



Tutorial: Processing MaxQuant- Data with Perseus

Perseus 1.5.1.6

What is Perseus?

- Powerful statistical software package developed by the Matthias Mann group (Freeware)
- Especially suited to analyze, evaluate and visualize MaxQuant-derived proteomic data

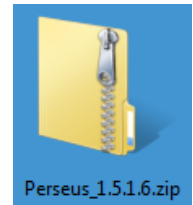
Installation

- Requirements:
 - Operating System: Microsoft Windows Vista or better (but can be run on a Mac via Parallels or Bootcamp etc.)
 - Preinstalled Software: Microsoft .NET Framework 4.5 (<http://www.microsoft.com/de-de/download>)
 - Perseus Registration Code (free-of-charge online-registration) → [click here](#)

Installation

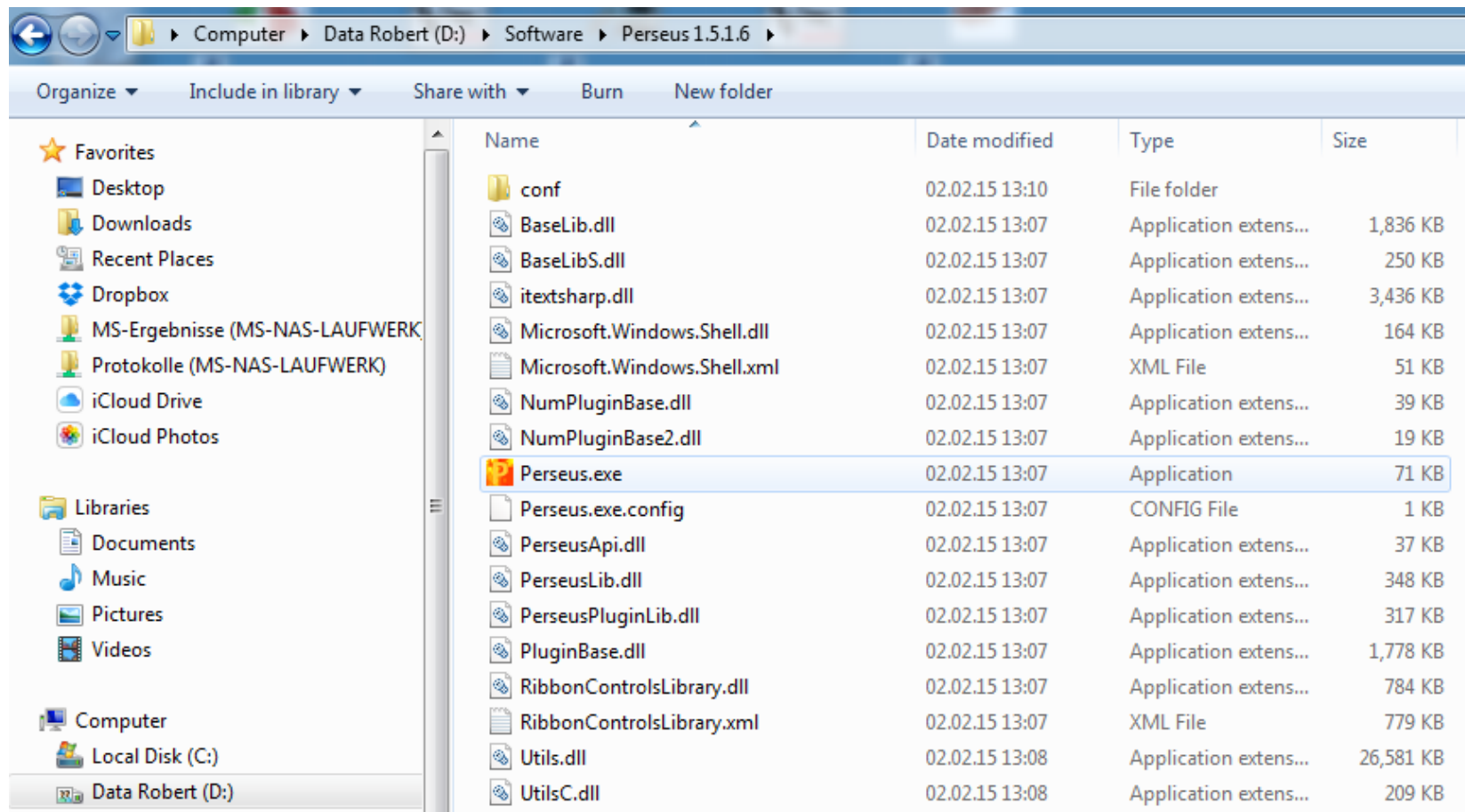
1. Download Perseus

- Perseus is provided as a single compressed file (.zip)
- You can download it by clicking [here](#) (Keep your registration code at hand)



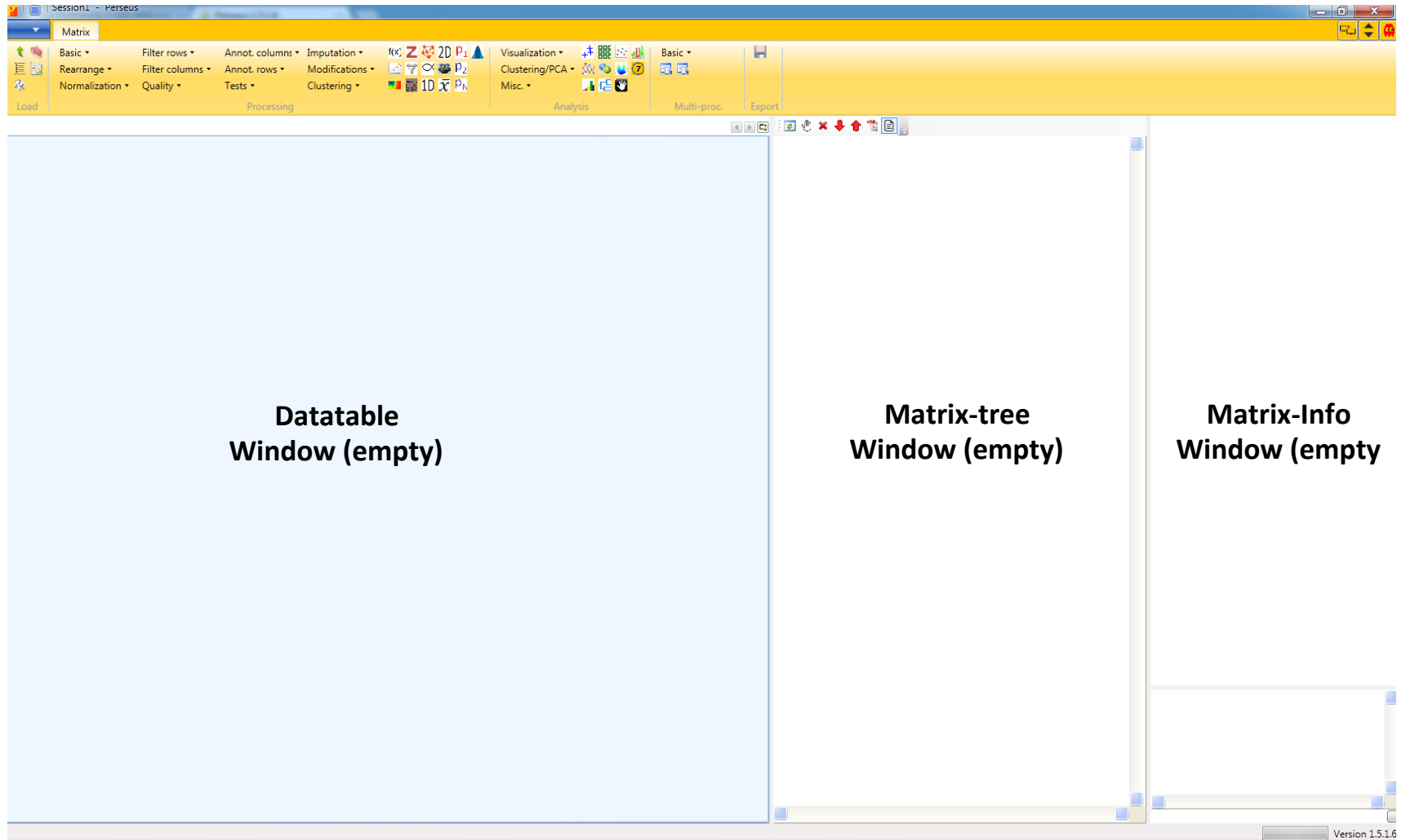
2. Uncompress the zip-file and move the containing Perseus folder to a destination of choice

