

# Package ‘rhdf5filters’

March 26, 2024

**Type** Package

**Title** HDF5 Compression Filters

**Version** 1.14.1

**Description** Provides a collection of additional compression filters for HDF5 datasets. The package is intended to provide seamless integration with rhdf5, however the compiled filters can also be used with external applications.

**License** BSD\_2\_clause + file LICENSE

**LazyLoad** true

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown, tinytest, rhdf5 (>= 2.34.0)

**SystemRequirements** GNU make

**URL** <https://github.com/grimbough/rhdf5filters>

**BugReports** <https://github.com/grimbough/rhdf5filters>

**LinkingTo** Rhdf5lib

**RoxygenNote** 7.2.3

**Encoding** UTF-8

**biocViews** Infrastructure, DataImport

**git\_url** <https://git.bioconductor.org/packages/rhdf5filters>

**git\_branch** RELEASE\_3\_18

**git\_last\_commit** 2a2e71e

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**Repository** Bioconductor 3.18

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available_filters	<i>Return a list of installed filters</i>
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**Description**

This function can be used to produce a vector of the installed filters.

**Usage**

```
available_filters()
```

**Value**

A character vector containing the names of the installed filters.

**Examples**

```
available_filters()
```

hdf5_plugin_path	<i>Return location of installed filters</i>
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**Description**

This function can be used to find the location of the installed filters. Setting the environment variable HDF5\_PLUGIN\_PATH to this value will allow other applications that require the the filters to use the versions distributed with this package.

**Usage**

```
hdf5_plugin_path()
```

**Value**

A character string containing the path where the compiled filters are located.

**Examples**

```
hdf5_plugin_path()
```

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rhdf5filters

*rhdf5filters*

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**Description**

This package provides several HDF5 compression filters for use with rhdf5 or other tools using HDF5.

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