# rnaspace.org - a web application for noncoding RNA identification

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# rnaspace.org

## a web application for noncoding RNA identification

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The increasing number of non-protein-coding RNA (ncRNA) discovered since 2000 and the lack of user friendly tools for finding and annotating them, have made necessary to propose to biologists an *in silico* environment allowing structural and functional annotations of these molecules. For the purpose, RNAspace is developed as a collaborative and open software allowing to:

- **run a variety of ncRNA gene finders in an integrated environment**,
- **explore computed results** with dedicated tools for comparison, combination, visualization, alignment and edition of putative ncRNAs,
- and **export** them in various formats (FASTA, GFF, CSV, RNAML).

The platform is a web application available for use on the web site **rnaspace.org** (with limitations on analyzed sequence size and execution time), and for local installation. It is written in Python language using CherryPy web framework (see cherrypy.org) and Cheetah template engine (see cheetahtemplate.org).

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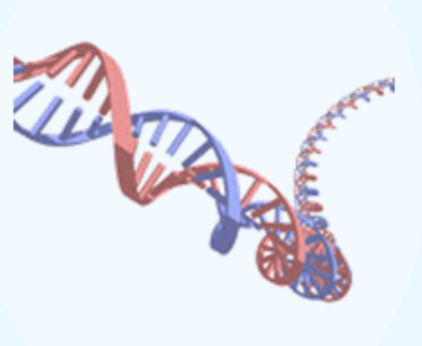
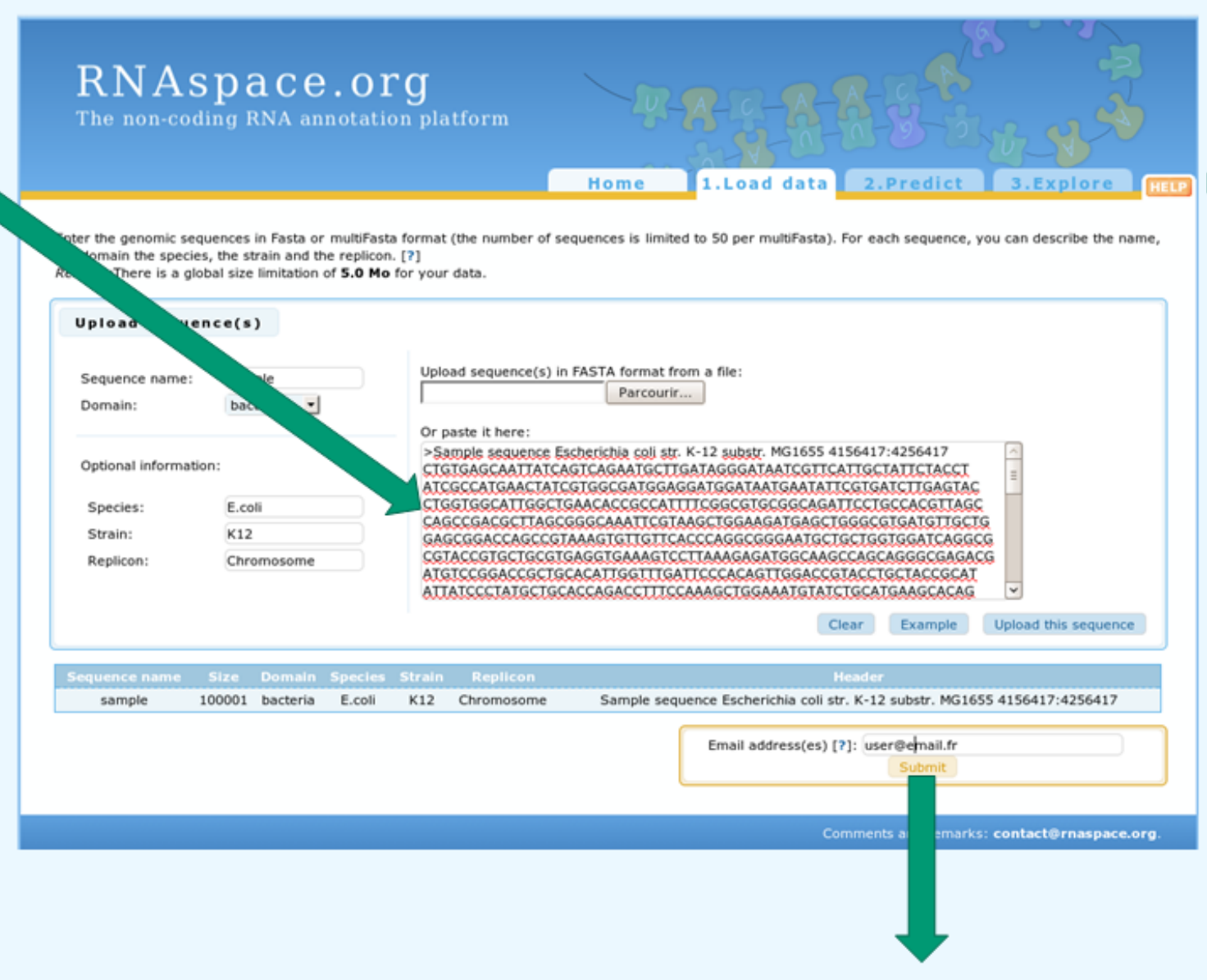
## General workflow