Start Perseus by double clicking Perseus.exe



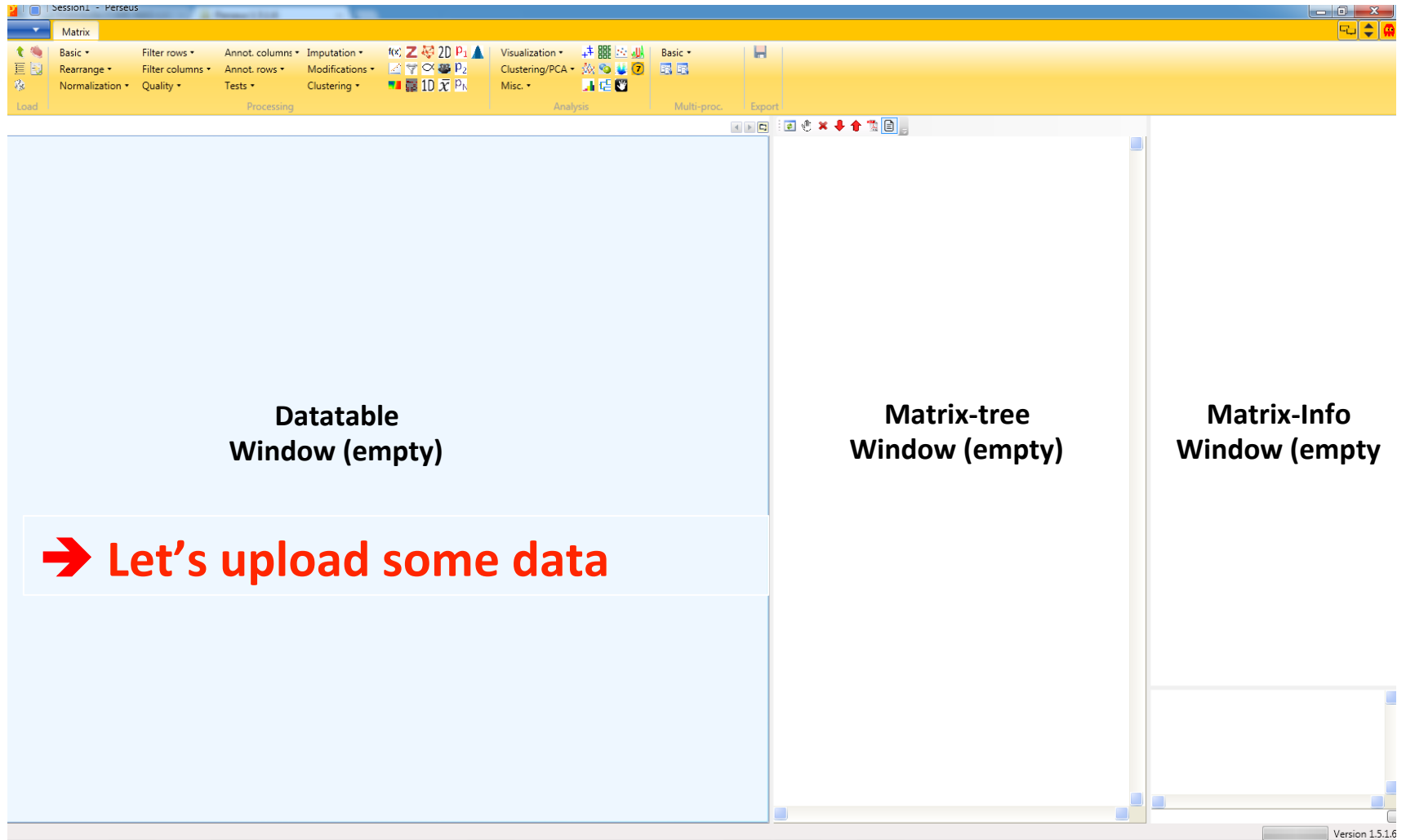
The software's main window opens

Main
Menu



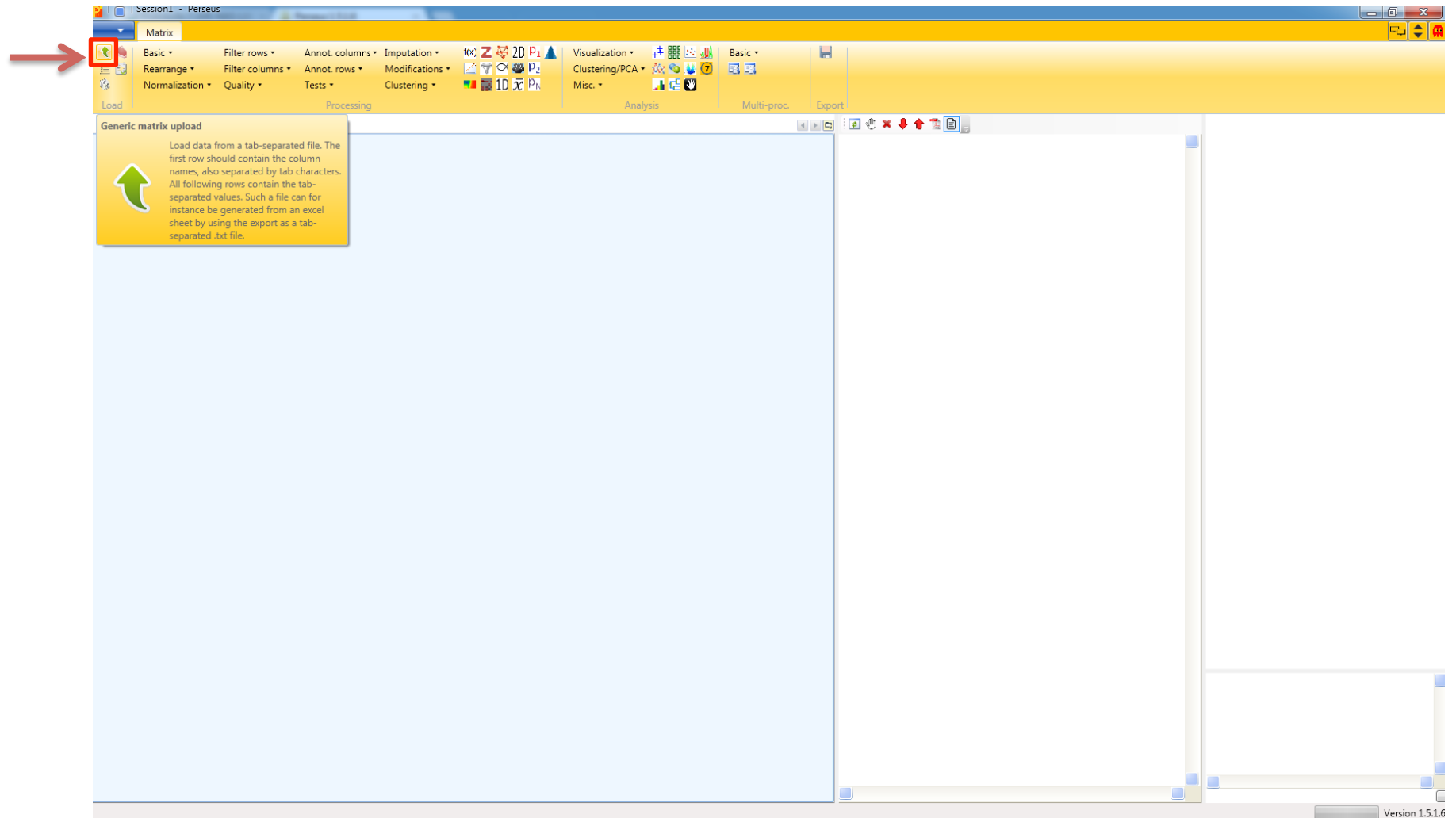
The software's main window opens

Main
Menu



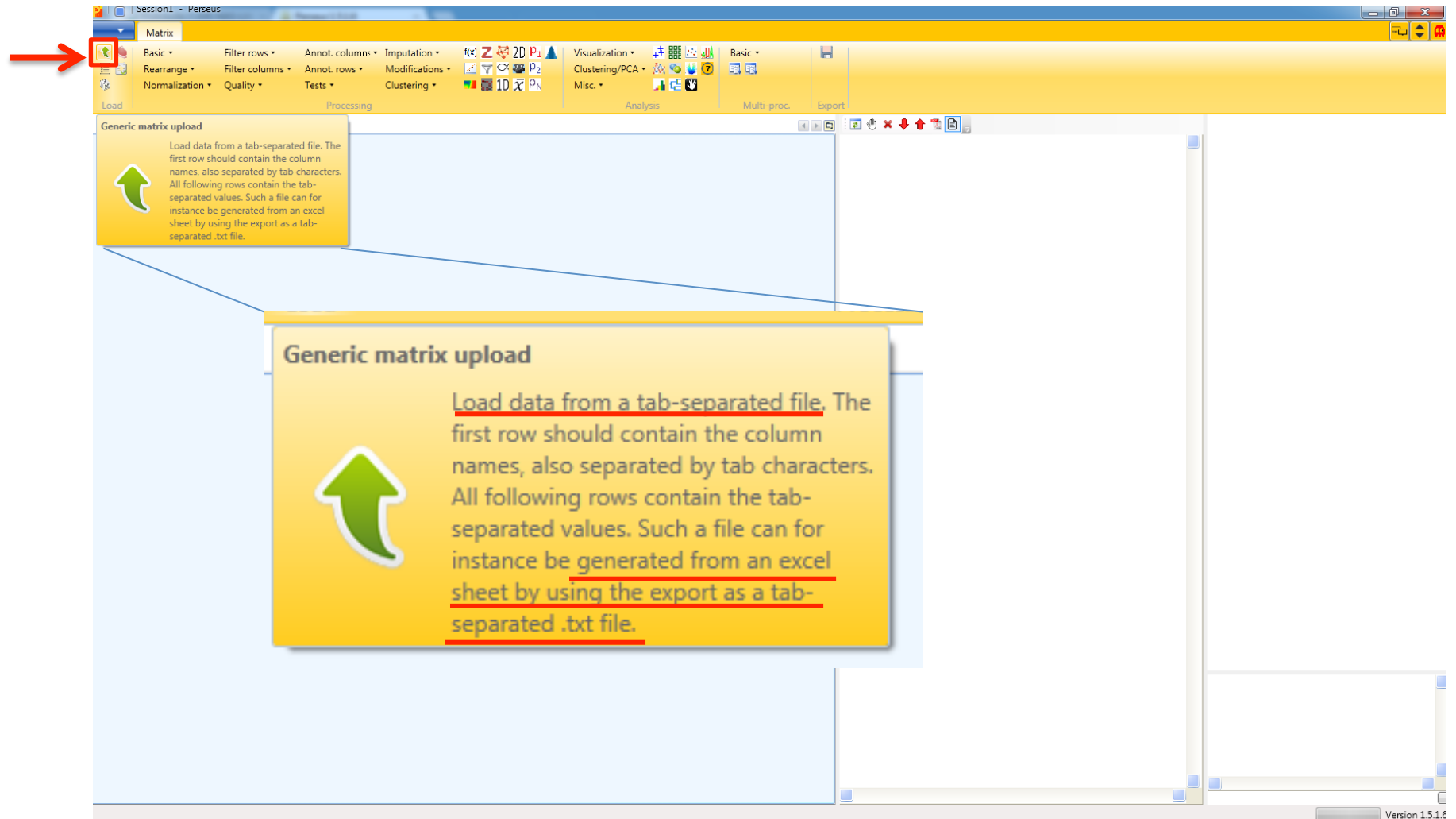
Data upload

Click on the small green arrow in the upper left corner

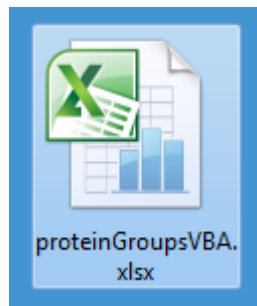


Data upload

The data is needed in a tab-separated format → Data export from Excel



1.Open Excel-file with protein/peptide results



Start

Einfügen

Seitenlayout

Formeln

Daten

Überprüfen

Ansicht

Acrobat

A198

P42212;CON_Q5U6Y5

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z
1	Protein IDs	Majority prot Peptide count Peptide count Peptide count Protein name Gene names Fasta header Number of p Peptides																								
2	T	N	N	N	N	T	T	T	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	
3	A0FGR8	A0FGR8	>sp	4	4	Extended sys ESYT2	>sp	A0FGR8	1	4	4	4	4	4	4	4	4.7	4.7	4.7	4.7	102.36					
4	A2RUC4	A2RUC4	1	1	1	tRNA wybut YW5	>sp	A2RUC4	1	1	1	1	1	1	1	1	4.8	4.8	4.8	4.8	36.547					
5	A4UGR9	A4UGR9	1	1	1	Xin actin-bin XIRP2	>sp	A4UGR9	1	1	1	1	1	1	1	1	0.7	0.7	0.7	0.7	382.3					
6	ASYYK6	ASYYK6	1	1	1	1 CR4-NOT R CNOT1	>sp	ASYYK6	1	1	1	1	1	1	1	1	0.6	0.6	0.6	0.6	266.94					
7	P0735S;A6NMV6	P0735S;A6N7	3	3	3	Annexin A2 ANXA2	>sp	P0735S	2	3	3	3	3	3	3	10.9	10.9	10.9	10.9	38.604						
8	P11231;B1NKU2;B1NK87;B1P12131;B1N1	P11231;B1N1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	>sp	P11231	1	1	1	1	1	1	1	1	1.9	1.9	1.9	1.9	103.75					
9	A8MP57	A8MP57	1	1	1	1 UPF0249 pro YDJC	>sp	A8MP57	1	1	1	1	1	1	1	1	4.3	4.3	4.3	4.3	34.466					
10	A8MV23	A8MV23	1	1	1	1 Serpin E3 SERPINE3	>sp	A8MV23	1	1	1	1	1	1	1	1	1.9	1.9	1.9	1.9	46.962					
11	CON_P00761	CON_P0076	2	2	2	>sp	P00761 SWI	1	2	2	2	2	2	2	2	7.8	7.8	7.8	7.8	24.409						
12	P02533;CON_P02533;Q0466 P02533;CON_13	P02533;CON_13	13;15;5;5;5;5;9;9;2;2;1;1;5;5;1;1;0;0;	Keratin, type KRT14	>sp	P02533	43	13	9	5	13	9	5	32.6	27.3	16.7	51.561									
13	P02538;CON_P02538;P4866 P02538;CON_13	P02538;CON_13	13;12;12;18;8;7;7;1;1;1;0;0;0;0;	Keratin, type KRT6A;KRT6B	>sp	P02538	9	13	8	1	13	8	1	27	18.1	18.1	60.044									
14	CON_P02662	CON_P0266	2	2	2	>sp	P02662 SWI	1	2	2	2	2	2	11.1	11.1	11.1	22.975									
15	CON_P02754	CON_P0275	1	1	1	>sp	P02754 SWI	1	1	1	1	1	1	8.6	8.6	8.6	18.281									
16	P08779;CON_P08779	P08779;CON_11	11	3	3	Keratin, type KRT16	>sp	P08779	2	11	3	3	11	3	26.6	10.8	10.8	51.267								
17	P13645;CON_P13645;CON_28	P13645;CON_28	28;9;3;3;3;22;22;5;1;1;0;	Keratin, type KRT10	>sp	P13645	12	28	28	22	28	22	53.1	53.1	46.7	58.826										
18	P13647;CON_P13647;CON_11	P13647;CON_11	11;1;2	5	3	Keratin, type KRT5	>sp	P13647	3	11	5	3	11	5	3	20.3	9.3	5.9	62.378							
19	P35527;CON_P35527	P35527;CON_23	23	22	22	Keratin, type KRT9	>sp	P35527	2	23	22	22	22	54.3	53.1	53.1	62.064									
20	P35908;CON_P35908;Q0155 P35908;CON_20	P35908;CON_20	20;20;3;2;2;2;18;18;3;2;2;2;13;10;0;0;0	Keratin, type KRT2	>sp	P35908	20	20	18	13	20	18	13	41.8	38.7	30.2	65.432									
21	CON_Q35ZHS	CON_Q35Z	1	1	1	>sp	Q35ZHS TRE	1	1	1	1	1	1	1	1	1.7	1.7	1.7	1.7	45.456						
22	Q5D862;CON_Q5D862	Q5D862;CON_1	1	1	1	Filaggrin-2 FLG2	>sp	Q5D862	2	1	1	1	1	1	0.5	0.5	0.5	0.5	248.07							
23	Q7Z794;CON_Q7Z794	Q7Z794;CON_2	1	1	1	Keratin, type KRT77	>sp	Q7Z794	1	2	1	2	1	3.8	1.7	1.7	61.901									
24	Q00148;Q13838	Q00148;Q13	1	1	1	ATP-depend DDX39A;DDX3	>sp	Q00148	1	1	1	1	1	2.3	2.3	2.3	49.129									
25	Q00165	Q00165	5	5	5	HCLS1-associ HAX1	>sp	Q00165	1	5	5	5	5	21.1	21.1	21.1	31.62									
26	Q00217	Q00217	1	1	1	1 NADH dehyd NDUF8	>sp	Q00217	1	1	1	1	1	4.3	4.3	4.3	23.705									
27	Q00264	Q00264	3	3	3	Membrane-c PRGMC1	>sp	Q00264	1	3	3	3	3	16.4	16.4	16.4	21.671									
28	Q00327	Q00327	1	1	1	1 Aryl hydroc ARNTL	>sp	Q00327	1	1	1	1	1	1.4	1.4	1.4	68.761									
29	Q00483	Q00483	3	3	3	3 NADH dehyd NDUF4	>sp	Q00483	1	3	3	3	3	37	37	37	37	9.3697								
30	Q00487	Q00487	1	1	1	1 26S proteas PSMD14	>sp	Q00487	1	1	1	1	1	4.2	4.2	4.2	34.577									
31	Q00571;Q15523;Q9NQ10	Q00571;Q15	6;4	6;4	6;4	ATP-depend DDX3X;DDX3	>sp	Q00571	3	6	6	6	6	11.6	11.6	11.6	73.243									
32	Q14654	Q14654	6	6	6	6 insulin rece IR54	>sp	Q14654	1	6	6	6	6	6.6	6.6	6.6	133.77									
33	Q14681	Q14681	2	2	2	2 Etoposide-in E124	>sp	Q14681	1	2	2	2	2	5.9	5.9	5.9	39.864									
34	Q14734	Q14734	1	1	1	1 Acyl-coenz y ACO8	>sp	Q14734	1	1	1	1	1	2.8	2.8	2.8	35.914									
35	Q14735	Q14735	2	2	2	2 CDP-diacyl CDIPT	>sp	Q14735	1	2	2	2	2	11.3	11.3	11.3	23.539									
36	Q14880	Q14880	2	2	2	2 Microsomal MGST3	>sp	Q14880	1	2	2	2	2	17.8	17.8	17.8	16.516									
37	Q14910;Q9NUP9;Q9HAP6	Q14910;Q9N	2;1	2;1	2;1	2 Protein lin-7 UNTA;UNTC	>sp	Q14910	3	2	2	2	2	9	9	9	25.996									
38	Q14925;Q5SRD1	Q14925;Q5S	7	7	7	7 Mitochondri TIMM23;TIM	>sp	Q14925	2	7	7	7	7	61.7	61.7	61.7	21.943									
39	Q14966;P57729;Q13637	Q14966	4;1	4;1	4;1	4 Ras-related RAB7L1	>sp	Q14966	3	4	4	4	4	23.2	23.2	23.2	23.155									
40	Q14967	Q14967	1	1	1	1 Calmegin CLGN	>sp	Q14967	1	1	1	1	1	1.8	1.8	1.8	70.038									
41	Q14980	Q14980	1	1	1	1 Exportin-1 XPO1	>sp	Q14980	1	1	1	1	1	1.1	1.1	1.1	123.38									
42	Q15120	Q15120	2	2	2	2 1-acyl-sn-glyc APAT2	>sp	Q15120	1	2	2	2	2	9.4	9.4	9.4	30.914									
43	Q15258	Q15258	1	1	1	1 Protein RER1 RER1	>sp	Q15258	1	1	1	1	1	5.6	5.6	5.6	22.958									
44	Q15260	Q15260	4	4	4	4 Surface lect LUSF4	>sp	Q15260	1	4	4	4	4	18.6	18.6	18.6	30.39									

