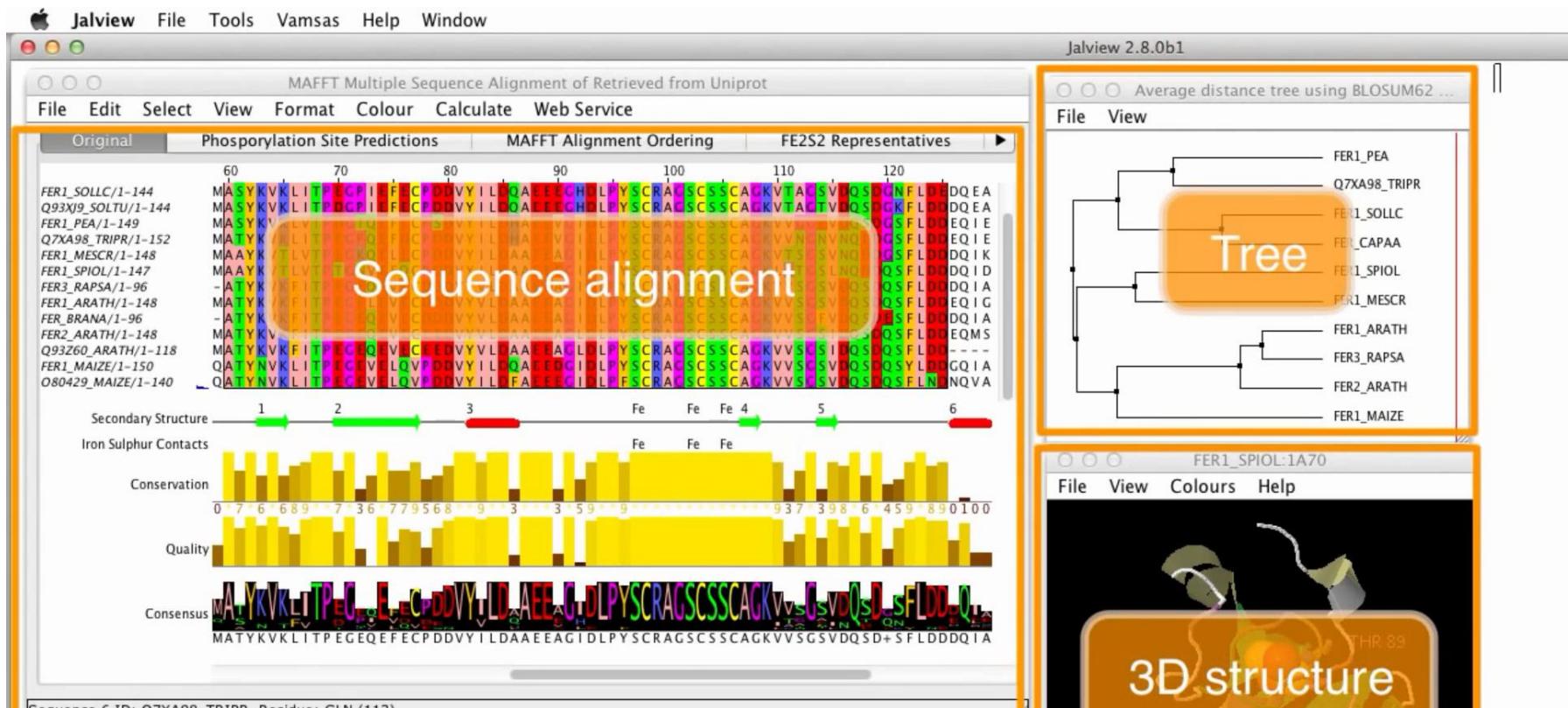


H3ABioNet

Pan African Bioinformatics Network for H3Africa

