Gget.muscle for multiple species alignment

We want to use gget.muscle for multiple species alignments. These multiple species have different length ensembl\_id/gene\_names. Therefore, they start at different places on the page.

* A screenshot of a computer screen

  Description automatically generated

Multiple species alignment with frog, zebrafish, mouse and human for PDCD4

* A screenshot of a computer code

  Description automatically generated

The ideal result would be that independent of gene name length the sequences would still start at the same place. This would make it easier to compare the sequences with each other.