

Our Animal DNA:

Comparing genes across the Tree of Life

Practical 2: align sequences with Clustal

Step 1: Fetch human sequence

First, we need to export our sequences from Ensembl. We already have our human sequence from Practical 1, which looks like this:

```
>ENSG00000139648:ENST00000267119.6 peptide: ENSP00000267119 pep:protein_coding
MSRQFTCKSGAAAKGGFSGCSAVLSSGGSSSSFRAGSKGLSGGFGSRSLSYSLGGVRSLNVA
SGSGKSGGYGFRGRASGFAGSMFGSVALGPVCTVCPGPGIHQVTVNESLLAPLNVELD
PEIQVRAQEREQIKALNNKFASFIDKVRFLQEQNVLETWKWELLQQLDLNCKNNLEPI
LEGYISNLRKQLETLSGDRVRLDSELNVRDVVEDYKKRYEEEINKRTAAENEFVLLKKD
VDAAYANKVELQAKVESMDQEI KFFRCLFEAEITQIQSHISDMSVILSMDNRRNLDSI
IDEVRTQYEEIALKSKAEAEALYQTKFQELQLAAGRHGDDLKNTKNEISELTRLIQIRIS
EIEENVKQASNLETAIADAEQRGNALKDARAKLDELEGALHQAKEELARMLREYQELMS
LKLALDMEIATYRKLESEECRMSGFPPSPVSIISIISSTSGGSVYGFPRPSMVSGGYVANS
SNCSIGVCSVRGEGRSRGSANDYKDTLKGSSLSAPSCKTSR
```

Header

Amino acid
1-letter
codes

If you have lost this sequence, follow steps 1 and 2 of the first practical to find it again

Copy and paste this into a document. To make it easier to see what's what, change the header (the line beginning >) to:

>human_KRT71

Make sure the header line starts with >, otherwise Clustal won't know it's the header and will try to read it as amino acid sequence. The amino acid lines should not have > at the beginning. Make sure you don't remove the newline between the header and the first line of sequence. Do not add any extra newlines between the header and the first line of the sequence. Do not have multiple lines starting with >.

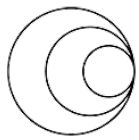
Step 2: Fetch other species sequences

Now you need to find the sequences from sea otter, black swan and Atlantic cod.

Go back to the tab with your BLAST results. Click on the identifier in the first column of the first row in the results table – this is the protein identifier.

Protein

Subject name	Gene hit	Subject start	Subject end	Subject ori	Genomic Location	Orientation	Query start	Query end	Length	Score	E-val	%ID
ENSGMOP00000026268	ENSGMOP00000014429	101	441	Forward	1:23583241-23621462 (Sequence)	Forward	102	444	343 (Sequence)	424	9e-142	58.31 (Alignment)
ENSGMOP00000039893	ENSGMOP00000014429	239	578	Forward	1:23583241-23621462 (Sequence)	Forward	102	443	342 (Sequence)	424	3e-140	58.48 (Alignment)
ENSGMOP00000038280	ENSGMOP00000014429	239	578	Forward	1:23583241-23621462 (Sequence)	Forward	102	443	342 (Sequence)	424	3e-140	58.48 (Alignment)
ENSGMOP00000043242	ENSGMOP00000014429	239	578	Forward	1:23583241-23621462 (Sequence)	Forward	102	443	342 (Sequence)	424	3e-140	58.48 (Alignment)



If you no longer have the BLAST results open, you can search for the IDs you noted down instead.

This will take you to a protein page. This page shows us the regions of the protein that are known to be involved in particular functions. These have been computed from the sequence, based on those functions in other proteins.

Location: 1:23,582,829-23,622,805 Gene: ENSGMOG00000014429 Trans: ENSGMOT00000033979 BLAST results

Transcript: ENSGMOT00000033979.1

Location Primary_assembly 1: 23,582,829-23,622,805 forward strand.

