

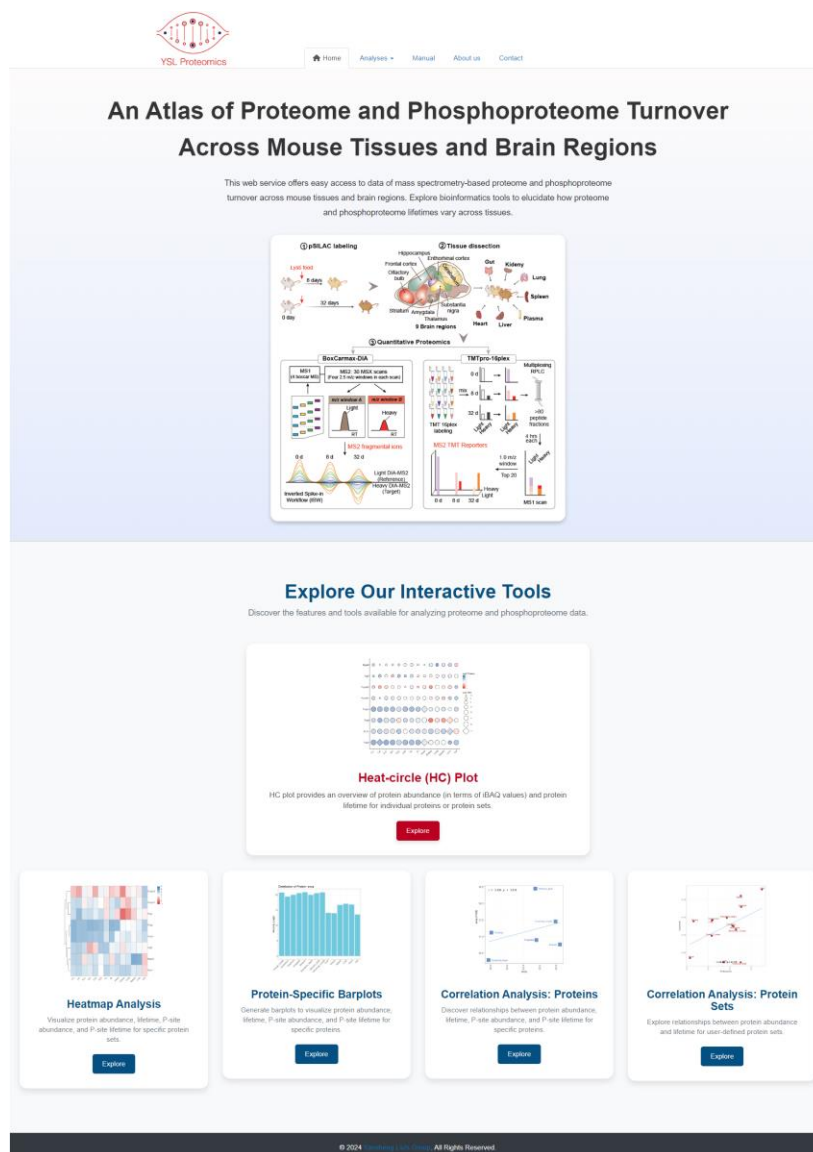
User Manual for Tissue Proteome and Phosphoproteome Turnover Web Application

Table of Contents

1. Data Preparation
2. Analysis modules
3. How to run this tool locally?

Tissue-PPT is a comprehensive resource that maps protein abundance (PA) and protein lifetime (PT) across eight mouse tissues and nine brain regions, providing in-depth insights into tissue-specific proteostasis. Using advanced proteomic techniques of data-independent acquisition (DIA) and tandem mass tagging (TMTpro), Tissue-PPT analyzed 11,000 proteins and 40,000 phosphosites with their PA and PT profiles, offering unmatched coverage and precision. Tissue-PPT uncovers e.g., tissue-specific short- and long-lived proteins, the role of phosphorylation in regulating protein stability, and how protein-protein interactions and organellar localization influence proteostasis and protein lifetime. By integrating multi-omics datasets, Tissue-PPT provides a detailed atlas of protein dynamics and tissue-specific regulation, offering new therapeutic insights. Accessible through an interactive web portal, Tissue-PPT serves as a valuable tool for studying proteome and phosphoproteome turnover in health and disease.

Users are welcome to visit this web site: <https://yslproteomics.shinyapps.io/tissuePPT>. We provide the option for the users to install this tool locally (Please check “3. How to run this tool locally?” part below). Then the website homepage can be shown like this:



1. Data Preparation

Users could either paste/upload a list of proteins of interest (POIs) or type in a gene name/UniProt ID.

1.1. A list of POIs

POIs should be protein names, like below:

1	Names
2	Psmb2
3	Psmb4
4	Psma6
5	Psmb6
6	Psmb1
7	Psmb3
8	Psma4
9	Psma1
10	Psma3
11	Psma5

Or UniProt IDs, as below:

1	UniProtIDs
2	A8MPP1
3	B7ZQA6
4	C9JRZ8
5	O00193
6	O00743
7	O14791
8	O15504
9	O43731
10	O60293
11	O60487
12	O60675
13	O60927
14	O75177

All of these names or IDs can be saved in a .csv/.txt file. There is only one column in this file and each row is a protein name or UniProt ID. In addition, Tissue-PPT also supports users to paste these POIs as described in the “2. Import Data” part.

1.2. A gene name/UniProt ID

Herein, users could directly type in a gene name (e.g. Snca), or a UniProt ID (e.g. O55042).

2. Analysis modules

There are five main modules currently supported in this application:

2.1. Heat-circle (HC) Plot: Visualize protein abundance and lifetime across tissues.

2.2. Heatmap Analysis: Generate heatmaps for protein or phosphosite data.

2.3. Protein-Specific Barplots: Create barplots for abundance and lifetime data of specific proteins.

2.4. Correlation Analysis: Individual Proteins: Explore relationships between protein and phosphorylation datasets of abundance and lifetime for a single protein.

2.5. Correlation Analysis: Protein Sets: Analyze correlations between protein sets or between protein sets and or the proteome.

2.1. Heat-circle (HC) Plot

2.1.1. What is HC-Plot?

HC-plot provides a synchronized overview of protein abundance (PA, in terms of iBAQ values, relative iBAQ values or riBAQ, and MS-intensities) and protein lifetime (PT or protein T50 determined by pulsed SILAC labeling) for individual proteins or protein sets. This allows researchers to explore relationships between protein abundance and lifetime across tissues.

2.1.2. How to Use HC-Plot?



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Heat-circle (HC) plot across tissues ?

Left: Parameter Panel

☒ 1. Paste ☐ 2. Upload ☐ 3. Example data

Please Paste gene names/UniProt IDs here:

☒ 4. PA: $\log_2(\text{riBAQ in ppm})$

☐ 5. PA: $\log_2(\text{iBAQ})$

☐ 6. $\log_2(\text{MS-intensity})$

☐ 7. PT rank percentage in each tissue?

☐ 8. Change figure height?

[Download figure](#)

Right: Result Panel

☒ Uploaded gene names/Uniprot IDs ☐ Expression data ☐ HC plot

Show entries

Description

	Description
1	NO data here. Please paste the genes/IDs, or load the example data to check first.

Showing 1 to 1 of 1 entries

A. Parameters:

A.1. Paste. Users can paste the gene names/UniProt IDs directly here. We found this option very useful for direct inspection of PA and PT values for given genes/proteins.

A.2. Upload. This means users can upload the gene names/UniProt IDs in a .csv file.

A.3. Example data. Here shows an example data for users.

A.4. PA: $\text{Log}_2(\text{riBAQ in ppm})$. riBAQ mean relative iBAQ. ppm means the relative contribution of iBAQ values to the total protein amount. If users select this parameter, this tool will transform the iBAQ values (log_2) into ppm (log_2). The values where $\text{Log}_2(\text{riBAQ in ppm}) < -1$ or $\text{Log}_2(\text{riBAQ in ppm}) > 9$ are defined as outliers.

A.5. PA: $\text{Log}_2(\text{iBAQ})$. If users select this parameter, this tool will match the iBAQ values (log_2) for the input gene names/UniProt IDs.

A.6. $\text{Log}_2(\text{MS-intensity})$. If users select this parameter, this tool will match the protein intensity (log_2) for the input gene names/UniProt IDs.

A.7. PT rank percentage in each tissue? If true, this tool will calculate the rank of the protein lifetime value and normalize every rank to the maximum rank in terms of rank percentage (0-100%) for each tissue.

A.7.1. Row scaled across tissues? If true in A.7. above, users will see this parameter, which means this tool will additionally scale the rank percentage value across all tissues for the current gene/protein list (Z score across tissues).

A.8. Change figure height? If enabled, users can manually adjust the figure height using the parameter A.8.1 (described below). If disabled, the tool will automatically adjust the figure height based on the number of input gene names or UniProt IDs.

A.8.1. Figure Height. This parameter adjusts the height of the plot.

B. Results:

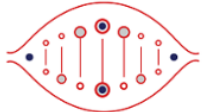
B.1. Uploaded gene names/Uniprot IDs. Here shows the input gene names/Uniprot IDs. If users input nothing, it shows 'NO data here. Please paste the genes/IDs, or load the example data to check first.'

B.2. Expression data. Here shows the matched results of the input gene names/Uniprot IDs, including protein iBAQ values and protein lifetime values. Please note that if users select parameters 4, 5, and/or 6 mentioned above, the corresponding results will be displayed based on the selected parameters.

B.3. HC plot. Here shows the HC plot based on the matched results.

2.1.3. Example Output

Users can choose the '3. Example data' in the left parameter panel. Shown as below:



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Heat-circle (HC) plot across tissues ?

☐ 1. Paste

☐ 2. Upload

☒ 3. Example data

Download example data

☒ 4. PA: Log₂(riBAQ in ppm)

☐ 5. PA: Log₂(iBAQ)

☐ 6. Log₂(MS-intensity)

☐ 7. PT rank percentage in each tissue?

☐ 8. Change figure height?