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ProteinGroups

Parameters

Minimum 5 peptides

Minimum 2 peptides (2)

Bereit

Mittelwert: 39601.29156

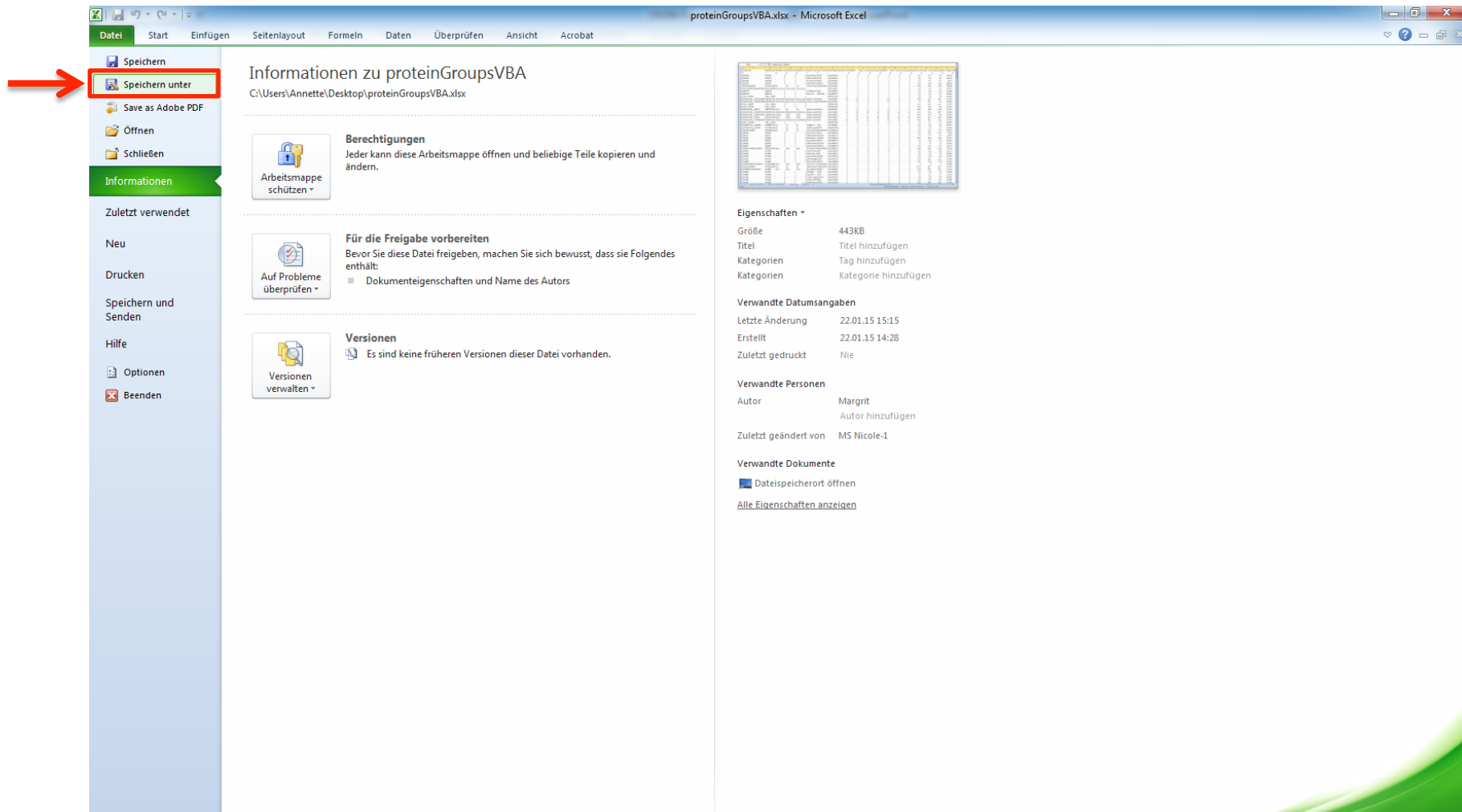
Anzahl: 82

Summe: 2.25727E+11

100 %

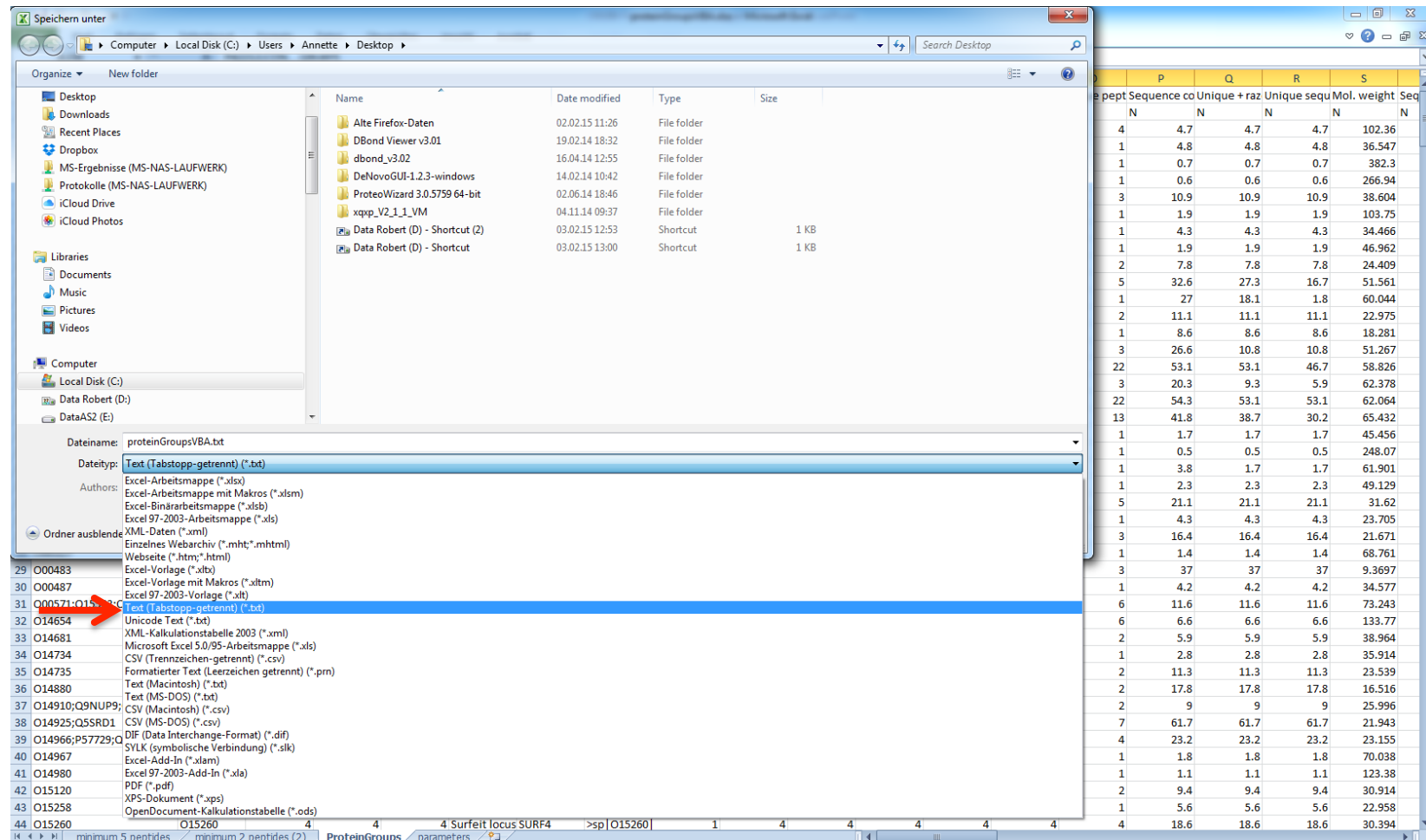
Data export from Excel

2.Click on File (Datei) ➔ Save as (Speichern unter)



Data export from Excel

3. As file format (Dateityp) choose "Text (Tab delimited) (*.txt)"



Data export from Excel

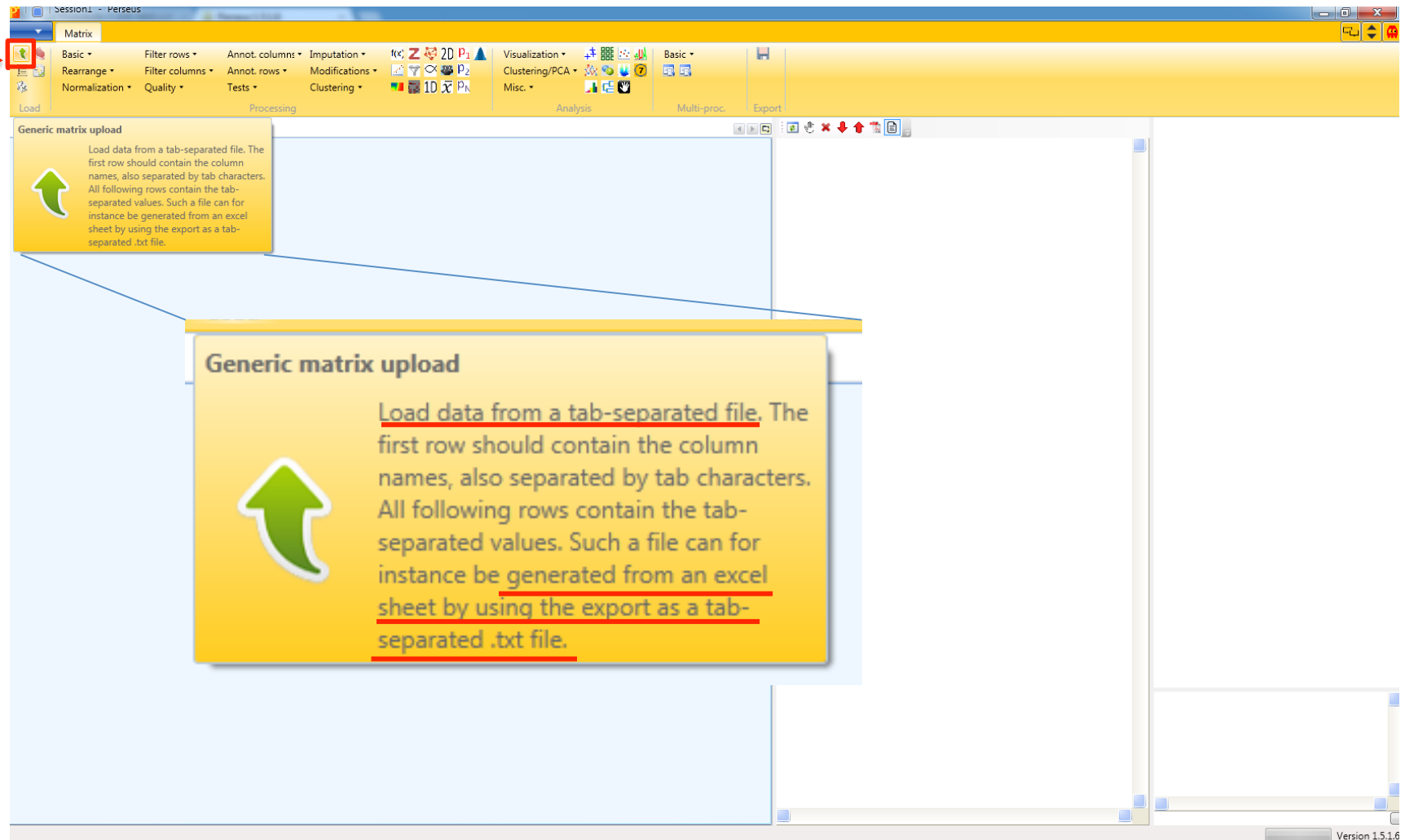
4. Confirm export by clicking OK ➔ Note that only the currently selected datasheet is exported

The screenshot shows a Microsoft Excel window with a spreadsheet titled "proteinGroupsVBA.xlsx". The spreadsheet contains a table with columns A through S, representing various protein and peptide data. A dialog box is open in the center, titled "Microsoft Excel", with a yellow warning icon. The text inside the dialog box reads: "Der ausgewählte Dateityp unterstützt keine Arbeitsmappen, die mehrere Blätter enthalten." Below this, there are two bullet points: "• Klicken Sie auf 'OK', wenn nur das aktuelle Blatt gespeichert werden soll." and "• Wenn alle Blätter in dieser Arbeitsmappe in dem ausgewählten Dateityp gespeichert werden sollen, wählen Sie jedes Blatt aus, und speichern Sie es als eigene Datei unter unterschiedlichen Namen, oder wählen Sie einen Dateityp, der mehrere Blätter unterstützt." At the bottom of the dialog box, there is a link "War diese Information hilfreich?". The "OK" button is highlighted with a red arrow, indicating the action to be taken to confirm the export of the currently selected datasheet.

