





Introduction to Bioinformatics Online Course: IBT

Multiple Sequence Alignment Building Multiple Sequence Alignment









COBALT

Constraint-based Multiple Alignment Tool

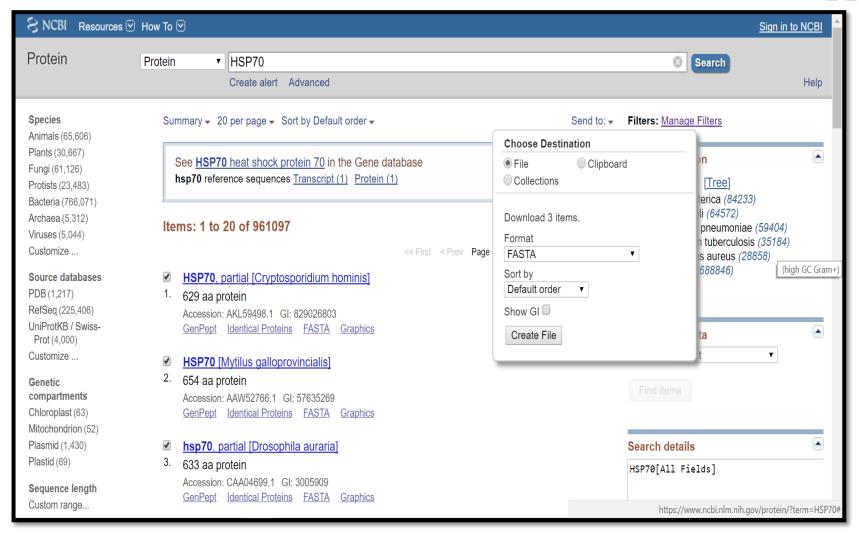
COBALT computes a multiple **protein** sequence alignment using **conserved domain** and **local sequence similarity** information.