Download figure

☒ Uploaded gene names/Uniprot IDs

☐ Expression data

☐ HC plot

Show

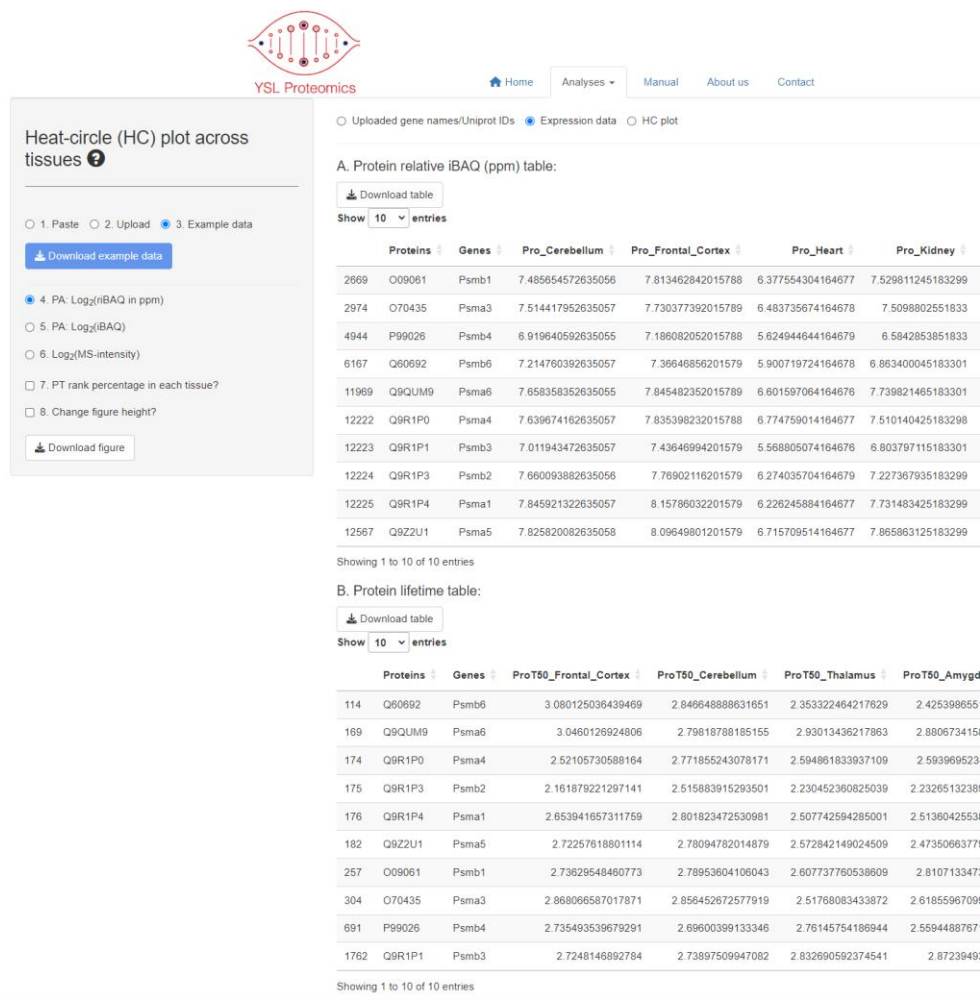
10

entries

	Names
1	Psmb2
2	Psmb4
3	Psma6
4	Psmb6
5	Psmb1
6	Psmb3
7	Psma4
8	Psma1
9	Psma3
10	Psma5

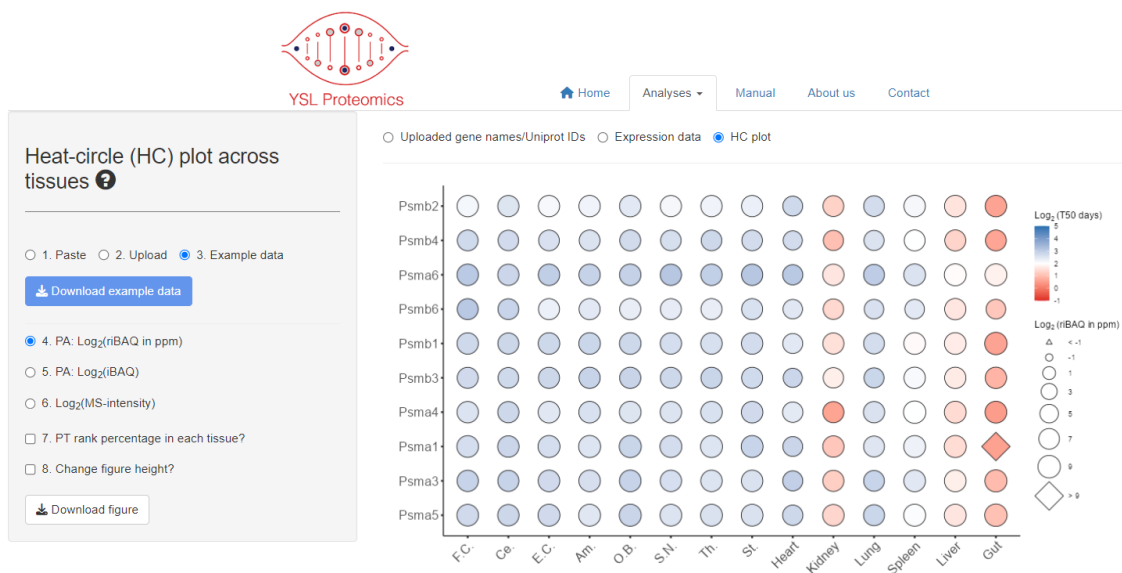
Showing 1 to 10 of 10 entries

Then users click 'Expression data', this tool will match relative iBAQ values in ppm (log2) and lifetime values (log2) for the input genes based on the default parameters, shown as below:



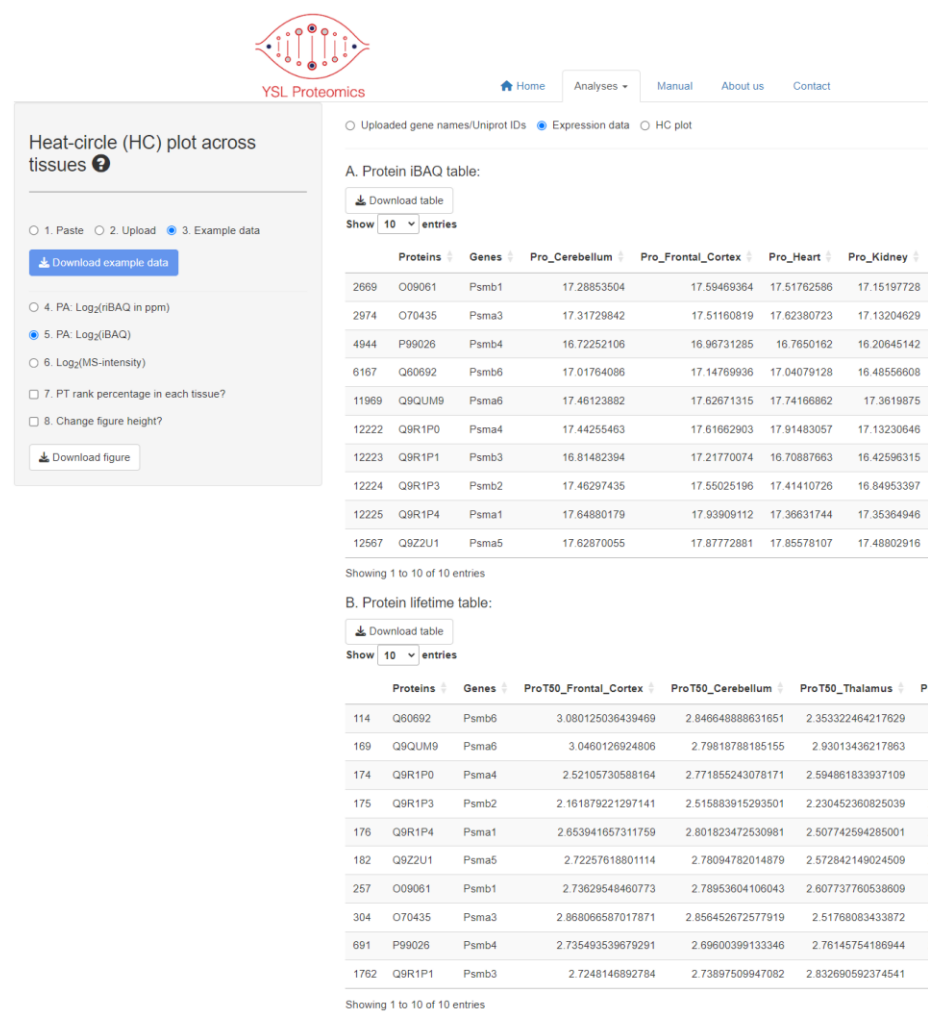
If users click the “Download table” button, the corresponding table will be downloaded to their local device.

The HC-plot based on these values is shown as below:



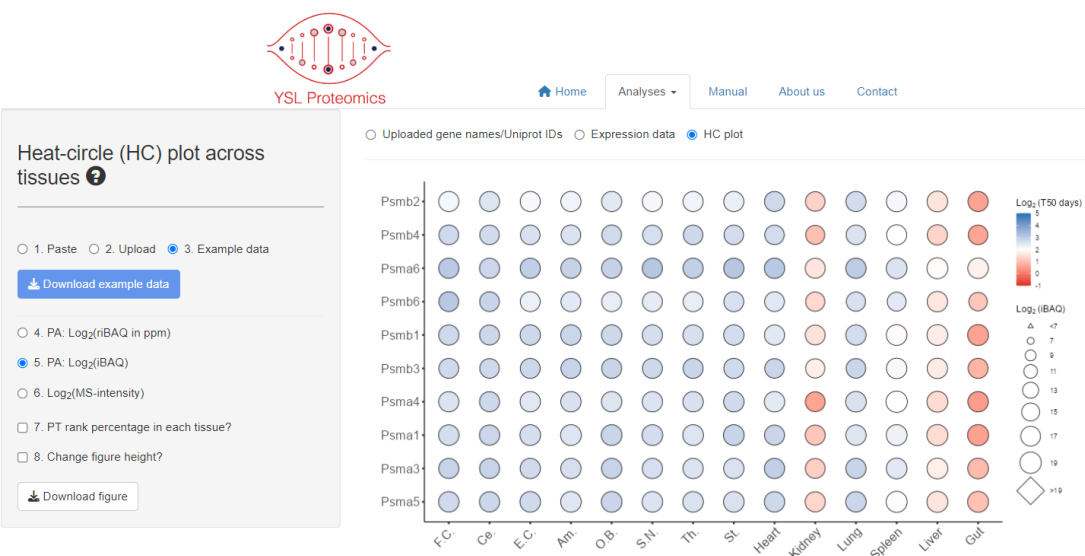
If users click the “Download figure” button, the corresponding figure will be downloaded to their local device.

If users choose '5. PA: Log2 (iBAQ)', this tool will match iBAQ values (log2) and lifetime values (log2) for the input genes, shown as below:



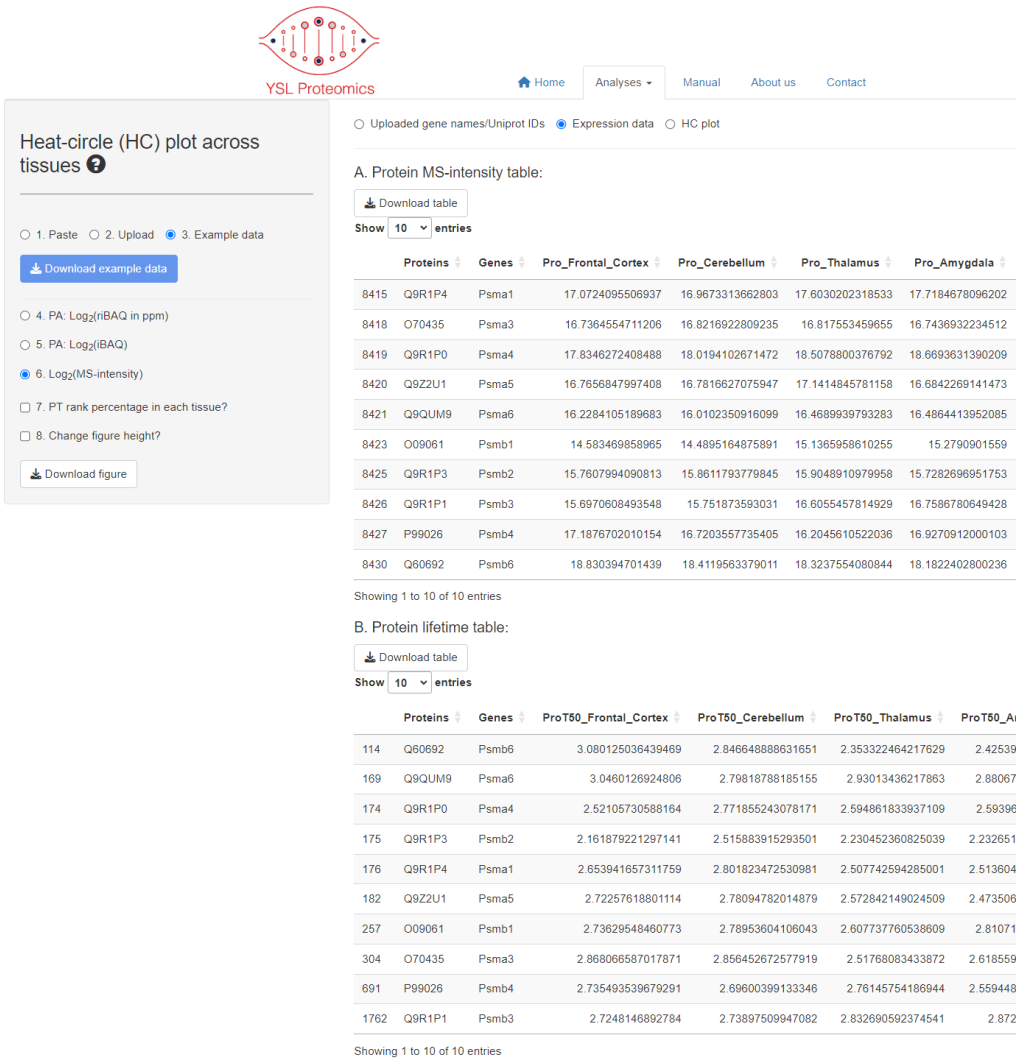
If users click the “Download table” button, the corresponding table will be downloaded to their local device.