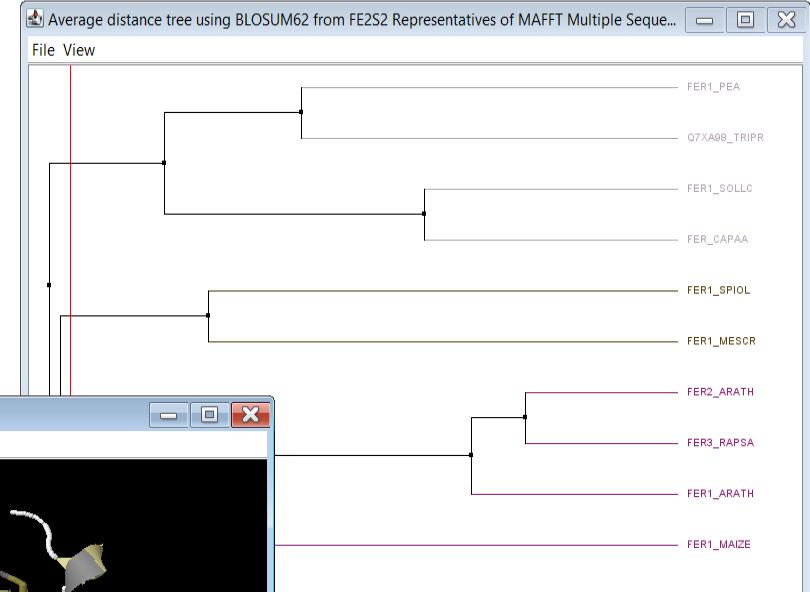
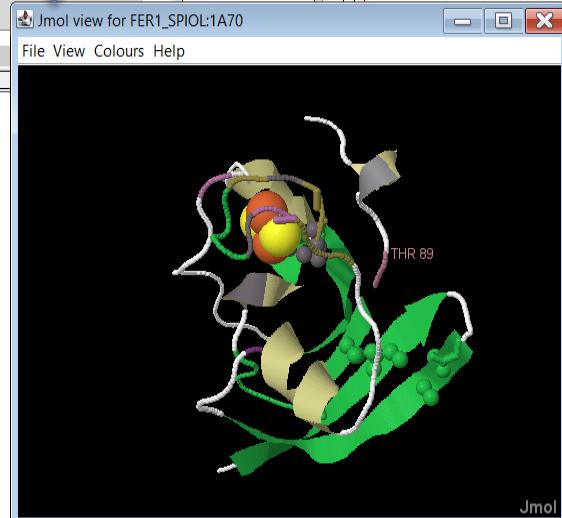
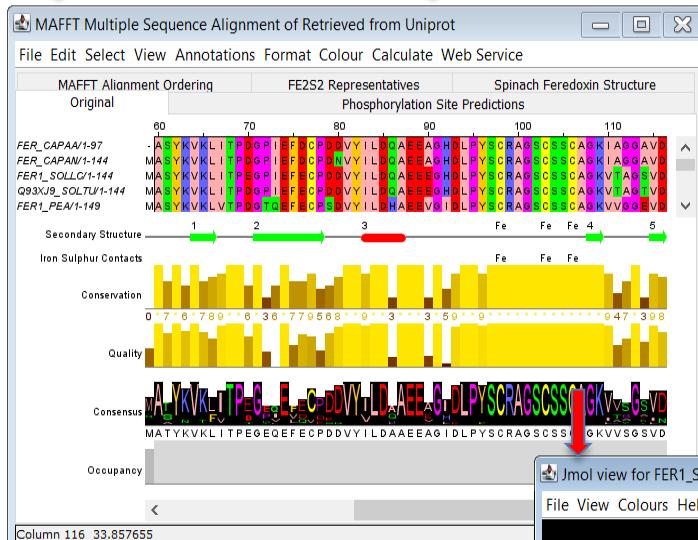


Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy



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

Jalview 2.11.1.0
File Tools Help Window



Source: Jalview Online Training

Video

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



H3ABioNet

Pan African Bioinformatics Network for H3Africa





Source: Jaview Online Training Video

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



Source: Jalview Online Training Video

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



H3ABioNet



Jalview Desktop Interface

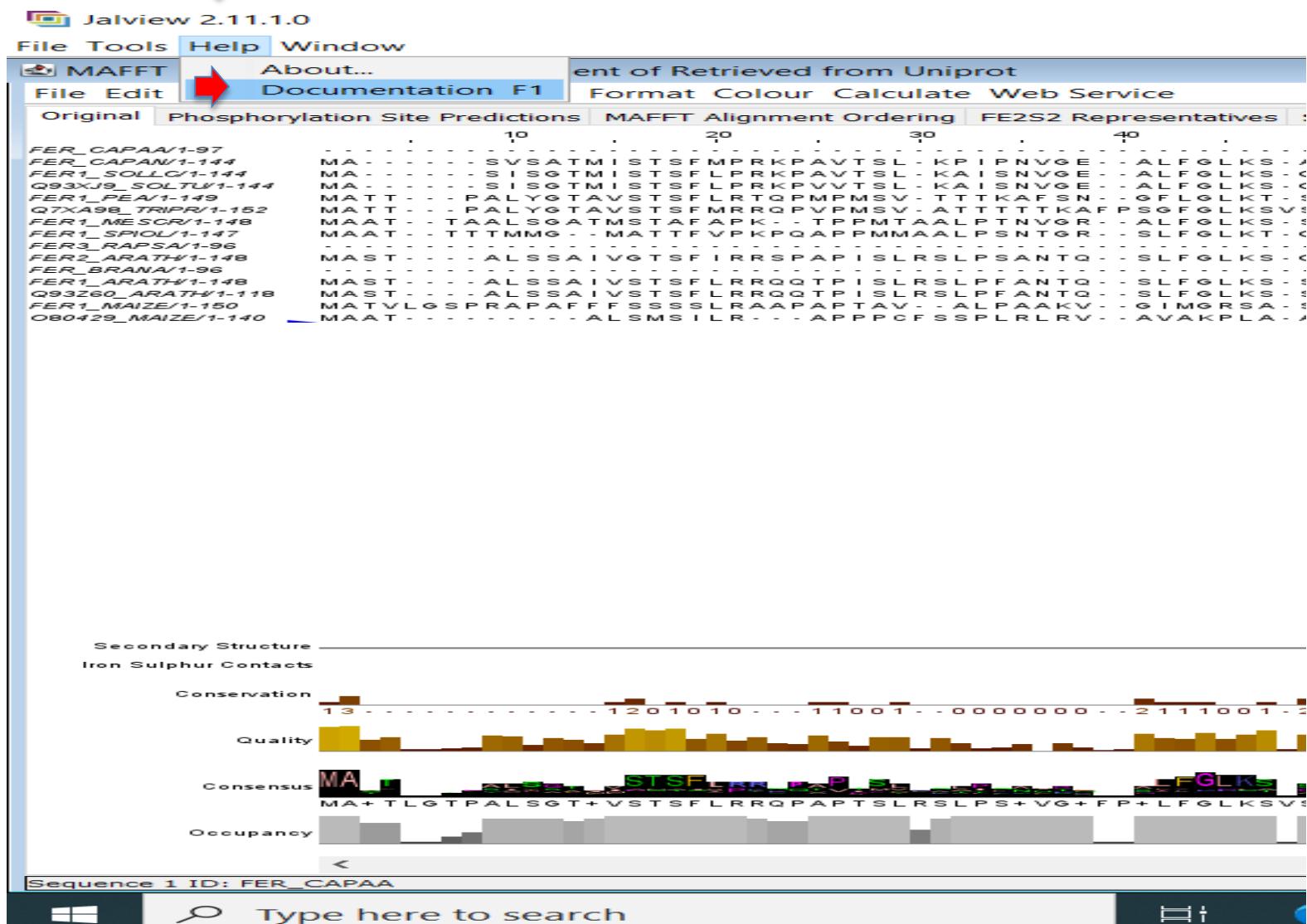


H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy





Jalview Documentation

Table Of Contents Search

Jalview

Welcome to Jalview's built in documentation.