1. Load genomic sequence

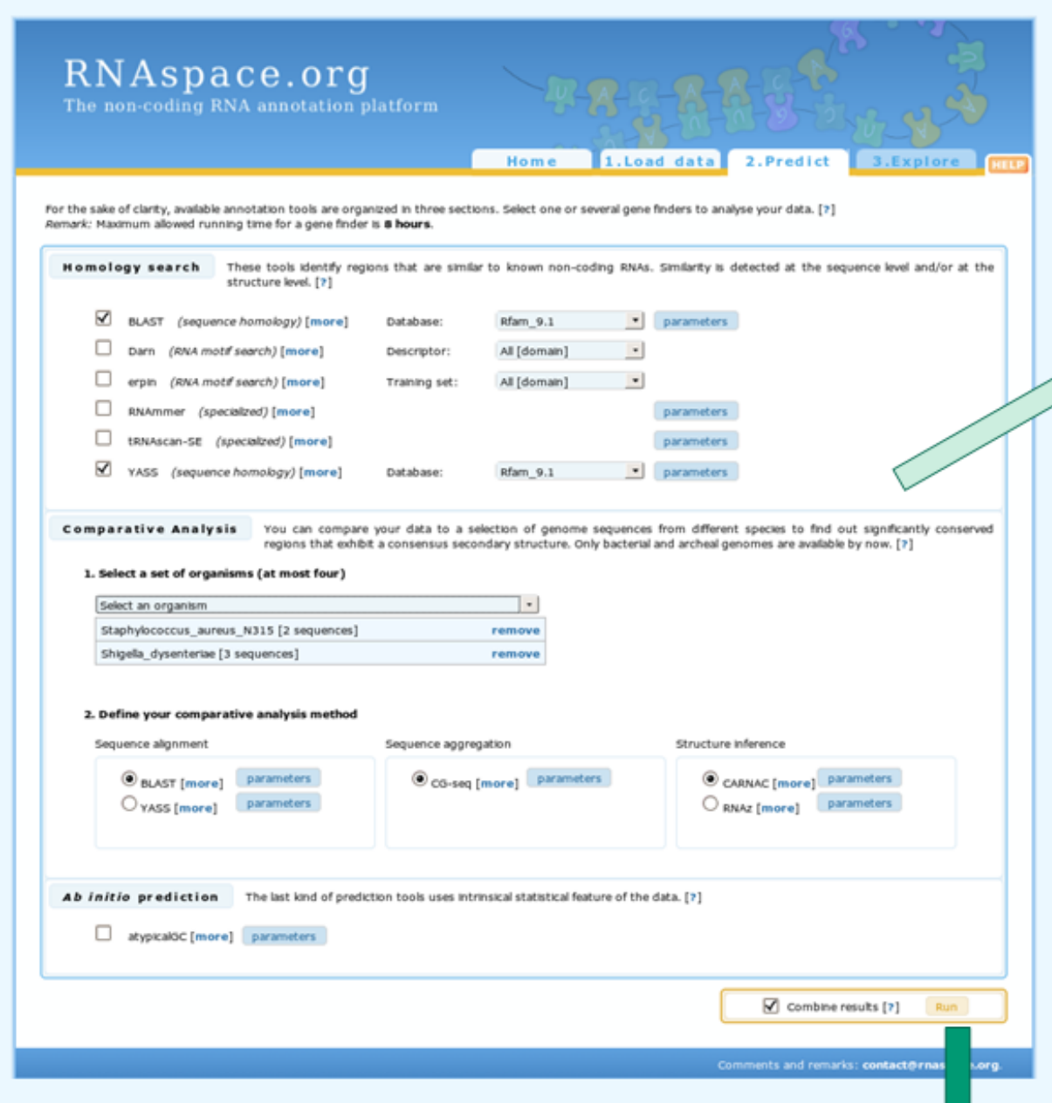


Get help

Gene finders are organized into 3 categories containing respectively:

- **known RNA based gene finders** including
  - (i) sequence homology search tools (BLAST[1], YASS[2]) on ncRNA databases (Rfam[3], miRBase[4], fRNAdb[5]),
  - (ii) general purpose RNA motif search tools (Darn[6], ERPIN[7]),
  - (iii) specialized search tools (RNAmmer[8] for ribosomal RNAs, tRNAscan_SE[9] for transfer RNAs)
- **comparative analysis gene finders** (an *ad hoc* pipeline has been implemented based on BLAST or YASS for similarities search and caRNAc[10] or RNAz[11] for consensus structure inference),
- ***ab initio* gene finders** (one based on detection of atypical GC% regions).

2. Choose and launch gene finders



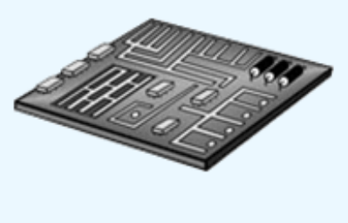
Optionallly, adapt parameters default values of gene finders

**Dynamic exploration (sorting and filtering) of putative ncRNAs** found on the genomic sequence. **Additional information can be computed and/or visualized [12, 13, 14] on line** (*e.g.*, secondary structure [15,16], alignment of predictions[15]) and **saved**.

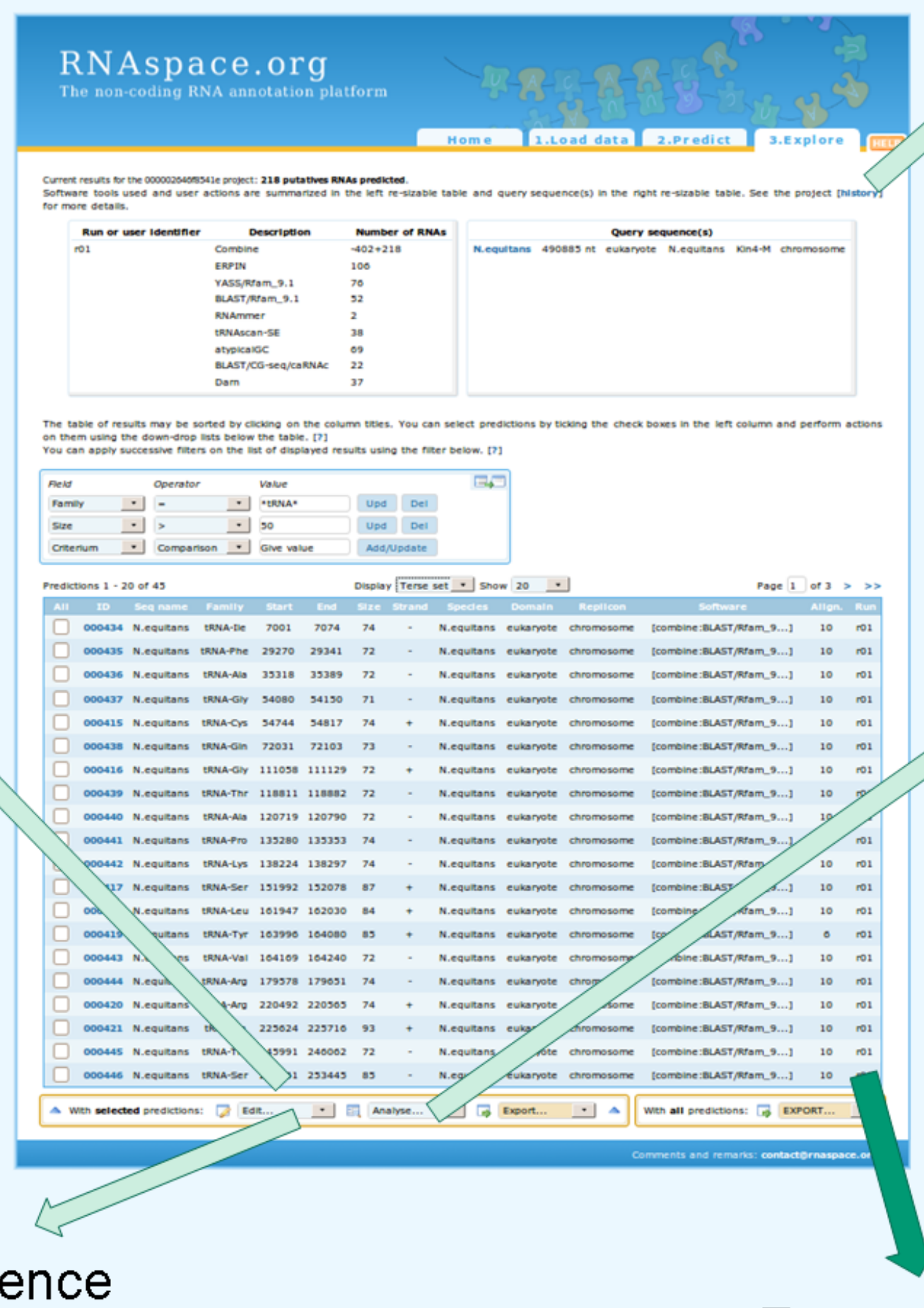
It is also possible to edit and to delete any putative ncRNA.