The HC-plot based on these values is shown as below:



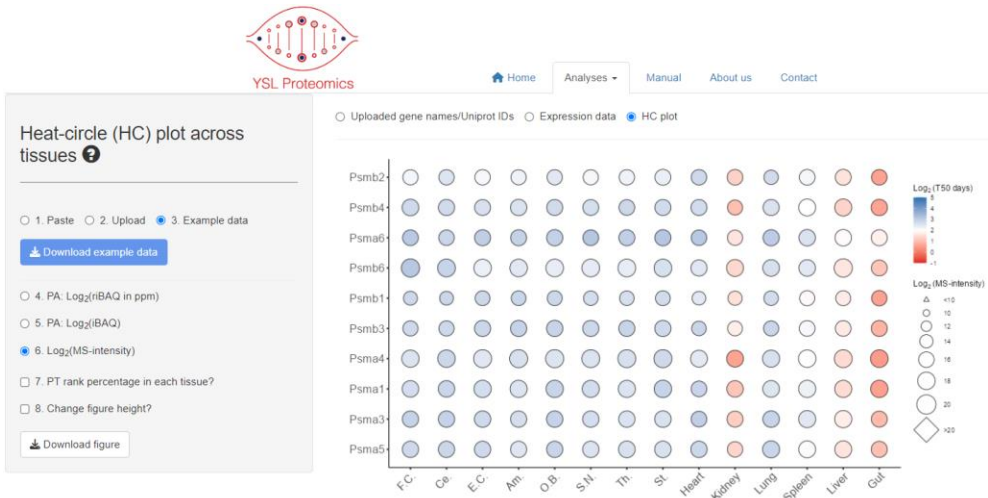
If users click the “Download figure” button, the corresponding figure will be downloaded to their local device.

If users choose '6. Log₂(MS-intensity)', this tool will match protein intensities (log₂) and lifetime values (log₂) for the input genes, shown as below:



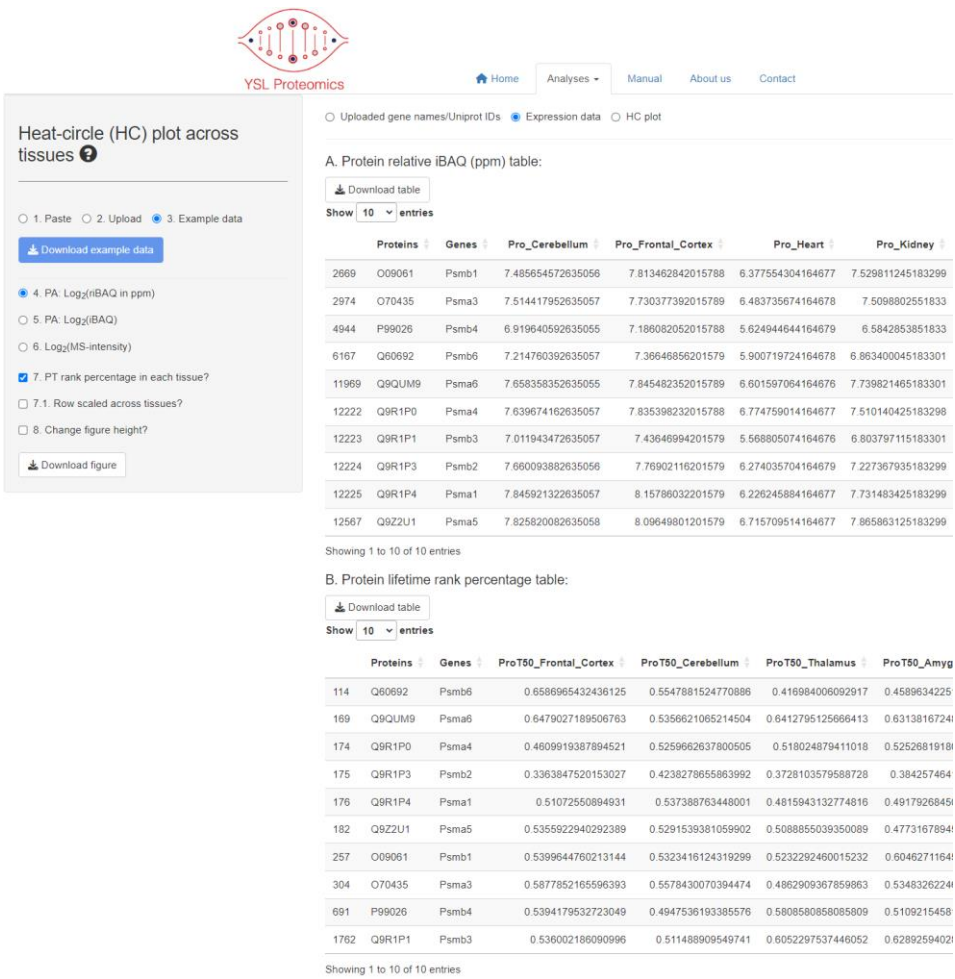
If users click the “Download table” button, the corresponding table will be downloaded to their local device.

The HC-plot based on these values is shown as below:



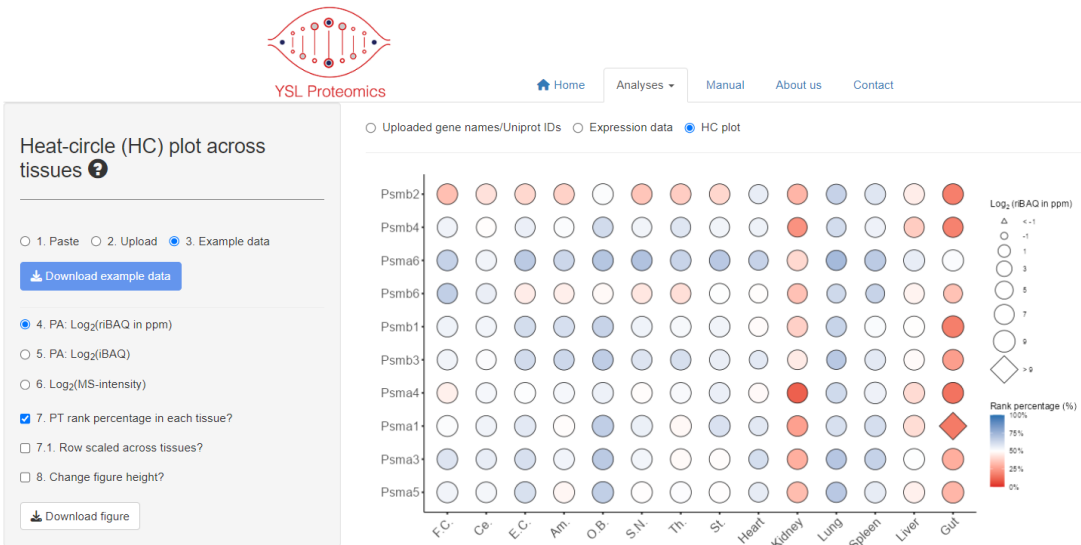
If users click the “Download figure” button, the corresponding figure will be downloaded to their local device.

If users choose '4. PA: Log2(riBAQ in ppm)' and '7. PT rank percentage in each tissue?', this tool will match relative iBAQ values in ppm (log2) and then calculate rank percentage of each protein lifetime value for each tissue, shown as below:



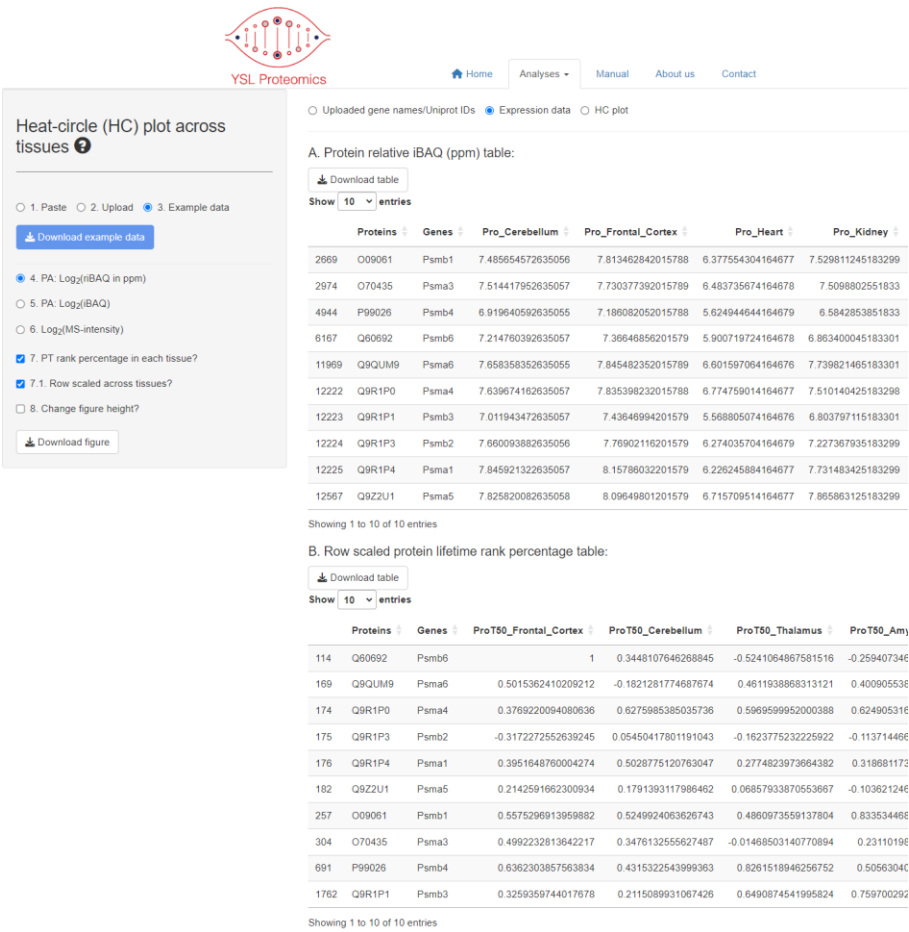
If users click the “Download table” button, the corresponding table will be downloaded to their local device.