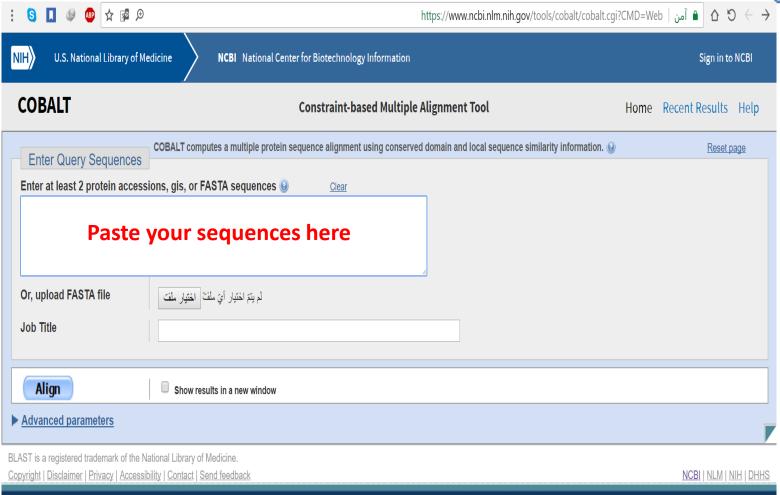










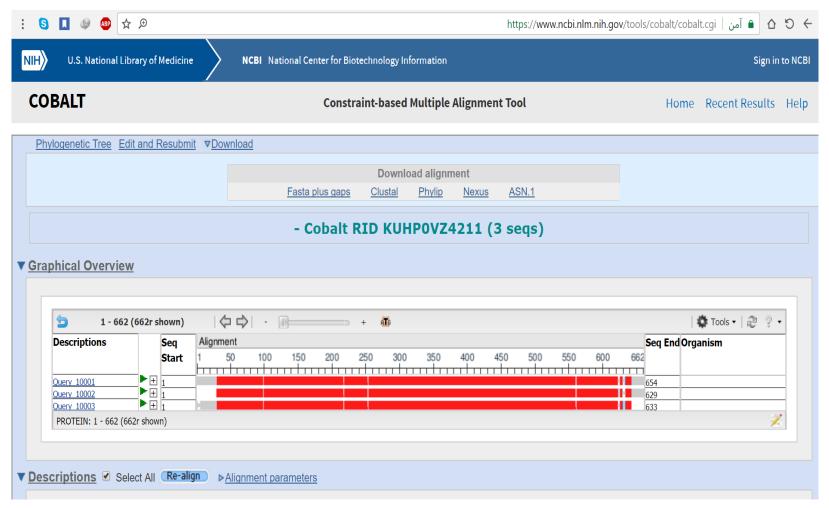










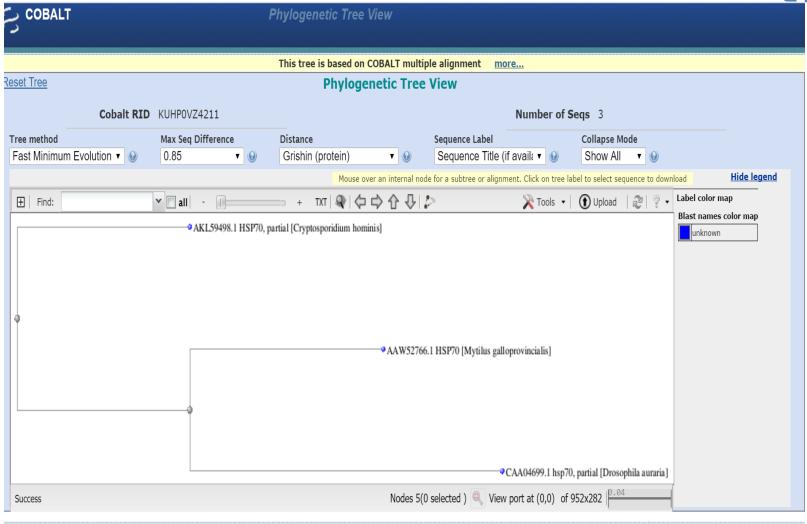










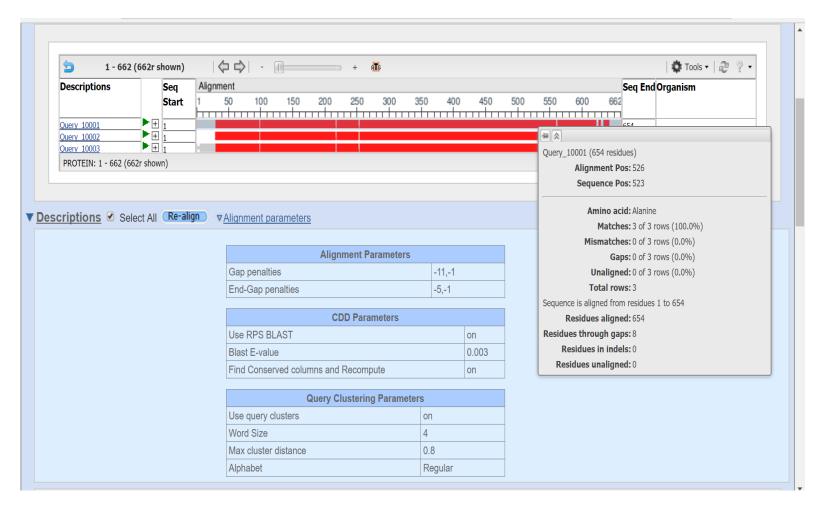










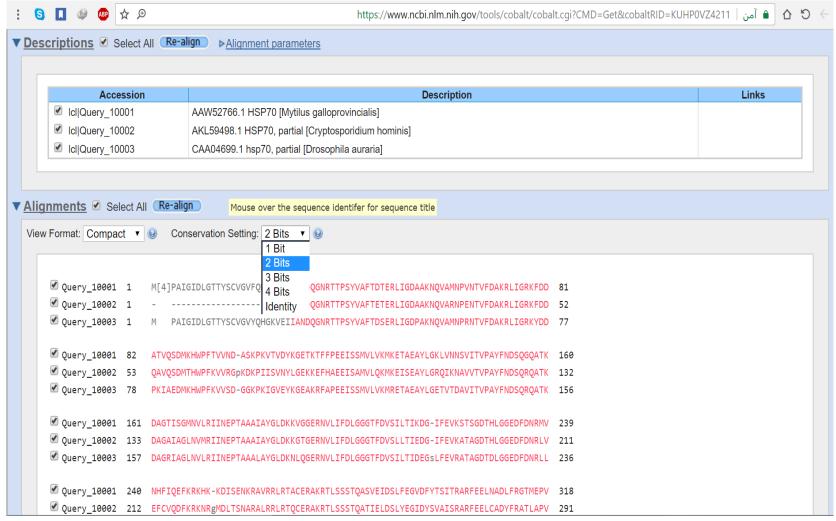




















Clustal Omega



Tools > Multiple Sequence Alignment > Clustal Omega









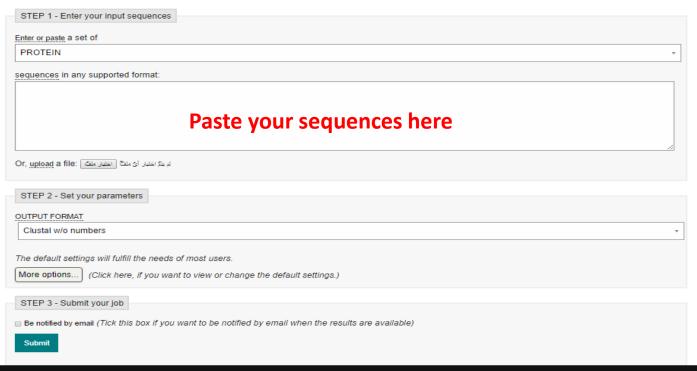


Tools > Multiple Sequence Alignment > Clustal Omega

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 between three or more sequences. For the alignment of two sequences please instead use our pairwise sequence alignment tools.

Important note: This tool can align up to 4000 sequences or a maximum file size of 4 MB.



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Clustal Omega

Input form

Web services

Help & Documentation

Tools > Multiple Sequence Alignment > Clustal Omega

Results for job clustalo-I20170611-151713-0223-46173747-pg

Alignments Result Summary Phylogenetic Tree Submission Details

Download Alignment File | Hide Colors | Send to Simple Phylogeny

CLUSTAL O(1.2.4) multiple sequence alignment

