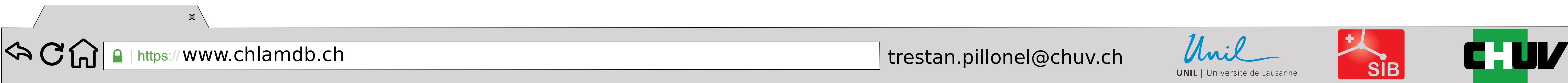


A comparative genomics database of the phylum Chlamydiae

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Summary of the method

1 Protein annotation

RefSeq
KEGG (KEGG Orthologs)
Interproscan (domains and signatures)
TCDB (transporters)
COG
SwissProt
DOOR operon database
STRING

2 Orthologs identification (OrthoFinder)

3 Identification of closest homologs in RefSeq and SwissProt databases (PLAST)

4 Phlogenetic reconstructions

- reference species pyhlogeny (FastTree)
- for each orthologous group (RaxML)
- for each orthologous group including closest RefSeq and Swissprot hits (RaxML)

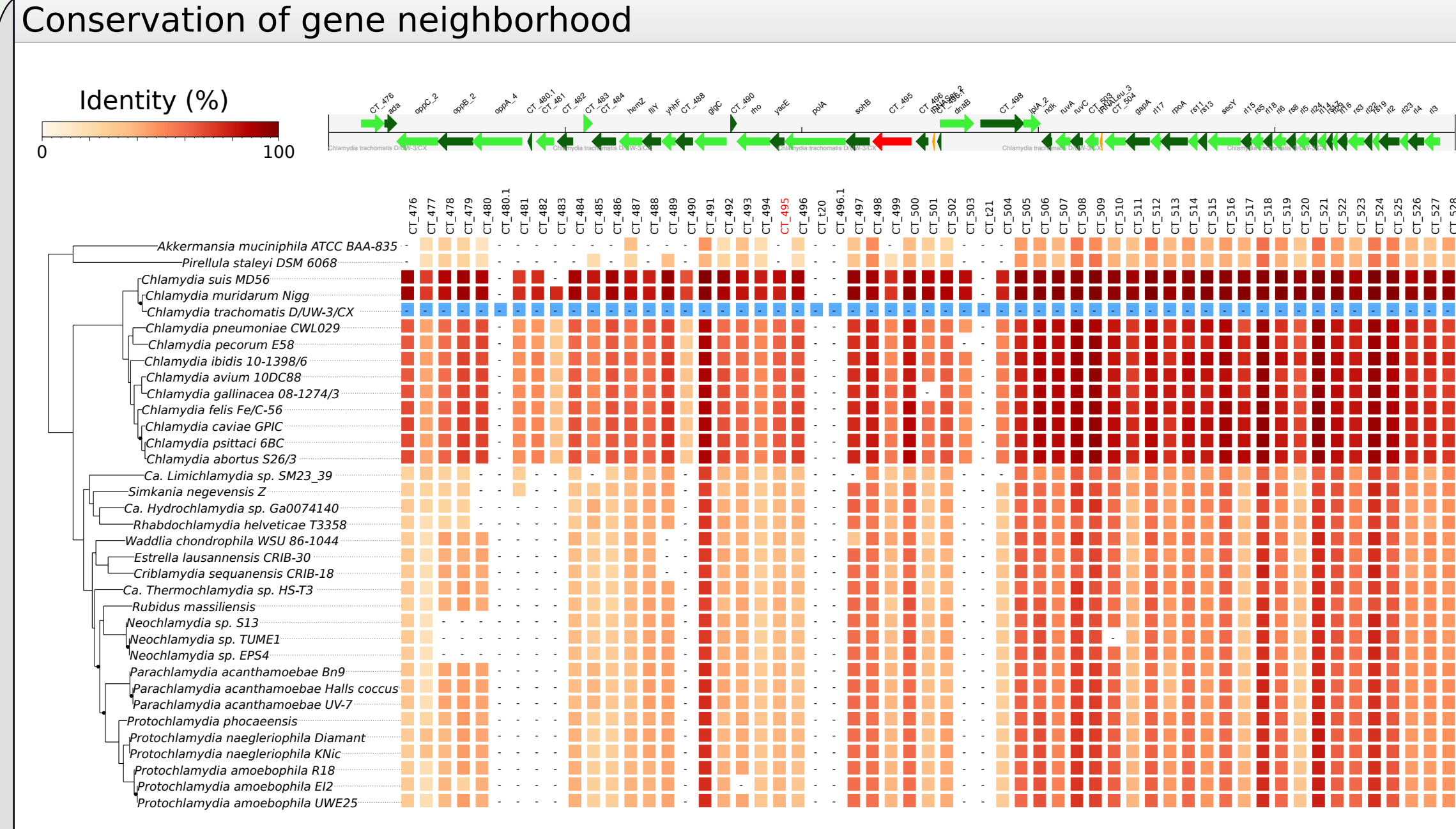
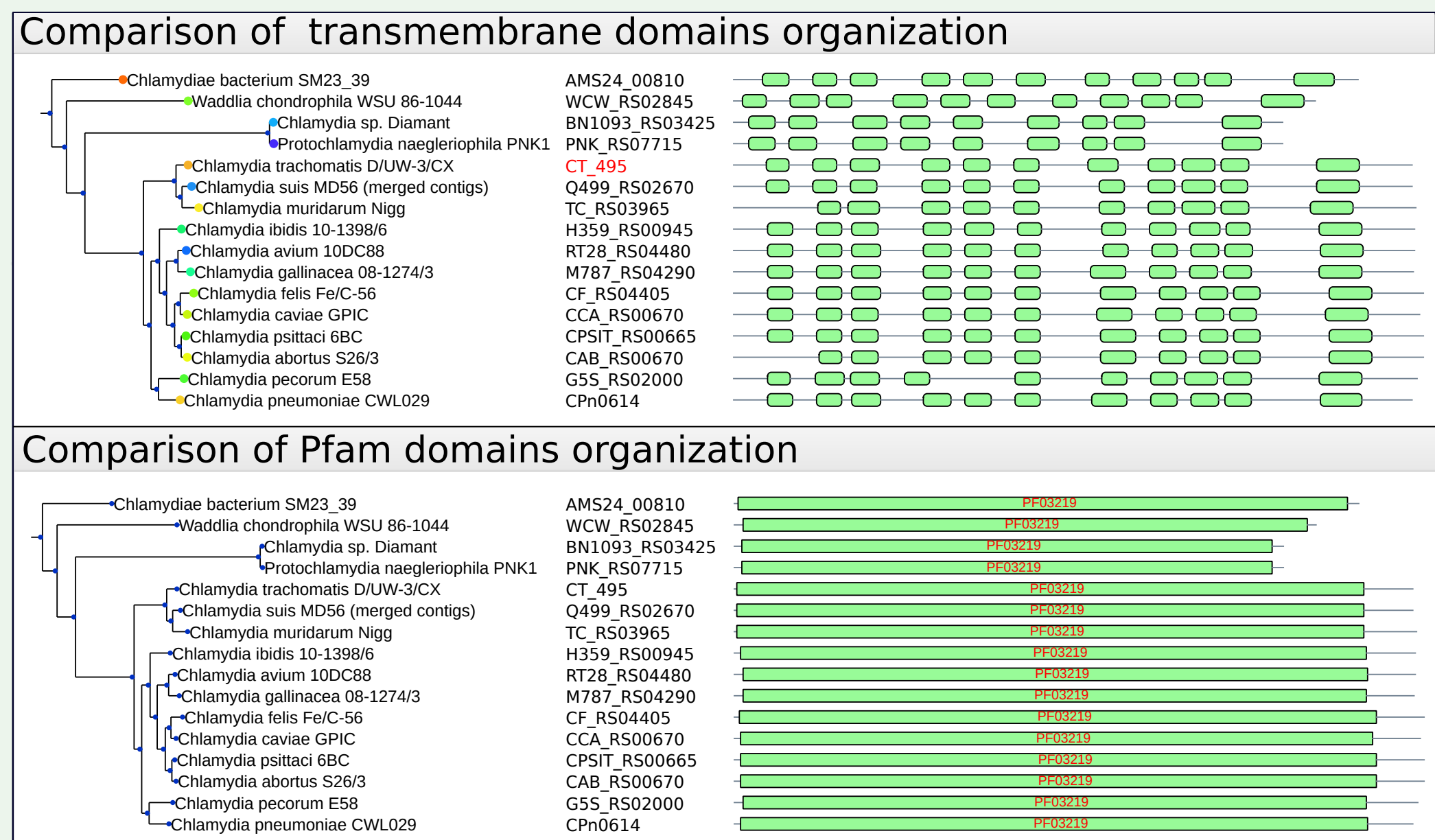
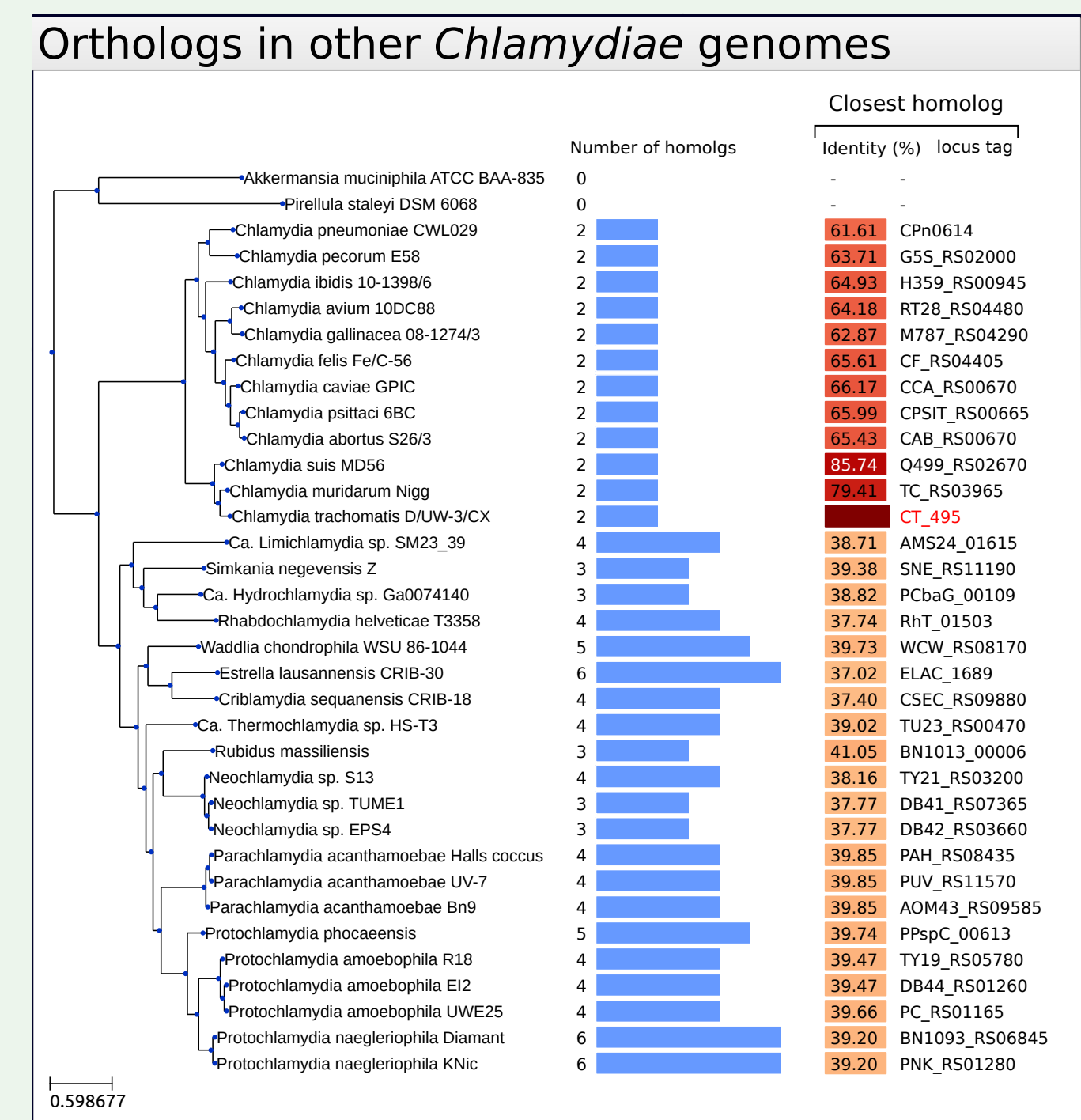
5 PFam domains taxonomic profiling (Interproscan, RefSeq)