Here are some good places to start:

- [What's new](#) summarises the new features in this release of Jalview.
- Learn how to [edit alignments](#) with Jalview.
- [Import and display sequence features on your alignment](#)
- Use [Imol](#) to view and superpose [3D structures](#) associated with sequences in the alignment

For more information, you might also want to take a look at the documentation section of the [Jalview website](#) (<http://www.jalview.org/about/documentation>).

If you are using the Jalview Desktop application and are looking for something specific, then try the search box (next to the print icon). If you're already viewing this in your web browser, then google the online version of these pages. If you don't find what you are looking for, or want to report a bug or make a feature request, then get in contact over at <http://www.jalview.org/community>.

Citing Jalview

If you use Jalview in your work, please cite the Jalview 2 paper in Bioinformatics:

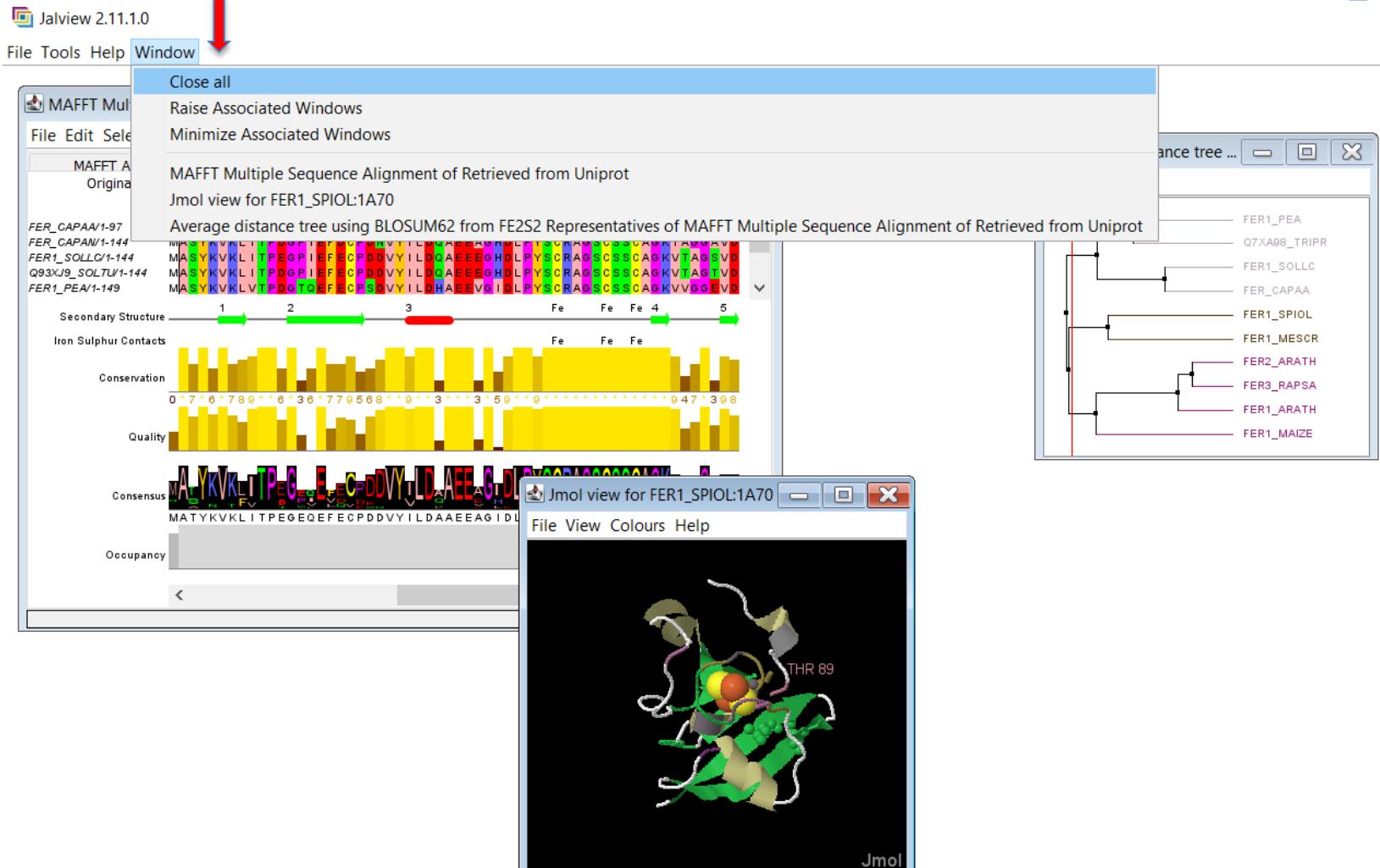
Waterhouse, A.M., Procter, J.B., Martin, D.M.A., Clamp, M., Barton, G.J. (2009), "Jalview version 2: A Multiple Sequence Alignment and Analysis Workbench," *Bioinformatics* 25 (9) 1189-1191 doi: 10.1093/bioinformatics/btp033

