Aryl malonate decarboxylase from *Bordetella bronchiseptica* (BbAMDase) is a enzyme that generates a wide spectrum of optically pure carboxylic acids, including several with anti-inflammatory activity such as flurbiprofen.

Group 1 (Blast & Foldseek)

Emilia Chua, Nikol Haxhi, Anna Hirschberger & Ivana Jelic

Find sequences related to the protein **Arylmalonate decarboxylase** from *Bordetella bronchiseptica*. The accession numbers are Q05115 UniProt and 3DTV_B / 3DTV from the PDB database.

Search for sequences NCBI and Foldseek.

We here are not is the most similar sequence but with similar function, which is often unknown. Use different algorithm data bases to search for sequences. Download 100 sequences each and upload them to github.

The presentation should contain a short introduction to the tool and how you used it for your need (what parameters did you change etc). You might also show some part on the computer if it does not take too much time. The presentations last year were all quite good .

A fasta containing the sequence is in the data_raw folder.

Group 2 (Alignment 1: mafft)

Selome Tamirat Desalegn, Theresa Leitner & Elin Kristina Muling Nielsen

Download and install mafft on your computer. Does is work? Tell us about the experience, trouble shooting, etc.

Align the sequences using mafft online at ebi and on your computer. Additionally align the sequences with the other tools from ebi.

The AMD sequence from *bb* has 4 cysteines. Do they align with the cysteines from the other sequences?

Group 3 (Alignment 1: muscle)

Bassam Ahmed Abdelrehim Ali Edrees, Leonard Jank, Aurora Valenzuela Romero

Download and install muscle on your computer. Does is work? Tell us about the experience, trouble shooting, etc.

Align the sequences using muscle online at ebi and on your computer. Additionally align the sequences with the other tools from ebi.

The AMD sequence from *bb* has 4 cysteines. Do they align with the cysteines from the other sequences?

Group 4 (Phylogenetic 1: phangorn)

Setayesh Basiri Tootkaboni, Milena Krennmayr, Jasmin Le, Alina Lisa Marie Riedl

Build a phylogenetic tree using the R package phangorn.

Group 5 (Phylogenetic 2: iqtree)

Uma Isaković, Andrej Nikolikj, Trivuna Radulović

Download and install iqtree on your computer. Does is work? Tell us about the experience, trouble shooting, etc. Build a phylogenetic tree using iqtree. Again using the online tool and the comand line version.

Group 5 (Ancestral sequence reconstruction using phangorn and grasp)

Philip Timothy John Hughes, Saya Maratova, Alexander Veith