For comparing clustal vs. muscle trees:

* Cox1\_min\_Cl
* Cox1\_min\_M
* Cox2\_min\_Cl
* Cox2\_min\_M

ClustalW – pairs sequences together based on similarity, then constructs the rest of the alignment based on the similarities between both individual sequences and pairs

Muscle – performs the multiple alignment first, comparing the similarity of all the sequences at once, then re-estimates and refines the possible arrangements down to the one that “makes the most sense” regarding similarity between pairs of sequences

For comparing tree type (max likelihood vs min evolution):

* Cox1\_max\_Cl
* Cox1\_min\_Cl
* Cox2\_max\_Cl
* Cox2\_min\_Cl

Maximum likelihood – constructed by looking at all possible tree structures and determining which is statistically most likely to occur

Minimum evolution – constructed based on which tree shows the minimum number of character state changes (optimizing for shortest branch length overall)

For comparing gene type (cox1 vs cox2):

* Cox1\_min\_Cl
* Cox2\_min\_Cl

Cox1 – regulates endogenesis in endothelial cells

Cox2 – involved in the production of prostaglandins that mediate pain and support the inflammatory process