

# Package: proteomicsCV (via r-universe)

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**Type** Package

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

**Version** 0.4.0

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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.

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**Encoding** UTF-8

**Imports** stats

**RoxygenNote** 7.3.2

**NeedsCompilation** no

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**Repository** CRAN

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### Description

Calculates the percentage CV for intensity based proteomic data.

### Usage

```
protLogCV(logData, base)
protCV(data)
```

### Arguments

data	input dataframe of the intensity values.
logData	input dataframe of the log transformed intensity values.
base	numerical base of the logarithm that was used to transform the data. Values that are accepted are 2 (for log2) and 10 (for log10)

### Value

returns a list containing the percentage CVs

### Author(s)

Alejandro J. Brenes

### References

<https://www.biorxiv.org/content/10.1101/2024.09.11.612398v1>

### Examples

```
library(proteomicsCV)
log_intensity_df<-data.frame(intensity1=c(16.93157,26.57542,19.90749,18.86056),
                             intensity2=c(17.16546,27.77706,19.45854,19.60721),
                             intensity3=c(17.04260,27.21697,19.70314,16.19530),
                             intensity4=c(17.08473,26.99766,17.93342,17.97693))

# log formula with the data already transformed to log2
cvs<-protLogCV(log_intensity_df, 2)
# log formula with the data not log transformed
not_log_intensity_df<-data.frame(intensity1=c(125000,100000000,983450,475987),
                                 intensity2=c(147000,230000000,720450,798656),
                                 intensity3=c(135000,156000000,853566,75036),
                                 intensity4=c(139000,134000000,250321,257986))
# base formula with raw intensity (no log transformation)
raw_cvs<-protCV(not_log_intensity_df)
```

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