BAB20284.1 MGSSHHHHHHHSSGLVPRGSHMLEMADSPAVGIDLGTTYSCVGVWKNDAVEIIANDQGNRT AAP40020.1 -----MGPAVGIDLGTTYSCVGIFREDRCDIIANDQGNRT AGY78334.1 -----MAKAPAIGIDLGTTYSCVGVFRHGQVEIIANDQGQRT AAW52766.1 -----MAKTGPAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRT AAX07834.1 -----MAPAKGVAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRT BAB20284.1 TPSYVAFTDTERLVGDAAKNQVARNPENTIFDAKRLIGRKFDDPSVQSDMKHWPFKVIAG AAP40020.1 TPSFVAFTDTERLIGDAAKNQVAMNPONTVFDAKRLIGRKFADPEVQADMKHFPFKVID-AGY78334.1 TPSYVAFTDTERLVGDAAKNQAAMNPENTVFDAKRLIGRRFDDSSVQADMKHWPFKVVN-AAW52766.1 TPSYVAFTDTERLIGDAAKNQVAMNPVNTVFDAKRLIGRKFDDATVQSDMKHWPFTVVN-AAX07834.1 TPSYVAFTDTERLIGDAAKNHLALNPSNTVFDAKRLIGRKMDDOVVOADMKHWPFKVVG-***.*******.*****.* ** **.*******.. * **.***..*.*. BAB20284.1 PGDKPLIEVTYQGEKKTFHPEEVSAMVLGKMKEIAEAYLGKEVKEAVITVLAYFNDSQRQ AAP40020.1 KNSKPVIEVEFKGEKKTFTPEEISSMVLTKMREAAEAYLGTTVNNAVITVPAYFNDSQRQ AGY78334.1 DGGKPKIQVQYKGETKTFAPEEISSMVLVKMKETAEAYLGQRVKDAVITVPAYFNDSQRQ AAW52766.1 DASKPKVTVDYKGETKTFFPEEISSMVLVKMKETAEAYLGKLVNNSVITVPAYFNDSQGQ AAX07834.1 DGGKPKIQVEYKGEDKTFYPEEISSMVLVKMKEIAEAYLGQQVSNAVITVPAYFNDSQRQ ** . * ..** *** ***.*. * ***** * ..**** * ***

