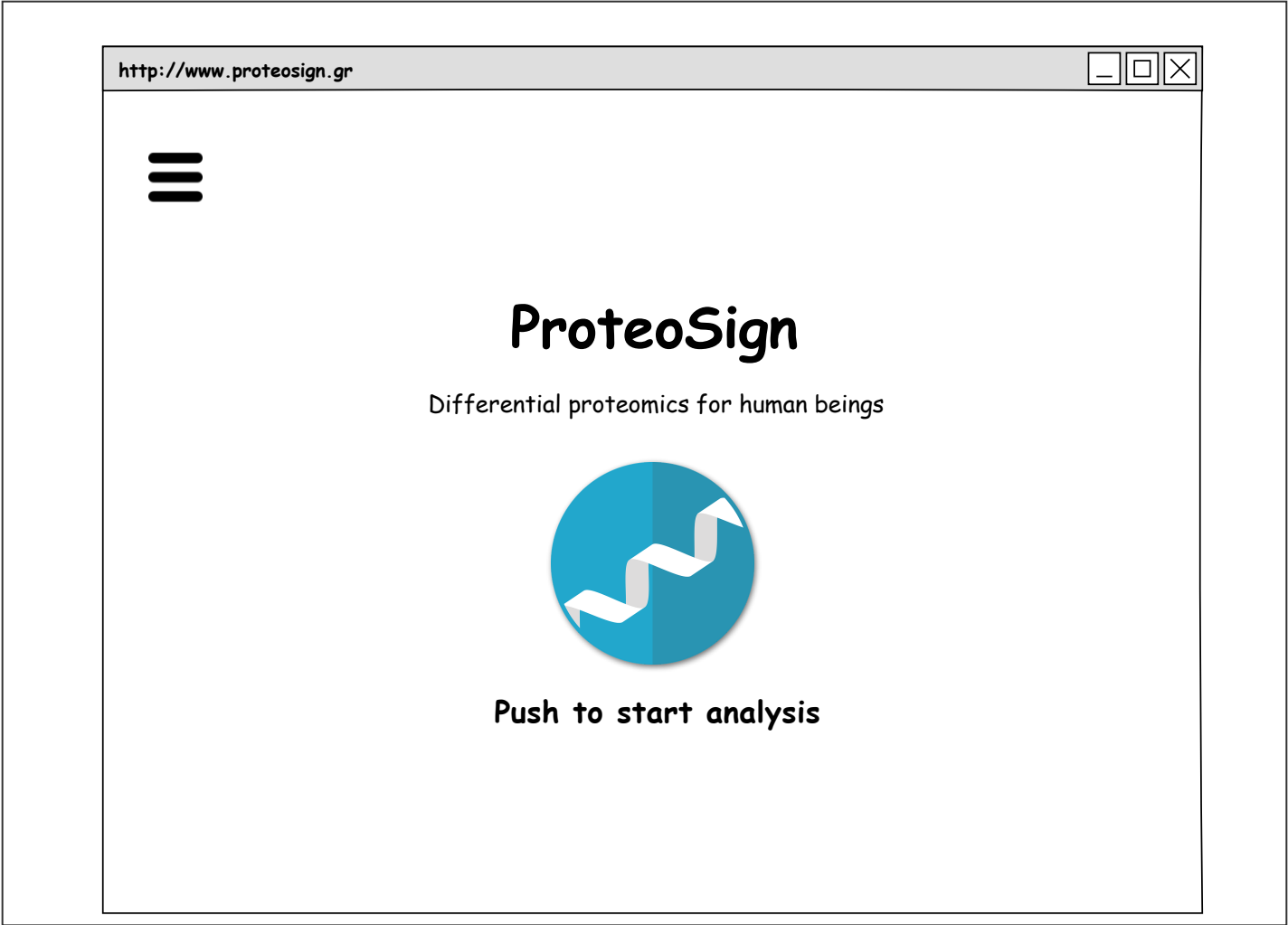




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ProteoSign

Differential proteomics for human beings



Push to start analysis

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 **Change Log**

12 December 2018: Added functionality for dwarves.

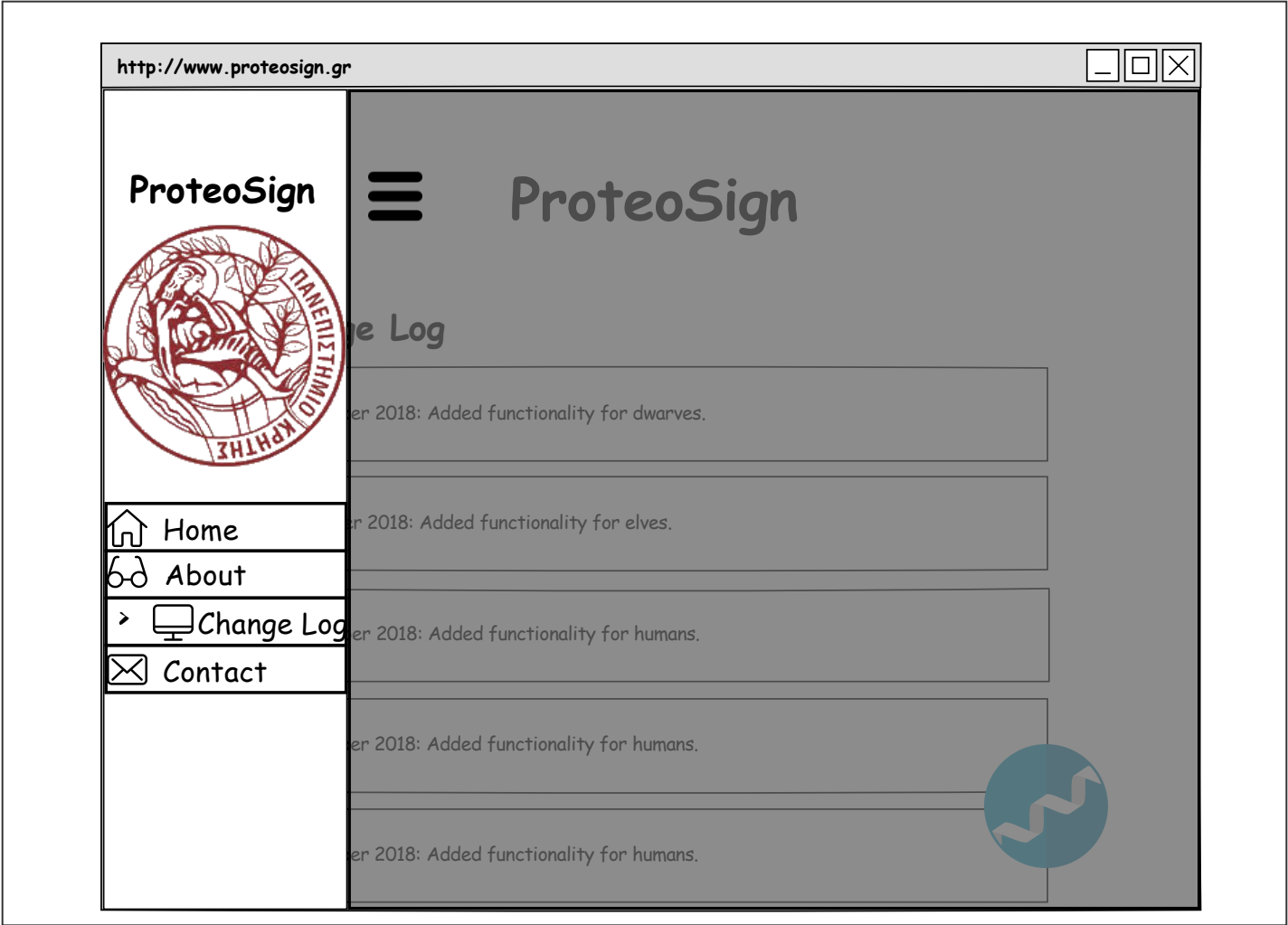
2 November 2018: Added functionality for elves.

21 Octomber 2018: Added functionality for humans.

21 Octomber 2018: Added functionality for humans.

21 Octomber 2018: Added functionality for humans.





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68 About

ProteoSign is an online service for protein **differential expression (or abundance) analysis** designed with the end-proteomics user in mind.

Borrowing from the experience of the microarray field, ProteoSign software utilizes the well-established [Linear Models For Microarray Data \(LIMMA\)](#) methodology for assessing statistical significance in protein abundance differences between two or more proteome states.

ProteoSign aims to fully automate the process of statistically evaluating differential expression in mass spectrometry-based bottom-up (shotgun) quantitative proteomics data by requiring **minimal user interaction time** and generating **publication-quality data plots**.

[Reference: This is a reference link](#)



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Step 1 of 6: Dataset Origin

Please choose the origin of the dataset

Proteome Discoverer

- or -

MaxQuant

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Step 2 of 6: Dataset Upload

Upload the Proteome Discoverer PSM file

First time here? Use a demo dataset!

Drag and drop or click to select files
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Step 2 of 6: Dataset Upload

Upload the ProteoSign dataset

Select dataset and press ok.
You can also download it to your machine!

Combo Box

Download

Cancel

OK

Drag and drop or click to select files
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Step 2 of 6: Dataset Upload

Upload the Proteome Discoverer PSM file

First time here? Use a demo dataset!

Drag and drop or click to select files
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Multiconsensus-psms.txt250 MBⓧ

Reset

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Step 2 of 6: Dataset Upload

Upload the Proteome Discoverer PSM file

First time here? Use a demo dataset!

Drag and drop or click to select files
(.txt only)

Multiconsensus-psms.txt250 MB

Reset

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Step 2 of 6: Dataset Upload

Upload the Proteome Discoverer PSM file

First time here? Use a demo dataset!

