

## How to navigate through the SpProtQuant website

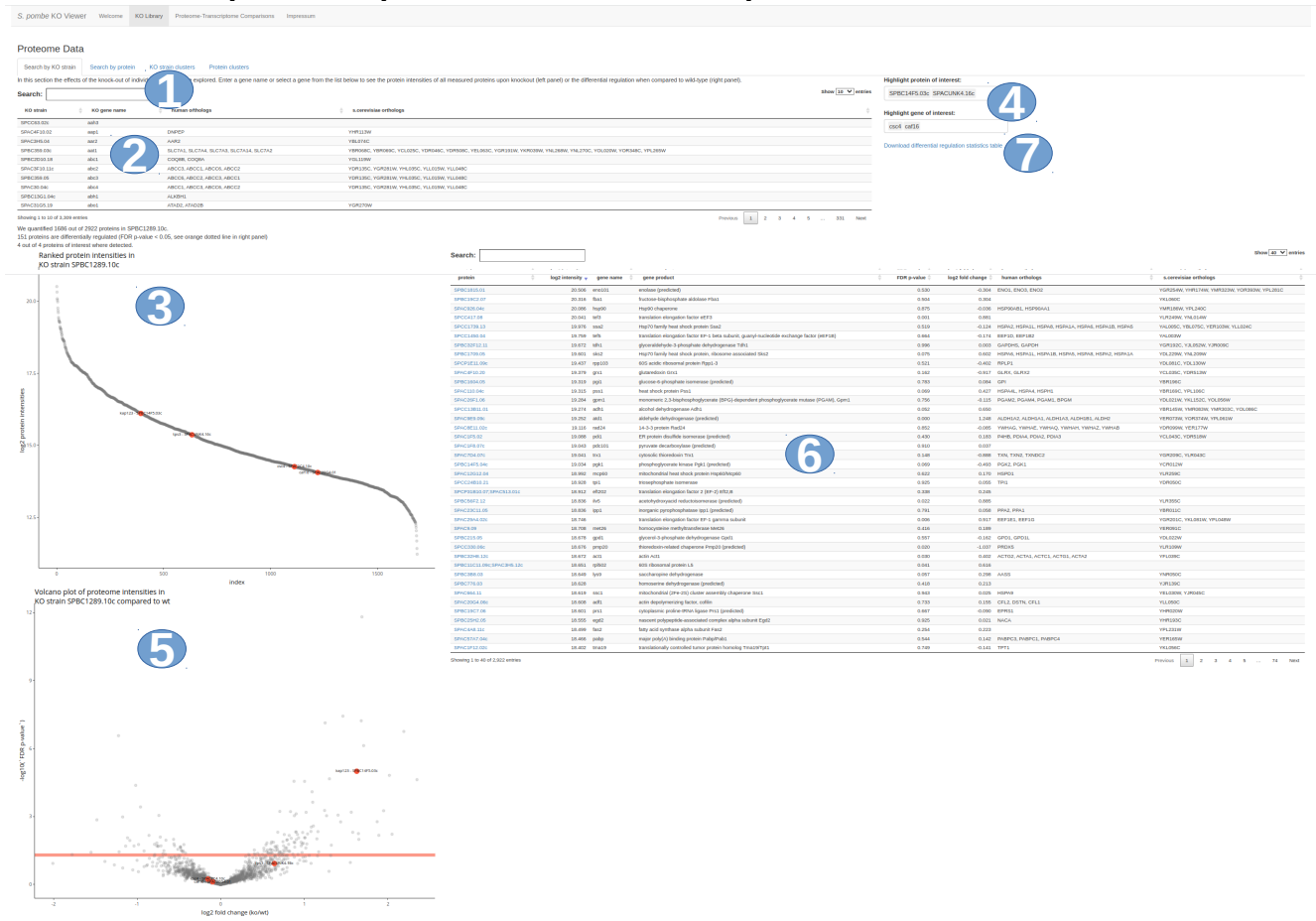
This manual shortly explains the main usage options of the website. The website has 5 main pages that represent different data sets from the paper:

**“Proteome effects of genome-wide single gene perturbations”** by Öztürk et al. Published 2022 in Nature Communications - <https://www.nature.com/articles/s41467-022-33814-8>

