Setting up BLAST search

Paste Tri12 sequences into BLAST input box

Select ToxGen

These are the finalized results of your BLAST run.
You can click here for a very condensed summary of the results

Click on the strain code to view strain metadata

# BLASTN 2.2.26 [Sep-21-2011]
# Database: data/dbs4plutof/tri12
# Mode: ultra condensed output

Additional UNITE taxon name is in gray colour.

Query - The name of the query (input) sequence
Reference - The name of the reference sequence
Score - The BLAST score
E-value - The BLAST E-value
Prent - Percent identity over the BLAST alignment
MisM - The number of mismatches over the BLAST alignment
Qstart - The position in the query sequence where the BLAST alignment starts
Qend - The position in the query sequence where the BLAST alignment ends
Rstart - The position in the reference sequence where the BLAST alignment starts
Rend - The position in the reference sequence where the BLAST alignment ends