

User Input Testing

This document displays a number of example searches that constitute user input data in different formats.

- i) [User input AZ20.tsv](#)
- ii) [User input AZ20.tsv, however missing the CV column](#)
- iii) [User input AZ20.tsv, however CV column is in a random location](#)
- iv) [User input AZ20.tsv, however the residue type and number does not contain any 'nones'](#)
- v) [User input AZ20.tsv, however the substrate name column has been placed as the final column](#)
- vi) [User input AZ20.tsv, however the substrate name column has been placed in a random position](#)
- vii) [User input AZ20.tsv, however the p values column is missing](#)
- viii) [User input AZ20.tsv, however the p values column is in a random column](#)
- ix) [User input AZ20.tsv, however the fold values column is missing](#)
- x) [User input AZ20.tsv, however the fold values column has been moved to a different column](#)

Test case scenario 1 = User input AZ20.tsv



Online analysis for your phospho-proteomics data

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A csv file of the analysed data is provided for download when the analysis is finished and individual data charts can be saved from the site.

Please see [the documentation](#) for information about how to format your datafile correctly and for further information about the analysis output results.

We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

Choose File az20.tsv

Upload

Data analysis takes some time - Please wait

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Results for AZ20.tsv are as follows with no error messages displayed.

File az20 successfully analysed

Phospho-proteomics Data Analysis Results

Processed Table

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Kinase & Substrate Frequencies

Kinase activities

Summary Charts

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General overview: This table corresponds to hits, whose corrected p-values meet an error rate threshold of ≤ 0.05 and have a CV of $\leq 25\%$. If the original upload table didn't include CV columns, then only the p-value threshold is applied.

Clickable entries: Try clicking entries in columns: *Substrate/Isoform in DB (gene name)*, *Phosphosite in DB (ID)* and *Kinase in DB (gene name)*. We guarantee a pleasant journey!

Intensity columns: Original intensity values were transformed by dividing each substrate/site intensity by the maximum intensity of the row (both conditions). This scaling allows the application of a heatmap to the cells, for visual clarification of intensity differences.

Log2 fold changes: Barplots are integrated into the column, that scale with the fold change values. *Note:* Cells that are fully coloured, denote hits detected in only one condition (see intensity columns).

Sorting: The Log2 fold changes are used, giving a gradated ordering of hits as you scroll through the table.

| Number | Substrate (gene name) | Phospho site ID | Substrate/Isoform in DB (gene name) | Phosphosite in DB (ID) | Kinase in DB (gene name) | Fold control intensity over maximum | Fold condition intensity over maximum | Log2 fold change - condition over control | corrected p-value |
|--------|-----------------------|-----------------|-------------------------------------|------------------------|--------------------------|-------------------------------------|---------------------------------------|---|-------------------|
| 1 | SYNE2 | S6361 | SYNE2 | S6361 | not in DB | 0 | 1 | | 0.00092 |
| 2 | GTF3C1 | S739 | GTF3C1 | S739 | not in DB | 0 | 1 | | 0.0012 |
| 3 | WWC3 | T909 | WWC3 | T909 | not in DB | 0 | 1 | | 0.0063 |
| 4 | PLEC | S4626 | PLEC | S4626 | not in DB | 0 | 1 | | 0.0085 |
| 5 | CTAGE5 | S559 | not in DB | not in DB | not in DB | 0 | 1 | | 0.0088 |
| 6 | SNRNP70 | S410 | SNRNP70 | S410 | not in DB | 0 | 1 | | 0.0091 |
| 7 | CC2D1A | S118 | CC2D1A | S118 | not in DB | 0 | 1 | | 0.011 |
| 8 | PACS1 | S430 | PACS1 | S430 | not in DB | 0 | 1 | | 0.014 |
| 9 | TMF1 | S112 | TMF1 | S112 | not in DB | 0 | 1 | | 0.014 |
| 10 | TRPS1 | S1041 | TRPS1 | S1041 | not in DB | 0 | 1 | | 0.015 |
| 11 | ZFHX3 | S2230 | ZFHX3 | S2230 | not in DB | 0 | 1 | | 0.021 |
| 12 | ZFHX3 | S2226 | ZFHX3 | S2226 | not in DB | 0 | 1 | | 0.021 |
| 13 | FOXK1 | T436 | FOXK1 | T436 | not in DB | 0.15 | 1 | 2.7 | 0.00048 |
| 14 | FOXK1 | S441 | FOXK1 | S441 | not in DB | 0.15 | 1 | 2.7 | 0.00048 |

Test case scenario 2 = User input AZ20.tsv, however missing the CV column



Online analysis for your phospho-proteomics data

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A csv file of the analysed data is provided for download when the analysis is finished and individual data charts can be saved from the site.

