Appendix B - Frequently Asked Questions (FAQ)

General

Where do I get an input file–a transcript annotation in GTF format?

There are multiple resources for annotations, most of them provide the information also in GTF format. One comfortable way is via the UCSC Table Browser. Select the species and genome version on which the annotation should be based on, and the annotation source ("track", for instance RefSeq). Select GTF as output format.

Troubleshooting