

**Input:** All candidate filtred aligned protein ORFs Clustering-2 Homemade python script Cluster1-Cluster2 Cluster3 Cluster4 **Input:** Clusters Amino acide alignment Clustalo v1.2.4 Default Input: Clusters **Trimming 8**) Trimal v1.4.rev22 | Automated1 **Input:** Clusters Concatenation Pal2nal sp5 Phylogeny 10 **Input:** Amino Acide Supermatrix IQ-TREE v2.1.2 | -m MFP -aIrt 5000 -bb 5000 -bnni -symtest-remove-bad