Please see [the documentation](#) for information about how to format your datafile correctly and for further information about the analysis output results.

We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

az20_no_cv.tsv

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Results for AZ20.tsv without the CV column. Here, the data analysis is still performed, however if the original file does not include a CV column, then only the p-value threshold is applied towards the calculation.

File az20_no_cv.s successfully analysed

Phospho-proteomics Data Analysis Results

Processed Table

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Kinase & Substrate Frequencies

Kinase activities

Summary Charts

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General overview: This table corresponds to hits, whose corrected p-values meet an error rate threshold of ≤ 0.05 and have a CV of $\leq 25\%$. If the original upload table didn't include CV columns, then only the p-value threshold is applied.

Clickable entries: Try clicking entries in columns: *Substrate/Isoform in DB (gene name)*, *Phosphosite in DB (ID)* and *Kinase in DB (gene name)*. We guarantee a pleasant journey!

Intensity columns: Original intensity values were transformed by dividing each substrate/site intensity by the maximum intensity of the row (both conditions). This scaling allows the application of a heatmap to the cells, for visual clarification of intensity differences.

Log2 fold changes: Barplots are integrated into the column, that scale with the fold change values. *Note:* Cells that are fully coloured, denote hits detected in only one condition (see intensity columns).

Sorting: The Log2 fold changes are used, giving a gradated ordering of hits as you scroll through the table.

| Number | Substrate (gene name) | Phospho site ID | Substrate/Isoform in DB (gene name) | Phosphosite in DB (ID) | Kinase in DB (gene name) | Fold control intensity over maximum | Fold condition intensity over maximum | Log2 fold change - condition over control | corrected p-value |
|--------|-----------------------|-----------------|-------------------------------------|------------------------|--------------------------|-------------------------------------|---------------------------------------|---|-------------------|
| 1 | SYNE2 | S6361 | SYNE2 | S6361 | not in DB | 0 | 1 | | 0.00092 |
| 2 | GTF3C1 | S739 | GTF3C1 | S739 | not in DB | 0 | 1 | | 0.0012 |
| 3 | WWC3 | T909 | WWC3 | T909 | not in DB | 0 | 1 | | 0.0063 |
| 4 | PLEC | S4626 | PLEC | S4626 | not in DB | 0 | 1 | | 0.0085 |
| 5 | CTAGE5 | S559 | not in DB | not in DB | not in DB | 0 | 1 | | 0.0088 |
| 6 | SNRNP70 | S410 | SNRNP70 | S410 | not in DB | 0 | 1 | | 0.0091 |
| 7 | CC2D1A | S118 | CC2D1A | S118 | not in DB | 0 | 1 | | 0.011 |
| 8 | PACS1 | S430 | PACS1 | S430 | not in DB | 0 | 1 | | 0.014 |
| 9 | TMF1 | S112 | TMF1 | S112 | not in DB | 0 | 1 | | 0.014 |
| 10 | TRPS1 | S1041 | TRPS1 | S1041 | not in DB | 0 | 1 | | 0.015 |
| 11 | ZFHX3 | S2230 | ZFHX3 | S2230 | not in DB | 0 | 1 | | 0.021 |
| 12 | ZFHX3 | S2226 | ZFHX3 | S2226 | not in DB | 0 | 1 | | 0.021 |
| 13 | VANGL1 | S86 | VANGL1 | S86 | not in DB | 0 | 1 | | 0.024 |
| 14 | VANGL1 | S88 | VANGL1 | S88 | not in DB | 0 | 1 | | 0.024 |
| 15 | RRP1B | S458 | RRP1B | S458 | not in DB | 0 | 1 | | 0.029 |

Test case scenario 3 = User input AZ20.tsv, however the CV column is in a random location



Online analysis for your phospho-proteomics data

All analysis on this website is done *on the fly*, therefore please do not click back or other links (in same tab) unless you have finished looking through your results.

A csv file of the analysed data is provided for download when the analysis is finished and individual data charts can be saved from the site.

Please see [the documentation](#) for information about how to format your datafile correctly and for further information about the analysis output results.

We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

az2o_cvs_asRandomColumn.tsv

Data analysis takes some time - Please wait

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Results for AZ20.tsv with the CV columns in a different location. Here, the data analysis does not perform, as it expects the CV columns to be at the end of the user data file.

