H3ABioNet

Bioinformatics Training Unit

H3ABioNet

Pan African Bioinformatics Network for H3Africa

Introduction to Bioinformatics online course: IBT

Multiple Sequence Alignment

Lec4: *From your favorite Aligner to Jalview*

By

Ahmed Mansour Alzohairy

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

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Collect Your Sequences in *FASTA* format in one text file

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ITS4 a
File Edit Format View Help
> Assiut121-ITS4_D07
NNNNNNGATCTACCTGATTTGAGGTCAACTTGTTTGTTATATTGTAAGGCCGAGCCTAGAATACCGAGAAATATACCATT
AAACTATTCAACGAGTTGGATAAACCTAATACATTGAAAGTCATATAGCACTATCCAGTACCACTCATGCCAATACATTT
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From your favorite Aligner

Login *Clustal Omega* and past your sequences and choose the type of your input

http://www.ebi.ac.uk/Tools/msa/clustalo/

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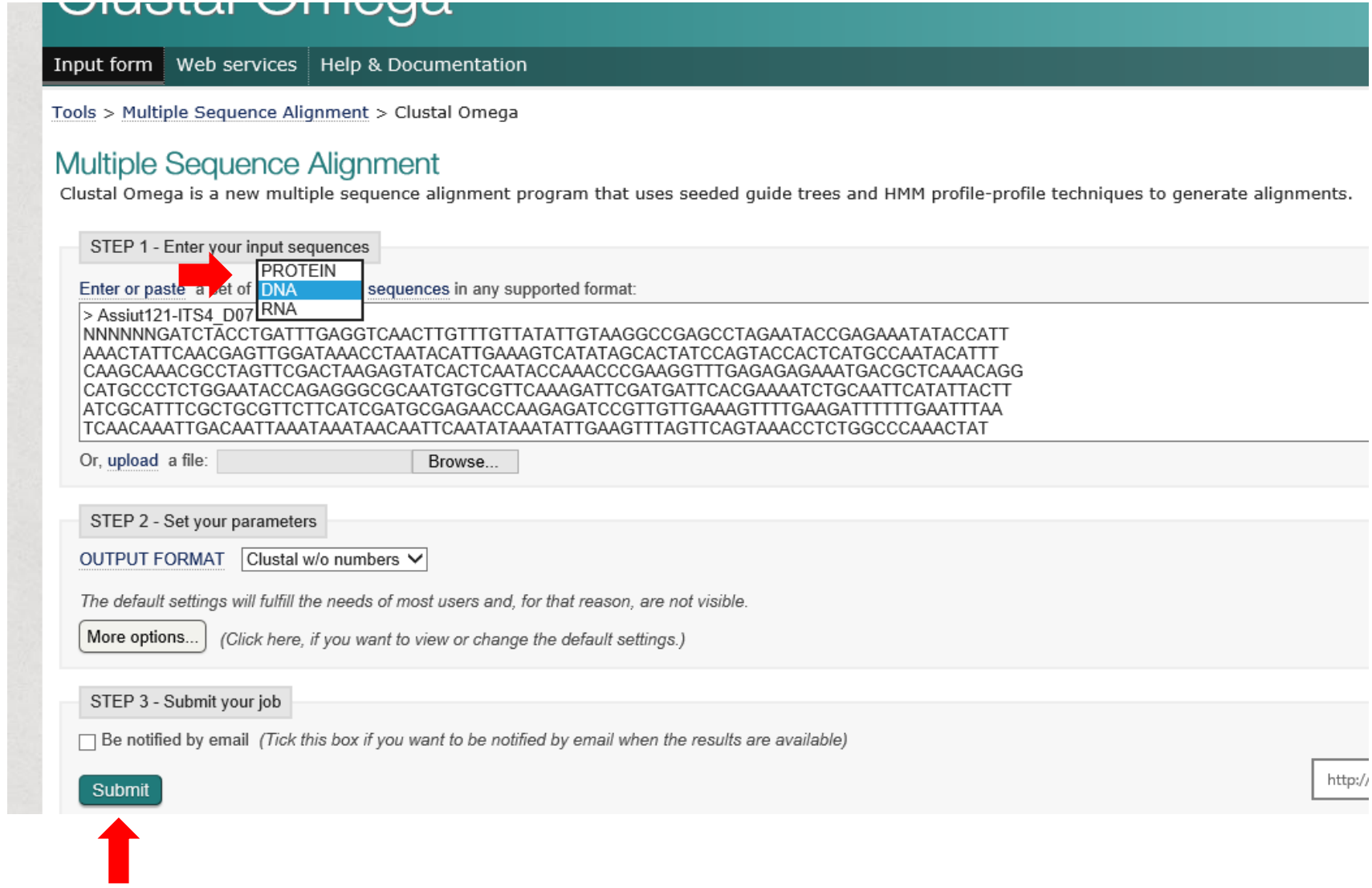
Input form
Web services
Help & Documentation
Tools > Multiple Sequence Alignment > Clustal Omega
Multiple Sequence Alignment
Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments.
STEP 1 - Enter your input sequences
PROTEIN
DNA
RNA
Enter or paste a set of sequences in any supported format:
> Assiut121-ITS4_D07
NNNNNNGATCTACCTGATTTGAGGTCAACTTGTTTGTTATATTGTAAGGCCGAGCCTAGAATACCGAGAAATATACCATT
AAACTATTCAACGAGTTGGATAAACCTAATACATTGAAAGTCATATAGCACTATCCAGTACCACTCATGCCAATACATTT
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TCAACAAATTGACAATTAAATAAATAACAATTCAATATAAATATTGAAGTTTAGTTCAGTAAACCTCTGGCCCAAACTAT
Or, upload a file:
Browse...
STEP 2 - Set your parameters
OUTPUT FORMAT
Clustal w/o numbers
The default settings will fulfill the needs of most users and, for that reason, are not visible.
More options...
(Click here, if you want to view or change the default settings.)
STEP 3 - Submit your job
Be notified by email (Tick this box if you want to be notified by email when the results are available)
Submit

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Download the alignment file on the Desktop

