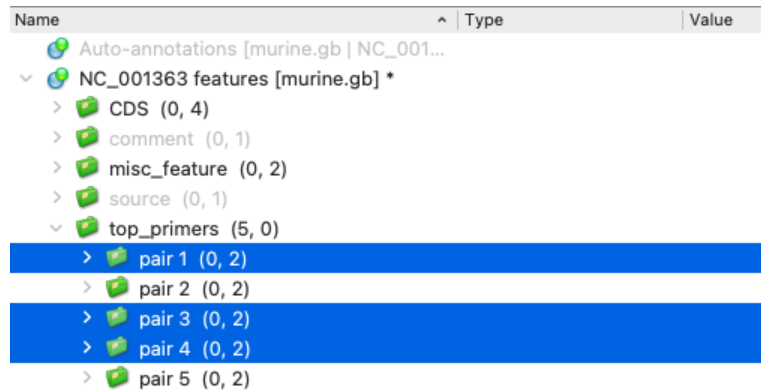


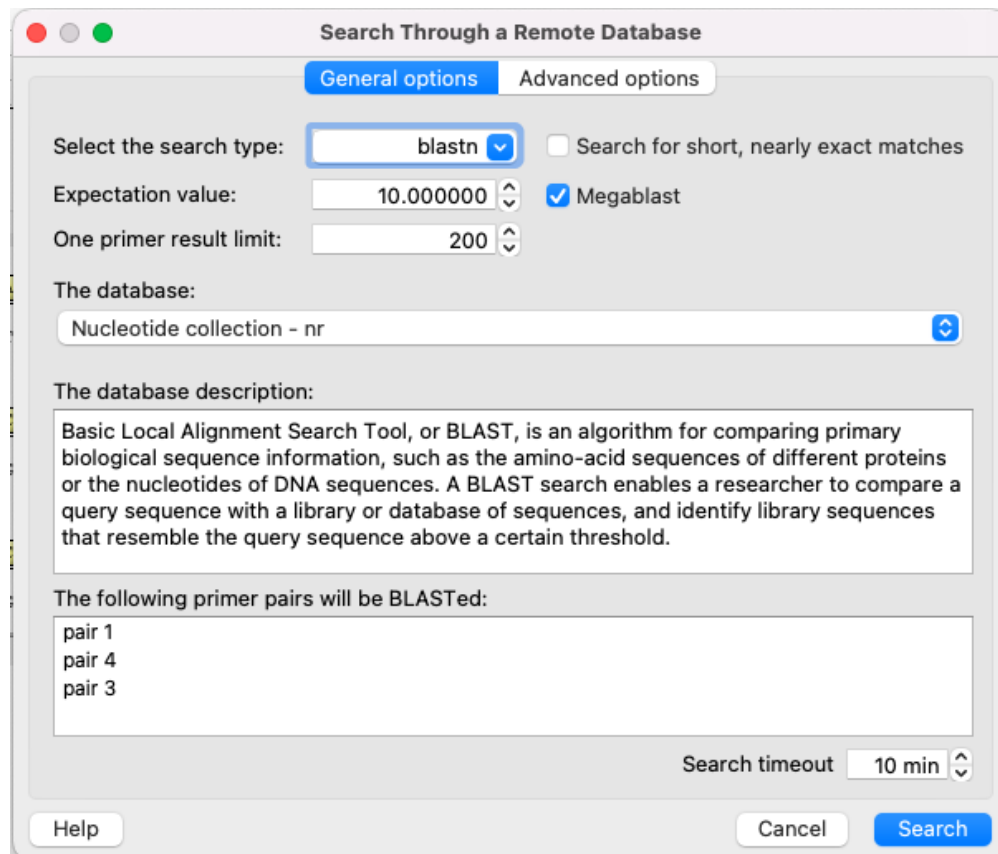
Primer-BLAST

You can run BLAST for primer pairs as in [the corresponding tool](#). This tool allows one to screen primers against user-selected database in order to avoid primer pairs that can cause non-specific amplifications. Your primers should have Primer3 UGENE format. Either get them using [Primer3/Primer3 \(no target sequence\)](#) or create by using the special [Transform into a primer pair](#) feature.

Select primer pairs you need to BLAST:



Click right mouse button Analyze Query NCBI BLAST database....



The following dialog has absolutely the same settings as the regular [Remote BLAST](#) tool, except:

- Instead of "Save annotation(s) to" and "Annotations parameters" settings you can see a list of selected primer pairs. That means, that BLAST will be run three times for three primer pairs - **pair 1**, **pair 4** and **pair 3**. All results will be stored to the annotation group with a primer pair, which was an input for this calculation.
- The "Megablast" option is enabled by default. Disable this option to get more results (it affects calculation time).