Anomaly detected..PhosphoQuest will self-destruct in T minus 10 seconds...just kidding! Please check your fold change calculations, a discrepancy has been detected.



Online analysis for your phospho-proteomics data

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We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

No file chosen

Data analysis takes some time - Please wait

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Test case scenario 4 = User input AZ20.tsv, however the residue type and number does not contain any 'nones'



Online analysis for your phospho-proteomics data

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A csv file of the analysed data is provided for download when the analysis is finished and individual data charts can be saved from the site.

Please see [the documentation](#) for information about how to format your datafile correctly and for further information about the analysis output results.

We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

Choose File az20_no_nones.tsv

Upload

Data analysis takes some time - Please wait

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Results for AZ20.tsv_noNones show that the analysis functions as normal and the lack of 'nones' within the substrate column does not affect the analysis.

File az20_no_nones successfully analysed

Phospho-proteomics Data Analysis Results

Processed Table

Volcano Plot

Kinase & Substrate Frequencies

Kinase activities

Summary Charts

Download data

General overview: This table corresponds to hits, whose corrected p-values meet an error rate threshold of ≤ 0.05 and have a CV of $\leq 25\%$. If the original upload table didn't include CV columns, then only the p-value threshold is applied.

Clickable entries: Try clicking entries in columns: *Substrate/Isoform in DB (gene name)*, *Phosphosite in DB (ID)* and *Kinase in DB (gene name)*. We guarantee a pleasant journey!

Intensity columns: Original intensity values were transformed by dividing each substrate/site intensity by the maximum intensity of the row (both conditions). This scaling allows the application of a heatmap to the cells, for visual clarification of intensity differences.

Log2 fold changes: Barplots are integrated into the column, that scale with the fold change values. *Note:* Cells that are fully coloured, denote hits detected in only one condition (see intensity columns).

Sorting: The Log2 fold changes are used, giving a graduated ordering of hits as you scroll through the table.

| Number | Substrate (gene name) | Phospho site ID | Substrate/Isoform in DB (gene name) | Phosphosite in DB (ID) | Kinase in DB (gene name) | Fold control intensity over maximum | Fold condition intensity over maximum | Log2 fold change - condition over control | corrected p-value |
|--------|-----------------------|-----------------|-------------------------------------|------------------------|--------------------------|-------------------------------------|---------------------------------------|---|-------------------|
| 1 | SYNE2 | S6361 | SYNE2 | S6361 | not in DB | 0 | 1 | | 0.00092 |
| 2 | GTF3C1 | S739 | GTF3C1 | S739 | not in DB | 0 | 1 | | 0.0012 |
| 3 | WWC3 | T909 | WWC3 | T909 | not in DB | 0 | 1 | | 0.0063 |
| 4 | PLEC | S4626 | PLEC | S4626 | not in DB | 0 | 1 | | 0.0085 |
| 5 | CTAGE5 | S559 | not in DB | not in DB | not in DB | 0 | 1 | | 0.0088 |
| 6 | SNRNP70 | S410 | SNRNP70 | S410 | not in DB | 0 | 1 | | 0.0091 |
| 7 | CC2D1A | S118 | CC2D1A | S118 | not in DB | 0 | 1 | | 0.011 |
| 8 | PACS1 | S430 | PACS1 | S430 | not in DB | 0 | 1 | | 0.014 |
| 9 | TMF1 | S112 | TMF1 | S112 | not in DB | 0 | 1 | | 0.014 |
| 10 | TRPS1 | S1041 | TRPS1 | S1041 | not in DB | 0 | 1 | | 0.015 |
| 11 | ZFHX3 | S2230 | ZFHX3 | S2230 | not in DB | 0 | 1 | | 0.021 |
| 12 | ZFHX3 | S2226 | ZFHX3 | S2226 | not in DB | 0 | 1 | | 0.021 |
| 13 | FOXK1 | T436 | FOXK1 | T436 | not in DB | 0.15 | 1 | 2.7 | 0.00048 |

Test case scenario 5 = User input AZ20.tsv, however the substrate name column has been placed as the final column



Online analysis for your phospho-proteomics data

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A csv file of the analysed data is provided for download when the analysis is finished and individual data charts can be saved from the site.

Please see [the documentation](#) for information about how to format your datafile correctly and for further information about the analysis output results.

We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

az20_substrateColumn_asFinalColumn.tsv

Data analysis takes some time - Please wait

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Results for AZ20.tsvsubstrateColumnasFinalColumn show that the current analysis requires the substrate name information to be as the first column of the user input file.