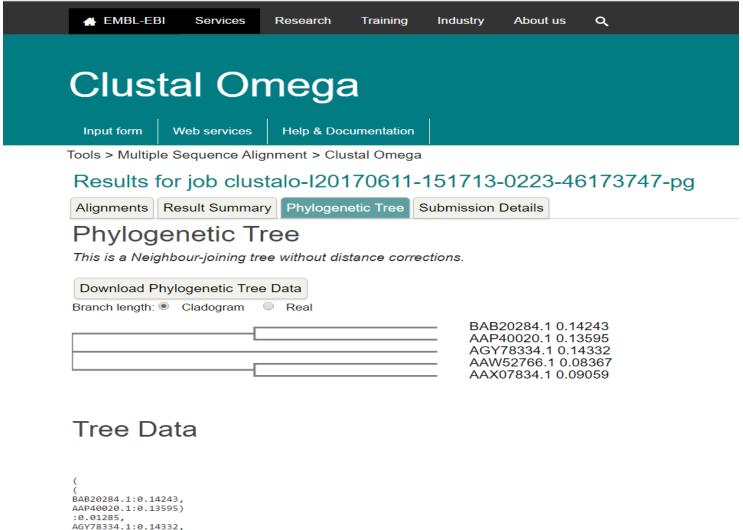
We want to improve your experience of this tool. Please fill in a short survey on SurveyMonkey to tell us about your experience of this tool. It will take you 2 minutes. Take this survey >





















Lec3: *Tcoffee and MUCLE in more details*

Aligning sequences and structures with Tcoffee

More accurate alignments at the cost of a slightly longer running time

Claverie J, Notredame C (2007). Bioinformatics for Dummies (2nd Edn). Wiley publishing, Inc. 436 pp.



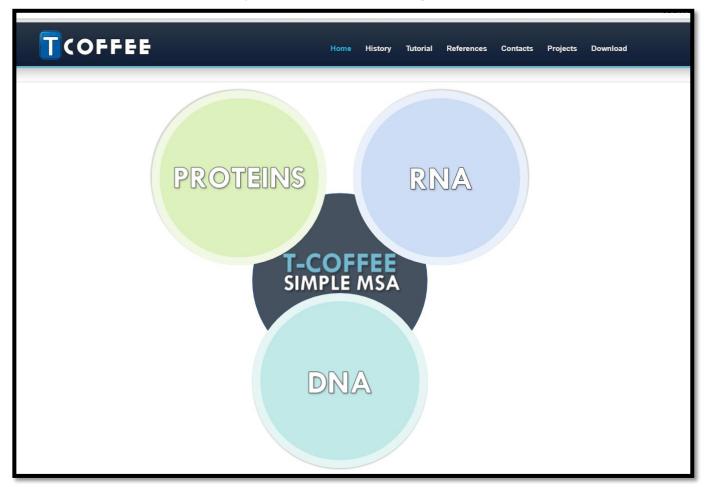








http://tcoffee.crg.cat/



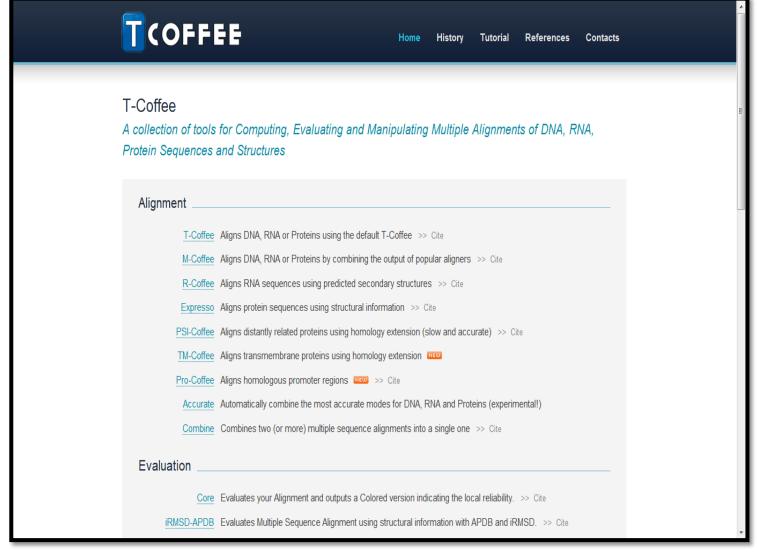






















TCOFFEE	Но	ome History	Tutorial	References	Contacts	
T-Coffee Aligns DNA, RNA or Prote	ins using the default T-Coffee					
Sequences input Paste or upload your set of sequences to align Click here to use the sample file	Past your sec	quenc	es he	ere	^	
Show more options						
Your email address						
	Submit Reset					
T-Coffee Server is hosted by the Centre	e for Genomic Regulation (CRG) of Barcelona				Back to top	











