

## ParR / ParS Genes in *Stenotrophomonas maltophilia* K279a and the RNAseq problema.

A wet lab group is studying the proteins ParR and ParS which are encoded in the genes *parR* and *parS* respectively, from *S. maltophilia* K279a. (the representative genome and reference strain)

As they have reported in this paper: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6262003/> those two proteins are involved, somehow, in antibiotic resistance in this organism.

They have contracted an external service to perform a [RNAseq](#) with this organism in conditions where they were expecting to see some changes in the expression of the previously mentioned genes. The results were delivered in a table sorted by the `locus_tag` of each gene. The external service people report that they have used the genome annotation from Ensembl bacteria obtained from a `gtf` formatted file. In case another annotation has to be used, it must be delivered to them in a `gtf` formatted file.

1. Check if those two genes / proteins are annotated with these names in the RefSeq and GenBank entry of *S. maltophilia* K279a complete genome.
2. Search in Uniprot for those two genes in any *S. maltophilia* strain.
3. Search in NCBI for ParR and ParS proteins from any strain of *S. maltophilia*
4. Use the sequences of those proteins to find them in the complete genome of *S. maltophilia* K279. Compare results in the `gbff` files from the GenBank annotation and the Refseq one.
5. Select the appropriate `locus_tag` and `old_locus_tag` for each gene/protein.
6. Get the `gtf` formatted file from ensemble bacteria for *S. maltophilia* K279a. Check the date when the data on it was annotated and if you could find in it the two previously mentioned genes.
7. Get the `gtf` formatted file for *S. maltophilia* K279a from NCBI Refseq database and check the date and the two genes.
8. Compare the alphafold predicted structures for the proteins located in the identified regions of the genome for both annotations (GenBank and Refseq)

ParS gene is the locus\_tag Smlt3730, however Smlt3729 is not the ParR, it is a wrongly annotated gene in the complementary strain. This has been corrected in further reannotations carried out in the RefSeq genome of *S. maltophilia* K279a, now you find the ParR gene with the /old\_locus\_tag="Smlt3730" and the /locus\_tag="SMLT\_RS17770" and the ParS gene without /old\_locus\_tag and with /locus\_tag="SMLT\_RS17765".