Protein IDs	Majority pro	Peptide cou	Peptide cou	Peptide cou	Protein nam	Gene names	Fasta header	Number of p	Peptides	Razor + uniq	Unique pept	Peptides 1	Razor + uniq	Unique pept	Sequence co	Unique + raz	Unique sequ	Mol. weight	Seq
T	N	N	N	N	T	T	T	N	N	N	N	N	N	N	N	N	N	N	N
A0FGR8	A0FGR8	4	4	4	Extended syi	ESYT2	>sp A0FGR8	1	4	4	4	4	4	4	4.7	4.7	4.7	102.36	
A2RUC4	A2RUC4	1	1	1	tRNA wybuti	TYW5	>sp A2RUC4	1	1	1	1	1	1	1	4.8	4.8	4.8	36.547	
A4UGR9	A4UGR9	1	1	1	Xin actin-bin	XIRP2	>sp A4UGR9	1	1	1	1	1	1	1	0.7	0.7	0.7	382.3	
ASYYK6	ASYYK6	1	1	1	CCR4-NOT tr	CNOT1	>sp ASYYK6	1	1	1	1	1	1	1	0.6	0.6	0.6	266.94	
P07355;A6NMY6	P07355;A6NMY6	3;3	3;3	3;3	Annexin A2;	ANXA2;ANX	>sp P07355	2	3	3	3	3	3	3	10.9	10.9	10.9	38.604	
P11231;B1NKT8;B1	P11231;B1NKT8;B1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	1;1;1;1;1;1	>sp P11231	7	1	1	1	1	1	1	1.9	1.9	1.9	103.75	
A8MPS7	A8MPS7	1	1	1	UPF0249 pro	YDJC	>sp A8MPS7	1	1	1	1	1	1	1	4.3	4.3	4.3	34.466	
A8MV23	A8MV23	1	1	1	Serpin E3	SERPINE3	>sp A8MV23	1	1	1	1	1	1	1	1.9	1.9	1.9	46.962	
CON_P00761	CON_P00761	2	2	2			>P00761 SWI	1	2	2	2	2	2	2	7.8	7.8	7.8	24.409	
P02533;CON_P02533;Q046	P02533;CON_P02533;Q046	13;13;5;5;5;5	9;9;2;2;1;1;1	5;5;1;1;0;0	Keratin, type	KRT14	>sp P02533	43	13	9	5	13	9	5	32.6	27.3	16.7	51.561	
P02538;CON_P02538;P4866	P02538;CON_P02538;P4866	13;13;12;12;18;8;7;7;1;1	1;1;0;0;0;0;0	Keratin, type	KRT6A;KRT6	>sp P02538	9	13	8	1	13	8	1	27	18.1	1.8	60.044		
CON_P02662	CON_P02662	2	2	2			>P02662 SWI	1	2	2	2	2	2	2	11.1	11.1	11.1	22.975	
CON_P02754	CON_P02754	1	1	1			>P02754 SWI	1	1	1	1	1	1	1	8.6	8.6	8.6	18.281	
P08779;CON_P08779	P08779;CON_P08779	3;3	3;3	3;3	Keratin, type	KRT16	>sp P08779	2	11	3	3	11	3	3	26.6	10.8	10.8	51.267	
P13645;CON_P13645;CON_P13645;CON_28;28;9;3;3	P13645;CON_P13645;CON_P13645;CON_28;28;9;3;3	28;28;9;3;3	22;22;5;1;1	Keratin, type	KRT10	>sp P13645	12	28	28	28	22	28	28	22	53.1	53.1	46.7	58.826	
P13647;CON_P13647;CON_P13647;CON_11;11	P13647;CON_P13647;CON_P13647;CON_11;11	11;11													20.3	9.3	5.9	62.378	
P35527;CON_P35527	P35527;CON_P35527	23;23													54.3	53.1	53.1	62.064	
P35908;CON_P35908;Q015	P35908;CON_P35908;Q015	20;20													41.8	38.7	30.2	65.432	
CON_Q35ZHS	CON_Q35ZHS														1.7	1.7	1.7	45.456	
Q5D862;CON_Q5D862	Q5D862;CON_Q5D862	1													0.5	0.5	0.5	248.07	
Q7Z794;CON_Q7Z794	Q7Z794;CON_Q7Z794	2;2													3.8	1.7	1.7	61.901	
O00148;Q13838	O00148;Q13838	1;1													2.3	2.3	2.3	49.129	
O00165	O00165														21.1	21.1	21.1	31.62	
O00217	O00217														4.3	4.3	4.3	23.705	
O00264	O00264	3	3	3	Membrane-z	PGRMC1	>sp O00264	1	3	3	3	3	3	3	16.4	16.4	16.4	21.671	
O00327	O00327	1	1	1	Aryl hydroca	ARNTL	>sp O00327	1	1	1	1	1	1	1	1.4	1.4	1.4	68.761	
O00483	O00483	3	3	3	NADH dehyd	NDUFA4	>sp O00483	1	3	3	3	3	3	3	37	37	37	9.3697	
O00487	O00487	1	1	1	26S proteas	PSMD14	>sp O00487	1	1	1	1	1	1	1	4.2	4.2	4.2	34.577	
O00571;O15523;Q9NQJ0	O00571;O15523;Q9NQJ0	6;4;1	6;4;1	6;4;1	ATP-depend	DDX3X;DDX3	>sp O00571	3	6	6	6	6	6	6	11.6	11.6	11.6	73.243	
O14654	O14654	6	6	6	Insulin rece	IRS4	>sp O14654	1	6	6	6	6	6	6	6.6	6.6	6.6	133.77	
O14681	O14681	2	2	2	Etoposide-in	EI24	>sp O14681	1	2	2	2	2	2	2	5.9	5.9	5.9	38.964	
O14734	O14734	1	1	1	Acyl-coenzy	ACOT8	>sp O14734	1	1	1	1	1	1	1	2.8	2.8	2.8	35.914	
O14735	O14735	2	2	2	CDP-diacylg	CDIPT	>sp O14735	1	2	2	2	2	2	2	11.3	11.3	11.3	23.539	
O14880	O14880	2	2	2	Microsomal	MGST3	>sp O14880	1	2	2	2	2	2	2	17.8	17.8	17.8	16.516	
O14910;Q9NUP9;Q9HAP6	O14910;Q9NUP9;Q9HAP6	2;1;1	2;1;1	2;1;1	Protein lin-7	LIN7A;LIN7C	>sp O14910	3	2	2	2	2	2	2	9	9	9	25.996	
O14925;Q5SRD1	O14925;Q5SRD1	7;5	7;5	7;5	Mitochondri	TIMM23;TIM	>sp O14925	2	7	7	7	7	7	7	61.7	61.7	61.7	21.943	
O14966;P57729;Q13637	O14966;P57729;Q13637	4;1;1	4;1;1	4;1;1	Ras-related	RAB7L1	>sp O14966	3	4	4	4	4	4	4	23.2	23.2	23.2	23.155	
O14967	O14967	1	1	1	Calmequin	CLGN	>sp O14967	1	1	1	1	1	1	1	1.8	1.8	1.8	70.038	
O14980	O14980	1	1	1	Exportin-1	XPO1	>sp O14980	1	1	1	1	1	1	1	1.1	1.1	1.1	123.38	
O15120	O15120	2	2	2	2-acyl-sn-gly	AGPAT2	>sp O15120	1	2	2	2	2	2	2	9.4	9.4	9.4	30.914	
O15258	O15258	1	1	1	Protein RER1	RER1	>sp O15258	1	1	1	1	1	1	1	5.6	5.6	5.6	22.958	
O15260	O15260	4	4	4	Surfeit locus	SURF4	>sp O15260	1	4	4	4	4	4	4	18.6	18.6	18.6	30.394	

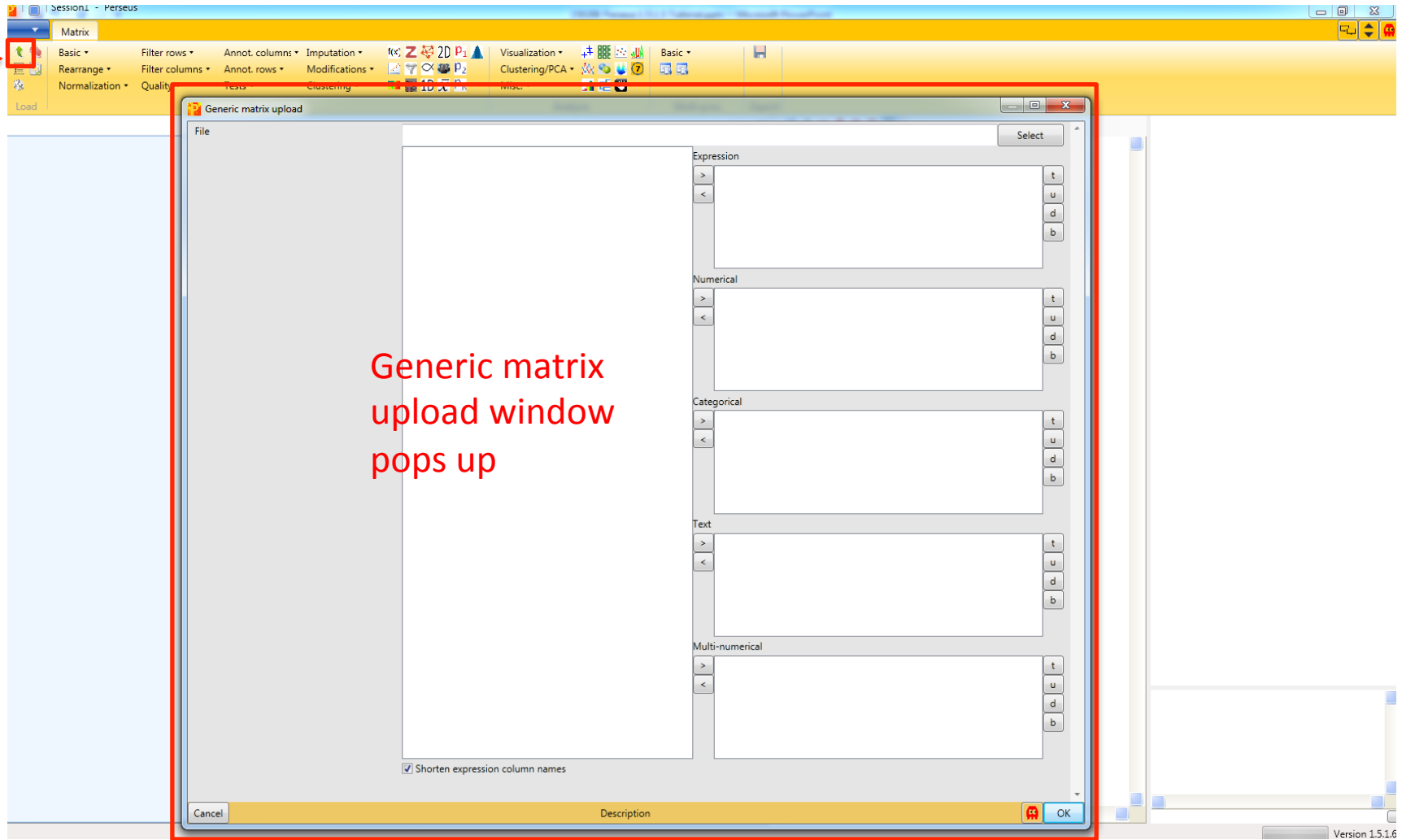
Back to Perseus - Data upload

Click
here!



Data upload

Click
here!



Data upload

Generic matrix upload

File

Expression

Numerical

Categorical

Text

Multi-numerical

☒ Shorten expression column names

Cancel Description OK

Select

Click here and select txt-file!

Data upload

Generic matrix upload

File: C:\Users\Annette\Desktop\proteinGroupsVBA.txt

Expression

- > Ratio M/L normalized
- < Ratio H/L normalized
- Ratio H/M normalized

Numerical

- > PEP
- < Sequence coverage [%]
- Unique + razor sequence coverage [%]
- Unique sequence coverage [%]
- Mol. weight [kDa]
- Peptides
- Razor + unique peptides
- Unique peptides

Categorical

- > Only identified by site
- < Reverse
- Potential contaminant

Text

- > Protein IDs
- < Majority protein IDs
- Protein names
- Gene names

Multi-numerical

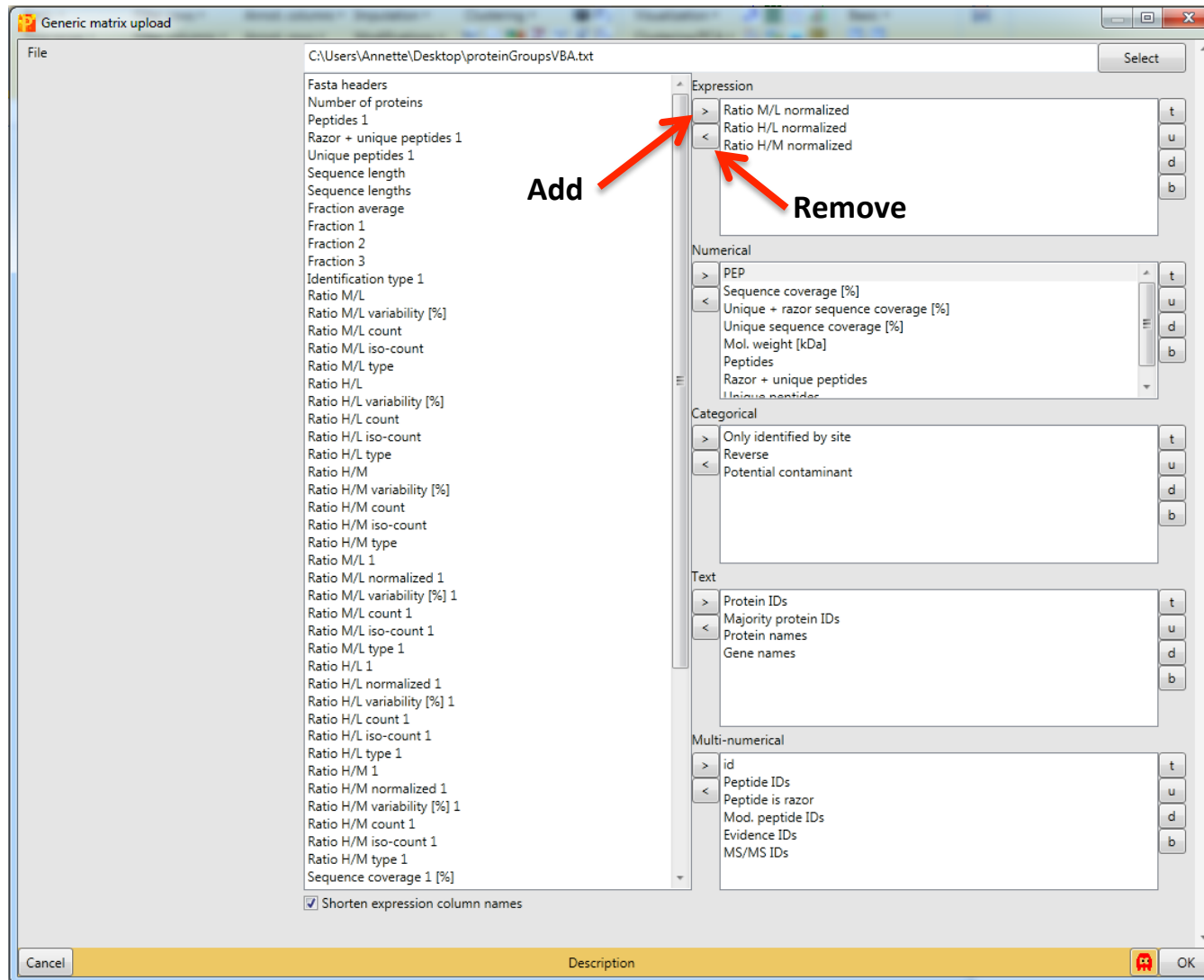
- > id
- < Peptide IDs
- Peptide is razor
- Mod. peptide IDs
- Evidence IDs
- MS/MS IDs