The HC-plot based on these values is shown as below:



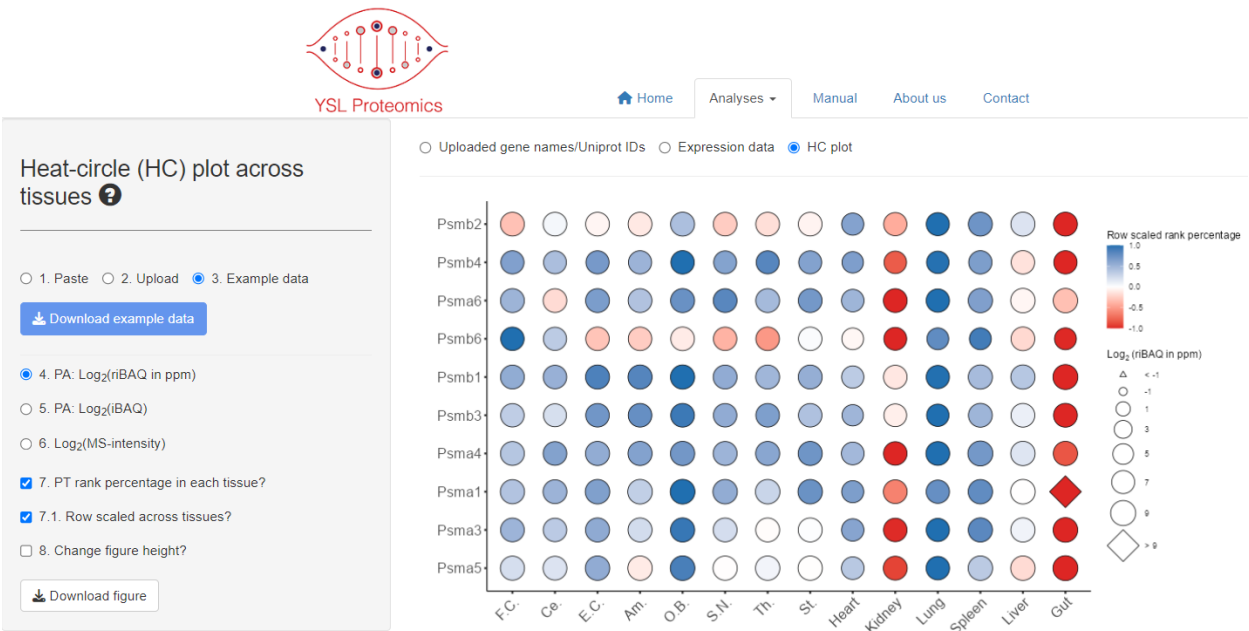
If users click the “Download figure” button, the corresponding figure will be downloaded to their local device.

If users choose '7.1. Row scaled across tissues?', this tool will scale the rank percentage of each protein lifetime value across all tissues for the current gene/protein list, shown as below:



If users click the “Download table” button, the corresponding table will be downloaded to their local device.

The HC-plot based on these values is shown as below:



If users click the “Download figure” button, the corresponding figure will be downloaded to their local device.

2.2. Heatmap Analysis

2.2.1. What is Heatmap Analysis?

Visualize protein abundance, lifetime, phospho abundance, and phospho lifetime across tissues with heatmaps. This module provides a rapid and comprehensive view of data trends for protein sets.

2.2.2. How to Use Heatmap Analysis?

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Heatmap analysis for protein sets

Left: Parameter Panel

☒ 1. Paste ☐ 2. Upload ☐ 3. Example data

Please Paste gene names/UniProt IDs here:

Figure Height: 1200

Download figure

Right: Result Panel

☒ Uploaded gene names/UniProt IDs ☐ Expression data ☐ Heatmap

Show 10 entries

Description

1	NO data here. Please paste the genes/IDs, or load the example data to check first.
---	--

Showing 1 to 1 of 1 entries

A. Parameters:

A.1. Paste. This means users can paste the gene names/UniProt IDs directly here.

A.2. Upload. This means users can upload the gene names/UniProt IDs in a .csv file.

A.3. Example data. Here shows an example data for users.

A.4. Figure Height. This parameter adjust the height of the plot.

B. Results:

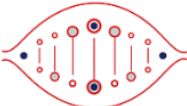
B.1. Uploaded gene names/UniProt IDs. Here shows the input gene names/UniProt IDs. If users input nothing, it shows 'NO data here. Please paste the genes/IDs, or load the example data to check first.'

B.2. Expression data. Here shows the matched results of the input gene names/UniProt IDs, including protein abundance (MS-intensities derived from BoxCarmax-DIA data), protein lifetime, phospho abundance, and phospho lifetime.

B.3. Heatmap. Here shows the Heatmap based on the matched results.

2.2.3. Example Output

Users can choose the '3. Example data' in the left parameter panel. Shown as below:



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Heatmap analysis for protein sets

1. Paste 2. Upload **3. Example data**

Download example data

Figure Height: 1200

Download figure

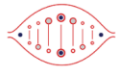
☒ Uploaded gene names/Uniprot IDs ☐ Expression data ☐ Heatmap

Show 10 entries

	Names
1	Psmb2
2	Psmb4
3	Psma6
4	Psmb6
5	Psmb1
6	Psmb3
7	Psma4
8	Psma1
9	Psma3
10	Psma5

Showing 1 to 10 of 10 entries

When users click on 'Expression data', the tool retrieves and matches four types of log2-transformed values for the input genes: Protein abundance, Protein lifetime, Phospho abundance, and Phospho lifetime. The matched data is displayed as shown below:



Heatmap analysis for protein sets



☐ 1. Paste ☐ 2. Upload ☒ 3. Example data

[Download example data](#)

Figure Height:

[Download figure](#)

☐ Uploaded gene names/Uniprot IDs ☒ Expression data ☐ Heatmap

A. Protein abundance table:

[Download table](#)

Show 10 entries

	Proteins	Genes	Frontal_Cortex	Cerebellum	Thalamus	Amygdala
8425	Q9R1P3	Psmb2	15.7807994090813	15.8611793779845	15.9048910979958	15.7282696951753
8427	P99026	Psmb4	17.1876702010154	16.7203557735405	16.2045610522036	16.9270912000103
8421	Q9QUM9	PsmA6	16.2284105189683	16.0102350916099	16.4689939793283	16.4864413952085
8430	Q60692	Psmb6	18.830394701439	18.4119563379011	18.3237554080844	18.1822402800236
8423	O09061	Psmb1	14.583469858965	14.4895164875891	15.1365958610255	15.2790901559
8426	Q9R1P1	Psmb3	15.6970608493548	15.751873593031	16.6055457814929	16.7586780649428
8419	Q9R1P0	PsmA4	17.8346272408488	18.0194102671472	18.5078800376792	18.6663631390209
8415	Q9R1P4	PsmA1	17.0724095506937	16.9673313662803	17.6030202318533	17.7184678096202
8418	O70435	PsmA3	16.7364554711206	16.8216922809235	16.817553459655	16.7436932234512
8420	Q9Z2U1	PsmA5	16.7656847997408	16.7816627075947	17.1414845781158	16.6842269141473

Showing 1 to 10 of 10 entries

B. Protein lifetime table:

[Download table](#)

Show 10 entries

	Proteins	Genes	Frontal_Cortex	Cerebellum	Thalamus	Amygdala
114	Q60692	Psmb6	3.080125036439469	2.846648888631651	2.353322464217629	2.42539865510E
169	Q9QUM9	PsmA6	3.0460126924806	2.79818788185155	2.93013436217863	2.88067341580E
174	Q9R1P0	PsmA4	2.52105730588164	2.771855243078171	2.594861833937109	2.593969523491
175	Q9R1P3	Psmb2	2.161879221297141	2.515883915293501	2.230452360825039	2.2326513238973
176	Q9R1P4	PsmA1	2.653941657311759	2.801823472530981	2.507742594285001	2.513604255387E
182	Q9Z2U1	PsmA5	2.72257619801114	2.78094782014879	2.572842149024509	2.4735086377907
257	O09061	Psmb1	2.73629548460773	2.78953604106043	2.607737780538609	2.810711334738E
304	O70435	PsmA3	2.868066587017871	2.856452672577919	2.51768083433872	2.6185596709032
691	P99026	Psmb4	2.735493539679291	2.69600399133346	2.76145754186944	2.559448876716E
1782	Q9R1P1	Psmb3	2.72481468892784	2.73897509947082	2.832690592374541	2.8723949353

Showing 1 to 10 of 10 entries

C. Phospho abundance table:

[Download table](#)

Show 10 entries

	Proteins	Genes	Peptides	PTMsite	Frontal_Cortex	Cereb
38926	Q60692	Psmb6	_AQS[Phospho (STY)]AFAFGPEALTPDWENR_	(S12)	14.0539186048421	14.393543
65703	Q9R1P4	PsmA1	_LVS[Phospho (STY)]LGSK_	(S110)	9.75685839146258	9.3665142
21728	O70435	PsmA3	_ES[Phospho (STY)]LKEEESDDNN[Oxidation (M)]_	(S243,M255)	11.7670244194209	13.430062
67149	Q9Z2U1	PsmA5	_GVNTFS[Phospho (STY)]PEGR_	(S16)	15.5587234345962	16.139936

Showing 1 to 4 of 4 entries

D. Phospho lifetime table:

[Download table](#)