The Jalview Authors

The following people have contributed to Jalview's development:

- Jalview 1
 - Michele Clamp
 - James Cuff
 - Steve Searle
 - David Martin
 - Geoff Barton
- Jalview 2
 - Jim Procter
 - Mungo Carstairs
 - Ben Soares
 - Kira Mourão
 - Tochukwu 'Charles' Ofoegbu
 - Andrew Waterhouse
 - Jan Engelhardt
 - Lauren Lui
 - Anne Menard
 - Natasha Sherstnev
 - Daniel Barton
 - David Roldan-Martinez
 - David Martin
 - Geoff Barton





Load your own sequences at the start up



H3ABioNet



Jalview 2.11.1.0

File Tools Help Window

Preferences

Show Memory Usage

Show Java Console

Show Jalview News

Collect Garbage

Groovy Console...

Enable experimental features

FER1_SOLL1-144

Q93XJ9_SOLL1-144

FER1_PEA1-149

MA5YKVKLITPECPDDVYILDAEEGLDA

Secondary Structure

Iron Sulphur Contacts

Conservation

Quality

Consensus

Occupancy

Format Retrieved from Uniprot

Colour Calculate Web Service

FE2S2 Representatives

Spinach Feredoxin Structure

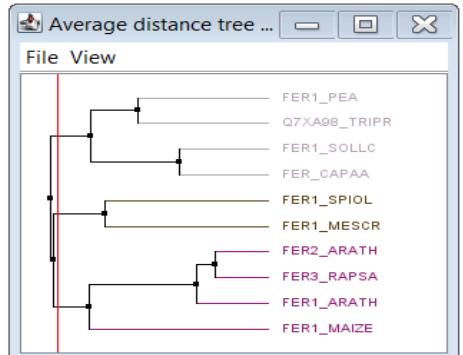
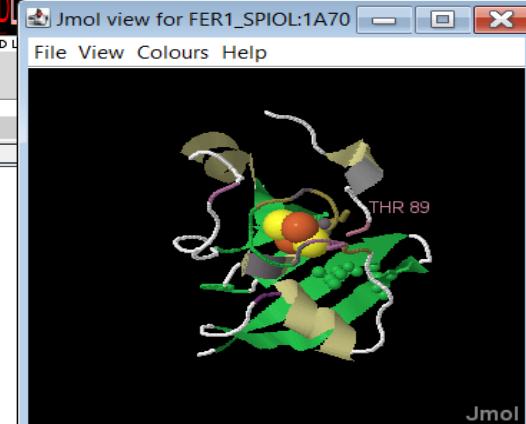
Phosphorylation Site Predictions