Drag and drop or click to select files
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Files Successfully Uploaded!

Reset

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Step 3 of 6: Experimental Setup

Fill the table with the information regarding the biological and technical replicates of the experiment. You can also import an experiment setup file by clickingthe import experimental setup button

Q

Search by raw file

Import Experimental Setup

☒	Raw Files	Biological Replicates	Technical replicates	Fraction
☒	Raw file 1	-	-	-
☒	Raw file 2	-	-	-
☒	Raw file 3	-	-	-
☒	Raw file 4	-	-	-
☒	Raw file 5	-	-	-
☒	Raw file 6	-	-	-
☒	Raw file 7	-	-	-
☒	Raw file 8	-	-	-
☒	Raw file 9	-	-	-
☒	Raw file 10	-	-	-

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Step 4 of 6: Experimental Setup

Fill t
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Search by

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☒	R
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☒	Raw file 7
☒	Raw file 8
☒	Raw file 9
☒	Raw file 10

technical
t setup

Experimental Setup
Fraction
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-

Import Experiment Setup File

Drag and drop or click to select files
(.csv only)

Download Experimental Empty Template

Upload

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Step 4 of 6: Experimental Setup

Fill the table with the information regarding the biological and technical replicates of the experiment. You can also import an experiment setup file by clicking the import experimental setup button

Q

Search by raw file

Import Experimental Setup

☒	Raw Files	Biological Replicates	Technical replicates	Fraction
☒	Raw file 1	1	1	1
☒	Raw file 2	2	1	1
☒	Raw file 3	3	1	1
☒	Raw file 4	4	1	1
☒	Raw file 5	5	1	1
☒	Raw file 6	6	1	1
☒	Raw file 7	7	1	1
☒	Raw file 8	8	1	1
☒	Raw file 9	9	1	1
☒	Raw file 10	10	1	1

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Step 4 of 6: Experimental Setup

Fill the table with the information regarding the biological and technical replicates of the experiment. You can also import an experiment setup file by clickingthe import experimental setup button

Search by raw file

Import Experimental Setup

	Raw Files	Biological Replicates	Technical replicates	Fraction	Condition
	Raw file 1	1	1	1	Wild
	Raw file 2	2	1	1	Wild
	Raw file 3	3	1	1	Wild
	Raw file 4	4	1	1	Wild
	Raw file 5	5	1	1	Wild
	Raw file 6	1	1	1	Mutant
	Raw file 7	2	1	1	Mutant
	Raw file 8	3	1	1	Mutant
	Raw file 9	4	1	1	Mutant
	Raw file 10	5	1	1	Mutant

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Step 5 of 6: Analysis Parameters

Conditions to compare

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Analysis parameters 

Parameter	Value
Analysis Name	ProteoSign-Analysis
Minimum Peptide's detections	1
Minimum Peptides per protein	2
Minimum Valid values percentance	50.0
Plots format	JPEG
Error Correction Method	Benjamini-Hochberg
Fold Change cutoff	1.5
FDR	0.05



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Push to start Analysis

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ProteoSign

Step 5 of 6: Analysis Parameters

Conditions to compare

Provide Custom Parameters

Parameter	Value
Analysis Name	ProteoSign-Analysis
Minimum Peptide's detections	1
Minimum Peptides per protein	2
Minimum Valid values percentance	50.0
Plots format	JPEG
Error Correction Method	Benjamini-Hochberg
Fold Change cutoff	1.5
FDR	0.05

or

Drag and drop or click to select file
(.csv only)

Download Parameters Empty Template

experimental-structure.csv
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ProteoSign

Step 5 of 6: Analysis Parameters

Conditions to compare

Provide Custom Parameters

Parameter	Value
Analysis Name	ProteoSign-Analysis
Minimum Peptide's detections	1
Minimum Peptides per protein	2
Minimum Valid values percentance	50.0
Plots format	JPEG
Error Correction Method	Benjamini-Hochberg
Fold Change cutoff	1.5
FDR	0.05

Parameters Successfully Set

Reset

Confirm

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Step 5 of 6: Analysis Parameters

Conditions to compare

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or

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Step 6 of 6: Analysis

1. Data Import 
2. Data Wrangling
3. Filtering of Contaminants/Reverse Sequences
4. Normalization
5. Imputation
6. Aggregation
7. Differential Expression Analysis
8. Plot Generation

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Step 6 of 6: Analysis

1. Data Import 
2. Data Wrangling 
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7. Differential Expression Analysis
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Step 6 of 6: Analysis

1. Data Import ✓
2. Data Wrangling ✓
3. Filtering of Contaminants/Reverse Sequences ✓
4. Normalization ✓
5. Imputation ✓
6. Aggregation ✓
7. Differential Expression Analysis ✓
8. Plot Generation ✓

View Results

