Construction of Phylogenetic Tree

1. Fasta (Peptide) Sequences of Functional ORs were obtained from HORDE database. (<https://genome.weizmann.ac.il/horde/>).
2. The fasta file was loaded in Sea VIew (1:4.6.4-1).
3. All ORs were aligned using MUSCLE method.
4. After alignment, PhyML was run using Alignment Muscle.
5. This analysis took 1hr 51min 12 s.
6. The unrooted tree file was saved and was used as an input for Interactive tree of life (iTOL) (<https://itol.embl.de/>)
7. The additional files under folder annotations were uploaded in the sequence of their numbers.