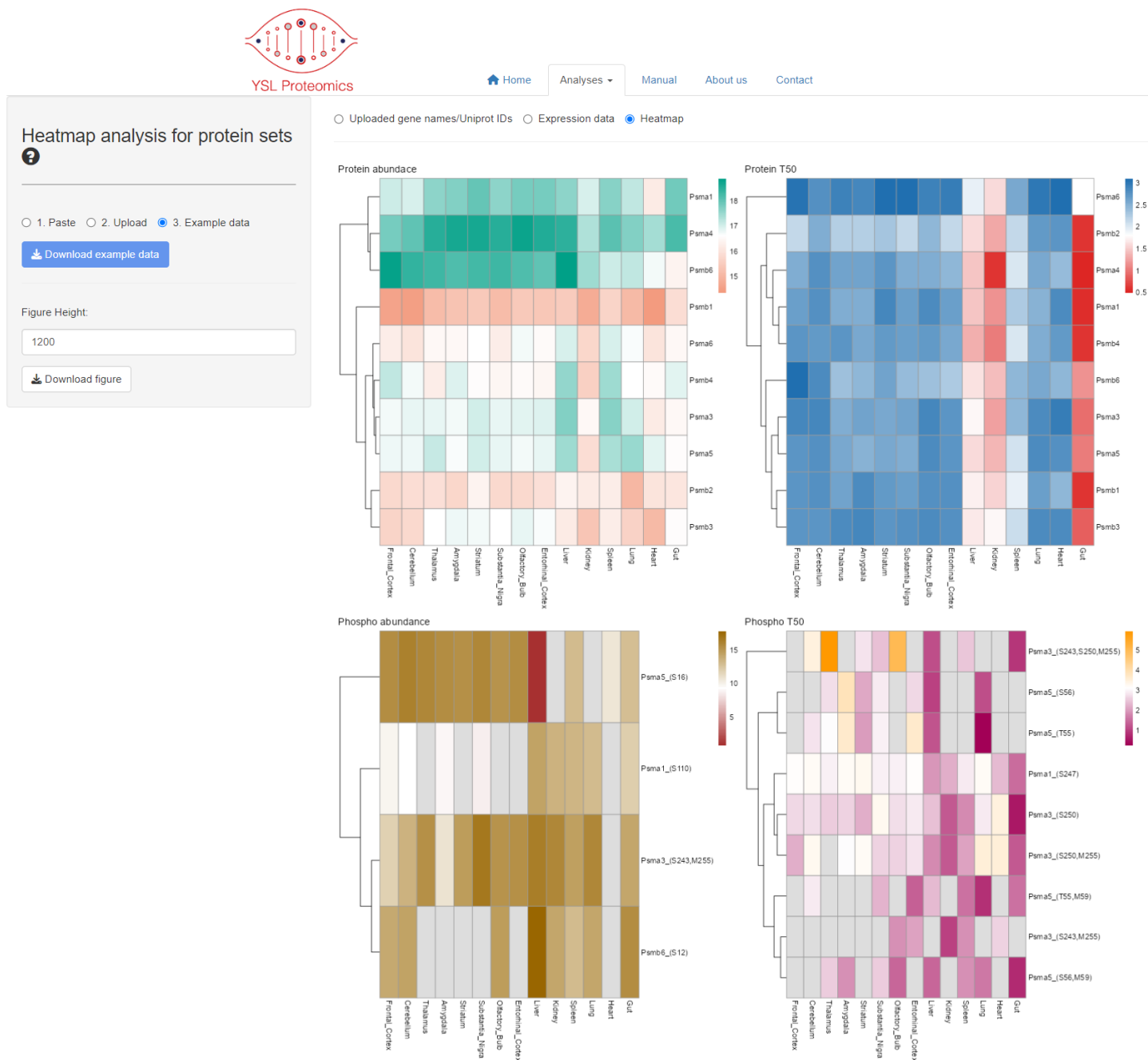
Show 10 entries

	Proteins	Genes	Peptides	PTMsite	Frontal_Cortex	Cereb
3030	Q9R1P4	PsmA1	_AQPS[Phospho (STY)]GAEEPAEK_	(S247)		3.15438
8466	O70435	PsmA3	_ES[Phospho (STY)]LKEEES[Phospho (STY)]DDNN[Oxidation (M)]_	(S243,S250,M255)		
8468	O70435	PsmA3	_ES[Phospho (STY)]LKEEESDDNN[Oxidation (M)]_	(S243,M255)		
8622	O70435	PsmA3	_ESLKEEES[Phospho (STY)]DDNN_	(S250)		2.64622
8623	O70435	PsmA3	_ESLKEEES[Phospho (STY)]DDNN[Oxidation (M)]_	(S250,M255)		2.18235
14376	Q9Z2U1	PsmA5	_IT[Phospho (STY)]SPLM[Oxidation (M)]EPSSIEK_	(T55,M59)		
14431	Q9Z2U1	PsmA5	_ITS[Phospho (STY)]PLM[Oxidation (M)]EPSSIEK_	(S56,M59)		
24500	Q9Z2U1	PsmA5	_RIT[Phospho (STY)]SPLMEPSIEK_	(T55)		
24502	Q9Z2U1	PsmA5	_RITS[Phospho (STY)]PLMEPSIEK_	(S56)		

Showing 1 to 9 of 9 entries

If users click the “Download table” button, the corresponding table will be downloaded to their local device.

The Heatmap based on these values is shown as below:



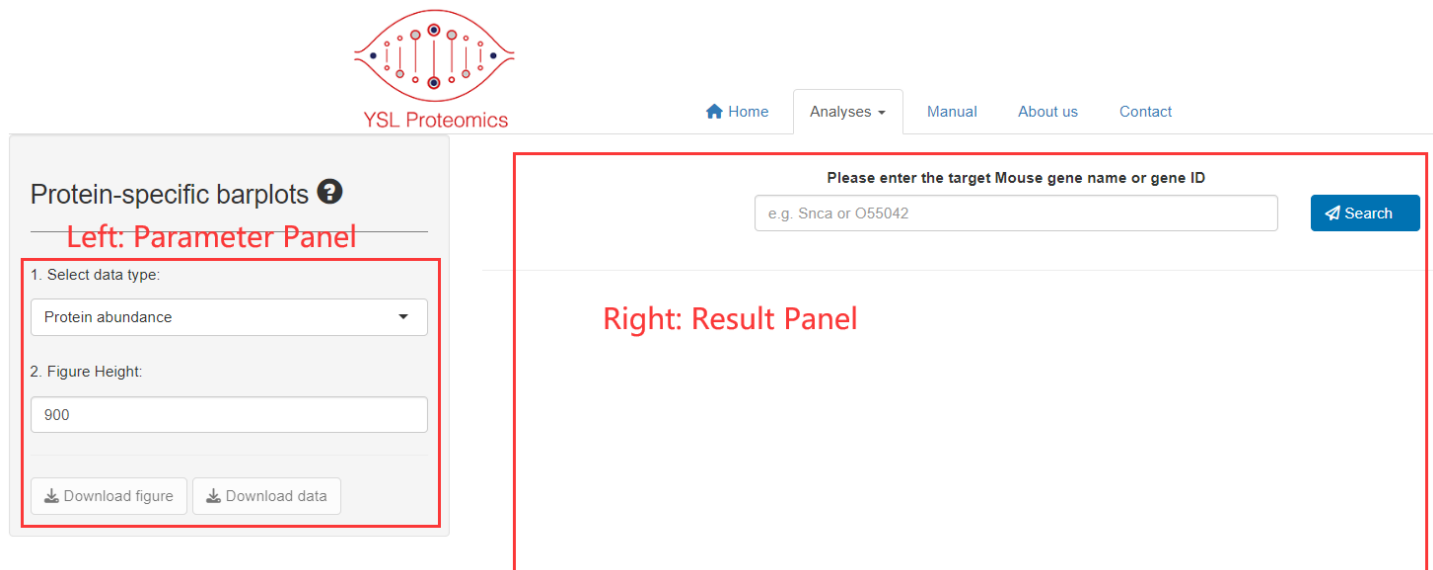
If users click the “Download figure” button, the corresponding figure will be downloaded to their local device.

2.3. Protein-Specific Barplots

2.3.1. What is Protein-Specific Barplots?

Protein-Specific Barplots are visual tools designed to display the distribution of protein-related data, such as protein abundance, lifetime, phosphosite abundance, or phosphosite lifetime, across different tissues for a specific protein. These barplots allow researchers to analyze and compare how a particular protein's characteristics vary across multiple tissues. By entering a protein's name or ID, users can generate detailed plots that summarize the protein's behavior, making it easier to identify patterns, trends, or anomalies in the data.

2.3.2. How to Use Protein-Specific Barplots?



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Protein-specific barplots ?

Left: Parameter Panel

1. Select data type:

Protein abundance

2. Figure Height:

900

Download figure Download data

Please enter the target Mouse gene name or gene ID

e.g. Snca or O55042 Search

Right: Result Panel

A. Parameters:

A.1. Select data type. There are four types of datasets, including Protein abundance (MS-intensities derived from BoxCarmax-DIA data), Protein lifetime, Phosphosite abundance, and Phosphosite lifetime. Users should choose one of them.

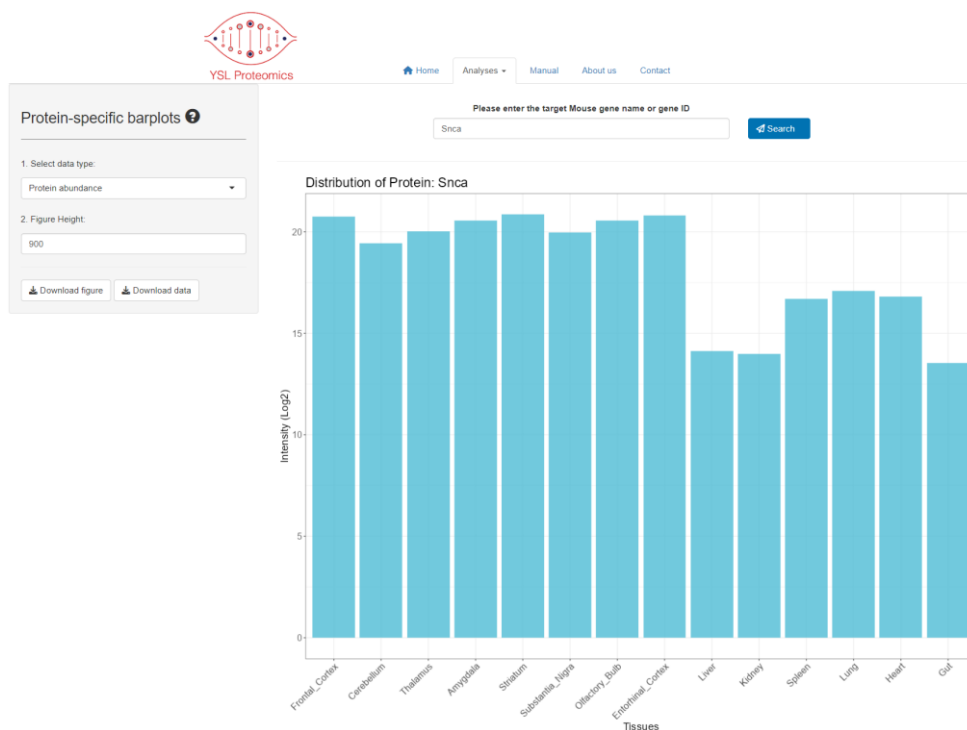
A.2. Figure Height. This parameter adjusts the height of the plot.

B. Results:

Please enter the target Mouse gene name or gene ID. Here users should type in a mouse gene name or UniProt ID that they want to check, for example, Snca or O55042. Case does not matter.

2.3.3. Example Output

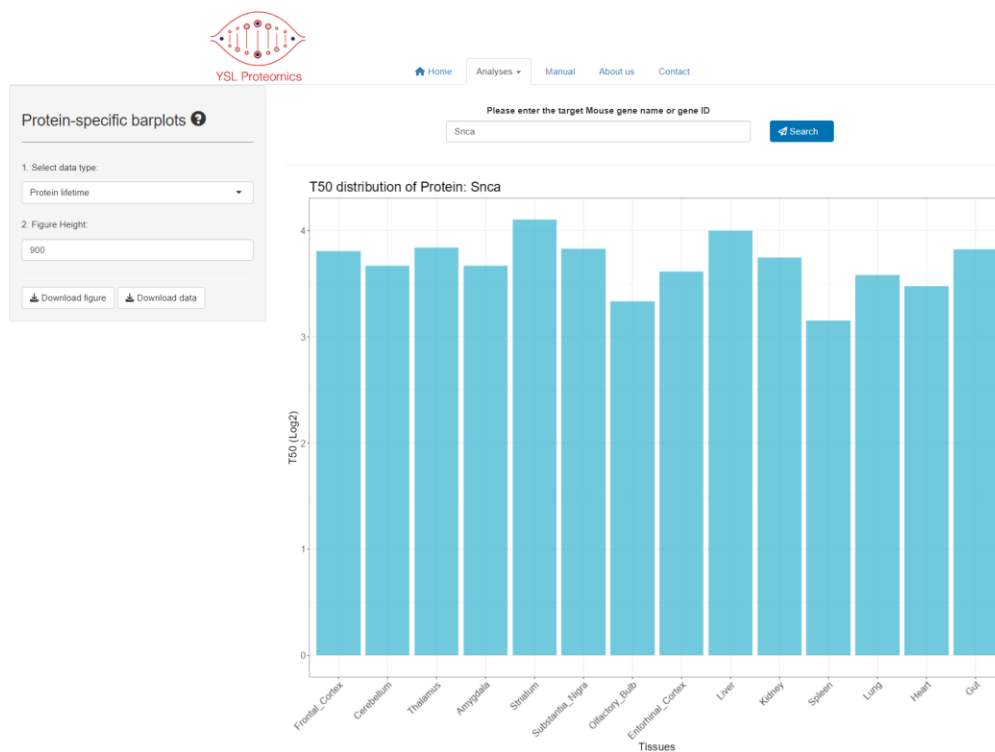
Users can type in a mouse gene name or UniProt ID that they want to check, for example, Snca. Then click the 'Search' button and the results are shown as below:



If users click the “Download figure” button, the corresponding figure will be downloaded to their local device.