About this transcript This transcript has 9 exons and is annotated with 27 domains and features.

Gene This transcript is a product of gene ENSGMOG00000014429.2 [Show transcript table](#)

Protein summary

Protein domains for ENSGMOP00000026268.1

ENSGMOP00000026268.1
MobiDB lite
Low complexity (Seq)
Coiled-coils (Ncoils)
Superfamily
SMART
Pprints
Pfam
keratin type II head
keratin, type II
intermediate filament, rod domain
intermediate filament, rod domain
intermediate filament, rod domain
intermediate filament protein, coiled-coil
P1TRR45616:329
P1TRR45616
intermediate filament, rod domain, coil 1B
1:205-170
1:205-300

Scale bar 0 60 120 180 240 300 360 420 538

Export data

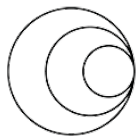
Functional regions of the protein

As before, we can export the sequence by clicking on the [Export data](#) button and selecting [Peptide sequence](#) only, ensuring that you select [None](#) under Genomic sequence. Refer back to step 2 of Practical 1 for more details and a screenshot of what to select.

Step 3: Make your sequence file

Copy and paste the sequence you get into the same document as the human protein sequence and change the name to give you the species again, making sure that you have > at the beginning of the header line and not at the beginning of the sequence lines.

Now do the same for the other two species. You should end up with a document containing four protein sequences, like this:



```
>human_KRT71
MSRQFTCKSGAAAKGGFSGCSAVLSGGSSSSFRAGSKGLSGGFGSRSLSLGGVRSLNVA
SGSGKSGGYGFRGRASGFAGSMFGSVALGPVCPTVCPGGIHQVTVNESLLAPLNVELD
PEIQKVRQAQEREQIKALNNKFASFIDKVRFLQEQNQVLETKWELLQQLDLNNCKNNLEPI
LEGYISNLRKQLETLSGDRVRLDSELNRVDRVVEDYKPKRYEEEINKRTAAENEFVLLKKD
VDAAYANKVELQAKVESMDQEIKFRCLEAEITQIQSHISDMSVILSMDNNRNLDLDSI