An error occurred please try again

could not convert string to float: '1A24_HUMAN(S356)'

Sadly the dragons ate your analysis

An error occurred



Please restart your PhosphoQuest.

[Try going back to analysis](#)

Test case scenario 6 = User input AZ20.tsv, however the substrate name column has been placed in a random position



Online analysis for your phospho-proteomics data

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We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

az20_substrateColumn_asRandomColumn.tsv

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Results for *AZ20.tsvsubstrateColumnasRandomColumn* show that the current analysis requires the substrate name information to be as the first column of the user input file.

An error occurred please try again

could not convert string to float: '1A24_HUMAN(S356)'

Sadly the dragons ate your analysis

An error occurred



Please restart your PhosphoQuest.

[Try going back to analysis](#)

Test case scenario 7 = User input AZ20.tsv, however the p values column is missing



Online analysis for your phospho-proteomics data

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A csv file of the analysed data is provided for download when the analysis is finished and individual data charts can be saved from the site.

Please see [the documentation](#) for information about how to format your datafile correctly and for further information about the analysis output results.

We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

az20_missingPvalues.tsv

Data analysis takes some time - Please wait

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Results for AZ20.tsv_missingP values show that the current analysis requires a P value column to be present for the analysis to be completed.

An error occurred please try again

single positional indexer is out-of-bounds

Sadly the dragons ate your analysis
An error occurred



Please restart your PhosphoQuest.
[Try going back to analysis](#)

Test case scenario 8 = User input AZ20.tsv, however the p values column is in a random column



Online analysis for your phospho-proteomics data

All analysis on this website is done *on the fly*, therefore please do not click back or other links (in same tab) unless you have finished looking through your results.

A csv file of the analysed data is provided for download when the analysis is finished and individual data charts can be saved from the site.

Please see [the documentation](#) for information about how to format your datafile correctly and for further information about the analysis output results.

We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

az20_Pvalues_asRandomColumn.tsv

Data analysis takes some time - Please wait

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Results for AZ20.tsv_missingPvalues show that the current analysis requires a P value column to be present for the analysis to be completed.

Anomaly detected...PhosphoQuest will self-destruct in T minus 10 seconds...just kidding! Please check your fold change calculations, a discrepancy has been detected.



Online analysis for your phospho-proteomics data

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We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

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Data analysis takes some time - Please wait

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Test case scenario 9 = User input AZ20.tsv, however the fold values column is missing



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We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

az20_missingFoldvalues.tsv

Data analysis takes some time - Please wait

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Results for AZ20.tsv_missingFoldvalues show that the current analysis requires a Fold value column to be present for the analysis to be completed.

An error occurred please try again

single positional indexer is out-of-bounds

Sadly the dragons ate your analysis
An error occurred



Please restart your PhosphoQuest.
[Try going back to analysis](#)

Test case scenario 10 = User input AZ20.tsv, however the fold values column has been moved to a different column



Online analysis for your phospho-proteomics data

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Please see [the documentation](#) for information about how to format your datafile correctly and for further information about the analysis output results.

We hope you enjoy your *PhosphoQuest*.

Upload data file for processing

az20_FoldValues_asRandomColumn.tsv

Data analysis takes some time - Please wait

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Results for AZ20.tsvFoldValuesasRandomColumn show that the current analysis requires a Fold value column to be present in the expected column.

Anomaly detected..PhosphoQuest will self-destruct in T minus 10 seconds...just kidding! Please check your fold change calculations, a discrepancy has been detected.



Online analysis for your phospho-proteomics data

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Upload data file for processing

No file chosen

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Summary

In this short user app testing, we have tested a number of different scenarios in relation to different user input files:-

- User input AZ20.tsv
- User input AZ20.tsv, however missing the CV column
- User input AZ20.tsv, however the CV column is in a random location
- User input AZ20.tsv, however the residue type and number does not contain any 'nones'
- User input AZ20.tsv, however the substrate name column has been placed as the final column
- User input AZ20.tsv, however the substrate name column has been placed in a random position
- User input AZ20.tsv, however the p values column is missing
- User input AZ20.tsv, however the p values column is in a random column
- Test case scenario 9 = User input AZ20.tsv, however the fold values column is missing
- Test case scenario 10 = User input AZ20.tsv, however the fold values column has been moved to a different column

We have tried to graphically illustrate the results of such searches and show that in each of the different

scenarios, the website does not crash, but the errors are captured in different ways. These error messages denote that there is something wrong with the input file in terms of order or columns of required information are missing. The user input testing also shows how missing CV columns can be accounted and the analysis completes without taking CVs into consideration.