If users click the “Download data” button, the corresponding data used for the barplot will be downloaded to their local device.

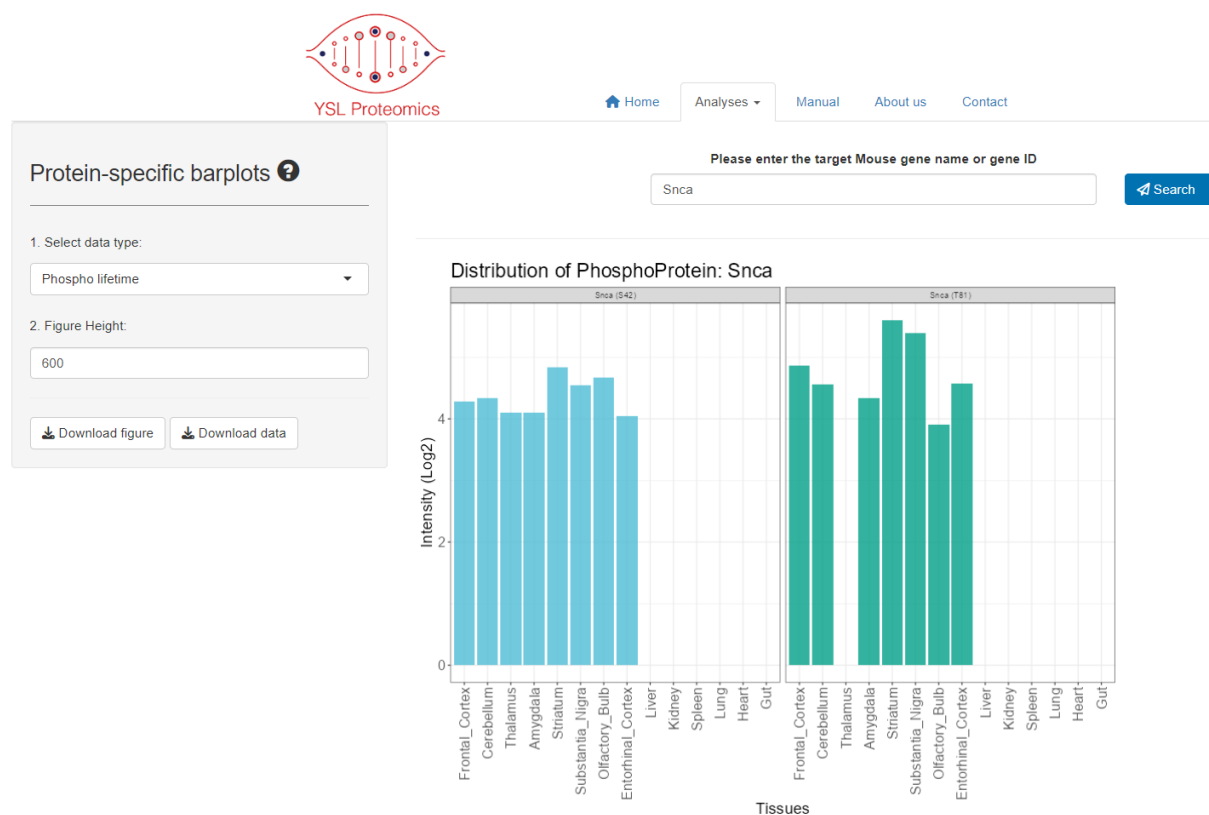
When users select 'Protein lifetime', the results are displayed as shown below:



When users select 'Phospho abundance', the results are displayed as shown below:



When users select 'Phospho lifetime', the results are displayed as shown below:

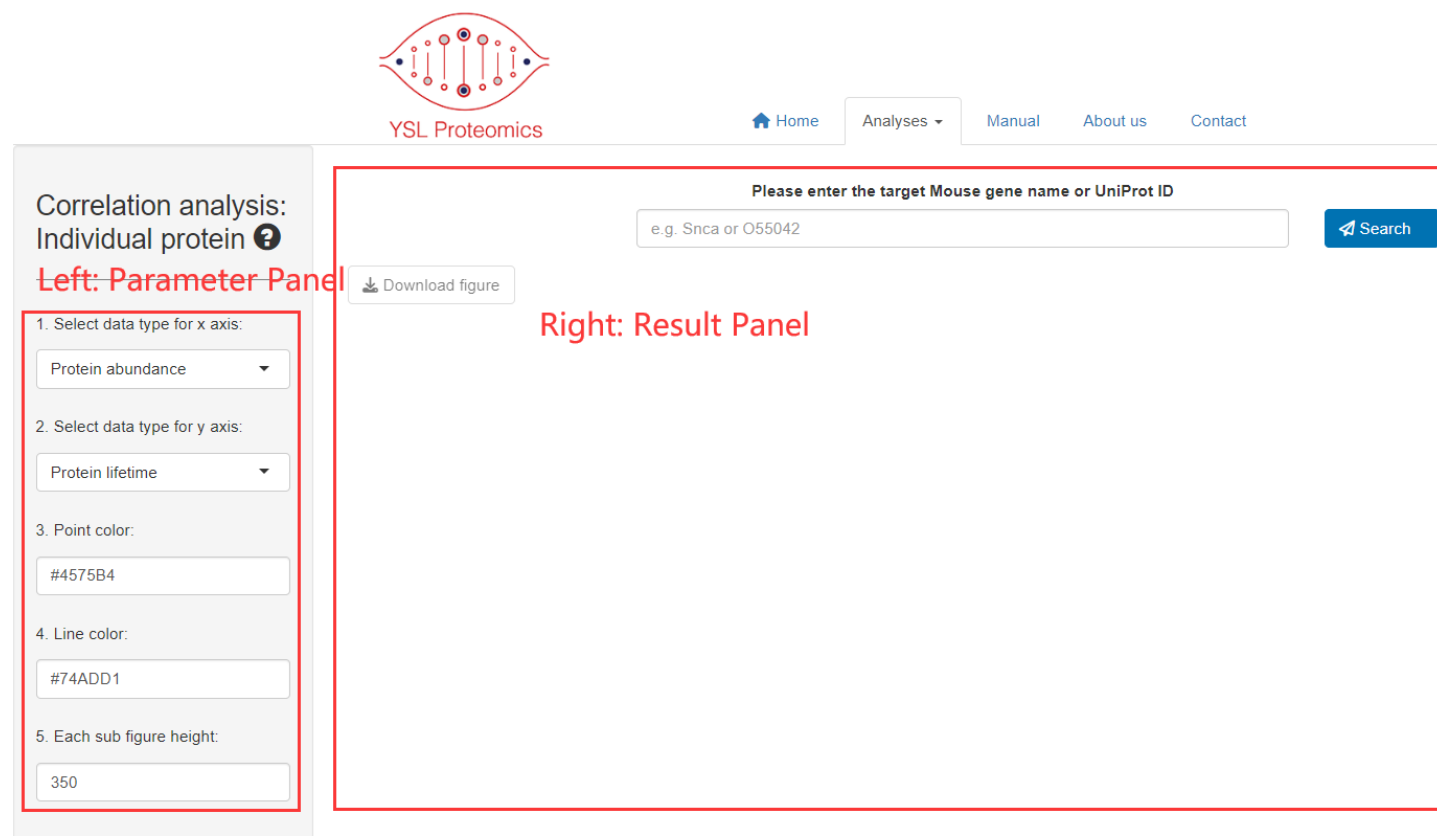


2.4. Correlation Analysis: Individual Proteins

2.4.1. What is Correlation Analysis: Individual Proteins?

Correlation Analysis: Individual Protein refers to a method for examining the relationship between a specific protein's abundance, lifetime, phospho abundance, or phospho lifetime across different tissues. By default, both Pearson and Spearman correlations are calculated for users. This analysis helps researchers understand how the behavior of an individual protein aligns with other variables or datasets. It provides valuable insights into tissue-specific dynamics, functional roles, or potential regulatory mechanisms associated with the protein, enabling a deeper understanding of its biological significance.

2.4.2. How to Use Correlation Analysis: Individual Proteins?



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Home Analyses Manual About us Contact

Correlation analysis: Individual protein ?

Left: Parameter Panel

1. Select data type for x axis:
Protein abundance

2. Select data type for y axis:
Protein lifetime

3. Point color:
#4575B4

4. Line color:
#74ADD1

5. Each sub figure height:
350

Right: Result Panel

Please enter the target Mouse gene name or UniProt ID

e.g. Snca or O55042

Search

Download figure

A. Parameters:

A.1. Select data type for x axis. There are four types of datasets, including Protein abundance, Protein lifetime, Phosphosite abundance, and Phosphosite lifetime. Users should choose one of them for x axis.

A.2. Select data type for y axis. Similar to above, but for y axis.

A.3. Point color. Users can type in a color name to change the point color in the correlation plot.

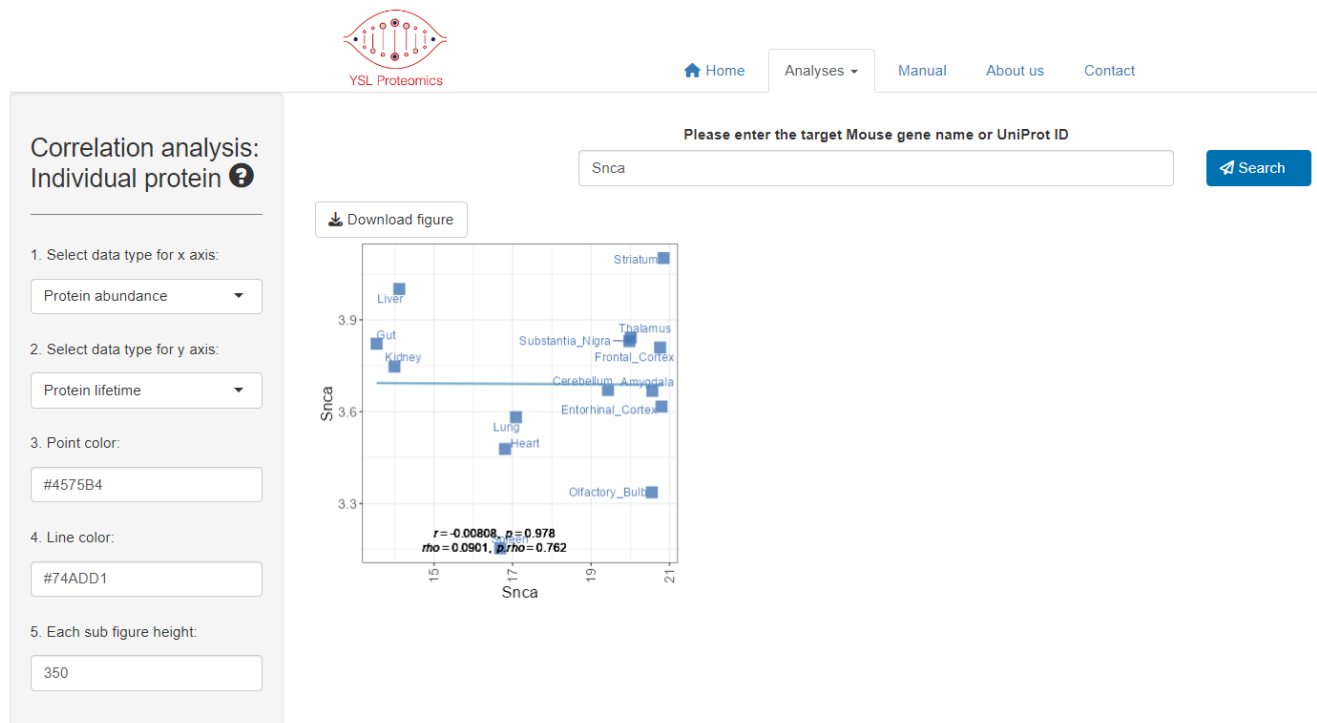
A.4. Line color. Users can type in a color name to change the line color in the correlation plot.