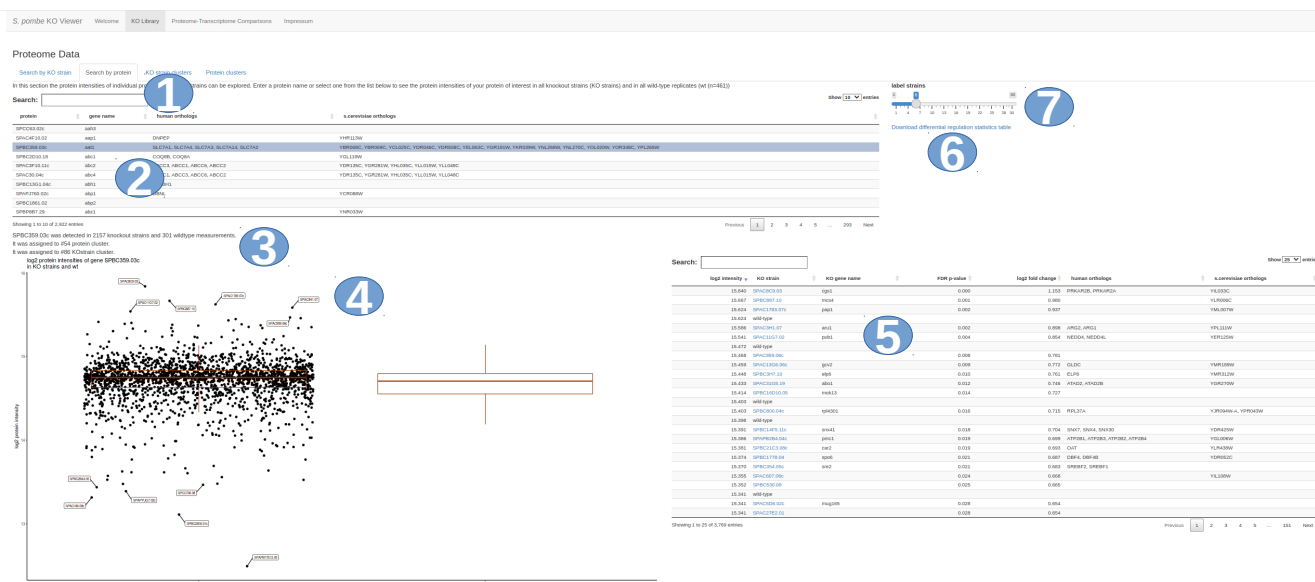
### **Contents:**

- Data sets include 5 partially interconnected sets:
  - Effect of the knockout of any gene of interest on the protein expression levels of other proteins
  - Changes in the expression of any protein of interest in different knockout strains
  - KO strain clusters
  - Protein cluster
  - Comparison of proteome and transcriptome changes upon knockout of any gene interest
- Web interface structure – on all pages a gene of interest can be entered as *S. pombe* protein ID, gene name and human or *S. cerevisiae* ortholog name and queried for the respective data
- Advanced settings can be adjusted to include more or less data – please see paragraphs below for more detailed information

# KO Library → Search by KO strain → Explore the effect of the knockout of your gene of interest on the protein expression levels of other proteins



# KO Library → Search by protein → Explore how your protein of interest changes in different knockout strains



1. Enter gene name of your gene of interest.
2. Select the respective gene – now all the data available for the KO strain of interest will be displayed.
3. Information about in how many of the knockout and wt strains the protein was detected and to which protein or knockout cluster it has been assigned. The clusters can be assessed on the pages 'KO strain clusters' and 'Protein clusters'.
4. Protein intensities of your protein of interest in all knockout strains (left panel) and a boxplot of intensities in wt strains included in the study (right panel).
5. Table including all the information for your protein of interest.
6. This table can also be downloaded.
7. How many of the most extreme strains you want to be highlighted.

# KO Library → KO strain clusters → Explore to which KO strain cluster your protein of interest belongs

**S. pombe KO Viewer** | Welcome | **KO Library** | Proteome-Transcriptome Comparisons | Impression

**Proteome Data**

Search by KO strain | Search by protein | **1** | Subjects | Protein clusters

Showing 1 to 10 of 344 results

| KO strain  | KO gene name | cluster number | human orthologs | submitter orthologs |
|------------|--------------|----------------|-----------------|---------------------|
| SPCC132.03 | gld8         | 41             |                 |                     |
| SPAC140.02 | hns1         | 82             | SNRP            | YHSC10              |
| SPAC154.04 | hns2         | 83             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 86             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 87             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 88             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 89             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 90             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 91             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 92             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 93             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 94             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 95             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 96             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 97             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 98             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 99             | SNRP            | YHSC10              |
| SPAC154.04 | hns1         | 100            | SNRP            | YHSC10              |

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5. Same as 4. but bigger. Grey lines represent interactions described in STRING.
6. List of KO strains included in the respective KO strain clusters.
7. List of Gene Ontology (GO) terms enriched in generally down regulated or up regulated proteins in the KO strains of the respective cluster.
8. This data can also be downloaded as a table including information for all clusters.

[illegible]

1. Enter gene name of your gene of interest.
2. Select the respective gene – now all the data available for the gene of interest will be displayed.
3. Alternatively you can select any protein cluster and see cluster information.
4. Protein cluster network figure including all proteins that belong to this cluster (and show similar protein intensities across KO strains). Grey lines represent interactions described in STRING.
5. Same as 4. but bigger. Grey lines represent interactions described in STRING.
6. List of proteins included in the respective protein clusters.
7. This data can also be downloaded as a table including information for all clusters.

# Proteome-Transcriptome Comparison



1. Enter gene name of your gene of interest.
2. Select the respective gene – now all the data available for the gene of interest will be displayed.
3. Plot including all fold changes at the transcriptome level plotted versus the fold changes at the proteome level. The plot also displays the Pearson's correlation coefficient between these two levels.
4. Distribution of the Pearson's correlation coefficients between fold changes at the transcriptome and proteome levels of all proteins that were detected in the 94 strains.
5. Threshold for the differential regulation p-values can be adjusted to exclude certain genes from the plot.
6. Additional genes of interest can be highlighted in plot 3.