COFFEE		Home	History	Tutorial	References	Contacts	
M-Coffee Aligns DNA, RNA or Prote	ins by combining the outpu	ıt of popular	r aligners				
Sequences input Paste or upload your set of sequences to align Click here to use the sample file	Paste you	r seqı	uenc	es h	ere	^	
Show more options							
Your email address							
T-Coffee Server is hosted by the Centre	Submit Reset Performed Genomic Regulation (CRG) of Barcelet	ona				Back to top	











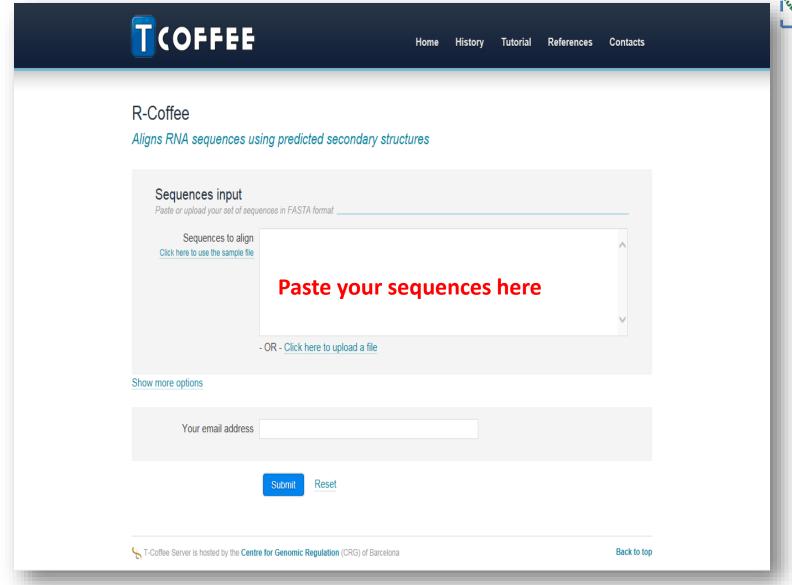
RNA Alignment























SARA-Coffee

Aligns RNA sequences using tertiary structure (new)

Sequences input Paste or upload your set of sequences	ences in FASTA format	
Sequences to align Click here to use the sample file	Paste your sequences here	^ V
Show more options	- OR - Click here to upload a file	
Snow more opnoris		
Your email address		
	Submit Reset	
T-Coffee Server is hosted by the Centr	e for Genomic Regulation (CRG) of Barcelona	Back to top











Protein Alignment











COFFEE	Home History Tutorial	References Contacts
Expresso Aligns protein sequences to	sing structural information	
Sequences input Paste or upload your set of seque Sequences to align Click here to use the sample file	Paste your sequences he	ere
Show more options Your email address	One of the control of	
	Submit Reset	
T-Coffee Server is hosted by the Centre	for Genomic Regulation (CRG) of Barcelona	Back to top











COFFEE		Home	History	Tutorial	References	Contacts	
PSI-Coffee Aligns distantly related prote	eins using homology extensio	n (slow	and accu	ırate)			
Sequences input Paste or upload your set of sequence Sequences to align Click here to use the sample file	Paste your s	sequ	uenc	es he	ere	^	
Show more options Your email address							
	Submit Reset						
T-Coffee Server is hosted by the Centre for	or Genomic Regulation (CRG) of Barcelona					Back to top	

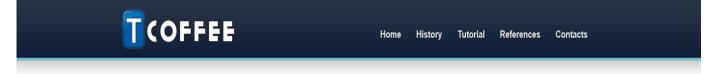












TM-Coffee

Aligns transmembrane proteins using homology extension (new)

Sequences input Paste or upload your set of sequ Sequences to align Click here to use the sample file	Paste your sequences here	^
	- OR - Click here to upload a file	
Show more options		
Your email address		
	Submit Reset	
T-Coffee Server is hosted by the Centr	re for Genomic Regulation (CRG) of Barcelona	Back to top













History

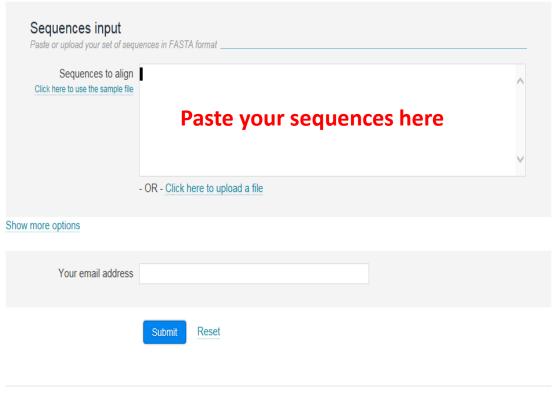
Tutorial

References

Contacts

Pro-Coffee

Aligns homologous promoter regions (new)



















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Histor

Tutoria

References

Contact

Accurate

Automatically combine the most accurate modes for DNA, RNA and Proteins (experimental!)