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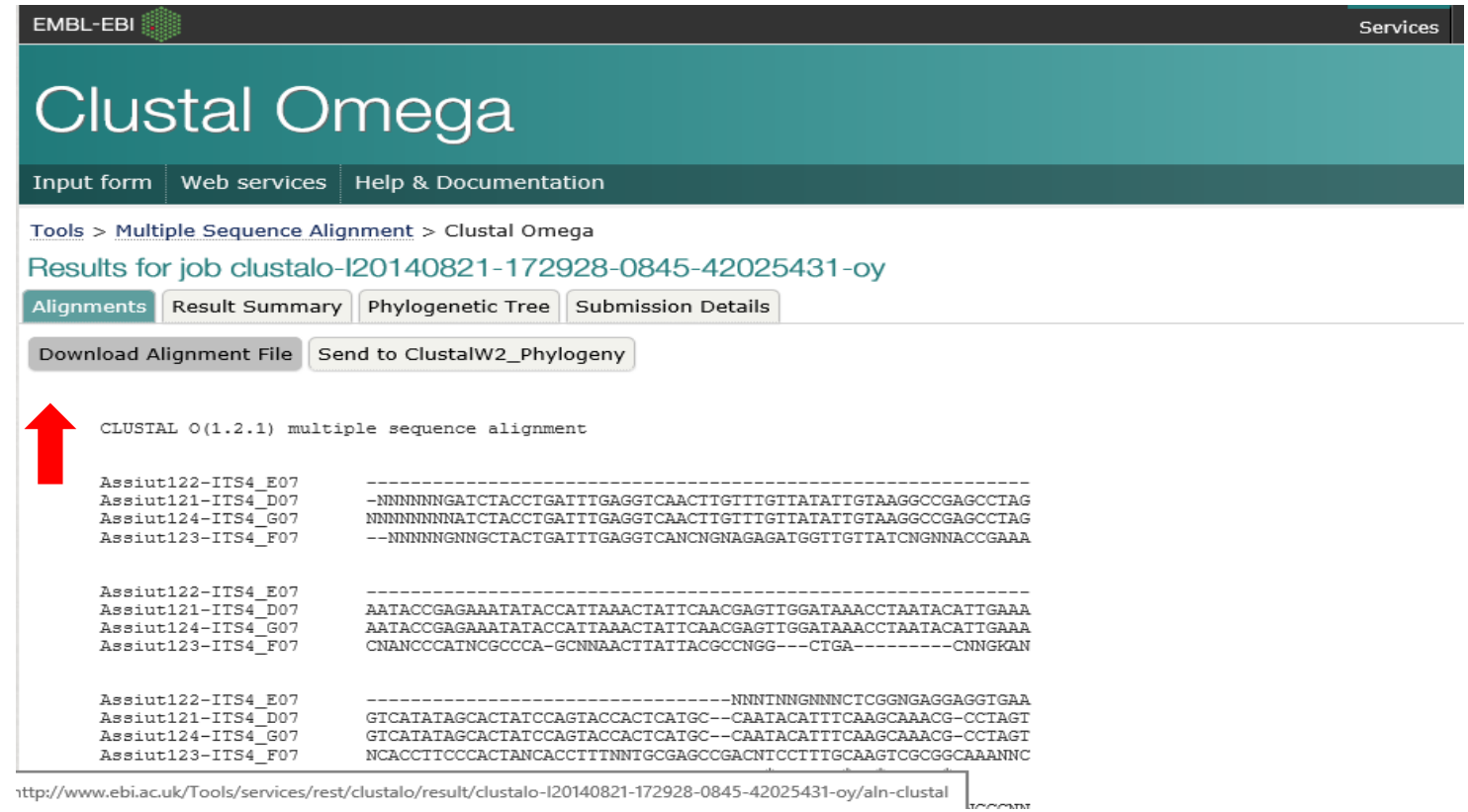

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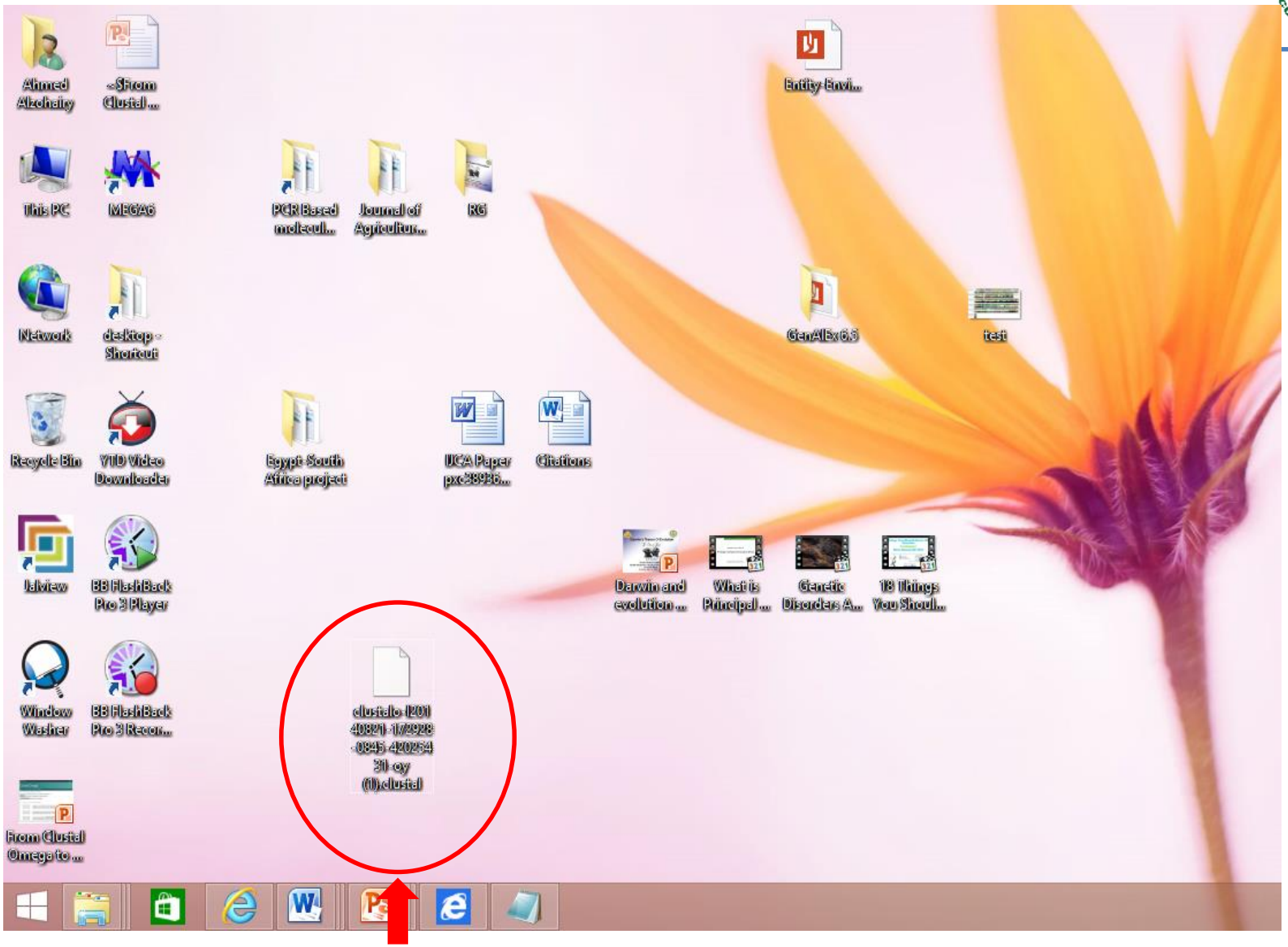
Ahmed Alzohairy
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MEGA6
PCR Based molecul...
Journal of Agricultur...
RG
Network
desktop - Shortcut
GenAlEx 6.5
test
Recycle Bin
YTD Video Downloader
Egypt-South Africa project
IJCA Paper pxc38936...
Citations
Jalview
BB FlashBack Pro 3 Player
Darwin and evolution ...
What is Principal ...
Genetic Disorders A...
18 Things You Shoul...
Window Washer
BB FlashBack Pro 3 Recor...
clustalo-I201 40821-172928 -0845-420254 31-oy (1).clustal
From Clustal Omega to ...

