







Functional analysis





Miscellaneous



Quality control



Relative  
quantification



MS  
stats

The logo features a stylized blue wave graphic on the left, composed of multiple overlapping, slightly offset lines that create a sense of depth and movement. To the right of the wave, the letters "MS" are displayed in a large, bold, blue serif font. Below "MS", the word "stats" is written in a smaller, grey, lowercase sans-serif font. The entire logo is set against a white background with a light grey shadow at the bottom.

antsQuantification(“config.yaml”)









Input Files



keys.txt



evidence.txt

contrast.txt

config.yaml

# artMS

**Analytical R Tools  
for Mass Spectrometry**

<http://artms.org>



> |

```
> artmsQuantification(yaml_config_file = "config-phgglobal.yaml")
```

## artMS: Relative Quantification using MSstats

---

```
>> Reading the configuration file
-- Folder: [quant-phglobal-pre] created
>> LOADING DATA
>> MERGING FILES
>> FILTERING
-- Contaminants CON__IREV__ removed
-- Removing protein groups
---- Use <Leading.razor.protein> as Protein ID
>> CONVERTING THE DATA TO MSSTATS FORMAT
-- Selecting Sequence Type: MaxQuant 'Modified.sequence' column
-- Adding NA values for missing values (required by MSstats)
-- Write out the MSstats input file (-mss.txt)
>> RUNNING MSstats (it usually takes a 'long' time: please, be patient)
      (MSstats messages are turned off.
      Select <display_msstats = TRUE> to activate MSstats outputs)
>> MSstats done
>> ANNOTATING THE RESULTS (adding gene symbols and protein names)
-- Selected hits for plots with LFC between -0.58 and 0.58 at 0.05 FDR:1207
>> PLOTTING HEATMAP FOR SIGNIFICANT CHANGES
>> PLOTTING VOLCANO PLOT
quant-phglobal-pre/phglobal-results-volcano.pdf is ready
>> ANALYSIS COMPLETED
```



# artMS

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Input Files

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Quality control



Relative  
quantification

**artmsQuantification("config.yaml")**

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Console

Terminal x

~/

```
> artmsQuantification(yaml_config_file = "config-phgglobal.yaml")
```

-----  
artMS: Relative Quantification using MSstats  
-----

>> Reading the configuration file

-- Folder: [quant-phgglobal-pre] created

>> LOADING DATA

>> MERGING FILES

>> FILTERING

-- Contaminants CON\_\_IREV\_\_ removed

-- Removing protein groups

---- Use <Leading.razor.protein> as Protein ID

>> CONVERTING THE DATA TO MSSTATS FORMAT

-- Selecting Sequence Type: MaxQuant 'Modified.sequence' column

-- Adding NA values for missing values (required by MSstats)

-- Write out the MSstats input file (-mss.txt)

>> RUNNING MSstats (it usually takes a 'long' time: please, be patient)  
(MSstats messages are turned off.

Select <display\_msstats = TRUE> to activate MSstats outputs)

>> MSstats done

>> ANNOTATING THE RESULTS (adding gene symbols and protein names)

-- Selected hits for plots with LFC between -0.58 and 0.58 at 0.05 FDR:1207

>> PLOTTING HEATMAP FOR SIGNIFICANT CHANGES

>> PLOTTING VOLCANO PLOT

quant-phgglobal-pre/phgglobal-results-volcano.pdf is ready

>> ANALYSIS COMPLETED

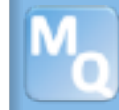
# artMS

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**artmsQuantification("config.yaml")** →

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