Sequences to align Click here to use the sample file		^
	Paste your sequences here	<u> </u>
	- OR - Click here to upload a file	
how more options		
Your email address		
	Submit Reset	

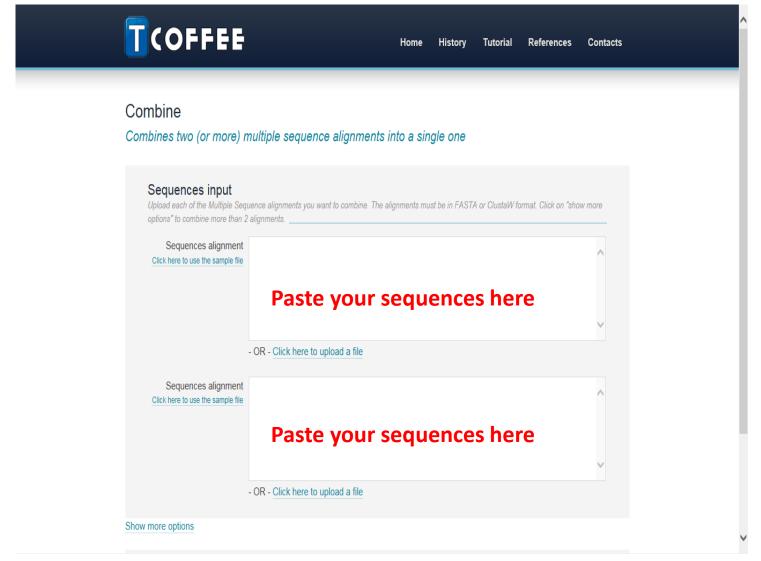






















Evaluation











- Give TCOFFEE a multiple alignment that you generated with your favorite method, and you can ask Tcoffee to evaluate the quality of this multiple sequence alignment for you.
- You can use any of the most common formats (MSF, ALN, FASTA, and PIR).













Core

Evaluates your Alignment and outputs a Colored version indicating the local reliability.

	equence Alignment in CLUSTAL format.	
Alignment Click here to use the sample file	Paste your sequences here	
	- OR - Click here to upload a file	
Show more options		
Your email address		
	Submit Reset	
T-Coffee Server is hosted by the Centr	e for Genomic Regulation (CRG) of Barcelona	Back to top













iRMSD-APDB

Evaluates Multiple Sequence Alignment using structural information with APDB and iRMSD.

Alignment Click here to use the sample file		^
	Paste your sequences here	~
	- OR - Click here to upload a file	
ow more options		
Your email address		
	Submit Reset	













T-RMSD

Allows fine-grained structural clustering of a given group of related protein domains (new)

Sequences to align Click here to use the sample file		^
	Paste your sequences here	V
	- OR - Click here to upload a file	
w more options		
Your email address		
	Submit Reset	
-Coffee Server is hosted by the Centr	e for Genomic Regulation (CRG) of Barcelona	Back to top













Strike

Evaluation of protein MSAs using a single 3D structure

Sequences input Paste or upload your set of sequences to align Click here to use the sample file	Paste your sequences here	^
	- OR - <u>Click here to upload a file</u>	V
Show more options		
Your email address		
	Submit Reset	
T-Coffee Server is hosted by the Centr	re for Genomic Regulation (CRG) of Barcelona	Back to top











Advanced







T-Coffee advanced



Run your alignment using full featured T-Coffee options.

