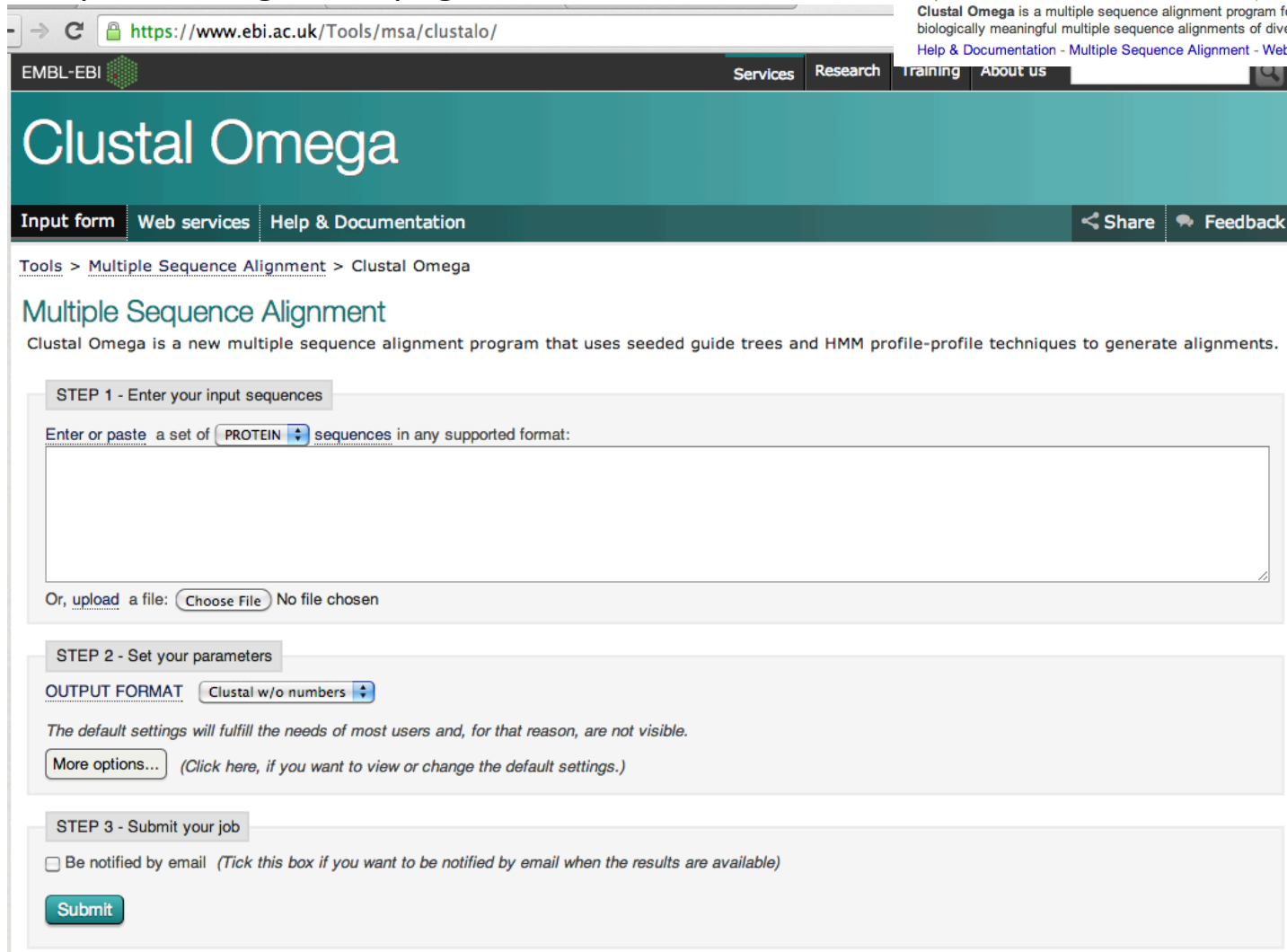
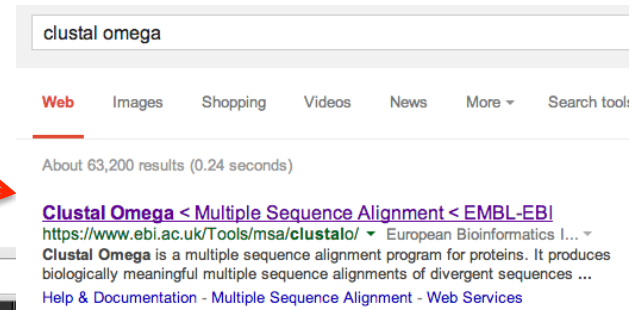


Clustal Omega: Align two or more DNA or Protein Sequences

Step 1. Internet search “clustal omega” →

Step 2. Click this link. →

Step 3. You’ll get this page:



Step 4. Find some sequence data to align.

Here is a text file with 3 DNAs in FASTA format.