☒ Shorten expression column names

Cancel Description OK

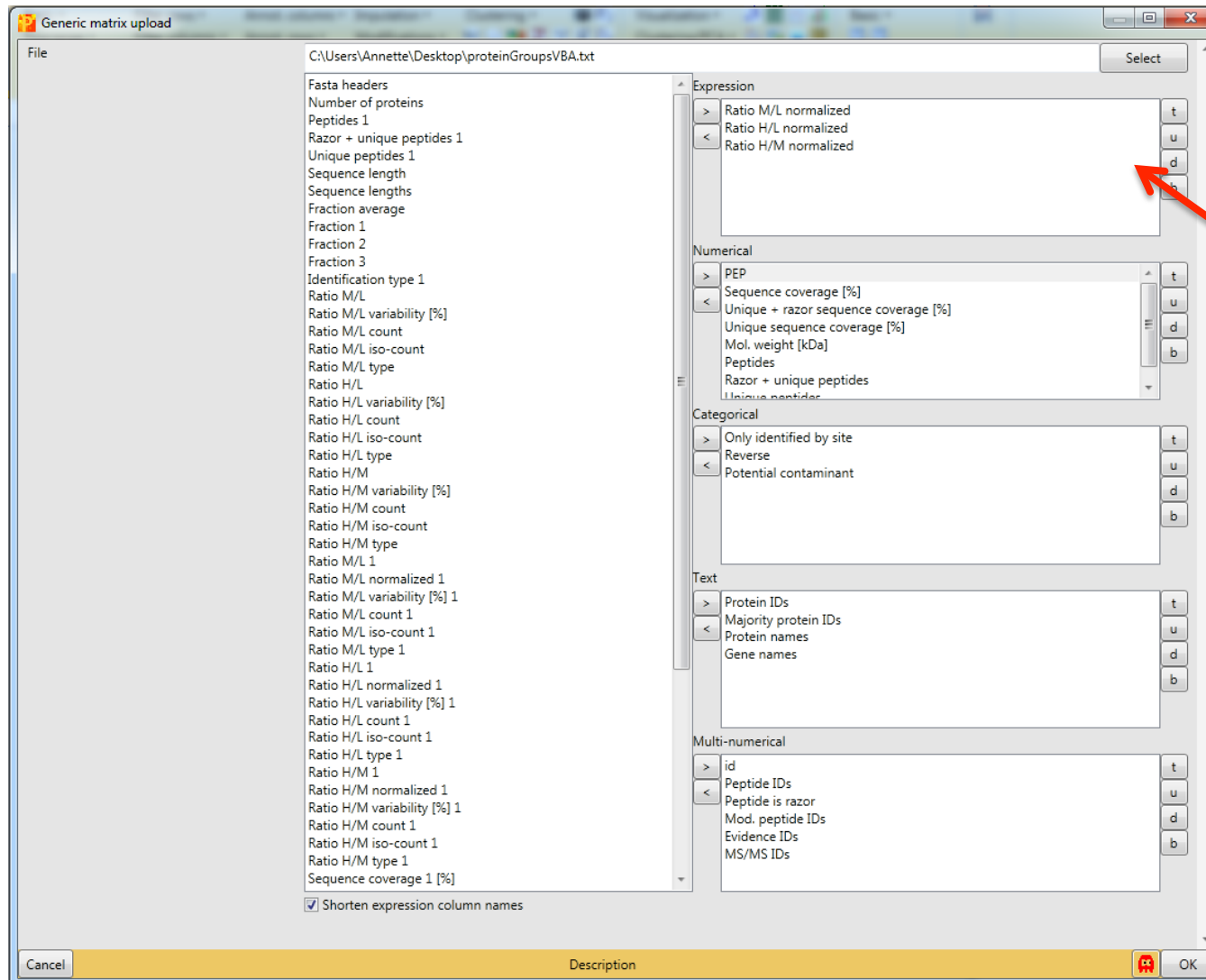
Now you have to define which data columns should be imported into Perseus. You must also define which type of data each column contains.

Data upload



Data is added or removed by clicking on the respective buttons.

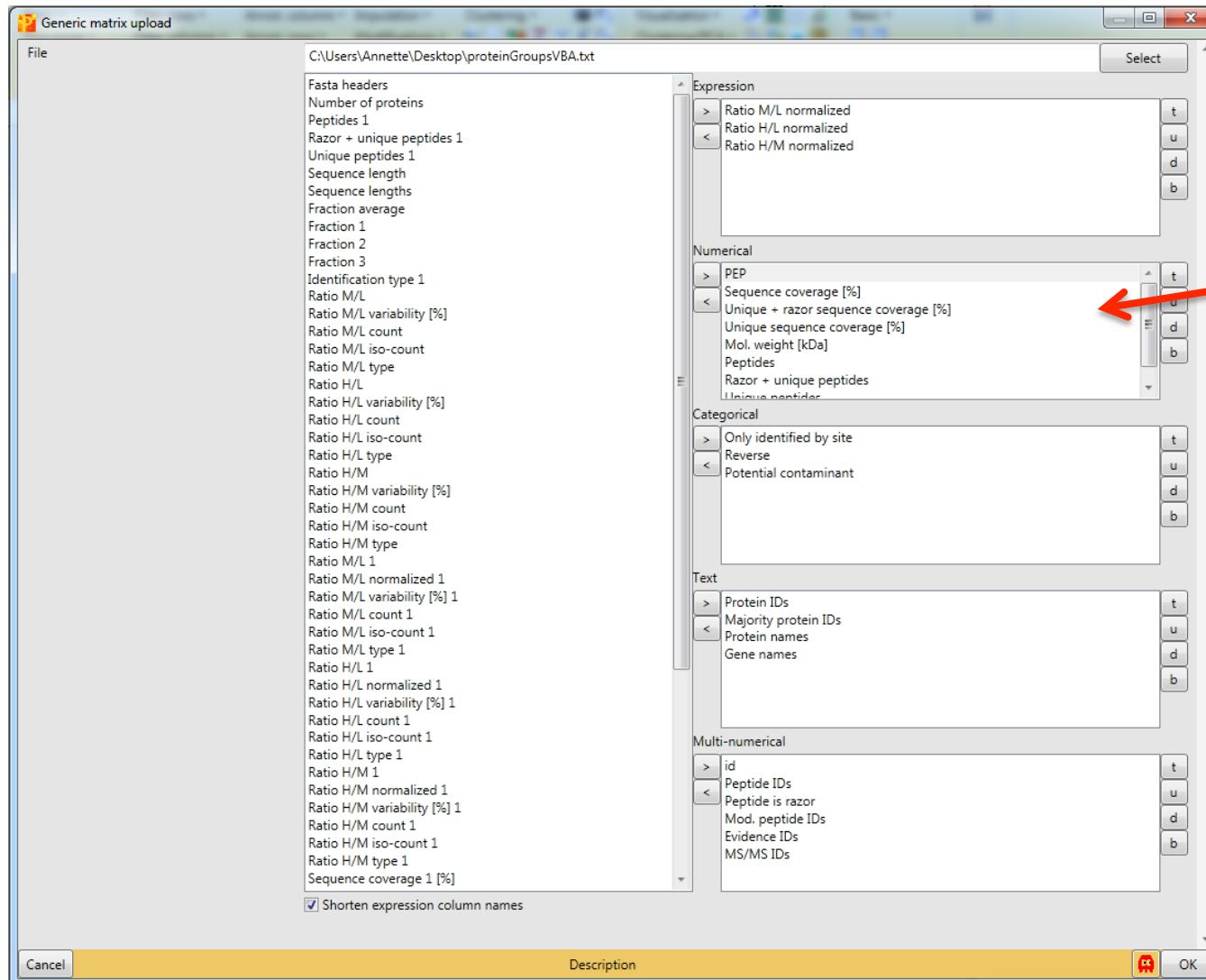
Data upload



There are five data types:

1. Expression data
= H/L-ratios, Label-free quantification values, Isobaric-label intensities etc.

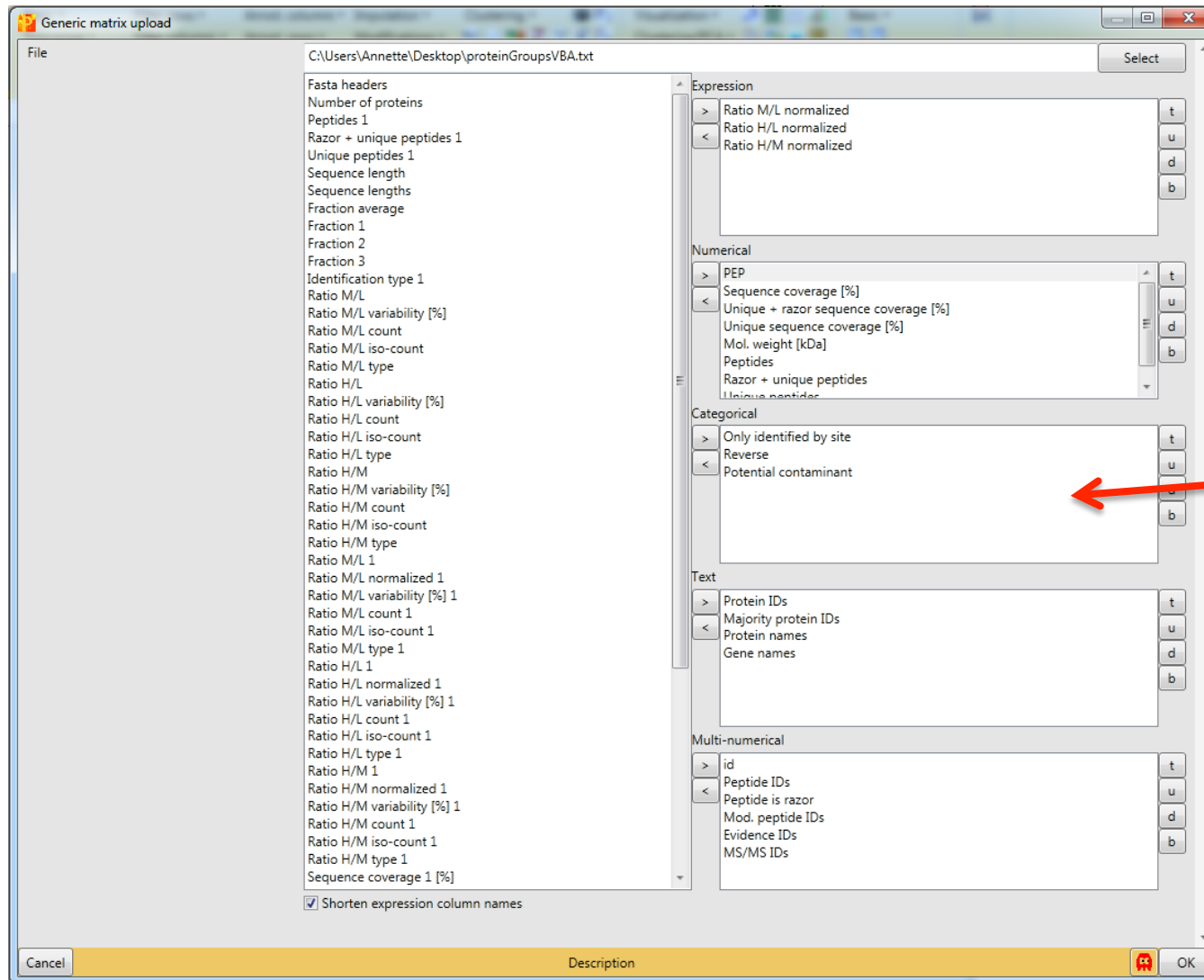
Data upload



There are five data types:

2. Numerical data =
Every column that contains single number values, like: Peptides, Mol. weight, Sequence coverage (%)

Data upload



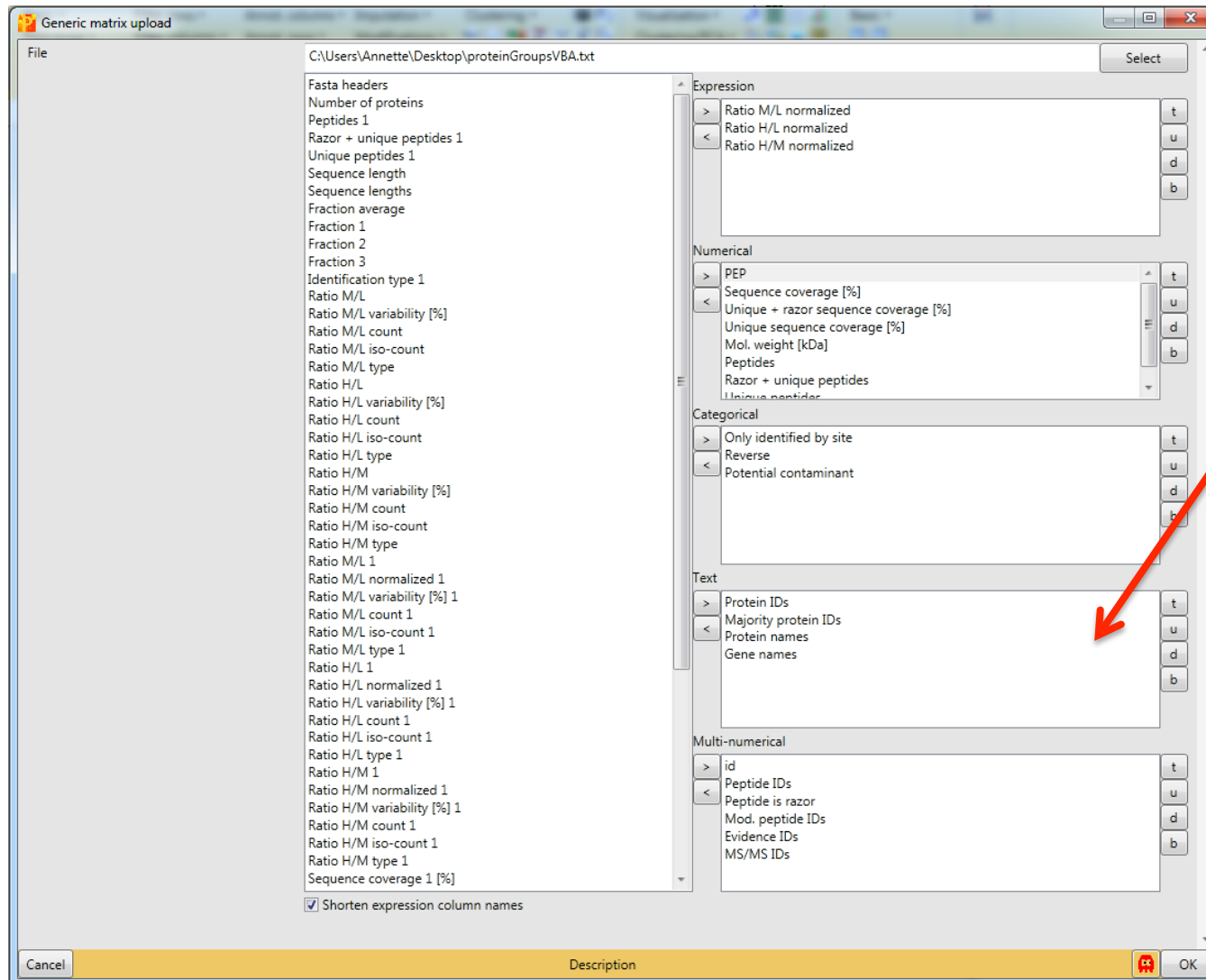
There are five data types:

