

MAFFT version 7

Multiple alignment program for amino acid or nucleotide sequences



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The pre-compiled packages ([for Macintosh](#), [for Windows](#)) are much easier to install than this!

Source

Download

- [mafft-7.471-with-extensions-src.tgz](#)
(supports RNA structural alignments as well as protein/DNA/RNA sequence alignments; [license notice](#))
- [mafft-7.471-without-extensions-src.tgz](#)
(supports protein/DNA/RNA sequence alignments only; [license notice](#))



Versions 7.380–7.392 had [a bug](#) in the `--add` and `--merge` options.
Versions 7.396–7.468 also had [a bug](#) in parsing input filename.
Please update to version 7.470 or higher.

Installation to /usr/local/ (root account is required)

This procedure requires root access, as programs are installed into `/usr/local/bin/` and `/usr/local/libexec/mafft/` by default. If you want to install MAFFT without being root, [see here](#).

1. Untar the package.

```
% gunzip -cd mafft-x.x-src.tgz | tar xfv -  
% cd mafft-x.x/core/
```

2. (optional) To enable [DASH](#), uncomment the following line in **Makefile**:

```
DASH_CLIENT = dash_client
```

3. Compile and install

```
% make clean  
% make  
% su  
# make install
```

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```
% make
% su
# make install
```

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Installation to a non-default location (root account is not required)

[See here.](#)