Web interface development with the python-based django framework

Data stored in a SQL database

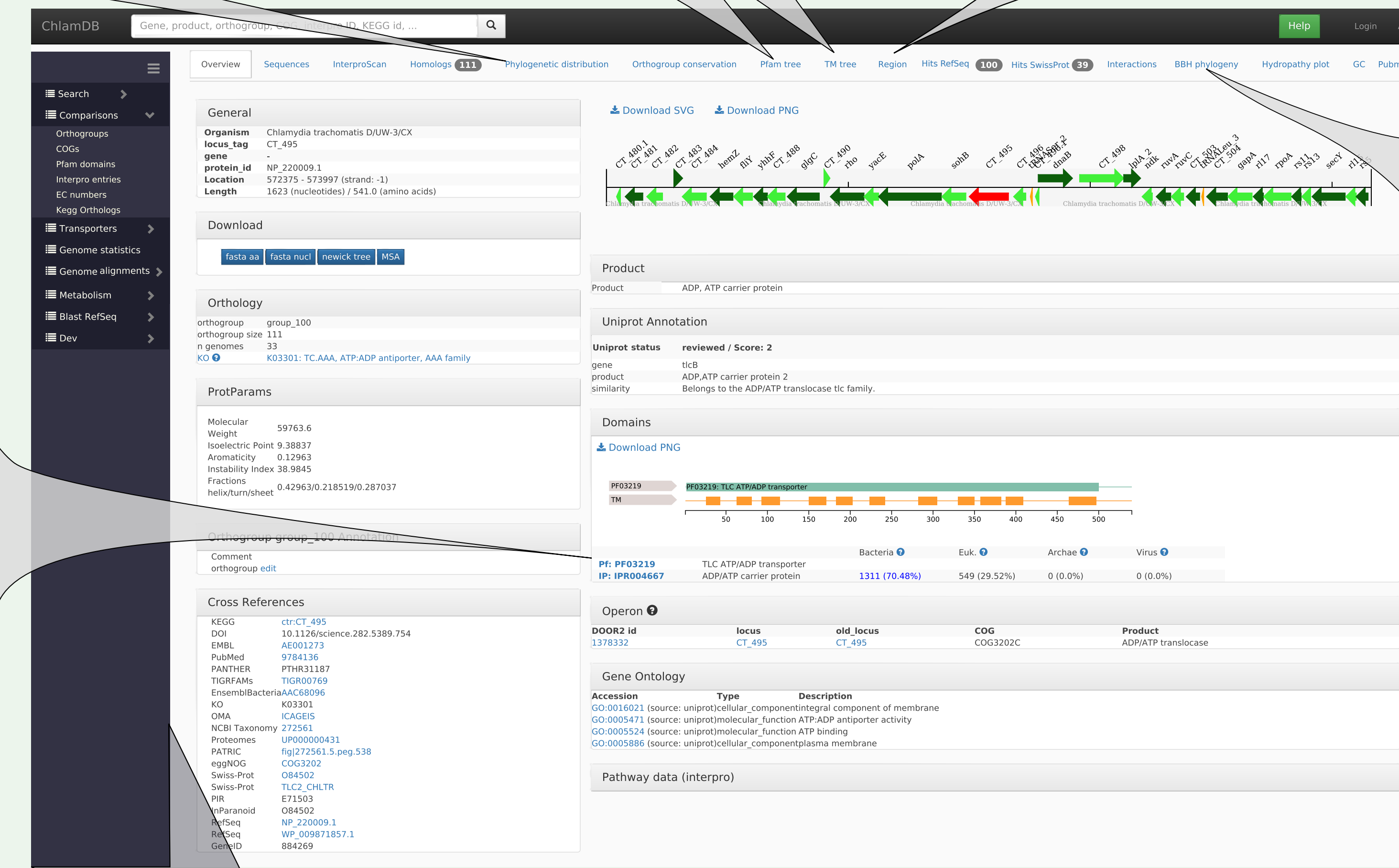
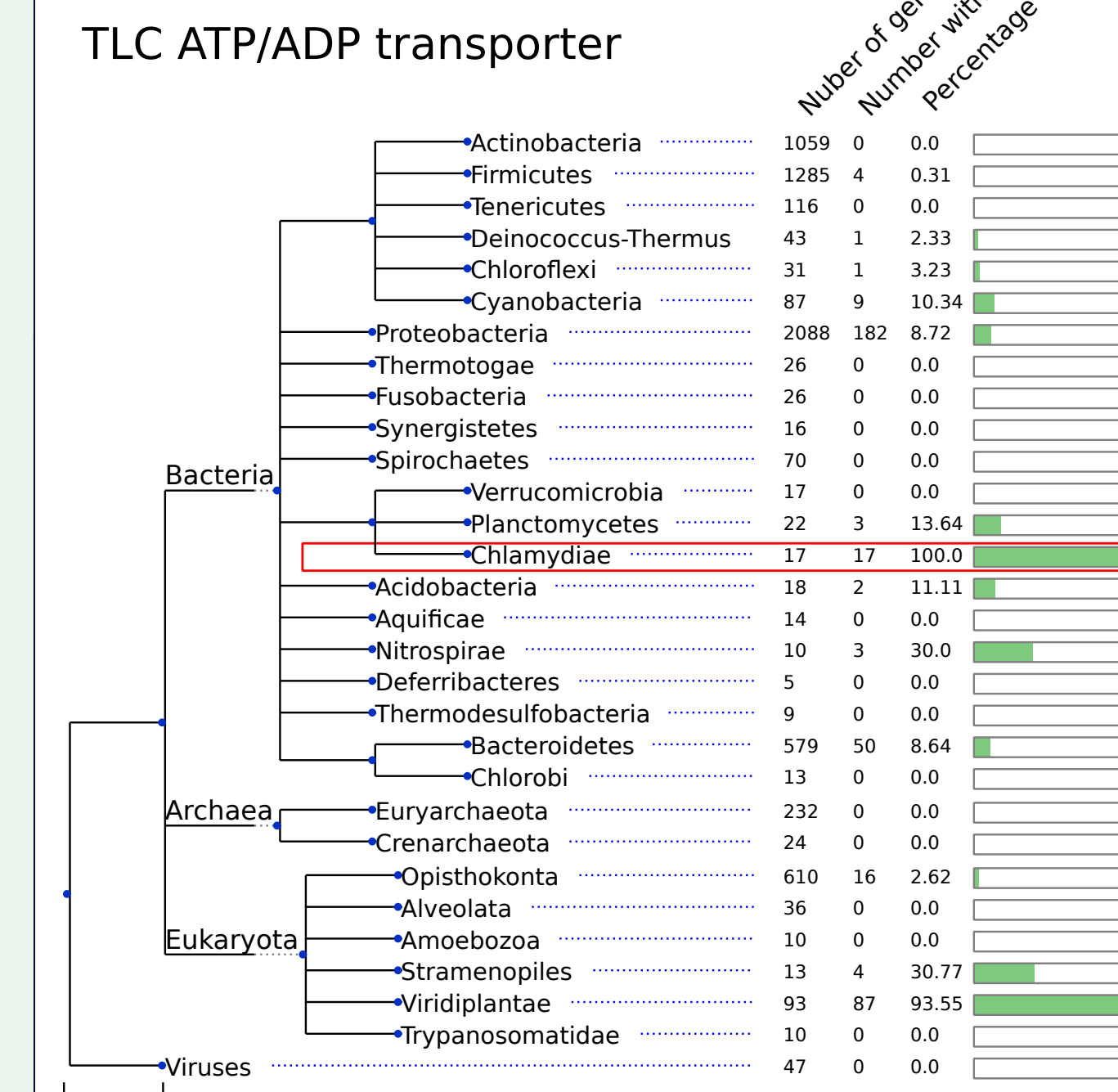