A.5. Each sub figure height. This parameter adjust the height of each subgraph.

B. Results:

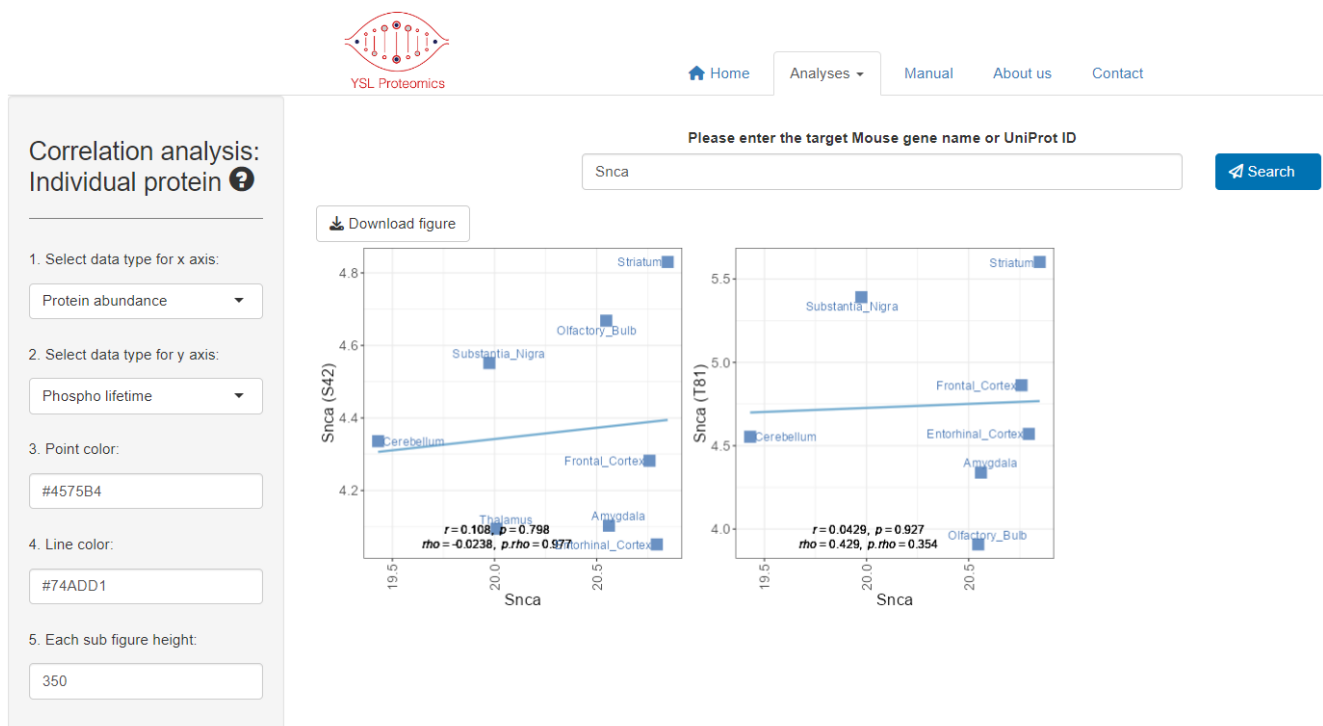
Please enter the target Mouse gene name or gene ID. Here users should type in a mouse gene name or UniProt ID that they want to check, for example, Snca or O55042. Case does not matter.

Users can type in a mouse gene name or UniProt ID that they want to check, for example, Snca. Then click the 'Search' button and the results are shown as below:



r means Pearson correlation coefficient, p means the p value of the correlation test with a pearson method. ρ means Spearman correlation coefficient, $p.\rho$ means the p value of the correlation test with a spearman method.

When users select 'Protein abundance' for x axis and 'Phospho lifetime' for y axis, the results are displayed as shown below:



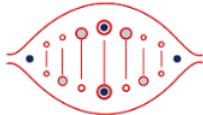
2.5. Correlation Analysis: Protein Sets

2.5.1. What is Correlation Analysis: Protein Sets?

Correlation Analysis: Protein Set supports discovery of relationship and dependency between protein abundance and protein lifetime for a given protein set or two protein sets or the averaged protein levels. By default, both Pearson and Spearman correlations are calculated for users.

2.5.2. How to Use Correlation Analysis: Individual Proteins?

I. One protein list. If users choose 'One protein list' here, they can input a single list of proteins, and this tool will perform correlation analysis between the proteins in the provided list and the entire proteome dataset integrated within the tool.



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Home Analyses Manual About us Contact

Correlation analysis: Protein sets

Left: Parameter Panel

☒ One protein list ☐ Two protein lists

☒ 1. Paste ☐ 2. Upload ☐ 3. Example data

Please Paste gene names/UniProt IDs here :

4. Select data type for x axis:

Protein set average abundance

5. Select data type for y axis:

Proteome average abundance

☐ 6. Change X axis and/or Y axis label or not?

Right: Result Panel

☒ Uploaded one protein list ☐ Expression data ☐ Correlation plot

Show 10 entries

Description

1	NO data here. Please paste the genes/IDs, or load the example data to check first.
---	--

Showing 1 to 1 of 1 entries

A. Parameters:

A.1. Paste. This means users can paste the gene names/UniProt IDs directly here.

A.2. Upload. This means users can upload the gene names/UniProt IDs in a .csv file.

A.3. Example data. Here shows an example data for users.

A.4. Select data type for x axis. There are four types of datasets, including Protein set average abundance (the average abundance of all proteins within the input protein set across different tissues), Protein set average lifetime (the average lifetime of all proteins within the input protein set across different tissues), Proteome

average abundance (the average abundance of all proteins within the whole integrated proteome dataset across different tissues), Proteome average lifetime (the average lifetime of all proteins within the whole integrated proteome dataset across different tissues). Users should choose one of them for x axis.

A.5. Select data type for y axis. Similar to above, but for y axis.

A.6. Change X axis and/or Y axis label or not? If true, users can define the X/Y axis label by themselves.

A.7. Point color. Users can type in a color name to change the point color in the correlation plot.

A.8. Line color. Users can type in a color name to change the line color in the correlation plot.

A.9. Each sub figure height. This parameter adjust the height of each subgraph.

B. Results:

B.1. Uploaded one protein list. Here shows the input one list of proteins. If users input nothing, it shows 'NO data here. Please paste the genes/IDs, or load the example data to check first.'

B.2. Expression data. Here shows the matched results of the input gene names/Uniprot IDs.

B.3. Correlation plot. Here shows the Correlation plot based on the matched results.

II. Two protein lists. Users can input two lists of proteins, and this tool will perform correlation analysis between the two lists of proteins.

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Home Analyses Manual About us Contact

Correlation analysis: Protein sets

Left: Parameter panel

☐ One protein list ☒ Two protein lists

☒ 1. Paste ☐ 2. Upload ☐ 3. Example data

Please Paste protein list 1:

Please Paste protein list 2:

Right: Result Panel

☒ Uploaded two protein lists ☐ Expression data ☐ Correlation plot

Protein list 1:

Show 10 entries

	Description
1	NO data here. Please paste the genes/IDs, or load the example data to check first.

Showing 1 to 1 of 1 entries

Protein list 2:

Show 10 entries

	Description
1	NO data here. Please paste the genes/IDs, or load the example data to check first.

Showing 1 to 1 of 1 entries

A. Parameters:

A.1. Paste. This means users can paste the gene names/UniProt IDs directly here. Please note, users should input two lists of proteins here.

A.2. Upload. This means users can upload the gene names/UniProt IDs in a .csv file. Please note, users should upload two lists of proteins here.

A.3. Example data. Here shows two example data for users.

A.4. Other parameters are similar to above.

B. Results:

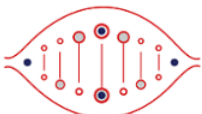
B.1. Uploaded two protein lists . Here shows the input two lists of proteins. If users input nothing, it shows 'NO data here. Please paste the genes/IDs, or load the example data to check first.'

B.2. Expression data. Here shows the matched results of the two lists of proteins.

B.3. Correlation plot. Here shows the Correlation plot based on the matched results.

2.5.3. Example Output

If users choose 'One protein list', and click '3. Example data', the 'Uploaded one protein list' will be shown as below, which means the example dataset contains 17 proteins:



YSL Proteomics

[Home](#) [Analyses](#) [Manual](#) [About us](#) [Contact](#)

Correlation analysis: Protein sets

☒ One protein list ☐ Two protein lists

☐ 1. Paste ☐ 2. Upload ☒ 3. Example data

[Download example data](#)

4. Select data type for x axis:
Protein set average abundance

5. Select data type for y axis:
Proteome average abundance

☐ 6. Change X axis and/or Y axis label or not?