IDEVRTQYEEIALKSKAEAEALYQTKFQELQLAAGRHGDDLKNTKNEISELTRLIQRIRS
EIENVKQASNLETAIADAEQRGDNALKDARAKLDELEGALHQAKEELARMLREYQELMS
LKLALDMEIATYRKLESEECRMSGEFSPVSIISSTSGGSVYGFPRSMVSGGYVANS
SNCISGVCSVRGGEGRSRGSANDYKDTLGGKSSLSAPSCKTSR
```

```
>swan
MSRQSTVRIQRGRSGFSAASAIVPNTCRTSFSSRSVTRVSGCNAGSGFSRVGGGFGSKSL
YNVGGCKRISVAGRGGGFYGPAGFGGAGSVYGC GGFGMPANLVSVNQSL LKPLNLEID
PSIQIRKEEKEQIKTLNNKFASFIDKVRFLQEQNKVLETKWELLQEQGMKTVKNNLEPL
FETYINNLRMQLNSLLSDKGRLEGEVNTQYLVEDFKKKYEDEINRRTVAENEFVTLKKD
VDASYMKNVELQAKVDALTEEINFLRALYEAELSQMOTQISDTSVVL TMDNNRNLDLDSI
ISEVKAQYEDIANRSRAEAESWYQTKYEELQATAGRHGDDL RNTKQEI SELNRHVQRLRS
EIDSVKKQCANLKAATAEAERGELALKDAKAKLAELEDALQAKADLARQLREYQELMN
VKLALDIEIATYRKLEEGEECRWVGNTLLVLVLEDPTQVLVMLGISEMHMLNGVSRGRG
KGCLVNSVTL
```

```
>otter
MSRQFTCKSGAATKGGFSGCSAVLSGGSSSSYRAGGKGISGGFGSRSLSLGGIRNISFN
MTSGSGKSGGYGFRGRASGFAGSMFGSVALGPVCPVCPGGIHQVTVNESLLAPLNVE
LDPEIQKVRQAQEREQIKALNNKFASFIDKVRFLQEQNQVLETKWELLQQLDLNNCKNNLE
PILEGYISNLRKQLETLSGDRVRLDSELRSVRDVEDYKPKRYEEEINRRTAAENEFVLLK
KDVAAYANKVELQAKVDSMDQEIKFCKLYEAEIAQIQSHISDMSVILSMDNNRDLNLD
SIIDEVRAQYEEIALKSKAEAEALYQTKFQELQLAAGRHGDDLKNTKNEISELTRLIQRI
RSEIENVKQASNLETAIADAEQRGDNALKDARAKLDELESALHQAKEELARMLREYQEL
MSLKLALDMEIATYRKLESEECRMSGEFSPVSIISSTSGSGGYGFRPSSVSGGYVA
SSSSCISGVCSVRGGDVRGRGSSSDYKDTLGRGSSQSTS SSKKASR
```

```
>cod
MSRQFTCKSGAATKGGFSGCSAVLSGGSSSSYRAGGKGISGGFGSRSLSLGGIRNISFN
MTSGSGKSGGYGFRGRASGFAGSMFGSVALGPVCPVCPGGIHQVTVNESLLAPLNVE
LDPEIQKVRQAQEREQIKALNNKFASFIDKVRFLQEQNQVLETKWELLQQLDLNNCKNNLE
PILEGYISNLRKQLETLSGDRVRLDSELRSVRDVEDYKPKRYEEEINRRTAAENEFVLLK
KDVAAYANKVELQAKVDSMDQEIKFCKLYEAEIAQIQSHISDMSVILSMDNNRDLNLD
SIIDEVRAQYEEIALKSKAEAEALYQTKFQELQLAAGRHGDDLKNTKNEISELTRLIQRI
RSEIENVKQASNLETAIADAEQRGDNALKDARAKLDELESALHQAKEELARMLREYQEL
MSLKLALDMEIATYRKLESEECRMSGEFSPVSIISSTSGSGGYGFRPSSVSGGYVA
SSSSCISGVCSVRGGDVRGRGSSSDYKDTLGRGSSQSTS SSKKASR
```