Get history of actions

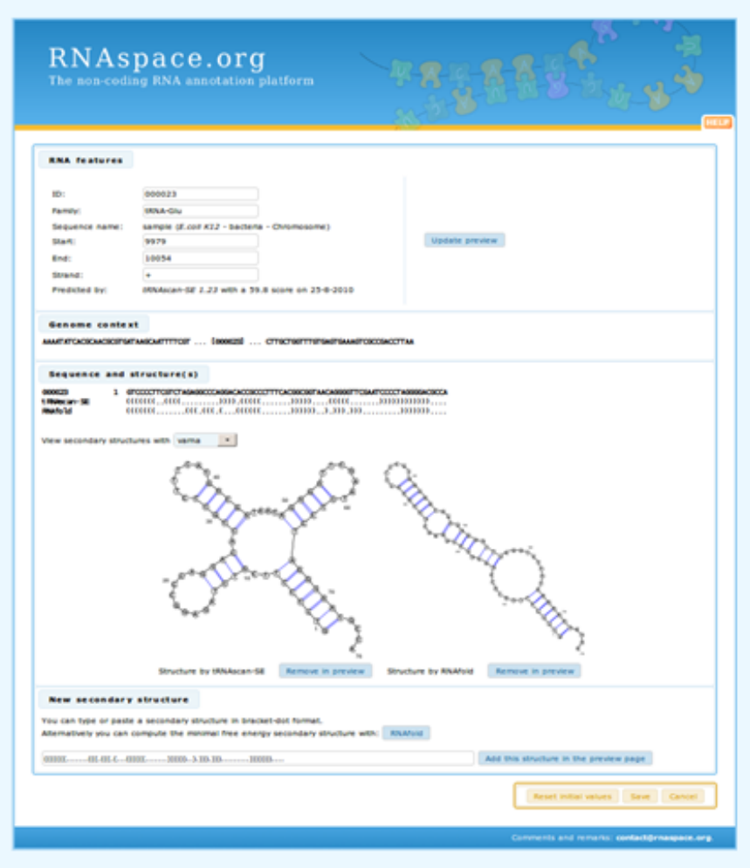
*Computational cluster*



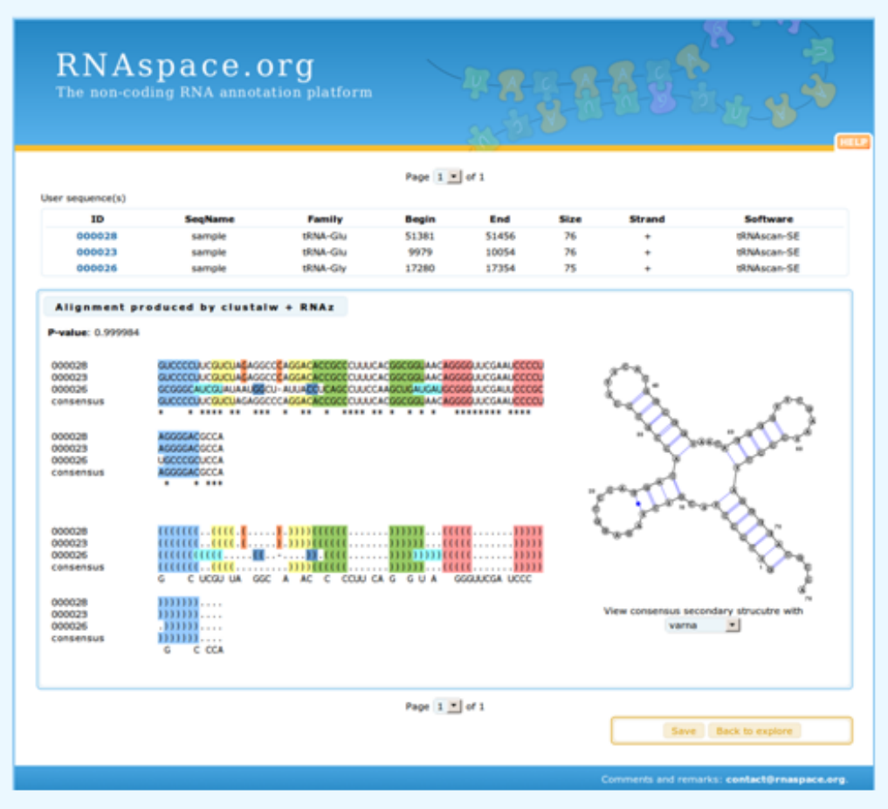
3. Explore ncRNA predictions



