

# Package ‘cytolib’

March 31, 2025

**Type** Package

**Title** C++ infrastructure for representing and interacting with the gated cytometry data

**Version** 2.18.2

**Date** 2017-08-07

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**Description** This package provides the core data structure and API to represent and interact with the gated cytometry data.

**License** AGPL-3.0-only

**License\_restricts\_use** no

**LazyLoad** yes

**Imports** RProtoBufLib

**Depends** R (>= 3.4)

**Suggests** knitr, rmarkdown

**LinkingTo** BH(>= 1.84.0.0), RProtoBufLib(>= 2.13.1), Rhdf5lib

**biocViews** ImmunoOncology, FlowCytometry, DataImport, Preprocessing, DataRepresentation

**VignetteBuilder** knitr

**SystemRequirements** GNU make, C++11

**RoxygenNote** 7.1.2

**Biarch** TRUE

**git\_url** <https://git.bioconductor.org/packages/cytolib>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** 77ce963

**git\_last\_commit\_date** 2025-01-20

**Repository** Bioconductor 3.20

**Date/Publication** 2025-03-31

## Contents

cytolib_LdFlags . . . . .	2
<b>Index</b>	<b>3</b>

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cytolib_LdFlags	<i>Output the LD flags for building against cytolib. These flags are propagated to sourceCpp via the inlineCxxPlugin (defined below) and to packages via a line in Makevars[.win] like this:</i>
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**Description**

```
PKG_LIBS += $(shell "$R_HOME/bin/$R_ARCH_BIN/Rscript.exe" -e "cytolib::cytolib_LdFlags()")
```

**Usage**

```
cytolib_LdFlags()
```

# Index

cytolib\_LdFlags, [2](#)