IEFDCPDVYILDAEEAHDLPYSCRAGSCSCAGKIAGGAVD
IEFDCPDVYILDAEEAHDLPYSCRAGSCSCAGKIAGGAVD
MASYKVKLITPEGPQEFCPDDVYILDAEEAGIDL

80 90 100 110

Fe Fe Fe 4 Fe

5



H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy



H3ABioNet



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

MAFFT Alignment Ordering FE2S2 Representatives Spinach Feredoxin Structure

Original Phosphorylation Site Predictions

FER_CAPAA/1-97
FER_CAPAN/1-144
FERI_SOLOC/1-144
Q93XJ9_SOLTU/1-1
FER1_PEA/1-149

Secondary Str
Iron Sulphur Co
Conserv
Conser
Conser
Occup
Sequence 1 ID: f

Preferences

Visual Colours Overview Structure Connections Backups Links Output Editing Web Services

Open new alignment

Maximize Window Show annotations Quality
Open Overview Conservation Consensus Occupancy
Full Sequence Id Show Group: Conservation Consensus
Right Align Ids Consensus: Histogram Logo

Font: SansSerif 10 plain

Show Unconserved Sequence ID Tooltip
Italic Sequence Ids List Database References
Smooth Font List Non-positional Features

Scale Protein to cDNA
Gap Symbol -
Wrap Alignment
Sort alignment by No sort
Sort annotations by No sort Autocalculated first

Open file http://www.jalview.org/examples/exampleFile_2_3.jar

OK Cancel

Average distance tree ... File View

EA
LTRIPR
OLLC
PAA
PIOL
ESCR
RATH
APSA
RATH
AIZE



H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy



H3ABioNet



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

MAFFT Alignment Ordering FE2S2 Representatives Spinach Ferredoxin Structure
Original Phosphorylation Site Predictions

FER_CAPAA/1-97
FER_CAPAN/1-144
FER1_SOLLC/1-144
Q93XJ9_SOLTU/1-1
FER1_PEA/1-149

Secondary Str Iron Sulphur Co Conserved Occupancy

Sequence 1 ID: FER_CAPAA/1-97

Preferences

Visual Colours Overview Structure Connections Backups Links Output Editing Web Services

Open new alignment

Show annotations Quality
Conservation Consensus Occupancy
Show Group: Conservation Consensus
Consensus: Histogram Logo

Font: SansSerif 10 plain

Show Unconserved Italic Sequence Ids Smooth Font
List Database References List Non-positional Features

Scale Protein to cDNA Gap Symbol
Wrap Alignment Sort alignment by No sort
Sort annotations by No sort Autocalculated first

Open file http://www.jalview.org/examples/exampleFile12_3.jar

OK Cancel

Average distance tree ...

File View

LEA
TRIPR
DLLO
PAA
PIOL
ESCR
RATH
APSA
RATH
AIZE

Select startup file

Look in: Desktop

Recent Items

Desktop

Documents

This PC

Network

Genomics

Intra-African Mobility grant 2020

Ismail Atia

May Presentation

NCBI

Photos

File name:

Files of type: All Files

Open Cancel



H3ABioNet

Pan African Bioinformatics Network for H3Africa



Introduction to Bioinformatics Online Course:IBT
Multiple Sequence Alignment | Prof. Ahmed M. Alzohairy

Practical

'to try in your own time'

- Download and install Jalview



BTU BIOINFORMATICS TRAINNING UNIT

1st Module | What Bioinformatics Can Do for You

2nd Module | Manipulation of Biological Sequences

3rd Module | Working with single DNA sequence

4th Module | How to Build a Multiple Sequence Alignment?

5th Module | Inferring Phylogenetic analysis using Jalignview

6th Module | Advanced Molecular Concepts

7th Module | Inferring Protein Sequence (Structure & Function)

8th Module | RNAanalysis and Function

9th Module | Editing and Publishing Alignments in your Manuscript

10th Module | Building and Publishing Phylogenetic Trees

11th Module | Working with Protein 3-D Structures

12th Module | Advanced Bioinformatics Using R

Bioinformatics Workshops Series

EST by, Dr. Ahmed Mansour Alzohairy

Call us: 01026060324 / 01000727270

Facebook: <https://www.facebook.com/Bioinformaticsunit>

Design by, Mohamed Tarek, 010220000224