7. Point color:
darkred

8. Line color:
#74ADD1

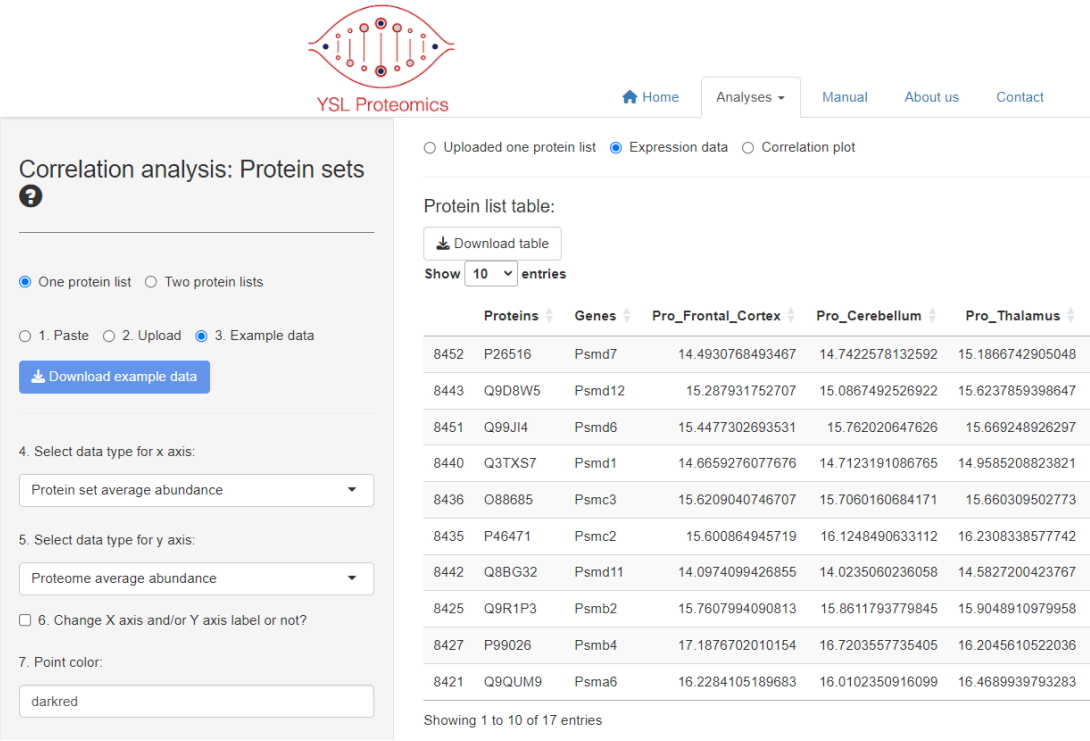
☒ Uploaded one protein list ☐ Expression data ☐ Correlation plot

Show 10 entries

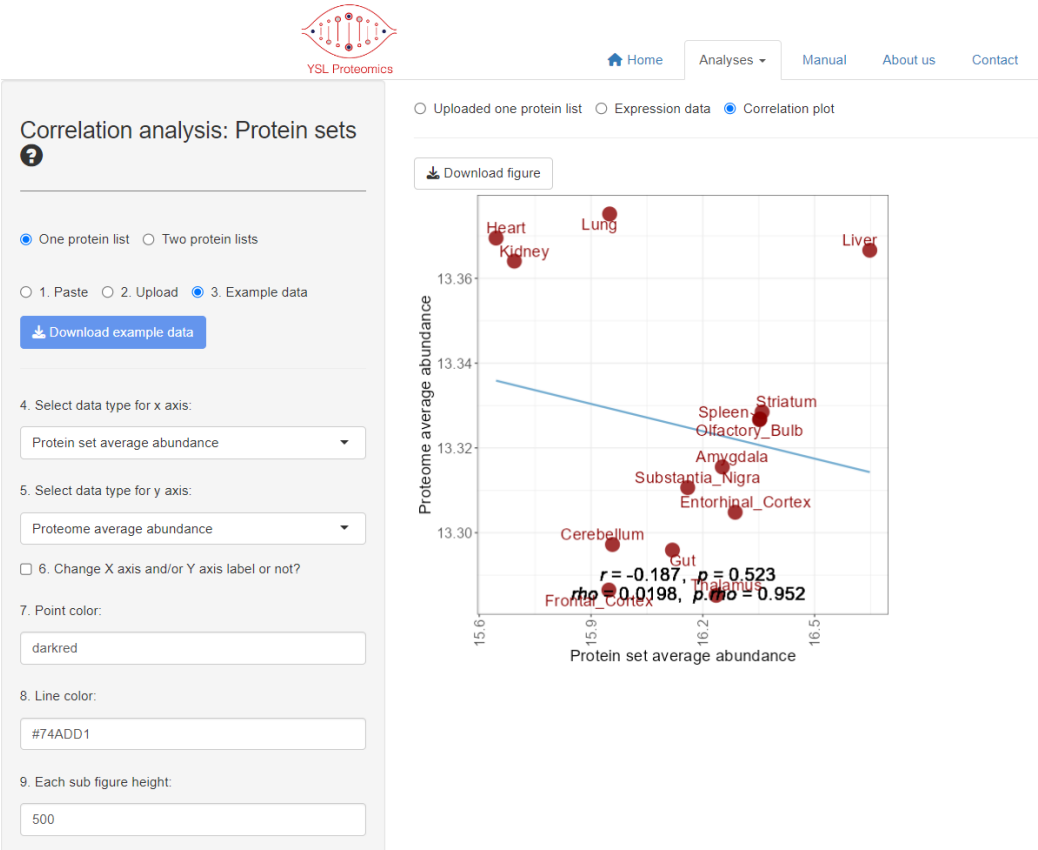
	IDs
1	Psmid7
2	Psmid12
3	Psmid6
4	Psmid1
5	Psmc3
6	Psmc2
7	Psmid11
8	Psmb2
9	Psmb4
10	Psma6

Showing 1 to 10 of 17 entries

Then users can click 'Expression data', below shows the matched results for the input 17 proteins.

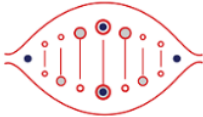


When users click 'Correlation plot', here shows the correlation plot as below. Users can choose the parameter “6. Change X axis and/or Y axis label or not?” to rename the protein lists.



r means Pearson correlation coefficient, p means the p value of the correlation test with a pearson method. ρ means Spearman correlation coefficient, $p.\rho$ means the p value of the correlation test with a spearman method.

If users choose 'Two protein lists', and click '3. Example data', the 'Uploaded two protein lists' will be shown as below, there are two example datasets here:



[Home](#)

Analyses ▾

[Manual](#)[About us](#)[Contact](#)

Correlation analysis: Protein sets

?

☐ One protein list

☒ Two protein lists

☐ 1. Paste

☐ 2. Upload

☒ 3. Example data

Download example 1

Download example 2

4. Select data type for x axis:

Protein set 1 average abundance ▾

5. Select data type for y axis:

Protein set 2 average abundance ▾

☐ 6. Change X axis and/or Y axis label or not?

7. Point color:

darkred

8. Line color:

#74ADD1

9. Each sub figure height:

700

☒ Uploaded two protein lists

☐ Expression data

☐ Correlation plot

Protein list 1:

Show 10 ▾ entries

	IDs
1	Psmid7
2	Psmid12
3	Psmid6
4	Psmid1
5	Psmc3
6	Psmc2
7	Psmid11
8	Psemb2
9	Psemb4
10	Psma6

Showing 1 to 10 of 17 entries

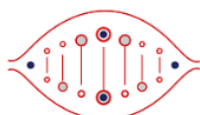
Protein list 2:

Show 10 ▾ entries

	IDs
1	Man2b1
2	Ctsf
3	Pla2g15
4	Rab9a
5	Dpp7
6	Vps16
7	Mtor
8	Arsa
9	Pon2
10	Lamp1

Showing 1 to 10 of 22 entries

Then users can click 'Expression data', below shows the matched results for the two lists of proteins.



YSL Proteomics

[Home](#)

Analyses ▾

Manual

[About us](#)

Contact

Correlation analysis: Protein sets



☐ One protein list ☒ Two protein lists

☐ 1. Paste ☐ 2. Upload ☒ 3. Example data

 Download example 1

 Download example 2

4. Select data type for x axis:

Protein set 1 average abundance

5. Select data type for y axis:

Protein set 2 average abundance

☐ 6. Change X axis and/or Y axis label or not?

7. Point color:

darkred

8. Line color:

#74ADD1

9. Each sub figure height:

700

☐ Uploaded two protein lists ☒ Expression data ☐ Correlation plot

Protein list 1 table:

Download table

Show 10 entries

	Proteins 🔄	Genes 🔄	Pro_Frontal_Cortex 🔄	Pro_Cerebellum 🔄	Pro_Thalamus 🔄
8452	P26516	Psmd7	14.4930768493467	14.7422578132592	15.1866742905048
8443	Q9D8W5	Psmd12	15.287931752707	15.0867492526922	15.6237859398647
8451	Q99JI4	Psmd6	15.4477302693531	15.762020647626	15.669248926297
8440	Q3TXS7	Psmd1	14.6659276077676	14.7123191086765	14.9585208823821
8436	O88685	Psmd3	15.6209040746707	15.7060160684171	15.660309502773
8435	P46471	Psmd2	15.600864945719	16.1248490633112	16.2308338577742
8442	Q8BG32	Psmd11	14.0974099426855	14.0235060236058	14.5827200423767
8425	Q9R1P3	Psmb2	15.7607994090813	15.8611793779845	15.9048910979958
8427	P99026	Psmb4	17.1876702010154	16.7203557735405	16.2045610522036
8421	Q9QUM9	Psma6	16.2284105189683	16.0102350916099	16.4689939793283

Showing 1 to 10 of 17 entries

Protein list 2 table:

Download table

Show 10 entries

	Proteins	Genes	Pro_Frontal_Cortex	Pro_Cerebellum	Pro_Thalam
5674	O09159	Man2b1	11.7166049068879	12.4784974770713	12.0657810
2351	Q9R013	Ctsf	13.3846818898471	13.9342108281897	13.35732715
7956	Q8VEB4	Pla2g15	13.1124280206316	12.1563169246892	12.823678647
8664	Q9R0M6	Rab9a	14.7332105298215	15.0768371990956	15.671133271
2861	Q9ET22	Dpp7	13.8622039959427	14.3744125813642	13.800906315
11614	Q920Q4	Vps16	13.5595324411342	13.3662082664782	13.896620872
6264	Q9JLN9	Mtor	14.3848529362463	14.2087521428589	14.450898183
894	P50428	Arsa	14.2328356359768	15.2380045628869	14.663150131
8142	Q62086	Pon2	12.7470735702032	13.5021439335074	13.621022236
5337	P11438;Q9DC13	Lamp1	16.7779213232078	17.3028013956936	17.188529636

Showing 1 to 10 of 22 entries

When users click 'Correlation plot', here shows the correlation plot as below. Users can choose the parameter “6. Change X axis and/or Y axis label or not?” to rename the protein lists.



r means Pearson correlation coefficient, p means the p value of the correlation test with a pearson method. ρ means Spearman correlation coefficient, $p.\rho$ means the p value of the correlation test with a spearman method.

3. How to run this tool locally?

Tissue-PPT is an open source application and all codes can be also obtained on our GitHub: <https://github.com/yslproteomics/tissuePPT>. If users want to run Tissue-PPT on their own computer, they should operate as below:

As this tool was developed with R, you may:

- a) Install R. You can download R from here: <https://www.r-project.org/>.
- b) Install RStudio. (Recommendatory but not necessary). You can download RStudio from here: <https://www.rstudio.com/>.
- c) Check packages. After installing R and RStudio, you should check whether you have installed these packages (shiny, shinyjs, shinyWidgets, shinyBS, DT, data.table, ggsci, ggplot2, ggrepel, patchwork, dplyr, openxlsx, cowplot, grid, ggpubr, impute, pheatmap, ggplotify). You may run the codes below to check them:

```
if(!require(pacman)) install.packages("pacman")
pacman::p_load(shiny, shinyjs, shinyWidgets, shinyBS, DT, data.table, ggsci, ggplot2, ggrepel, patchwork,
dplyr, openxlsx, cowplot, grid, ggpubr, impute, pheatmap, ggplotify)
```

Please note, if you find some packages cannot be installed directly using the above command, you can find them in the GitHub source and install them by, for example:

```
library(devtools)
install_github("yslproteomics/tissuePPT")
```

- d) Run this tool locally

```
if(!require(tissuePPT)) devtools::install_github("yslproteomics/tissuePPT")
library(tissuePPT)
tissuePPT_app()
```