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Open Jalview and load your sequence file

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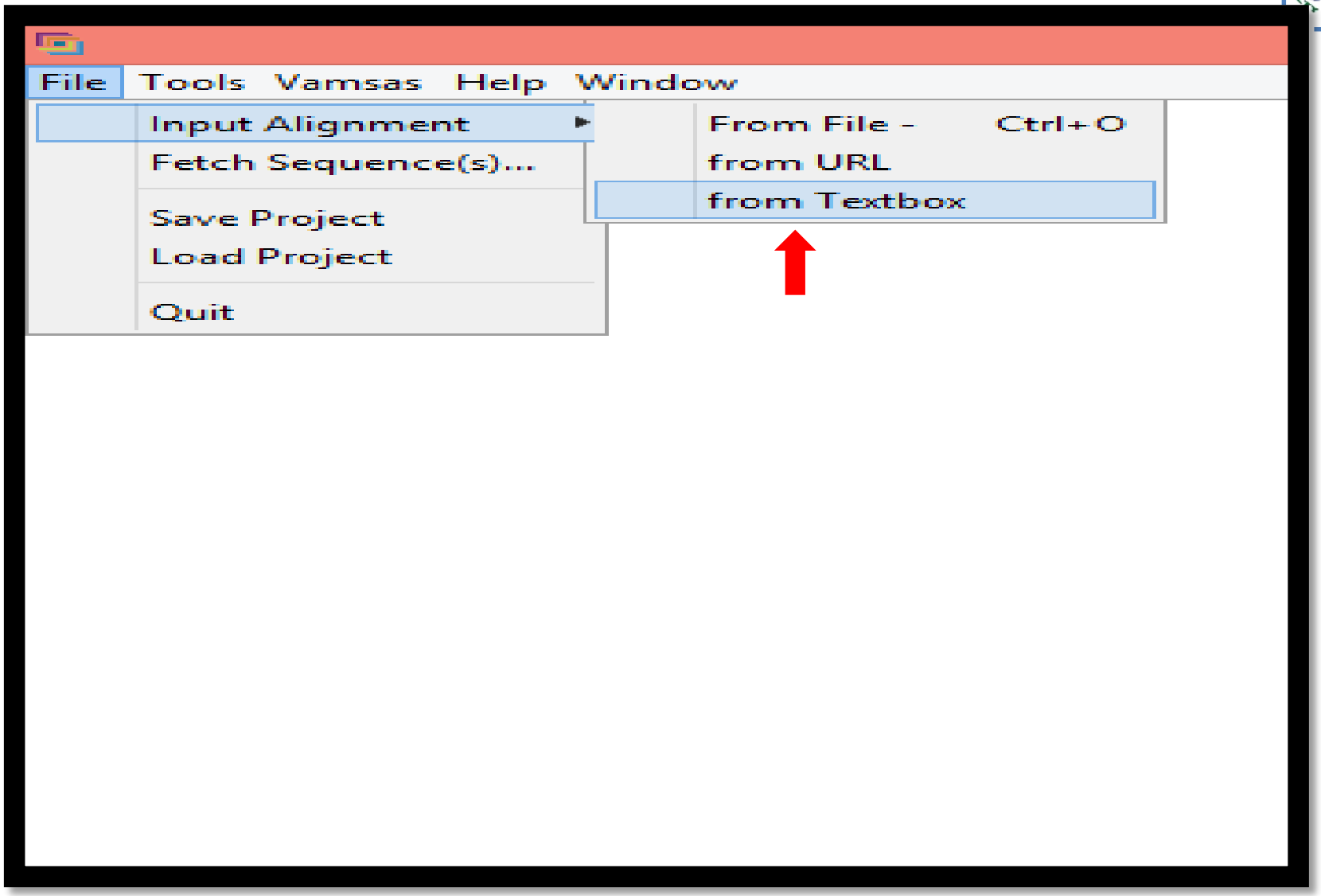
File
Tools
Vamsas
Help
Window
Input Alignment
Fetch Sequence(s)...
Save Project
Load Project
Quit
From File - Ctrl+O
from URL
from Textbox