3. Categorical data

= This is a yes or no data. Every protein group that belongs to a certain category is marked with a plus (+). MaxQuant automatically assigns some of the identified protein groups to three categories:

1. Only identified by site
2. Potential contaminant
3. Reverse

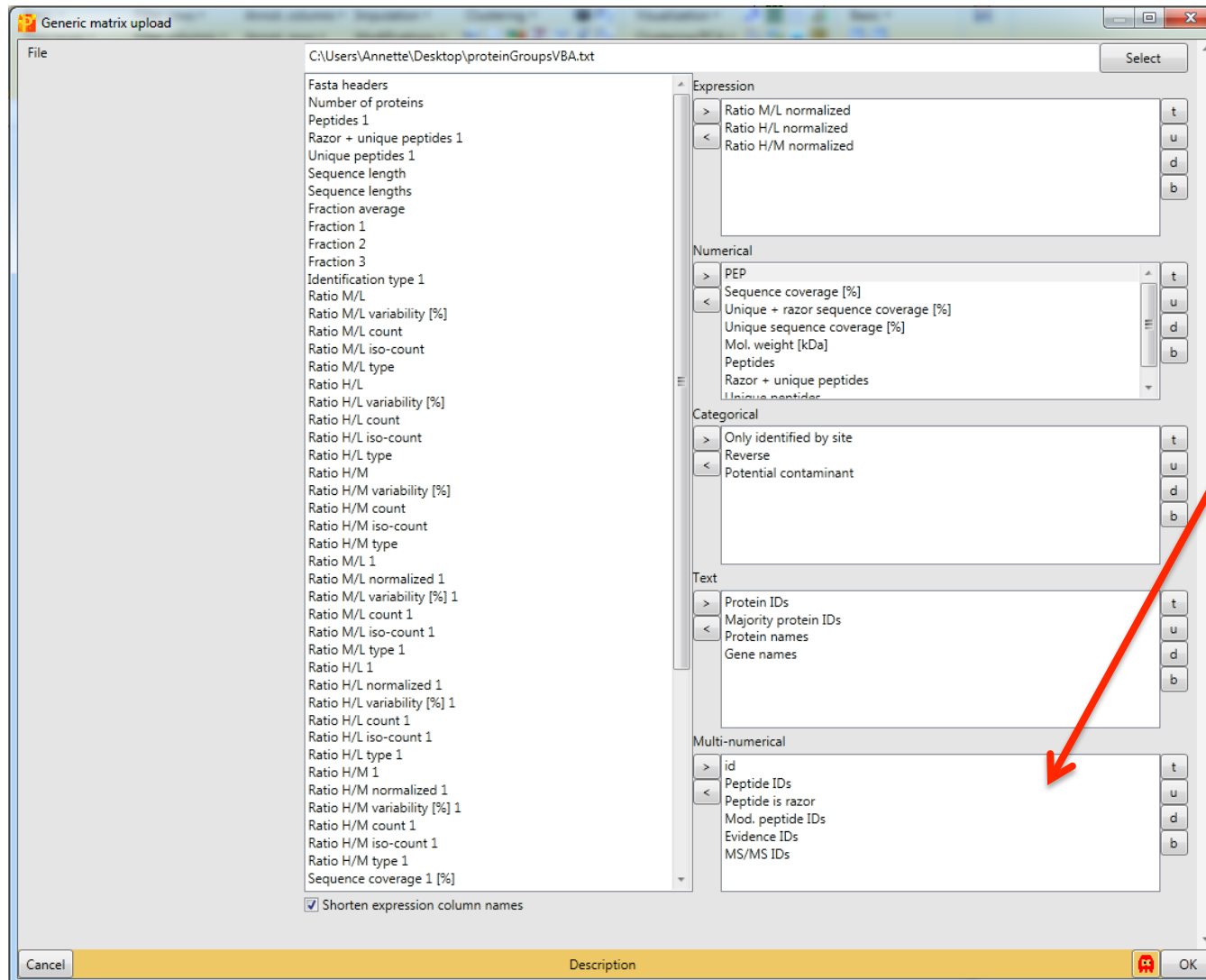
Data upload



There are five data types:

4. Text data =
Everything that is not a number e.g. Protein IDs (Accession), Protein names, Gene names etc.

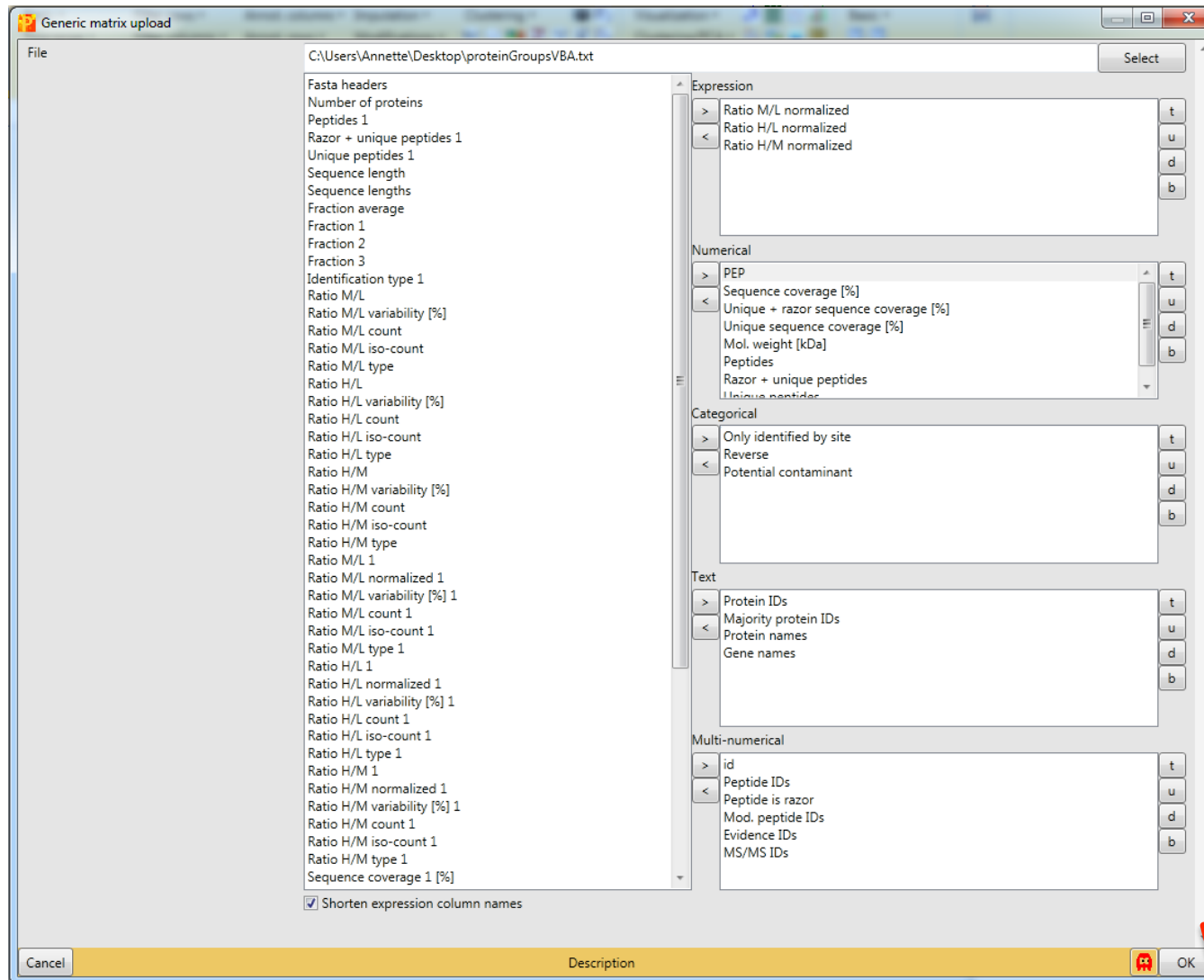
Data upload



There are five data types:

5. Multi-numerical data = Every column that contains more than one single number. Usually these numbers are separated by a semicolon. Examples are the different ID-Columns with link to other files generated by MaxQuant (MS/MS-lists etc.)

Data upload



After data selection
click OK!

First steps

Data is imported into Perseus in a so-called **matrix**.

The screenshot displays the Perseus software interface. The main window is titled 'Session1 - Perseus'. Below the menu bar, there is a toolbar with various icons for data manipulation. The 'Data' window is open, showing a table with columns: Type, A, B, C, Only identifi... by site, Reverse, Potential contam..., Q-value, Score, Intensity, Intensity L, Intensity H, Peptides A, and Peptides B. The table contains 32 rows of data. A red arrow points from the word 'matrix' in the text above to the 'matrix1' tab in the 'Matrix-tree' window. Another red arrow points from the word 'matrix' in the text above to the 'matrix1' tab in the 'Matrix-Info' window.

Data window

Type	A	B	C	Only identifi... by site	Reverse	Potential contam...	Q-value	Score	Intensity	Intensity L	Intensity H	Peptides A	Peptides B
	Expres...	Expres...	Expression	Catego...	Catego...	Catego...	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric
1	NaN	NaN	0.80343				0	4.0745	188920...	9885200	9006800	0	0
2	NaN	NaN	0.64703				0.0034...	1.4653	183450...	124320...	5912800	0	1
3	NaN	0.50649	0.81553				0	6.6682	931260...	667470...	263780...	1	5
4	NaN	NaN	1.1326				0	14.438	968950...	496020...	472930...	0	1
5	NaN	NaN	NaN				0.0014...	1.9054	960480	832250	128230	0	1
6	NaN	NaN	NaN				0.0078...	1.1743	1918800	1124800	793970	1	0
7	NaN	NaN	NaN				0	5.6441	1161600	1156300	5326.8	0	0
8	NaN	NaN	NaN				0.0095...	0.99659	254400	254400	0	0	0
9	NaN	NaN	NaN				0.0077...	1.1381	128280	128280	0	0	0
10	NaN	0.33634	0.5571				0	4.9443	374210...	305720...	6849100	0	2
11	NaN	NaN	0.14989				0	26.421	296510...	251130...	4537400	0	2
12	NaN	NaN	NaN				0	21.108	8887900	5066000	3821900	0	1
13	NaN	NaN	0.75698				0	3.1953	135380...	8140000	5397600	0	0
14	0.60601	1.0407	0.7331				0	57.426	663490...	420780...	242710...	7	4
15	NaN	NaN	NaN				0	4.5381	3446500	1936500	1510000	0	0
16	0.0810...	3.3769	1.283				0	191.38	464670...	254420...	210260...	20	25
17	NaN	NaN	NaN				0.0094...	0.94881	7212000	2895100	4316900	0	0
18	NaN	NaN	0.59947				0	4.8189	124850...	7841100	4643800	0	0
19	NaN	NaN	NaN				0	3.4842	513390...	425040...	8834400	0	2
20	1.0224	0.46729	0.67218				0	84.494	446610...	320330...	126280...	3	6
21	NaN	NaN	NaN				0.0014...	1.7605	1550900	1295900	254970	0	1
22	NaN	NaN	0.037928				0	54.024	5748300	5706900	41385	0	0
23	NaN	NaN	0.88542				0	2.965	6351000	3160500	3190500	0	0
24	NaN	NaN	0.90245				0	5.0359	193560...	134310...	5924700	0	1
25	NaN	2.0667	NaN				0	4.787	266540...	102710...	163830...	1	3
26	NaN	NaN	0.61849				0	5.9197	104520...	6450000	4002100	0	0
27	NaN	NaN	1.4144				0	3.3244	103470...	4940000	5407100	0	0
28	0.96779	0.39904	NaN				0	3.0785	100530...	850920...	154400...	2	2
29	0.97586	0.90167	0.81699				0	202.54	213370...	132590...	807790...	13	26
30	NaN	NaN	NaN				0	2.6081	5259800	3040000	2219800	0	0
31	0.84727	0.60973	0.36602				0	20.291	100360...	713550...	290030...	4	4
32	NaN	NaN	2.8061				0.0014...	1.6726	117460...	386590...	787980...	1	1

1628 items

Matrix-tree window (lists all matrices contained in a Perseus project)

Matrix-Info window (contains information about the currently selected matrix)

matrix1
Creator: Annette
02/18/2015 18:02:58
Origin: D:\SILAC Workshop 2015\combined\txt\p
File: proteinGroups.txt
Quality: (small values are good.)
Rows (1628)
Expression columns (3)
Categorical columns (3)
String columns (4)
Numerical columns (17)
Multi-numerical columns (8)
Categorical rows (0)
Numerical rows (0)

Version 1.5.1.6

First steps

Every time you change something a new **matrix** is created. This way you can always go back to a previous processing stage.