(Go to http://en.wikipedia.org/wiki/FASTA_format for more info on fasta files.)

```
>NucSeq1
ATGAACGACGAAACACAATTTACAAATAAGGCCAACGAAATTATCCGTTTGGCCCAGAAATTGGCTCAGG
ATCACAGACATGCTCAGTTACAACCAATTCACCTACTTGCTGCATTTGTTGAGCCAAACGAGGATGGTTC
>NucSeq2
ATGGCTGATTATCCTTTTACTGACAAAGCCGCAAAGACATTGTCTGATGCGTACTCAATTGCACAATCTT
ATGGTCATTACAATTAACCCCTATTACATTGCTGCTGCTCTTTTGTCCGACAGTGACAGTAACGGTAC
>NucSeq3
ATGAACGACGAAACGAAGTTTACGAACAAAGCTCTCGATATCATCACCATTGCACAGAACTAGCACAGG
ACCACCAGCATTTCGACGCTGGTGCCTCTACACGTGCTTGCAGCGTTCGTAGAGACACCTGCTGATGGTAG
```

Step 5. Copy and Paste the data into the input window.

(You can also upload a text file with the data.)

Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and HI

STEP 1 - Enter your input sequences

Enter or paste a set of sequences in any supported format:

```
>NucSeq1
ATGAACGACGAAACACAATTTACAAATAAGGCCAACGAAATTATCCGTTTGGCCCAGAAATTGGCTCAGG
ATCACAGACATGCTCAGTTACAACCAATTCACCTACTTGCTGCATTTGTTGAGCCAAACGAGGATGGTTC
>NucSeq2
ATGGCTGATTATCCTTTTACTGACAAAGCCGCAAAGACATTGTCTGATGCGTACTCAATTGCACAATCTT
ATGGTCATTACAATTAACCCCTATTACATTGCTGCTGCTCTTTTGTCCGACAGTGACAGTAACGGTAC
>NucSeq3
```

Or, upload a file: No file chosen

Step 6. Because these are DNA sequences, select “DNA” in the pop-down menu.

Multiple Sequence Alignment

Clustal Omega is a new multiple sequence alignment program that uses seeded guide trees and H

STEP 1 - Enter your input sequences

Enter or paste a set of PROTEIN sequences in any supported format:

DNA
 RNA

```
>NucSeq1
ATGAACGACGAAACAAATAAGGCCAACGAAATTATCCGTTTGGCCCAGAAATTGGCTCAGG
ATCACAGACATGCTCAGTTACAACCAATCACTTACTTGCTGCATTTGTTGAGCCAAACGAGGATGGTTC
>NucSeq2
ATGGCTGATTATCCTTTTACTGACAAAGCCGCAAAGACATTGTCTGATGCGTACTCAATTGCACAATCTT
ATGGTCATTCACAATTAACCCCTATTACATTGCTGCTGCTCTTTTGTCCGACAGTGACAGTAACGGTAC
>NucSeq3
```

Step 7. Scroll Down and click the Submit button.

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

Step 8. Interpreting the output: After waiting a bit, the output will appear in the browse.

Clustal Omega

Input form | Web services | Help & Documentation

Tools > Multiple Sequence Alignment > Clustal Omega

Results for job clustalo-l20140211-234917-0285-23328113-es

Alignments | Result Summary | Phylogenetic Tree | Submission Details

Download Alignment File | Show Colors | Send to ClustalW2_Phylogeny

CLUSTAL O(1.2.0) multiple sequence alignment

```
NucSeq3      ATGAACGACGAAACGAAGTTTACGAACAAAGCTCT--CGATATCATCACCATTGCACAGA
NucSeq1      ATGAACGACGAAACACAATTTACAAATAAGGCCAA--CGAAATTATCCGTTTGGCCCAGA
NucSeq2      ---ATGGCTGATTATCCTTTTACTGACAAAGCCGAAAGACATTGTCTGATGCGT--ACT
              *: *. **::.. .. ***** .* **.*  .** ** .*  : * * :

NucSeq3      AACTAGCACAGGACCACCAGCATTTCGACGCTGGTGCCTCTACACGTGCTTGCAGCGTTCG
NucSeq1      AATTGGCTCAGGATCACAGACATGCTCAGTTACAACCAATTCACTTACTTGCTGCATTTG
NucSeq2      CAATTGCACAATCTTATGGTCATTACAAATTAACCCCTATTCACATTGCTGCTGCTCTTT
              .* * **::** . * . *** * ... * . **:.*:*** * ***:** *

NucSeq3      TAGAGACACCTGCTGATGGTAG-----
NucSeq1      TTGAGCCAAACGAGGAT-----GGTTC
NucSeq2      T--GTCCGACAGTGACAGTAACGGTAC
              * . .*... * ..:
```

Links to data, output, phylogeny.

Download to a text file.

The sequence alignment.

The Clustal format in “interleaved”: these alignments show 60 alignment positions for all sequences, then go to the next 60 until there is no more alignment.

More information about the alignment.

CLUSTAL O(1.2.0) multiple sequence alignment

```
NucSeq3   ATGAACGACGAAACGAAGTTTACGAACAAAGCTCT--CGATATCATCACCATTGCACAGA
NucSeq1   ATGAACGACGAAACACAATTTACAAATAAGGCCAA--CGAAATTATCCGTTTGGCCCAGA
NucSeq2   ---ATGGCTGATTATCCTTTTACTGACAAAGCCGCAAAGACATTGTCTGATGCGT--ACT
          *: *. **::. .. ***** .* **.**      .** ** .**  : *  *  :
```

↑
Gaps are “-” character.
The alignment put three gap characters in a row here.