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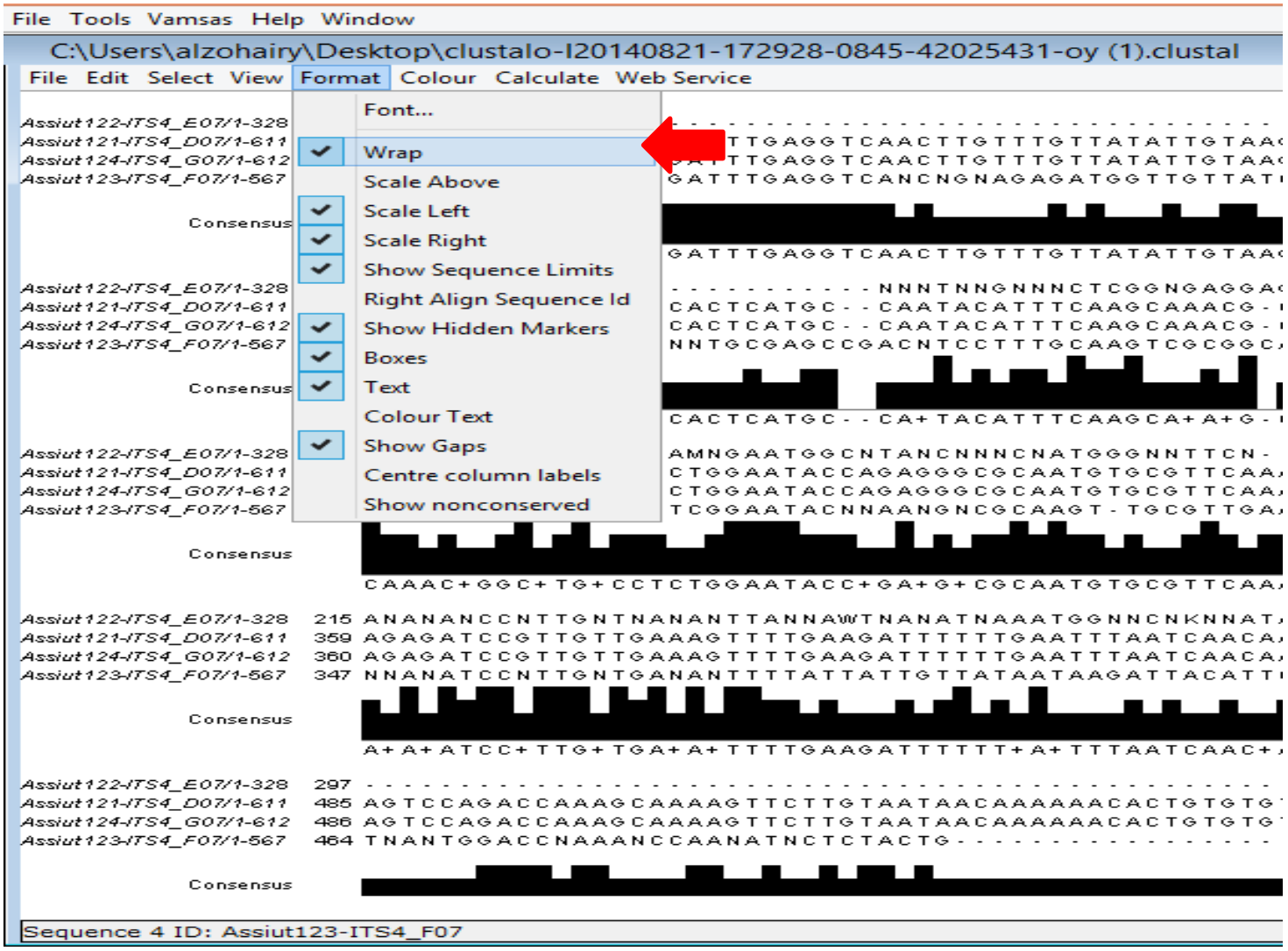
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File Edit Select View Format Colour Calculate Web Service
Font...
Wrap
Scale Above
Scale Left
Scale Right
Show Sequence Limits
Right Align Sequence Id
Show Hidden Markers
Boxes
Text
Colour Text
Show Gaps
Centre column labels
Show nonconserved
Assiut122-ITS4_E07/1-328
Assiut121-ITS4_D07/1-611
Assiut124-ITS4_G07/1-612
Assiut123-ITS4_F07/1-567
Consensus
Sequence 4 ID: Assiut123-ITS4_F07

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Choose the best colour to represent your sequence

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File Tools Vamsas Help Window
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File Edit Select View Format Colour Calculate Web Service
Apply Colour To All Groups
Colour Text...
None
Clustalx
BLOSUM62 Score
Percentage Identity
Zappo
Taylor
Hydrophobicity
Helix Propensity
Strand Propensity
Turn Propensity
Buried Index
Nucleotide
Purine/Pyrimidine
T-Coffee Scores
User Defined...
By Conservation
Modify Conservation Threshold...
Above Identity Threshold
Modify Identity Threshold...
by Annotation...
by RNA Helices
Assiut122-ITS4_E07/1-328
Assiut121-ITS4_D07/1-611
Assiut124-ITS4_G07/1-612
Assiut123-ITS4_F07/1-567
Consensus

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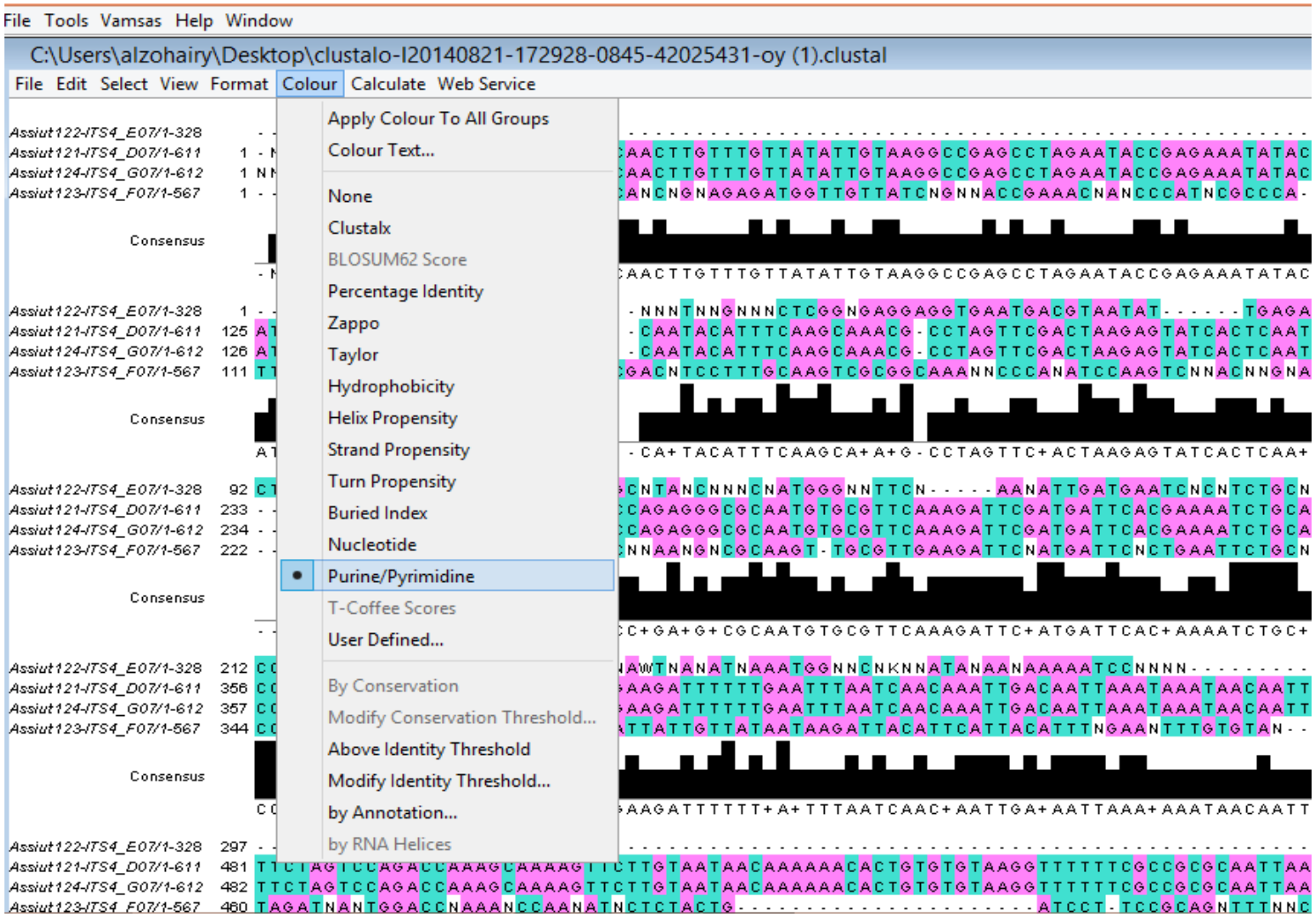
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Apply Colour To All Groups
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Clustalx
BLOSUM62 Score
Percentage Identity
Zappo
Taylor
Hydrophobicity
Helix Propensity
Strand Propensity
Turn Propensity
Buried Index
Nucleotide
Purine/Pyrimidine
T-Coffee Scores
User Defined...
By Conservation
Modify Conservation Threshold...
Above Identity Threshold
Modify Identity Threshold...
by Annotation...
by RNA Helices
Assiut122-ITS4_E07/1-328
Assiut121-ITS4_D07/1-611
Assiut124-ITS4_G07/1-612
Assiut123-ITS4_F07/1-567
Consensus

