



## Hands-On Nine The Big Jaw

CLUSTAL OMEGA is available at EMBL-EBI in the United Kingdom at: <http://www.ebi.ac.uk/Tools/msa/clustalo>.

The file “myh16\_sequences.txt” contains eight nucleotide sequences from the masticatory myosin heavy chain (MYH16). Copy and paste the 8 sequences in FASTA format into the CLUSTAL OMEGA data window. Make sure you have “DNA” from dropdown window in Step 1. Use the default conditions provided by the program, in STEP 2 and STEP 3 and click on “Submit” to align the eight sequences. Note that the eight sequences are:

- Accession Number: AY350716.1 Woolley monkey (*Lagothrix lagotricha*) masticatory myosin heavy chain (MYH16) gene, exon 18 and partial cds
- Accession Number: AY350717.1 Rhesus macaque (*Macaca nemestrina*) masticatory myosin heavy chain (MYH16) gene, exon 18 and partial cds
- Accession Number: AY350718.1 Pigtailed Macaque (*Macaca mulatta*) masticatory myosin heavy chain (MYH16) gene, exon 18 and partial cds
- Accession Number: AY350719.1 Orangutan (*Pongo pygmaeus*) masticatory myosin heavy chain (MYH16) gene, exon 18 and partial cds
- Accession Number: AY350720.1 Gorilla (*Gorilla gorilla*) masticatory myosin heavy chain (MYH16) gene, exon 18 and partial cds
- Accession Number: AY350721.1 Bonobo (*Pan paniscus*) masticatory myosin heavy chain (MYH16) gene, exon 18 and partial cds
- Accession Number: AY350722.1 Chimpanzee (*Pan troglodytes*) masticatory myosin heavy chain (MYH16) gene, exon 18 and partial cds
- Accession Number: BK001410 Human (*Homo Sapiens*), *Homo sapiens* myosin heavy chain (MYH16) pseudogene, exon 19 (nucleotides 36298-36383 from BK001410)

The alignment itself will appear under: CLUSTAL O(1.1.0) multiple sequence alignment.

- a) What kind of substitutions do we have? Look at the columns and count the number of transitions and the number of transversions.
- b) What kind of indels (deletions/insertions) can you see? What are the consequences of the indels? Fully explain your answer, knowing that the sequences are given in the first reading frame.

Note that by clicking on “Page Summary” at the top of the page, and by choosing the JAVA alignment viewer and editor “JalView”, we get to see a different way of showing the alignment of the eight sequences.