Check that:

1. All header lines start with >.
2. Each sequence has only one line of header.
3. The sequence lines do not start with >.
4. There are no extra lines between the header and sequence.

Step 4: Clustal input

You need to put these sequences into Clustal Ω. Go to <https://www.ebi.ac.uk/jdispatcher/msa/clustalo>



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Clustal Omega

[Input form](#) [Web services](#) [Help & Documentation](#) [Bioinformatics Tools FAQ](#) [Feedback](#) [Share](#)

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.

STEP 1 - Enter your input sequences

Enter or paste a set of

PROTEIN

sequences in any supported format:

 **Input**

Or, upload a file: No file chosen [Use a example sequence](#) | [Clear sequence](#) | [See more example inputs](#)

STEP 2 - Set your parameters

OUTPUT FORMAT


ClustalW with character counts

The default settings will fulfill the needs of most users.

(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)

 **Run**

Copy all four sequences into the input box on Clustal. Then click on [Submit](#).

Step 5: Clustal results

**Questions:**

1. Could you do this without a computer? How long do you think it would take to align all these sequences and spot similarities and differences between them by hand?
2. What if you had to do this for all 20,000 protein coding genes in a species?

Step 6: Change your view

There are other ways to see the alignments. Click on [Show colors](#).

Results for job clustalo-I20201015-095701-0397-7099231-p2m

Alignments Result Summary Guide Tree Phylogenetic Tree Results Viewers Submission Details

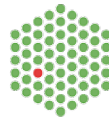
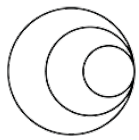
Download Alignment File Hide Colors

CLUSTAL O(1.2.4) multiple sequence alignment

human	MSRQFTCKSGAA---AKGGF-----SGCSAVLSGGSS----SSFAGSKGLSGG	42
sea	MSRQFTCKSGAA---TKGGF-----SGCSAVLSGGSS----SSYRAGKGIISGG	42
Atlantic	MSKRVTQTSYSVRSAPRNYSSASYSGPSMGGSRQSYARST--FGGASRGMGGGGGGG	58
black	MSRQ---STVRIQGRSGFSAASAIVPN--TCRTSPSSRSVTRVGSNCAGSGFSRVGGG	54
	**:: . : . : . * . * . . * . . **	
human	FGSRSLYSLGGVRSL--NVASGSGKSGGYGFRGRASGFAGSMFGSVALGPVCPVCPG	100
sea	FGSRSLYSLGGIRNIFNMTSGSGKSGGYGFRGRASGFAGSMFGSVALGPVCPVCPG	102
Atlantic	FISSSA-YGG-----MGLGSSMAGGGMGMGGGFGGGMGMG-----A	99
black	FGSKSLYNVGGCKRISV-AGRGGGFYGPAGFGGGAGSVY--GCGGGFG-----M	100
	* * * ** . . * * * * . . :	
human	GIHQVTVNESLLAPLNVELDPEIQKVRQAEREQIKALNNKFASPIDKVRFLEQQNQVLET	160
sea	GIHQVTVNESLLAPLNVELDPEIQKVRQAEREQIKALNNKFASPIDKVRFLEQQNQVLET	162
Atlantic	PITAVTVNKSLLAPLNLAIDPNIQAVRTHEKEQIKGLNNRFASPIDKVRFLEQQNKLET	159
black	PANLVSVNQSLKPLNLEIDPSIQIRKKEEKEIKTLNKNKFASPIDKVRFLEQQNKVLET	160
	*::** ** * : ** . ** : * . * : ** * : ** * : ** * : ** * : ** * : **	

The colours can make it easier to see similarities and differences – it is easy to spot a column of matching colours than to spot a column of matching letters. There are 20 different amino acids, and some are more similar than others. Chemically similar amino acids are coloured the same, so we can most easily identify changes that are likely to affect the protein.

For example, one column shows R, R, K and K, all in magenta. R and K are Arginine and Lysine, respectively, which are both alkaline. In contrast, another column shows E, E (blue), K (magenta) and Q (green), which represent Glutamic acid (acidic), Lysine (alkaline) and Glutamine (with an amide group).



Questions:

3. Can you find any sections in the alignment with long runs of matching sequence? What is the longest you can find?

4. Look at position 5 in the alignment. What amino acids can you see there? Why have these been coloured differently? This is a great chart to look at for amino acids: <https://www.compoundchem.com/2014/09/16/aminoacids/>

5. Why do you think that some parts of the protein have lots of similarity between species, and other parts do not?



Another option is to see a tree constructed from the sequences, showing us which sequences are most similar to each other. Click on [Phylogenetic tree](#) at the top of the page.

Results for job clustalo-l20201015-095701-0397-7099231-p2m


Alignments Result Summary Guide Tree **Phylogenetic Tree** Results Viewers Submission Details

Download Phylogenetic Tree Data

Phylogenetic Tree

This is a Neighbour-joining tree without distance corrections.

Branch length: Cladogram Real

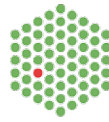


human	0.03735
sea	0.0334
Atlantic	0.25266
black	0.17114

Questions:

6. Which sequences are most similar to each other?

7. Why do you think this is?



Extended practical

Only if you have time or are particularly interested in this.

Why not see if you can find *KRT71* in more species and carry out an alignment of more sequences?

Why not find a different human gene and try searching for that?

Some genes to try:

ADAM30

NOTCH2NLR

PPIAL4A

LIX1L

GJA8