Upload your data Use the button below to uplod one or more files Click here to upload a file	
2. Enter the program options Specify in the below field the T-Coffee options as you would do using the command line	
You can enter any valid T-coffee command line options, for example -in your_input_file.fasta -mode expresso -output scorfasta_aln. You can find an introduction to command line options and syntax at the following T-Coffee tutorial. Also it may be useful T-Coffee Cheat Sheat and T-Coffee reference manual.	_
3. Email address Specify your email address if your want to be notified on alignment completion (optional)	
Submit Reset	











TCOFFEE results











T(OFFEE

Home History Tutorial References Contacts

T-Coffee alignment result













Useful links

Google Group Support and discussion group

tcoffee.org Find out more about T-Coffee project and documentation

Cedric Notredame Home page, Courses and Blog

Download Sources and binaries are available for download at this link

Twitter Check it out for latest T-Coffee developments and new tips

Facebook T-Coffee has a page on Facebook

ResearchGate Follow the discussion on on ResearchGate











Mirror sites



Vital-IT, Swiss Institute of Bioinformatics (SIB)



EBI, European Bioinformatics Institute



IGS lab., CNRS



Max-Planck Institute for Developmental Biology



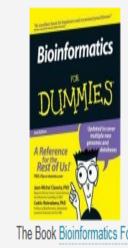
Cornell



EMBNet-Spain



Pasteur Institute



The Book Bioinformatics For Dummies contains a T-Coffee tutorial and many other online resources.







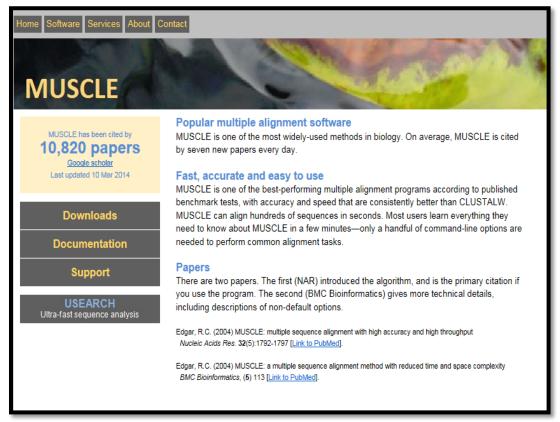








Crunching large datasets with MUSCLE



Claverie J, Notredame C (2007). Bioinformatics for Dummies (2nd Edn). Wiley publishing, Inc. 436 pp.











MUSCLE is a newcomer in the multiplesequence-alignment arena — but it is a remarkably efficient package for making fast, high-quality multiple sequence alignments. MUSCLE is ideal if you want to align several hundred sequences.



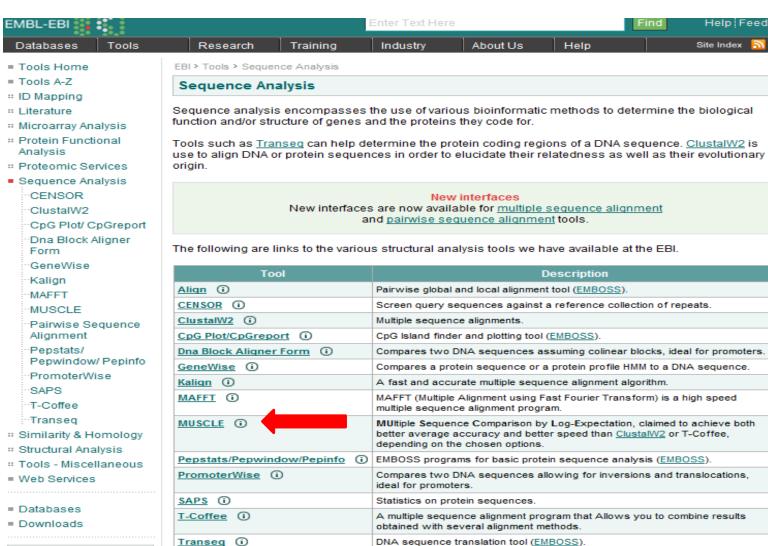








Site Index







webPRANK is a phylogeny-aware multiple sequence alignment program which makes use of evolutionary information to help place insertions and deletions