Protein coding sequences annotation

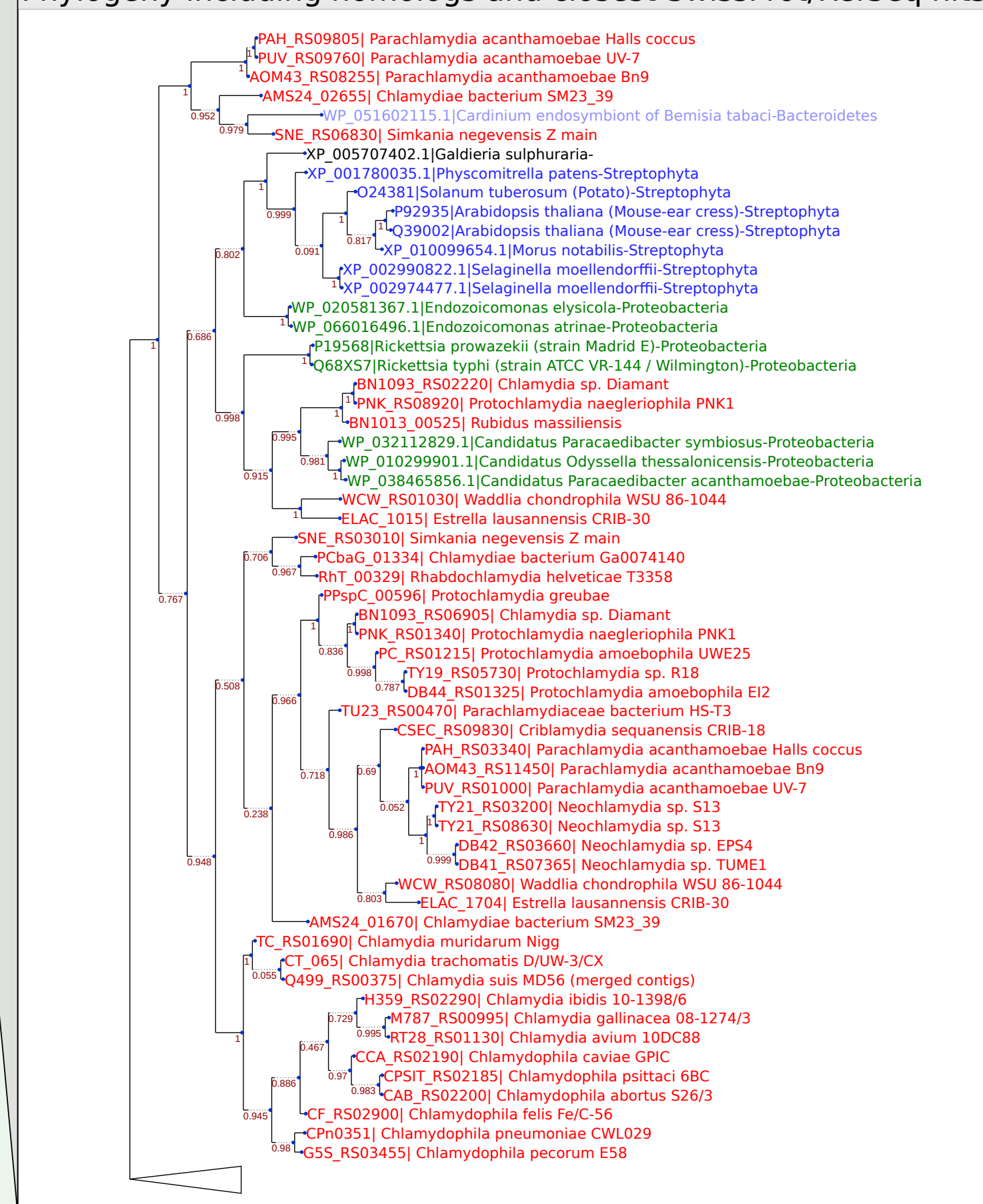


Taxonomic profile of Pfam domains

Based on >6000 RefSeq representative genomes

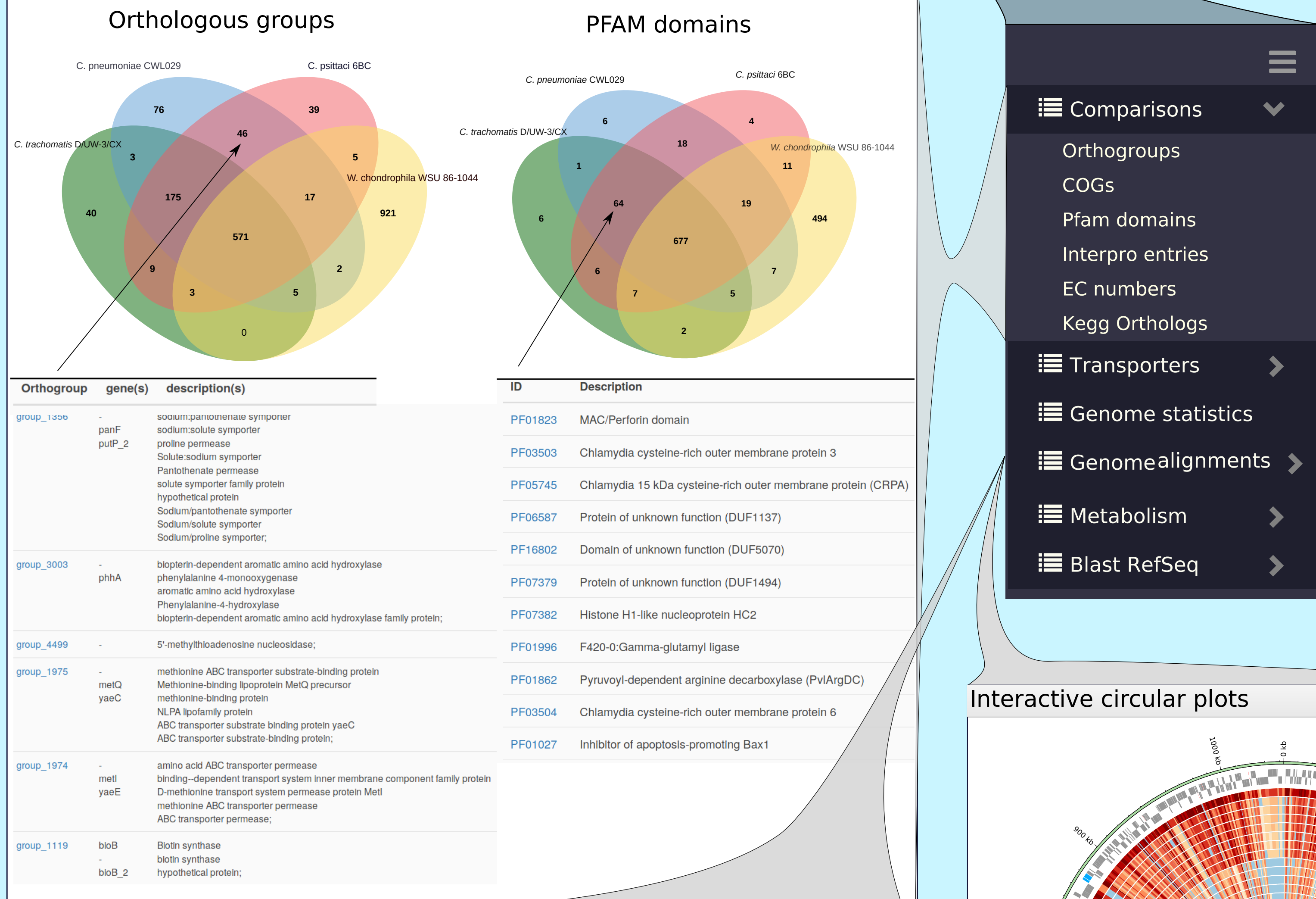


Phylogeny including homologs and closest SwissProt/RefSeq hits

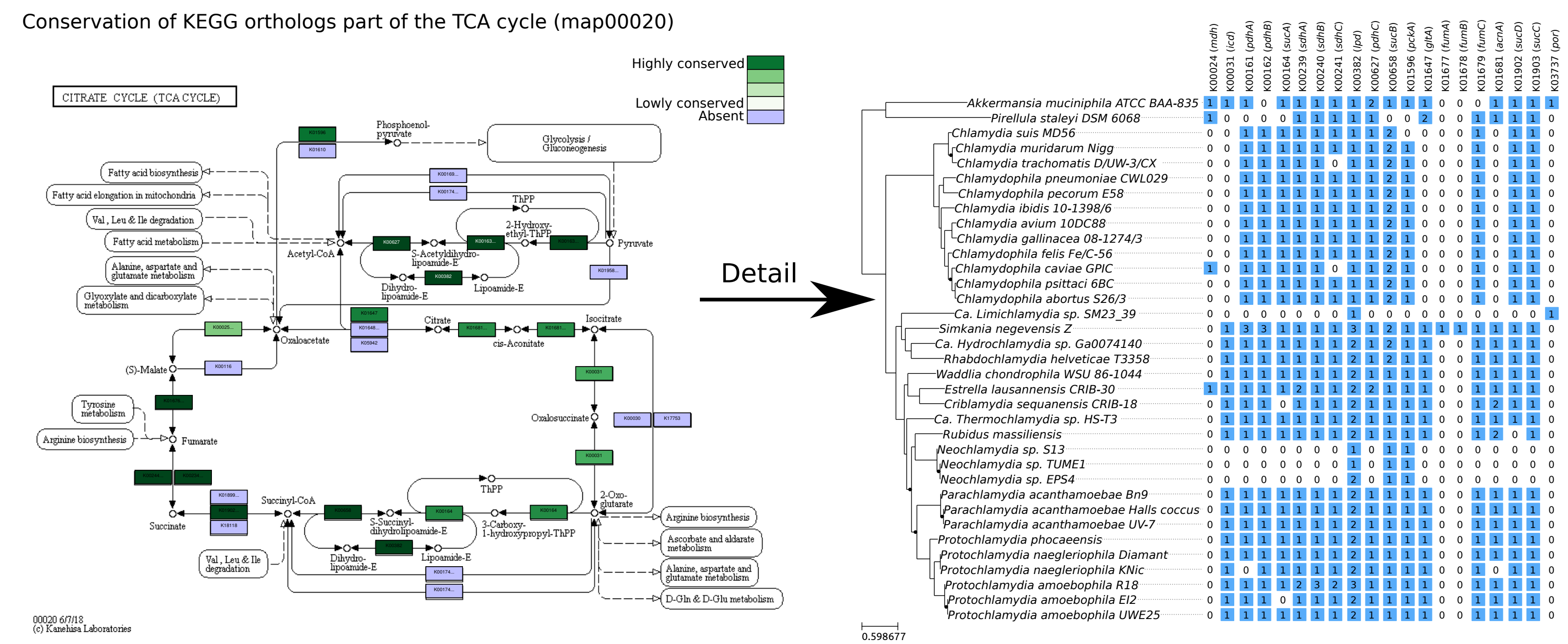


Toolbox for large scale comparative analyses

Whole genome comparative analyses



Comparative analyses of metabolic pathways based on KEGG annotation



Conclusion and perspectives