The screenshot displays the Perseus software interface. At the top, the 'Matrix' menu is open, showing various options like 'Basic', 'Filter rows', 'Annot. columns', etc. A red arrow points from the text 'back to a previous processing stage' to the 'matrix1' button in the 'Matrix' menu. Below the menu, the 'Data' table is visible, showing a list of 1628 items. A red arrow points from the text 'back to a previous processing stage' to the 'matrix1' button in the 'Matrix' menu. On the right side, the 'Matrix-tree' window is open, listing all matrices contained in a Perseus project. Below it, the 'Matrix-Info' window is open, containing information about the currently selected matrix.

Datatable Window

Type	A	B	C	Only Identifi...	Reverse	Potential	Q-value	Score	Intensity	Intensity	Intensity	Peptides	Peptides
	Expres...	Expres...	Expression	Catego...	Catego...	Catego...	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric
1	NaN	NaN	0.80343				0	4.0745	188920...	9885200	9006800	0	0
2	NaN	NaN	0.64703				0.0034...	1.4653	183450...	124320...	5912800	0	1
3	NaN	0.50649	0.81553				0	6.6682	931260...	667470...	263780...	1	5
4	NaN	NaN	1.1326				0	14.438	968950...	496020...	472930...	0	1
5	NaN	NaN	NaN				0.0014...	1.9054	960480	832250	128230	0	1
6	NaN	NaN	NaN				0.0078...	1.1743	1918800	1124800	793970	1	0
7	NaN	NaN	NaN				0	5.6441	1161600	1156300	5326.8	0	0
8	NaN	NaN	NaN				0.0095...	0.99659	254400	254400	0	0	0
9	NaN	NaN	NaN				0.0077...	1.1381	128280	128280	0	0	0
10	NaN	0.33634	0.5571				0	4.9443	374210...	305720...	6849100	0	2
11	NaN	NaN	0.14989				0	26.421	296510...	251130...	4537400	0	2
12	NaN	NaN	NaN				0	21.108	8887900	5066000	3821900	0	1
13	NaN	NaN	0.75698				0	3.1953	135380...	8140000	5397600	0	0
14	0.60601	1.0407	0.7331				0	57.426	663490...	420780...	242710...	7	4
15	NaN	NaN	NaN				0	4.5381	3446500	1936500	1510000	0	0
16	0.0810...	3.3769	1.283				0	191.38	464670...	254420...	210260...	20	25
17	NaN	NaN	NaN				0.0094...	0.94881	7212000	2895100	4316900	0	0
18	NaN	NaN	0.59947				0	4.8189	124850...	7841100	4643800	0	0
19	NaN	NaN	NaN				0	3.4842	513390...	425040...	8834400	0	2
20	1.0224	0.46729	0.67218				0	84.494	446610...	320330...	126280...	3	6
21	NaN	NaN	NaN				0.0014...	1.7605	1550900	1295900	254970	0	1
22	NaN	NaN	0.037928				0	54.024	5748300	5706900	41385	0	0
23	NaN	NaN	0.88542				0	2.965	6351000	3160500	3190500	0	0
24	NaN	NaN	0.90245				0	5.0359	193560...	134310...	5924700	0	1
25	NaN	2.0667	NaN				0	4.787	266540...	102710...	163830...	1	3
26	NaN	NaN	0.61849				0	5.9197	104520...	6450000	4002100	0	0
27	NaN	NaN	1.4144				0	3.3244	103470...	4940000	5407100	0	0
28	0.96779	0.39904	NaN				0	3.0785	100530...	850920...	154400...	2	2
29	0.97586	0.90167	0.81699				0	202.54	213370...	132590...	807790...	13	26
30	NaN	NaN	NaN				0	2.6081	5259800	3040000	2219800	0	0
31	0.84727	0.60973	0.36602				0	20.291	100360...	713550...	290030...	4	4
32	NaN	NaN	2.8061				0.0014...	1.6726	117460...	386590...	787980...	1	1

Matrix-tree Window (lists all matrices contained in a Perseus project)

Matrix-Info Window (contains information about the currently selected matrix)

matrix1
Creator: Annette
02/18/2015 18:02:58
Origin: D:\SILAC Workshop 2015\combined\txt\p
File: proteinGroups.txt
Quality: (small values are good.)
Rows (1628)
Expression columns (3)
Categorical columns (3)
String columns (4)
Numerical columns (17)
Multi-numerical columns (8)
Categorical rows (0)
Numerical rows (0)

Version 1.5.1.6

First steps

The Datable Window

Each column contains one type of data like SILAC ratios, sequence coverage, peptide numbers,...

Data type (as defined during upload)

Each row contains one identified protein group

Type	A	B	C	Only identifi... by site	Reverse	Potential contam...	Q-value	Score	Intensity	Intensity L	Intensity H	Peptides A	Peptides B	Peptides C	Razor + unique peptides	Razor + unique peptides	Razor + unique peptides	Unique peptides A	Unique peptides B	Unique peptides C
33	NaN	NaN	0.30486				0	8.1199	2024900	1443800	581170	0	0	4	0	0	4	0	0	3
34	1.8203	2.4858	0.50199				0	42.051	639440...	322480...	316960...	5	4	5	5	4	5	5	4	5
35	NaN	NaN	NaN				0	6.2465	394760	146850	247910	0	0	1	0	0	1	0	0	1
36	0.90953	0.64613	1.0638				0	194.74	262310...	154310...	108010...	16	16	25	16	16	25	16	16	25
37	NaN	0.43303	0.86671				0	14.748	787510...	452480...	335030...	1	1	2	1	1	2	1	1	2
38	NaN	NaN	NaN				0	3.2351	372240...	312520...	5972300	0	1	0	0	1	0	0	1	0
39	NaN	NaN	NaN				0	2.4933	855680	704330	151350	0	1	0	0	1	0	0	1	0
40	NaN	NaN	NaN				0.0094...	0.98022	4456000	4279700	176340	0	0	1	0	0	1	0	0	1
41	NaN	NaN	NaN				0	15.506	445940...	254500...	191440...	7	5	6	1	0	1	0	0	0
42	NaN	NaN	1.1788				0	7.0117	353700...	170680...	183020...	0	0	2	0	0	2	0	0	2
43	NaN	NaN	2.0128				0	2.6325	7071000	2341600	4729400	0	0	2	0	0	2	0	0	2
44	NaN	0.31979	1.2166				0	5.7233	247230...	168960...	7826800	0	2	2	0	2	2	0	2	2
45	NaN	0.53144	NaN				0	4.1807	353450...	299600...	5385100	0	2	0	0	2	0	0	2	0
46	NaN	NaN	2.0486				0	3.2423	194280...	5746100	136820...	0	0	2	0	0	2	0	0	2
47	0.59303	0.32887	0.50644				0	22.391	686870...	550940...	135930...	2	3	3	2	3	3	2	3	3
48	0.85755	1.114	NaN				0	3.6129	195420...	108570...	868580...	1	1	1	1	1	1	1	1	1
49	NaN	NaN	1.0721				0	4.066	230570...	120950...	109620...	1	0	2	1	0	2	1	0	2
50	0.75695	3.3265	0.83447				0	82.637	104120...	521480...	519760...	5	8	5	5	8	5	5	8	5
51	1.0146	0.6911	0.52887				0	14.384	137620...	904860...	471340...	2	3	4	2	3	4	2	3	4
52	0.88658	1.0667	0.67661				0	47.706	138550...	863300...	522210...	2	3	3	2	3	3	2	3	3
53	1.0051	0.42981	0.54816				0	52.193	281620...	208570...	730410...	2	5	3	2	5	3	2	5	3
54	NaN	NaN	0.68491				0	7.23	7553200	4582300	2970900	0	0	1	0	0	1	0	0	1
55	NaN	0.72979	NaN				0.0054...	1.3152	1935500	1330700	604750	0	1	0	0	1	0	0	1	0
56	1.0455	8.4935	1.2727				0	62.976	482640...	216930...	265710...	3	4	9	2	3	8	2	3	8
57	NaN	NaN	NaN				0	4.2367	2524200	969840	1554300	0	0	1	0	0	1	0	0	1
58	NaN	NaN	NaN				0	12.424	9841100	4284900	5556200	1	0	1	1	0	1	1	0	1
59	1.0577	0.44189	0.79827				0	96.342	139260...	108540...	307130...	6	10	6	6	10	6	6	10	6
60	NaN	0.45482	NaN				0	4.3987	5159100	3960300	1198800	0	3	0	0	3	0	0	3	0
61	NaN	NaN	NaN				0	4.1784	131890...	8631300	4557500	0	0	1	0	0	1	0	0	1
62	1.33	0.5061	0.80206				0	9.0007	146260...	110930...	353340...	2	4	2	2	4	2	2	4	2
63	NaN	NaN	1.297				0.0014...	1.8653	8683400	6083500	2599900	0	1	1	0	1	1	0	1	1
64	NaN	NaN	NaN				0	9.9793	8522600	4676000	1846700	0	0	1	0	0	1	0	0	1

Protein group???

- MaxQuant does not give you single protein identifications, but so-called protein groups.
- A group contains all the proteins and protein isoforms (present in the searched database), which can be explained by a given set of identified peptides.

First steps

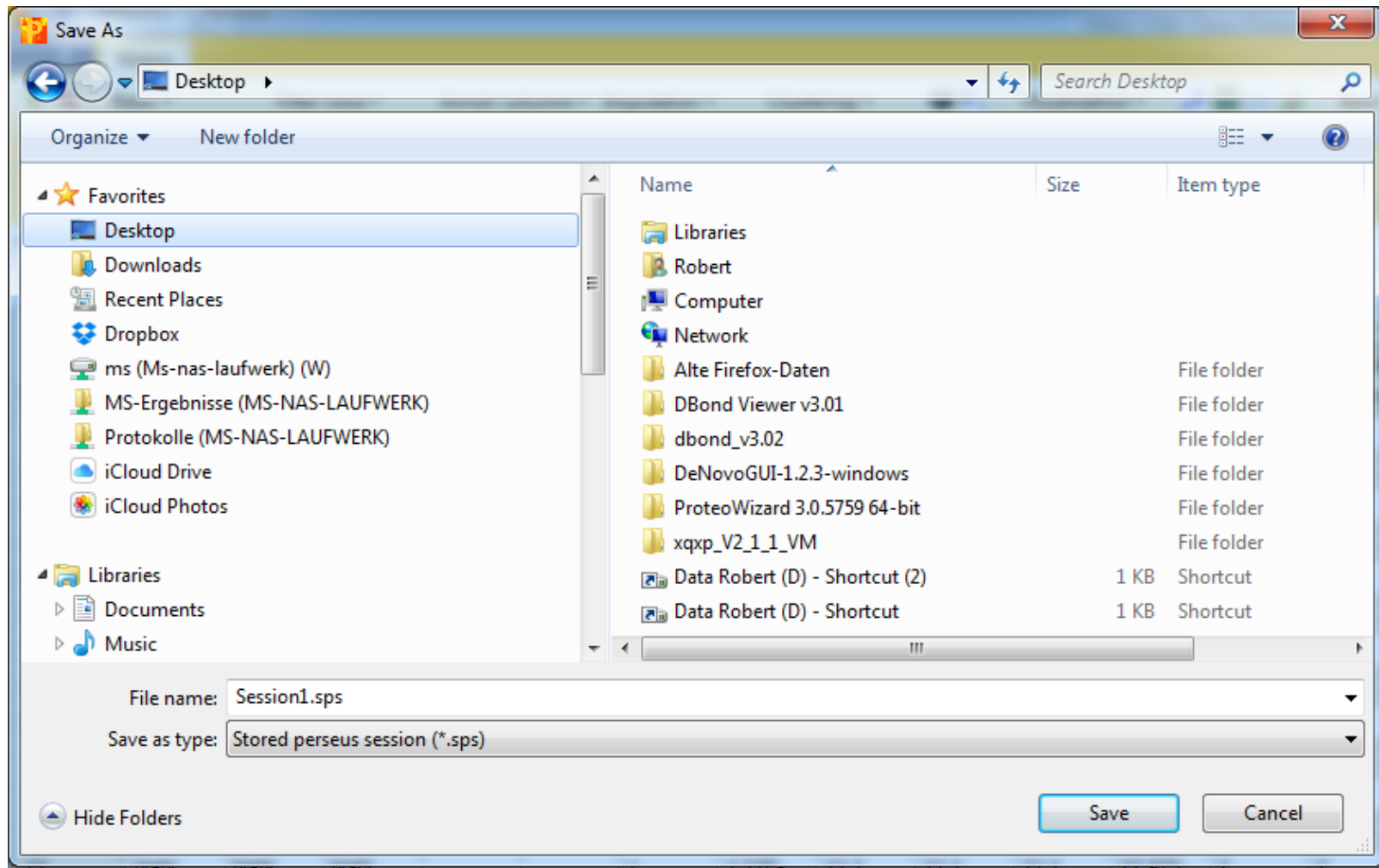
Before processing the data further, first save the Perseus project.

The screenshot displays the Perseus software interface. On the left, a menu is open with the 'Save' option highlighted by a red arrow. The menu includes options for 'Save', 'Save as', 'Save as PDF', 'Open', 'New', 'New window', 'Annotation download', 'Help', and 'Exit'. The main window shows a data table with columns: Unique + razor sequen..., Unique sequen..., Mol. weight [kDa], Peptides, Razor + unique peptides, Unique peptides, and Prot IDs. The table contains 553 rows of data. On the right, a panel shows the project details for 'matrix1', including the creator (Annette), date (02/16/2015 10:23:44), origin (C:\Users\Annette\Desktop\proteinGroupsVBA.txt), file (proteinGroupsVBA.txt), quality (small values are good.), and row count (553). The bottom status bar indicates '553 items' and 'Version 1.5.1.6'.