ClustalW2 is a general purpose multiple sequence

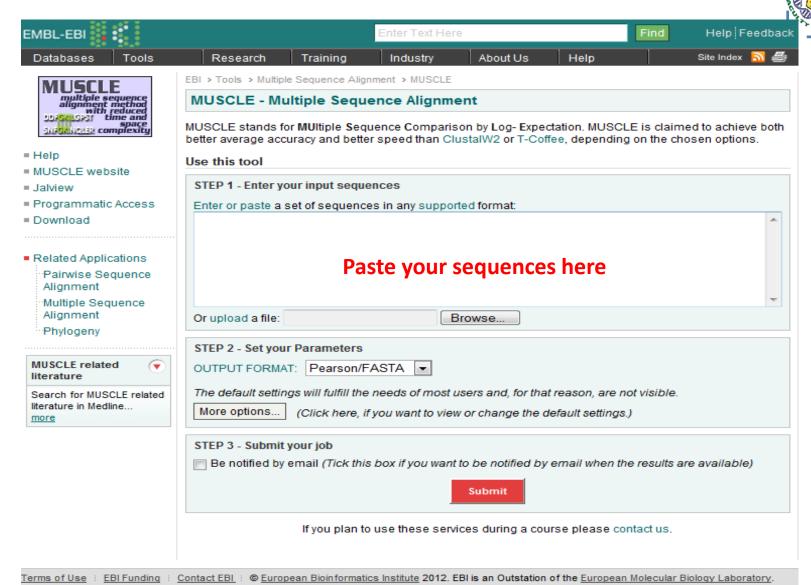
ClustalW2

-

webPRANK



















Your job is currently running... please be patient

The result of your job will appear in this browser window

Your Job output: toolresult.ebi?tool=muscle&jobld=muscle-I20120208-185741-0432-16229494-ov

Please note the following

- You may press Shift+Refresh or Reload on your browser at any time to check if results are ready.
 Should this window go blank please press the Shift+Refresh or Reload button on your browser.
- You may bookmark this page to view your results later if you wish.
- Results are stored for 7 days.

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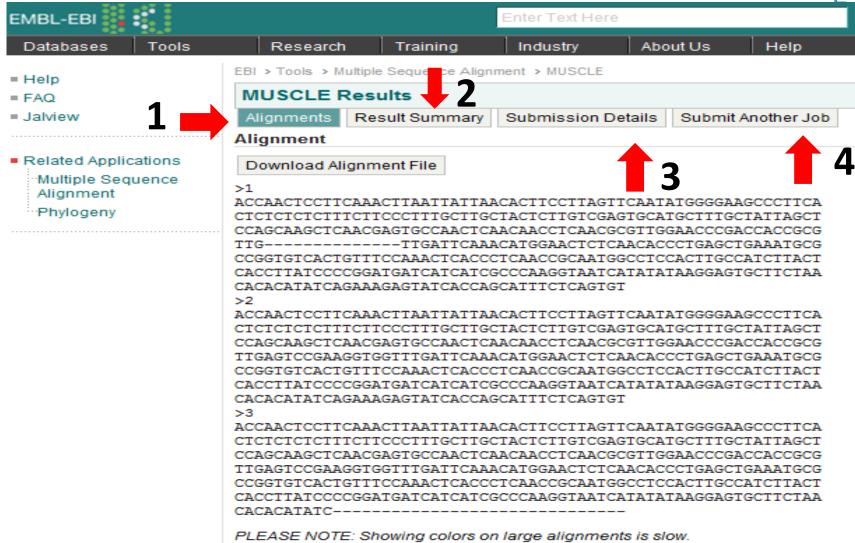






















Practical

'to try in your own time

- 1- For your set of HSF1 FASTA sequences, what are the right TCOFFEE flavor to align them?
- 2- For your set of HSF1 aligned sequences, use the right *TCOFFEE* flavor to evaluate your alignment?
- 3- Calculate the timing for Aligning your sequence collection using MUSCUL, TCOFFEE and Clustal Omega and order them based on their speed?













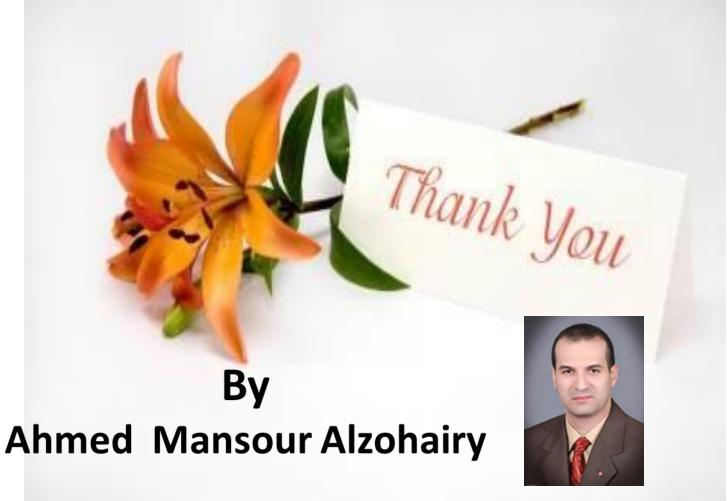












Department of Genetics, Zagazig University, Zagazig, Egypt