The *Chlamydiae* database provides a high-quality resource for the chlamydia research community.

It facilitates the access to protein annotations and allows retrieving evolutionary relationships between *Chlamydiae* orthologs and their closest homologs in public databases.

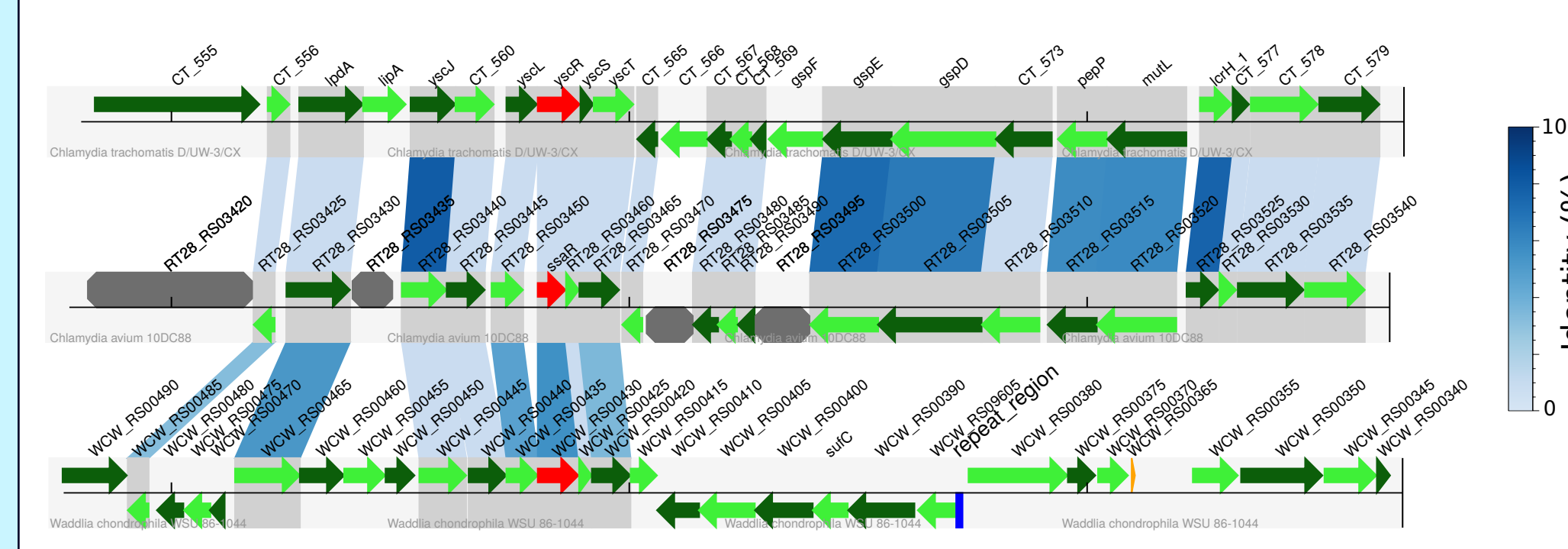
The database will be updated on a regular basis with newly sequenced chlamydial genomes.

Examples of publications using this database:

Environmental metagenomic assemblies reveal seven new highly divergent chlamydial lineages and hallmarks of a conserved intracellular lifestyle
T Pillonel et al., Frontiers in microbiology (2018)

Metagenomic Analysis of Fish-Associated *Ca. Parilichlamydiaceae* Reveals Striking Metabolic Similarities to the Terrestrial Chlamydiaceae
A Taylor-Brown et al., Genome biology and evolution (2018)

Multiple alignments centered on a target locus: example with CT_559 (Sct)



Interactive circular plots

