

# libGenome

## About libGenome

libGenome is a freely available toolkit for developing sequence analysis software in C++. It is intended to take the hassle out of performing common tasks on genetic sequence and annotation data.

Among other things, libGenome can help you:

Read and write Multi-FastA format files

Read and write GenBank flat file database entries

Append, chop, truncate, reverse, complement, translate, and otherwise mangle sequence data

Access annotation in GenBank flat files

libGenome is developed and maintained by Aaron Darling. Its design is based on concepts developed by Aaron Darling, Jason Christensen, Nicole T. Perna, and Bob Mau while working in Frederick R. Blattner's laboratory at the University of Wisconsin Madison.

## Documentation

API documentation for the latest libGenome is automatically generated nightly from our source code repository and available here: <http://gel.ahabs.wisc.edu/apidocs/libGenome>

## Source code repository

We maintain a subversion based source code repository for libGenome as part of the Mauve sourceforge project. The latest source code can be obtained with the following subversion command:

```
svn co https://mauve.svn.sourceforge.net/svnroot/mauve/libGenome/trunk libGenome
```

The source code repository can also be [browsed online](#).

## Download

The latest source code snapshot of libGenome is available from:

<http://gel.ahabs.wisc.edu/mauve/source/snapshots/libgenome-snapshot.tar.gz>

Although nightly snapshots of libGenome are not explicitly tested, they will likely work without issue because libGenome is stable and no longer under active development. Tested libGenome releases are generally made in conjunction with releases of the Mauve genome alignment software. Source code can be found in the versioned mauve release folders here:

<http://gel.ahabs.wisc.edu/mauve/source>