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Jalview 2.8.1
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File Edit Select View Format Colour Calculate Web Service
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Assiut121-ITS4_D07/1-611
Assiut124-ITS4_G07/1-612
Assiut123-ITS4_F07/1-567
Consensus
Sequence 4 ID: Assiut123-ITS4_F07 Nucleotide: Guanine (176)

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Export your Alignment to an Image for publication

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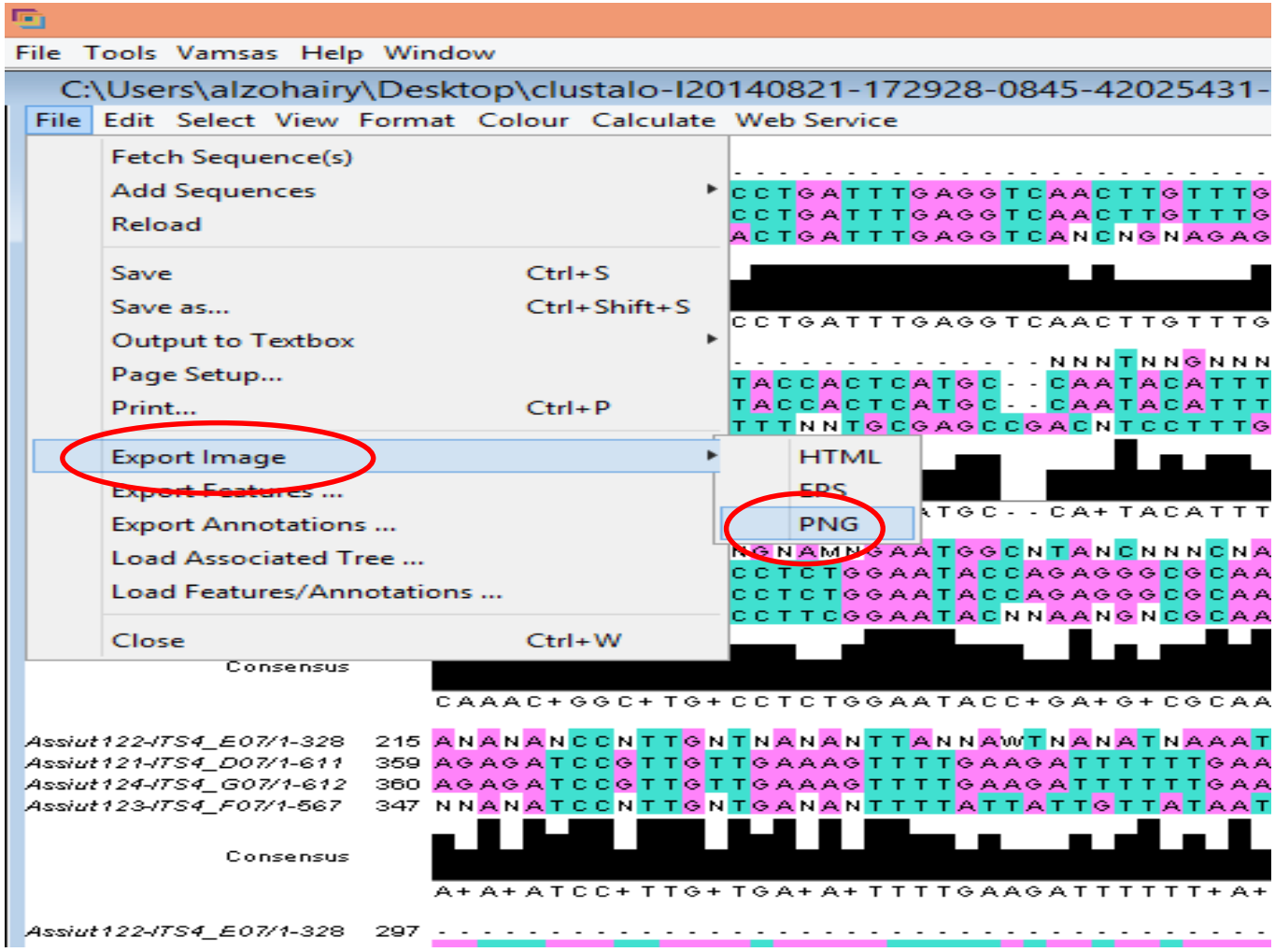
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File Edit Select View Format Colour Calculate Web Service
Fetch Sequence(s)
Add Sequences
Reload
Save Ctrl+S
Save as... Ctrl+Shift+S
Output to Textbox
Page Setup...
Print... Ctrl+P
Export Image
Export Features ...
Export Annotations ...
Load Associated Tree ...
Load Features/Annotations ...
Close Ctrl+W
HTML
EPS
PNG
Consensus
Assiut122-ITS4_E07/1-328 215
Assiut121-ITS4_D07/1-611 359
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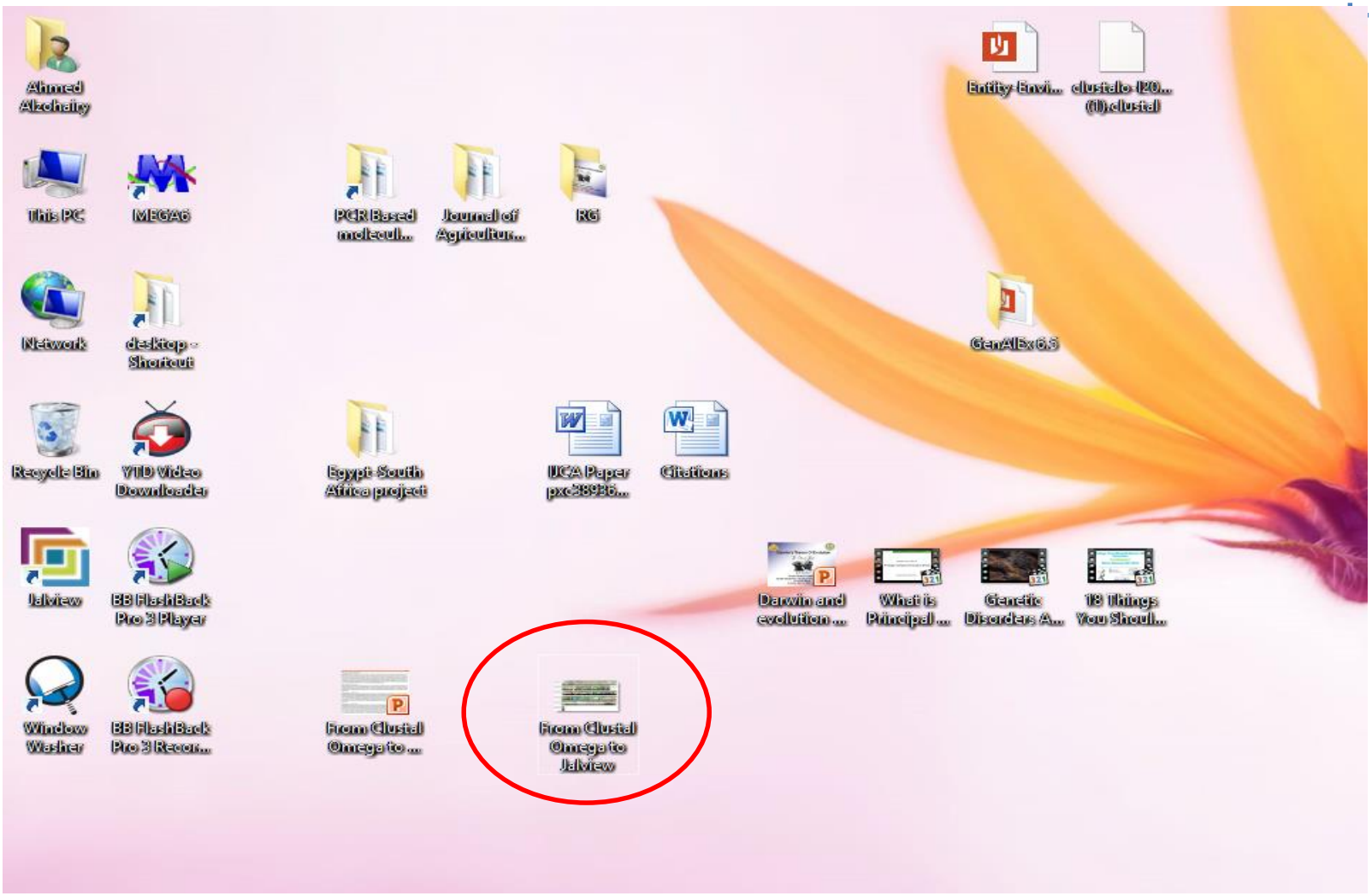
Ahmed Alzohairy
Entity-Envi...
clustalo-I20... (1).clustal
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PCR Based molecul...
Journal of Agricultur...
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desktop - Shortcut
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Recycle Bin
YTD Video Downloader
Egypt-South Africa project
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From Clustal Omega to ...
From Clustal Omega to Jalview

