





```
1 files:
2   evidence: evidence.txt
3   keys: keys.txt
4   contrasts: contrast.txt
5   summary: summary.txt
6   output: phglobal_results/phglobal-results.txt
7 qc:
8   basic: 1
9   extended: 1
10  extendedSummary: 1
11 data:
12   enabled: 1
13   fractions:
14     enabled: 0
15   silac:
16     enabled: 0
17   filters:
18     enabled: 1
19     contaminants: 1
20     protein_groups: remove
21     modifications: PH
22   sample_plots: 1
23 msstats:
24   enabled: 1
25   msstats_input:
26   profilePlots: none
27   normalization_method: equalizeMedians
28   normalization_reference:
29   summaryMethod: TMP
30   censoredInt: NA
31   cutoffCensored: minFeature
32   MBimpute: 1
33   feature_subset: all
34 output_extras:
35   enabled: 1
36   annotate:
37     enabled: 1
38     species: HUMAN
39   plots:
40     volcano: 1
41     heatmap: 1
42     LFC: -0.58 0.58
43     FDR: 0.05
44     heatmap_cluster_cols: 0
45     heatmap_display: log2FC
```

config.yaml

configuration

Files



Quality control



Relative  
quantification



Functional analysis



Miscellaneous



# artMS

**Analytical R Tools  
for Mass Spectrometry**

<http://artms.org>





Q

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