Package 'SHlite'

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Type Package

Title Advises the user on the quality of Seahorse data

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Description The main function sh_full() gives an overview of how often each well within the dataset deviates from the mean +- sd of the measurement.

License file LICENSE

Encoding UTF-8

LazyData true

Imports utils

R topics documented:

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sh_full	*Seahorse Full function*

Description

Gives an overview of how often each well within each group of the dataset deviates from the mean +- sd of the measurement.

Usage

```
sh_full(input, check.min=T, assay="ms", save.out=F, custom, save.name="output.txt")
```

Arguments

`input`	A .csv file containing all measurements for all wells of the groups to analyze.
`check.min`	A logical value indicating whether columns containing NA values should be removed. Default TRUE
`assay`	Either 'ms' for mitrostress, 'gs' for glucostress or 'custom'. Default 'ms'
`save.out`	Saves the output of the analysis to a .txt document. New results will be appended to the file. Default F
`custom`	Please fill in if assay = 'custom'. Has to be a numeric vector (e.g. custom = c(1:2,5:8))
`save.name`	A string to a .txt file to which the output should be appended. The default saves the output in the project folder, this can however be changes by adding other destinations. Default "output.txt"

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