

MMASS(3)

MMASS(3)

NAME

`mmass-modules` – a free mass spectrometry tool for proteomics — C-based extension modules

SYNOPSIS

`mmass-modules`

DESCRIPTION

This manual page briefly documents the **mmass-modules** package, a package that ships C-language extensions to the **mmass** package.

The **mmass-modules** package currently ships only one extension, the *calculations.so* extensions that is used to perform high performance calculations routines in the mass spectrum plotting module.

SEE ALSO

`mmass` (1), `mmass-doc`(7).

AUTHORS

Martin Strohalm <support@mmass.org>

Program author (contact him via <http://www.mmass.org> website's form).

Filippo Rusconi <rusconi-debian@laposte.net>

Man-page author for the Debian distribution.

COPYRIGHT

Copyright © 2005-2010 Martin Strohalm

Copyright © 2011 Filippo Rusconi

This manual page was written by Filippo Rusconi <rusconi-debian AT laposte DOT net> for the Debian system (but may be used by others). Permission is granted to copy, distribute and/or modify this document under the terms of the GNU General Public License, Version 3, published by the Free Software Foundation.

On a Debian system the complete text of the GNU General Public License version 3 can be found in the file *'/usr/share/common-licenses/GPL-3'*.