↑
A asterisk “*” indicates all the sequences have the same nucleotide.
Fully conserved.

↑ ↑ ↑
0 dots = no conservation.
1 dot “.” = some conservation.
2 dots “:” = all pyrimidines or all purines at position.

Clustal Omega Options

Clicking here



STEP 2 - Set your parameters

OUTPUT FORMAT

The default settings will fulfill the needs of most users and, for that reason, are not visible.

(Click here, if you want to view or change the default settings.)

Will allow you to change alignment settings.

Most important for most people is how to change output formats.

STEP 2 - Set your parameters

OUTPUT FORMAT

DEALIGN INPUT S

MAX GUIDE TREE

MBED-LIKE CLUSTERING GUIDE-

NUMBER of COMBINED ITERATIONS

HMM ITERATIONS

ORDER

- Clustal w/o numbers
- Clustal w/ numbers
- Pearson/FASTA
- MSF
- PHYLIP
- SELEX
- STOCKHOLM
- VIENNA

Aligning Protein Sequences

Step 1. Set to Protein.

Step 2. Paste in Data (or choose file).

Step 3. Submit.

STEP 1 - Enter your input sequences

Enter or paste a set of **PROTEIN** sequences in any supported format:

```
>LCseedSf1
MKKLTVAISAVAASVLMAMSAQAAEIYNKDSNKLDLYGKVNAKHYFSSNDADDG
LGFKGETQINDQLTGFGQWEYEFKGNRAESQGSSKDKTRLAFAGLKFGDYGSDI
GVAYDIGAVITDVLPEFGGDTWTQTDFVMTGRTTG VATYRNNDFFLVDGLNFA/
NDRTDVTENG DGFGFSTTYEYEGFGVGATYAKSDRTNDQVIYGNNSLNASGQI
AAGLKYDANNIYLATTYSETQNMTVFGNNHIANKAQNFEVVAQYQDFGLRPSV/
GKDLGAWGDQDLIEYIDVGATYYFNKNMSTFVDYKINLIDKSDFTKASGVATDDIV
```

Or, upload a file: No file chosen

STEP 2 - Set your parameters

OUTPUT FORMAT

The default settings will fulfill the needs of most users and, for that reason, are not visible.

(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)

Step. 4 Wait for alignment

Alignments Result Summary Phylogenetic Tree Submission Details

Download Alignment File Show Colors Send to ClustalW2_Phylogeny

CLUSTAL O(1.2.0) multiple sequence alignment

```
LCseedSf1          MKKLTVAISAVAASVLMAMSAQAAEIYNKDSNKLDLYGKVNAKHYFSSNDADDGDTTYVR
PhoEseedEco2      MKMKKSTLALVVMGIVASVSVQAAEIYNKDGKLDVYGKVKAMHYMSDNDSDKGDQSYIR
PhoEseedEco1      MKMKKSTLALVVMGIVASASVQAAEIYNKDGKLDVYGKVKAMHYMSDNDSDKGDQSYIR
PhoEseedEco4      --MKKSTLALVVMGIVASASVQAAEIYNKDGKLDVYGKVKAMHYMSDNDSDKGDQSYIR
PhoEseedSen1      --MNKSTLAI-VVSI IASASVHAAEVYNKNGNKLDVYGKVKAMHYMSDYDSKGDQSYVR
PhoEseedSen2      --MNKSTLAI-VVSI IASASVHAAEVYNKNGNKLDVYGKVKAMHYMSDYDSKGDQSYVR
                   .  :::  .  .::  :  *.:***:***:****:****:*  **:.  *.:***  ::*

LCseedSf1          LGFKGETQINDQLTGFGQWEYEFKGNRAESQGSSKDKTRLAFAGLKFGDYGSDYGRNYG
PhoEseedEco2      FGFKGETQINDQLTGYGRWEAEFAGNKAESDT-AQQKTRLAFAGLKYKDLGSDYGRNLG
PhoEseedEco1      FGFKGETQINDQLTGYGRWEAEFAGNKAESDT-AQQKTRLAFAGLKYKDLGSDYGRNLG
PhoEseedEco4      FGFKGETQINDQLTGYGRWEAEFAGNKAESDT-AQQKTRLAFAGLKYKDLGSDYGRNLG
PhoEseedSen1      FGFKGETQINDQLTGYGRWEAEFAGNKAESDS-SQQKNRLAFAGLKLDIGSDYGRNLG
PhoEseedSen2      FGFKGETQINDQLTGYGRWEAEFAGNKAESDS-SQQKTRLAFAGLKLDIGSDYGRNLG
                   :*****:*** ** ***:***:  :::******  * **:* ** *
```

As with DNA:

“-” still means a gap.

“*” means conserved.

“.” and “:” still mean slightly conserved.

However, the . and : indicate different properties of amino acids conserved at a position.