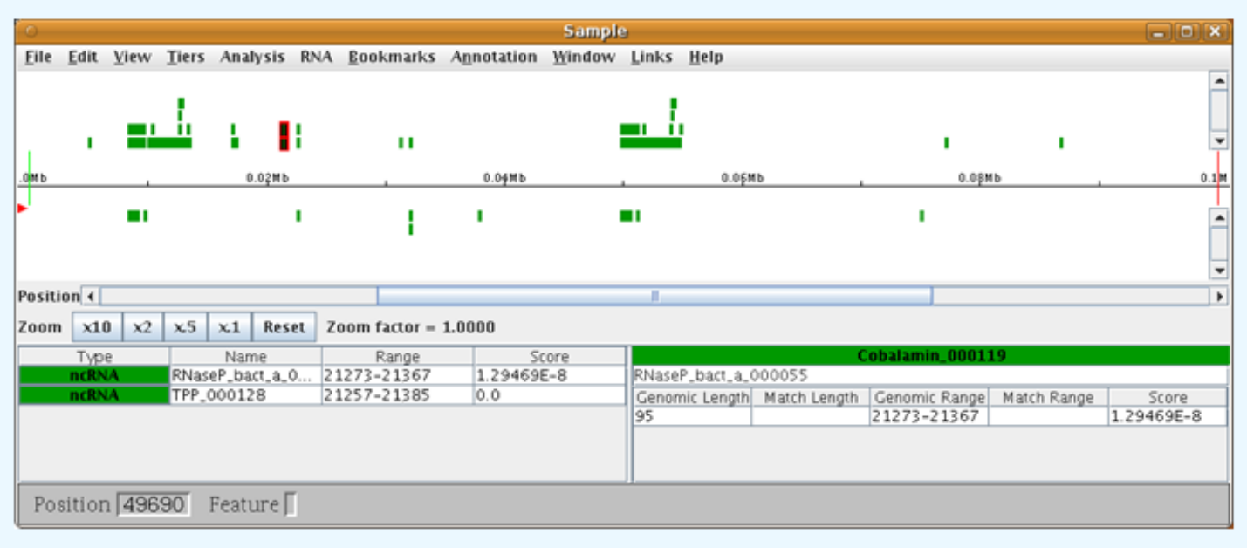
Edit ncRNA prediction

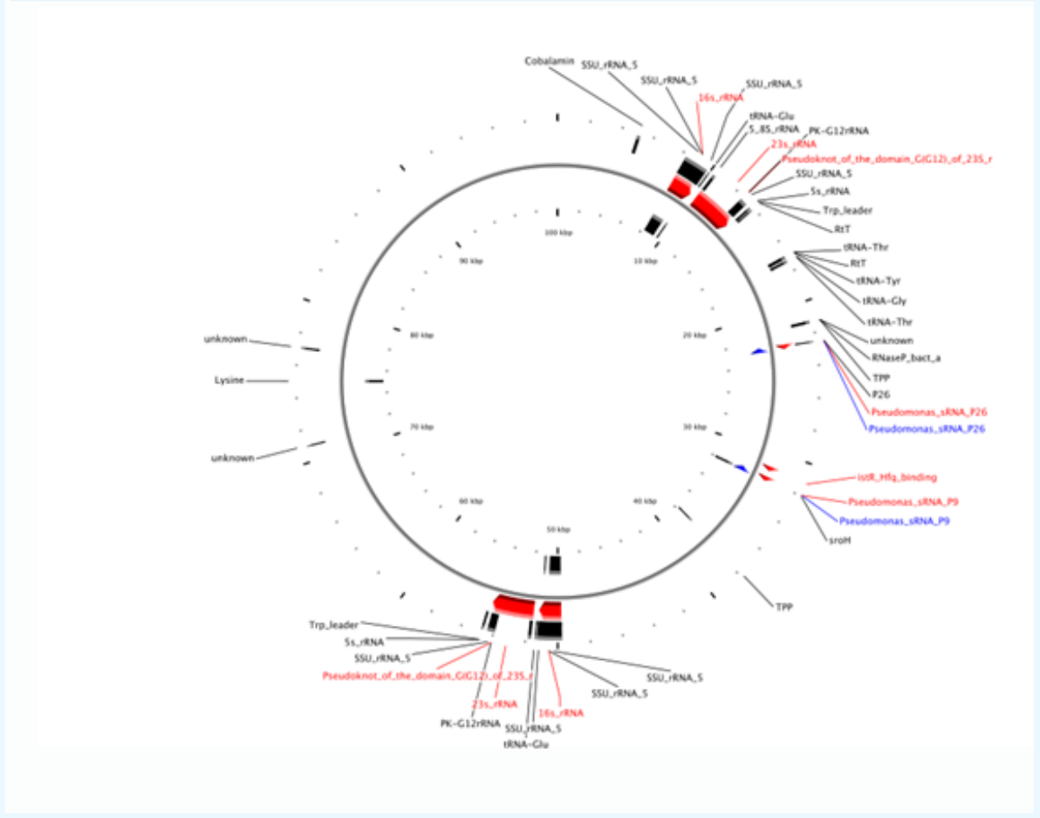


Align predictions

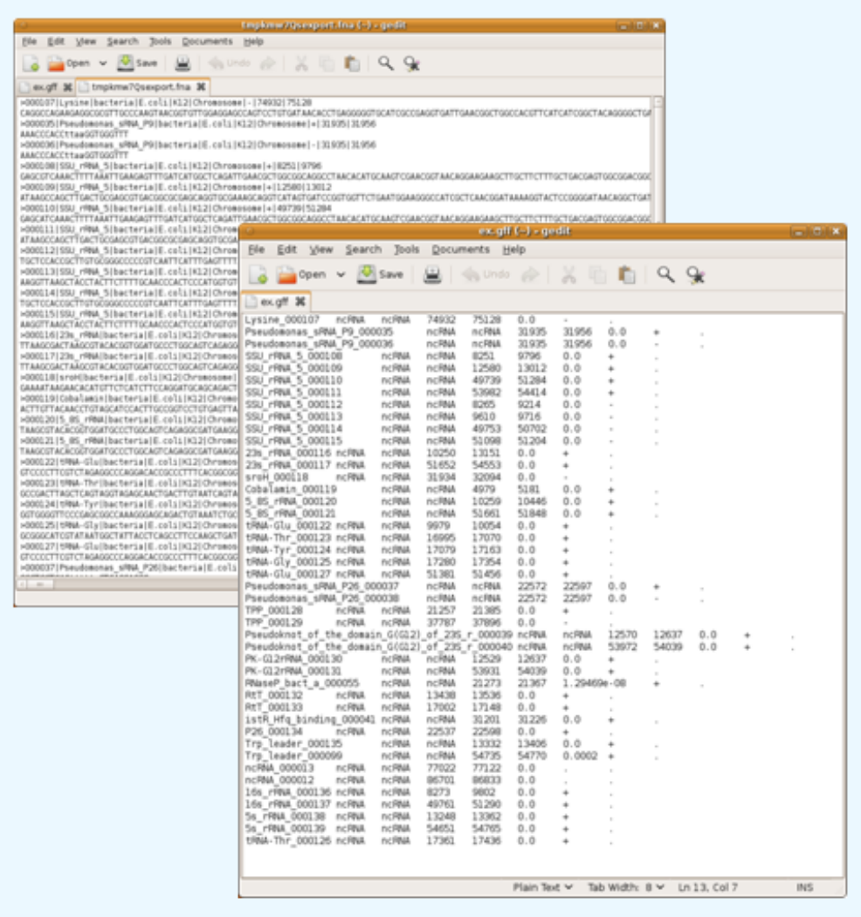


Visualize predictions on the genomic sequence





Export candidates in various formats



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