

libClustalW

About libClustalW

libClustalW is a refactorization of the popular Clustal-W 1.8.4 alignment software into a development library. By refactorizing Clustal-W into a library, the various functions implemented in Clustal-W can be called directly by C/C++ programs without forking a separate ClustalW process. In the process of refactorizing, we have attempted to make the fewest possible changes to the original Clustal W 1.8.4 source code.

Documentation

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

Source code repository

We maintain a subversion based source code repository for libClustalW 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/libClustalW/trunk libClustalW
```

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

Download

The latest source code snapshot of libClustalW is available from:

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

Although nightly snapshots of libClustalW are not explicitly tested, they will likely work without issue because libClustalW is stable and no longer under active development. Tested libClustalW 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>