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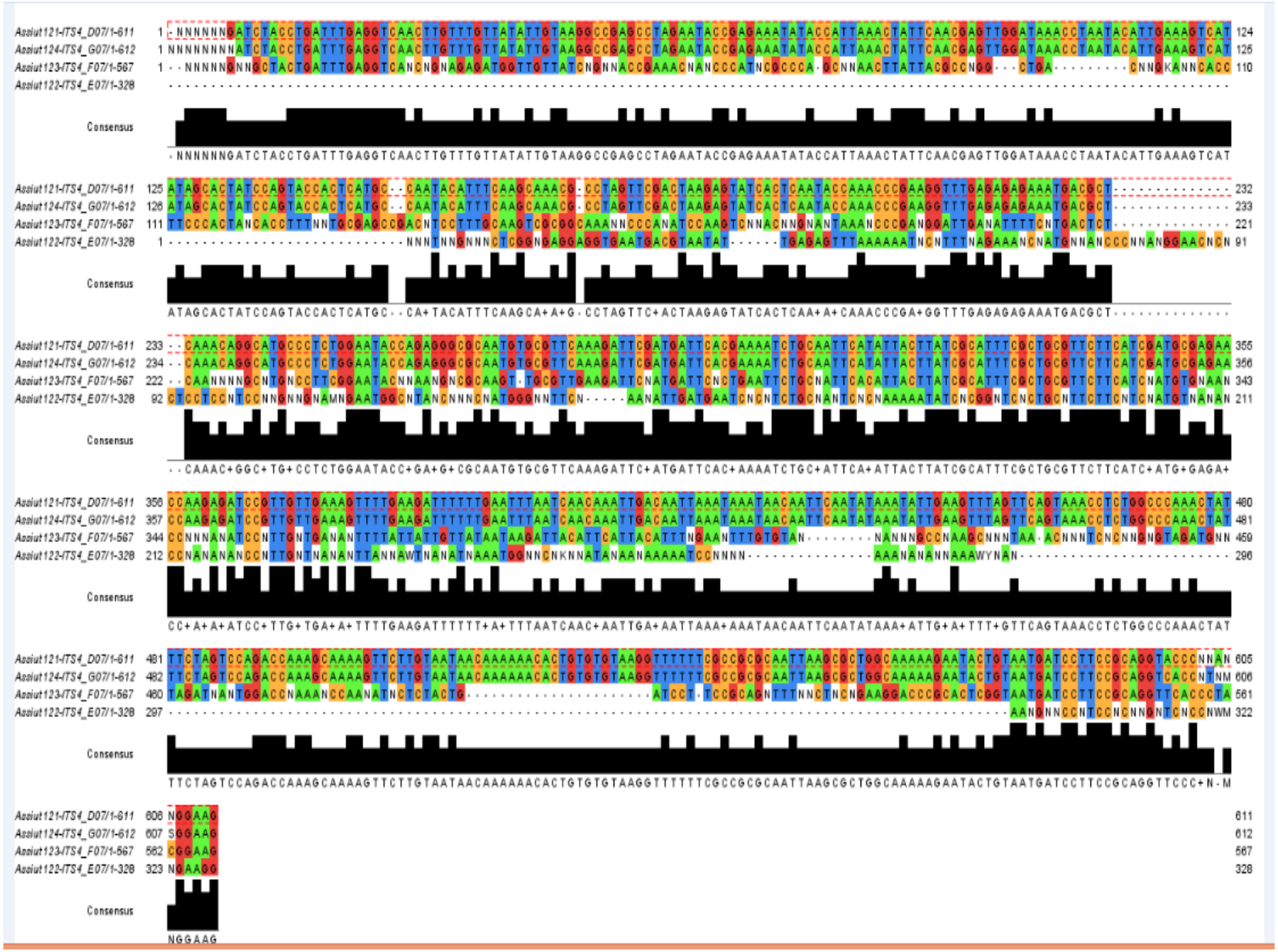
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Consensus

