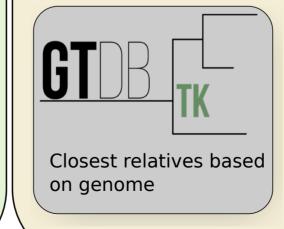




Ecology



Taxonomy

(based on 16S rRNA)

## Output

- -16S tree
- -Genome tree
- -GC (%) difference
- -ANI to closest relatives
- -POCP to closest relatives
- -CAZy profile

-16S rRNA identity to closest relatives -KEGG based; urease, oxidase, sulfide utilisation, ammonia utilisation, sulfate reduction, nitrogen fixation, flagella, vitamin biosynthesis, carbon source utilisation

## **Functional**



Carbohydrate degrading potential

