

# Package ‘proteomicsCV’

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**Type** Package

**Title** Calculates the Percentage CV for Mass Spectrometry-Based Proteomics Data

**Version** 0.2.5

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**Description** Calculates the percentage coefficient of variation (CV) for mass spectrometry-based proteomic data. The CV can be calculated with the traditional formula for raw (non log transformed) intensity data, or log transformed data. This package currently does not reference any academic publication.

**License** MIT + file LICENSE

**Encoding** UTF-8

**Imports** stats

**RoxygenNote** 7.2.3

**NeedsCompilation** no

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**Repository** CRAN

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## Description

Calculates the percentage CV for intensity based proteomic data.

**Usage**

```
protLogCV(data, log_transformed)
protCV(data)
```

**Arguments**

**data** input dataframe of the intensity values. These should be normalised already for optimal results.

**log\_transformed** 'no' for data that has not been log transformed. 'yes' for natural log transformed data. (log() function in R)

**Value**

returns a list of percentage CVs

**Author(s)**

Alejandro J. Brenes

**Examples**

```
library(proteomicsCV)
intensity_df<-data.frame(intensity1=c(23.88,23.55,23.41,23.15),
                          intensity2=c(23.98,23.56,23.43,23.29),
                          intensity3=c(23.94,23.635,23.37,23.21),
                          intensity4=c(23.81,23.57,23.54,23.08))

# log formula with the data already transformed to natural log
cvs<-protLogCV(intensity_df, "yes")
# log formula with the data not log transformed
not_log_intensity_df<-exp(1)^intensity_df
cvs<-protLogCV(not_log_intensity_df,"no")
# base formula with raw intensity (no log transformation)
raw_cvs<-protCV(not_log_intensity_df)
```

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