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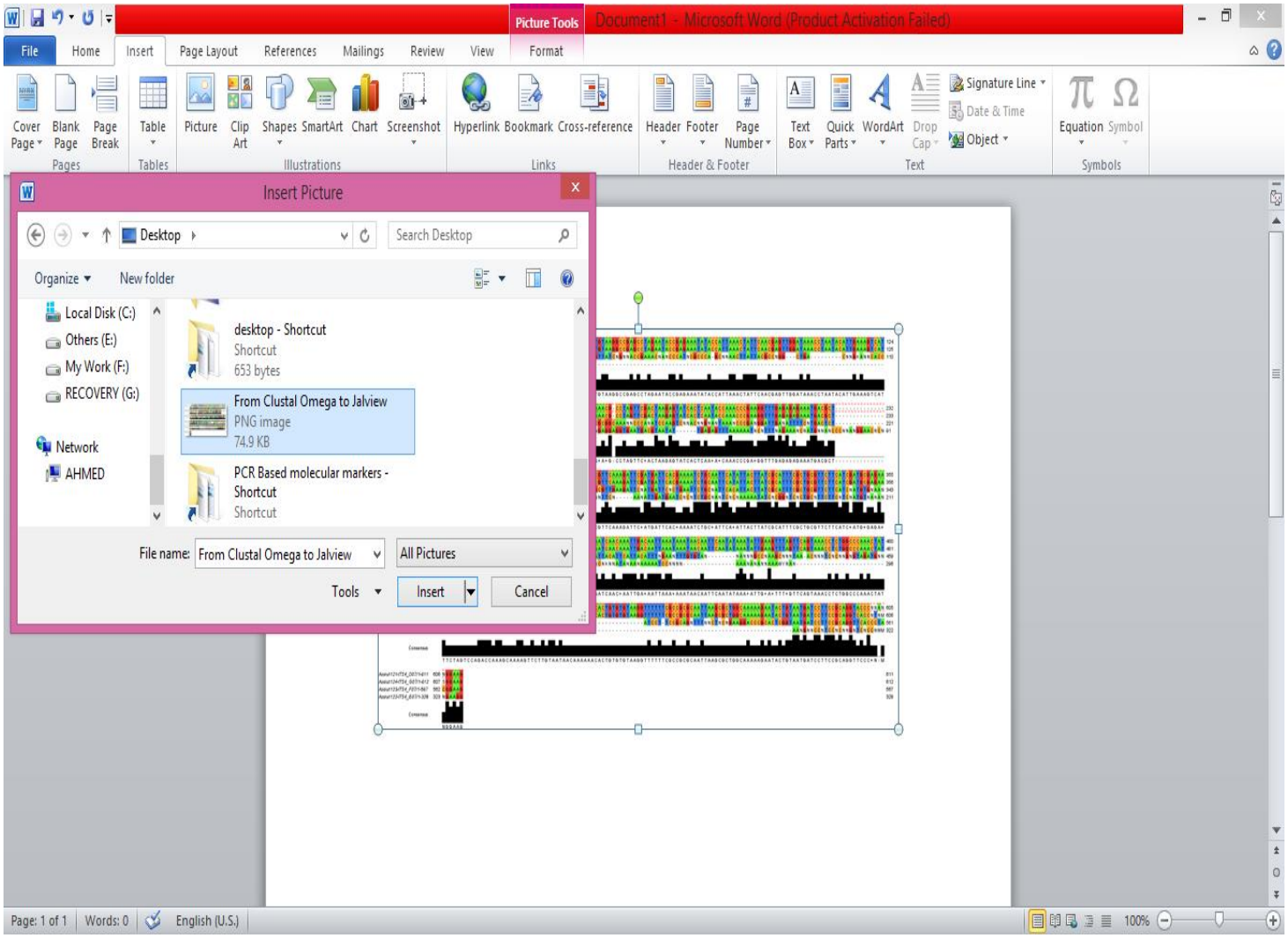
Picture Tools
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Page Layout
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Review
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Format
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Desktop
Search Desktop
Organize
New folder
Local Disk (C:)
Others (E:)
My Work (F:)
RECOVERY (G:)
Network
AHMED
desktop - Shortcut
Shortcut
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From Clustal Omega to Jalview
PNG image
74.9 KB
PCR Based molecular markers - Shortcut
Shortcut
File name: From Clustal Omega to Jalview
All Pictures
Tools
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Page: 1 of 1
Words: 0
English (U.S.)
100%

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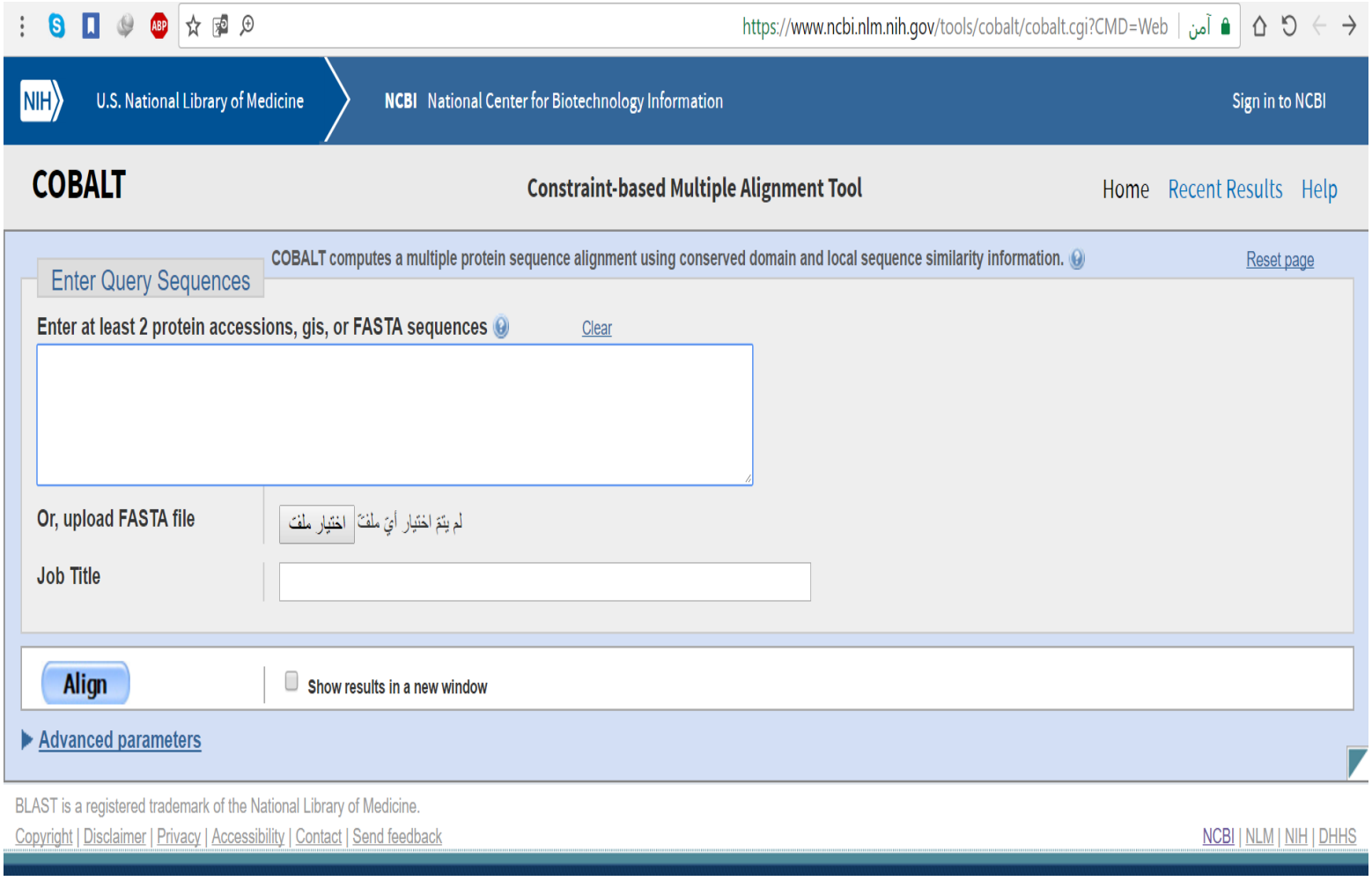
The same thing can be done by other sequences aligners



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GENOMICS
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 Phylogenetics analysis using Jalview
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
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11th Module Working with Protein 3-D Structures
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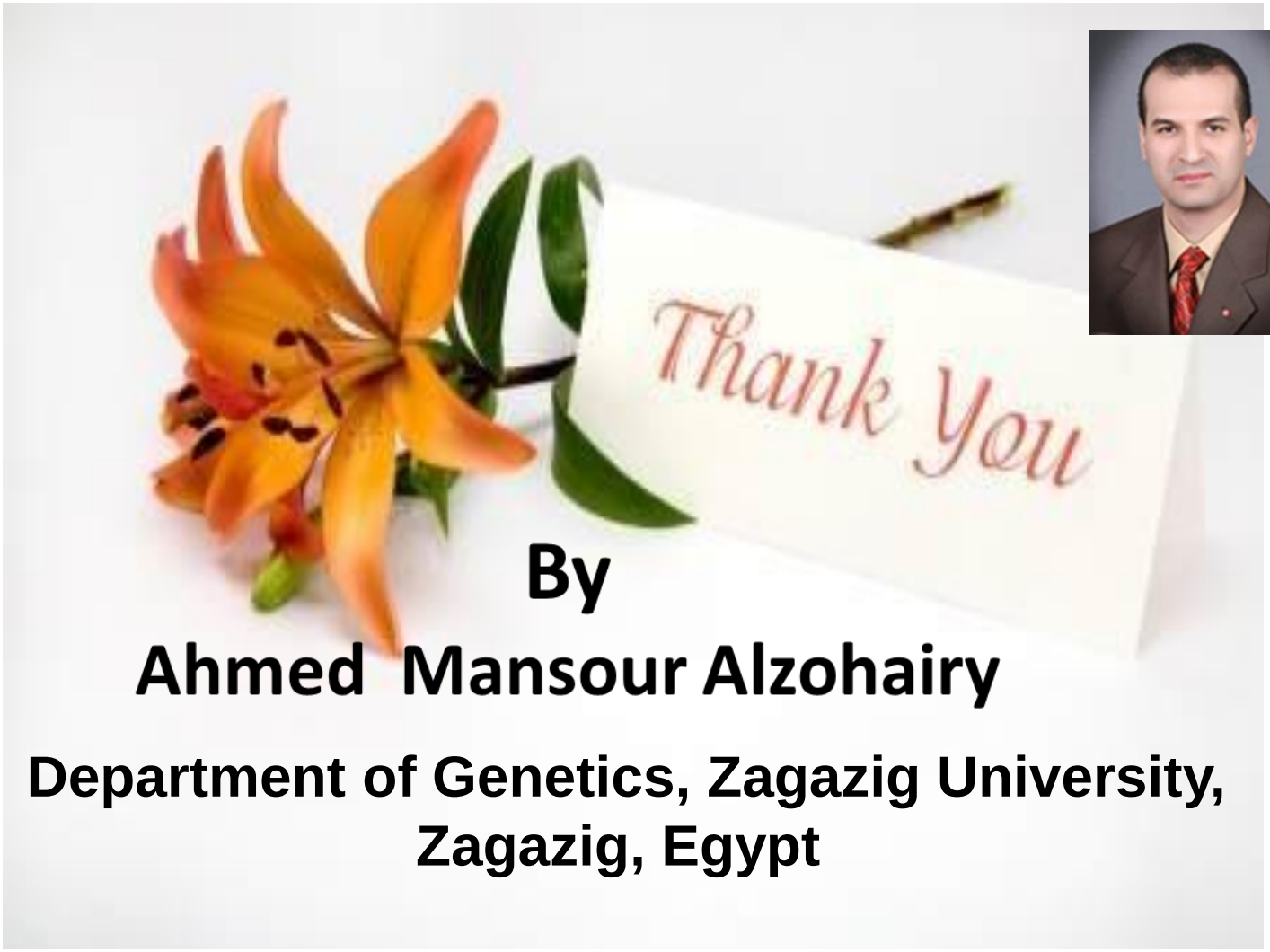

By

Ahmed Mansour Alzohairy

Department of Genetics, Zagazig University, Zagazig, Egypt