Unique + razor sequen...	Unique sequen...	Mol. weight [kDa]	Peptides	Razor + unique peptides	Unique peptides	Prot IDs
NaN	NaN	NaN	NaN	NaN	NaN	T
4.7	4.7	102.36	4	4	4	A0F
4.8	4.8	36.547	1	1	1	A2R
0.7	0.7	382.3	1	1	1	A4U
0.6	0.6	266.94	1	1	1	A5Y
10.9	10.9	38.604	3	3	3	P07
1.9	1.9	103.75	1	1	1	P11
4.3	4.3	34.466	1	1	1	A8M
1.9	1.9	46.962	1	1	1	A8M
0.11321	0.36557	1.125	+	2.56E...	32.6	27.3
2.259	0.20286	0.40328	+	1.87E...	27	18.1
NaN	NaN	NaN	+	1.31E...	11.1	11.1
NaN	NaN	NaN	+	0.0006...	8.6	8.6
NaN	NaN	NaN	+	9.7E-60	26.6	10.8
0.0636...	0.0748...	15.765	+	5.01E...	53.1	53.1
0.16413	0.75705	12.778	+	1.35E...	20.3	9.3
0.11225	0.20776	1.154	+	3.47E...	54.3	53.1
0.0903...	0.12433	1.4228	+	1.12E...	41.8	38.7
NaN	NaN	NaN	+	0.0233...	1.7	1.7
NaN	NaN	NaN	+	0.0022...	0.5	0.5
NaN	NaN	NaN	+	3.74E...	3.8	1.7
NaN	NaN	NaN		0.0018...	2.3	2.3
1.1107	2.4128	2.5822		1.38E...	21.1	21.1
NaN	NaN	NaN		0.0001...	4.3	4.3
0.74499	0.91574	1.1054		1.46E...	16.4	16.4
NaN	NaN	NaN		0.0249...	1.4	1.4
0.87934	1.0377	0.91532		3.73E...	37	37
NaN	NaN	NaN		0.02872	4.2	4.2
1.2975	0.978	1.0558		6.28E...	11.6	11.6
1.3502	1.0293	0.82036		3.03E...	6.6	6.6
NaN	NaN	NaN		0.0001...	5.9	5.9

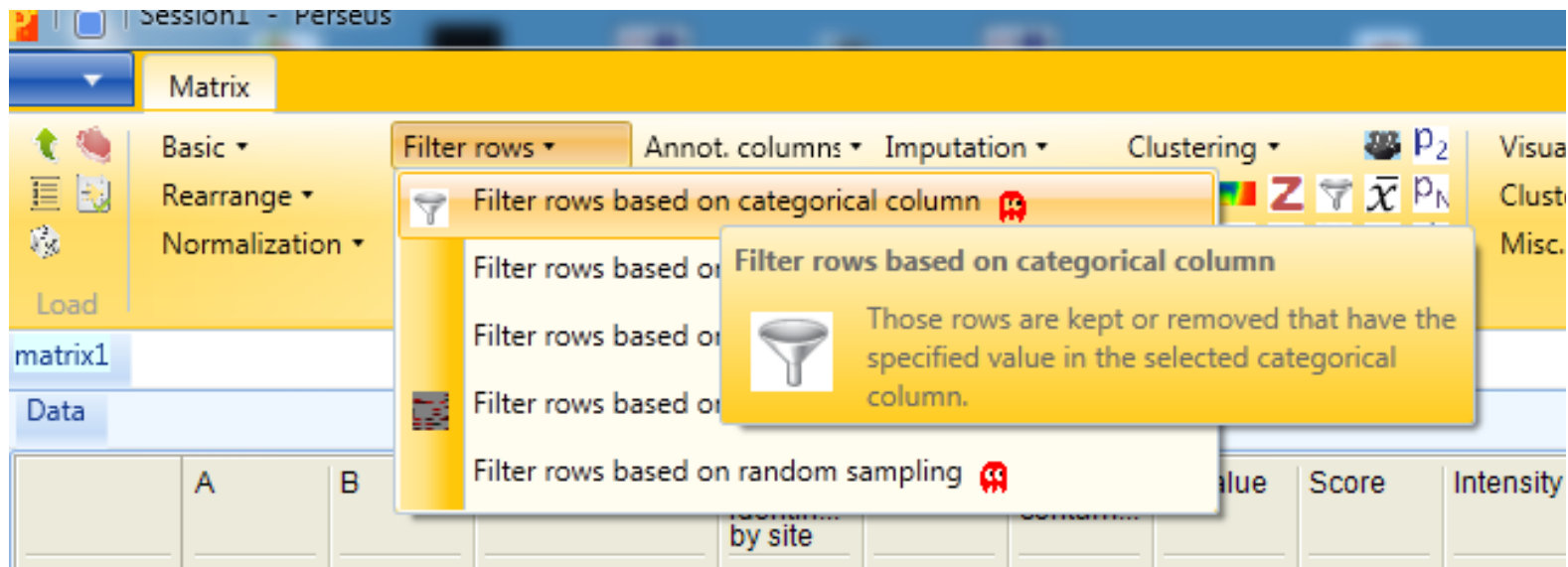
First steps

Perseus projects are saved as sps-files



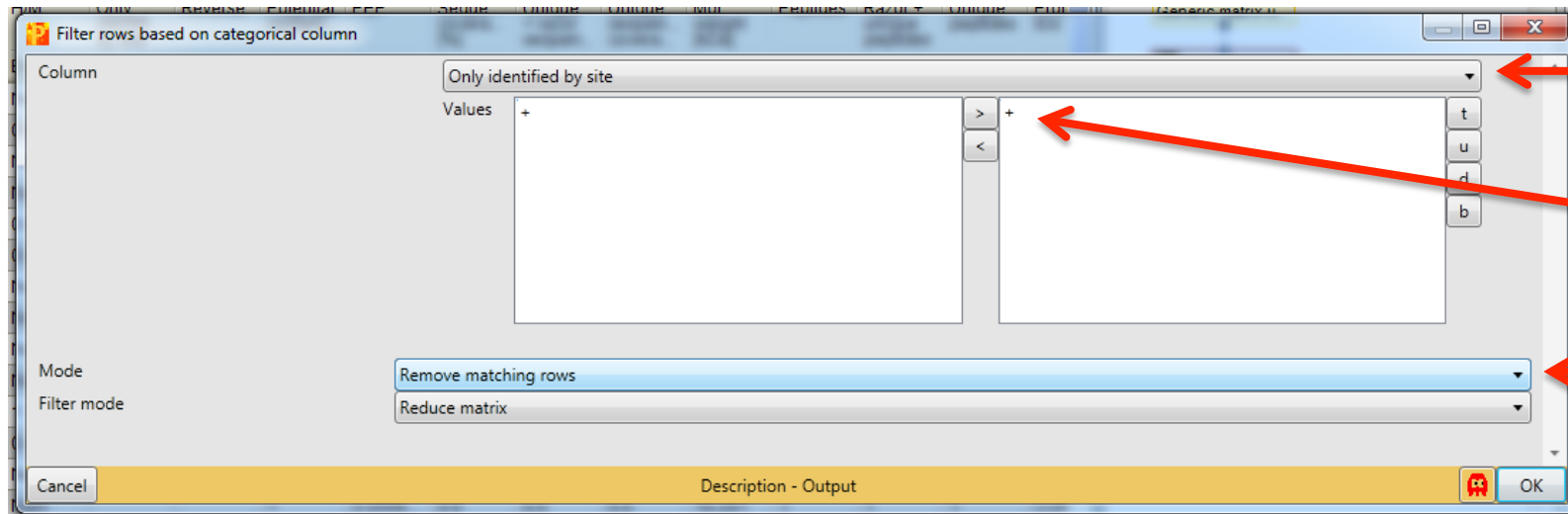
First steps

One now starts with the removal of usually irrelevant protein group identifications i.e. “Only identified by site”, “Reverse” and “Potential contaminants” → Click Filter rows - Filter rows based on categorical columns



First steps

Removal of usually irrelevant protein group identifications



Which column should be searched for?

What value should be looked for?

What should happen to columns matching the criteria?

First steps

Perseus now created a **matrix2** (in a new tab), in which all entries marked with a + in the “Only identified by site”-category have been removed

The screenshot displays the Perseus software interface. The main window shows a data table with columns for protein identification and quantification. The 'matrix2' tab is selected in the 'Data' panel. A red arrow points from the text above to the 'matrix2' tab. Another red arrow points from the 'Only identified by site' column header to the 'matrix2' tab in the workflow diagram on the right.

Type	A	B	C	Only identified by site	Reverse	Potential contaminant	Q-value	Score	Intensity	Intensity L	Intensity H	Peptides A	Peptides B	Peptides C	Razor unique peptides	Razor + unique peptides	Razor unique peptides
	Express...	Express...	Express...	Catego...	Catego...	Catego...	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Nu
1	NaN	NaN	0.80343				0	4.0745	188920...	9885200	9006800	0	0	3	0	0	
2	NaN	NaN	0.64703				0.0034...	1.4653	183450...	124320...	5912800	0	1	2	0	1	2
3	NaN	0.50649	0.81553				0	6.6682	931260...	667470...	263780...	1	5	3	1	5	3
4	NaN	NaN	1.1326				0	14.438	968950...	496020...	472930...	0	1	7	0	1	7
5	NaN	NaN	NaN				0.0014...	1.9054	960480	832250	128230	0	1	0	0	1	0
6	NaN	NaN	NaN				0.0078...	1.1743	1918800	1124800	793970	1	0	0	1	0	0
7	NaN	NaN	NaN				0	5.6441	1161600	1156300	5326.8	0	0	2	0	0	2
8	NaN	NaN	NaN				0.0095...	0.99659	254400	254400	254400	0	0	3	0	0	1
9	NaN	NaN	NaN				0.0077...	1.1381	128280	128280	0	0	0	2	0	0	1
10	NaN	0.33634	0.5571				0	4.9443	374210...	305720...	6849100	0	2	2	0	2	2
11	NaN	NaN	0.14989				0	26.421	296510...	251130...	4537400	0	2	4	0	0	2
12	NaN	NaN	NaN				0	21.108	8887900	5066000	3821900	0	1	2	0	0	1
13	NaN	NaN	0.75698				0	3.1953	135380...	8140000	5397600	0	0	1	0	0	1
14	0.60601	1.0407	0.7331				0	57.426	663490...	420780...	242710...	7	4	10	7	4	10
15	NaN	NaN	NaN				0	4.5381	3446500	1936500	1510000	0	0	1	0	0	1
16	0.0810...	3.3769	1.283				0	191.38	464670...	254420...	210260...	20	25	18	20	25	18
17	NaN	NaN	NaN				0.0094...	0.94881	7212000	2895100	4316900	0	0	1	0	0	1
18	NaN	NaN	0.59947				0	4.8189	124850...	7841100	4643800	0	0	1	0	0	1
19	NaN	NaN	NaN				0	3.4842	513390...	425040...	8834400	0	2	0	0	2	0
20	1.0224	0.46729	0.67218				0	84.494	446610...	320330...	126280...	3	6	10	3	6	10
21	NaN	NaN	NaN				0.0014...	1.7605	1550900	1295900	254970	0	1	0	0	1	0
22	NaN	NaN	0.0379...				0	54.024	5748300	5706900	41385	0	0	4	0	0	4
23	NaN	NaN	0.88542				0	2.965	6351000	3160500	3190500	0	0	1	0	0	1
24	NaN	NaN	0.90245				0	5.0359	193560...	134310...	5924700	0	1	1	0	1	1
25	NaN	2.0667	NaN				0	4.787	266540...	102710...	163830...	1	3	2	0	2	1
26	NaN	NaN	0.61849				0	5.9197	104520...	6450000	4002100	0	0	1	0	0	1
27	NaN	NaN	1.4144				0	3.3244	103470...	4940000	5407100	0	0	2	0	0	2
28	0.96779	0.39904	NaN				0	3.0785	100530...	850920...	154400...	2	2	0	2	2	0
29	0.97586	0.90167	0.81699				0	202.54	213370...	132590...	807790...	13	26	28	13	26	28
30	NaN	NaN	NaN				0	2.6081	5259800	3040000	2219800	0	0	1	0	0	1
31	0.84727	0.60973	0.36602				0	20.291	100360...	713550...	290030...	4	4	3	4	4	3
32	NaN	NaN	2.8061				0.0014...	1.6726	117460...	386590...	787980...	1	1	2	1	1	2

1607 items

Version 1.5.1.6

First steps

Now repeat the **filtering** for the other two categories!

The screenshot shows the Perseus software interface. The top menu bar includes options like Matrix, Basic, Rearrange, Normalization, Filter rows, Filter columns, Annot. columns, Annot. rows, Tests, Imputation, Modifications, Proteomic ruler, Clustering, Visualization, Clustering/PCA, Misc., Basic, Multi-proc., and Export. A red arrow points to the 'Filter rows' menu item. The main window displays a data matrix with columns for protein identification, quality scores, and expression levels. A sidebar on the right shows a workflow diagram with 'Generic matrix u...', 'matrix1', 'Filter rows based...', and 'matrix2' steps.

Type	A	B	C	Only identifi...	Reverse	Potential contam...	Q-value	Score	Intensity	Intensity L	Intensity H	Peptides A	Peptides B	Peptides C	Razor + unique peptides	Razor + unique peptides	Ra un pe
	Expres...	Expres...	Expres...	Catego...	Catego...	Catego...	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Numeric	Nu
1	NaN	NaN	0.80343				0	4.0745	188920...	9885200	9006800	0	0	3	0	0	3
2	NaN	NaN	0.64703				0.0034...	1.4653	183450...	124320...	5912800	0	1	2	0	1	2
3	NaN	0.50649	0.81553				0	6.6682	931260...	667470...	263780...	1	5	3	1	5	3
4	NaN	NaN	1.1326				0	14.438	968950...	496020...	472930...	0	1	7	0	1	7
5	NaN	NaN	NaN				0.0014...	1.9054	960480	832250	128230	0	1	0	0	1	0
6	NaN	NaN	NaN				0.0078...	1.1743	1918800	1124800	793970	1	0	0	1	0	0
7	NaN	NaN	NaN				0	5.6441	1161600	1156300	5326.8	0	0	2	0	0	2
8	NaN	NaN	NaN				0.0095...	0.99659	254400	254400	0	0	0	3	0	0	1
9	NaN	NaN	NaN				0.0077...	1.1381	128280	128280	0	0	0	2	0	0	1
10	NaN	0.33634	0.5571				0	4.9443	374210...	305720...	6849100	0	2	2	0	2	2
11	NaN	NaN	0.14989				0	26.421	296510...	251130...	4537400	0	2	4	0	0	2
12	NaN	NaN	NaN				0	21.108	8887900	5066000	3821900	0	1	2	0	0	1
13	NaN	NaN	0.75698				0	3.1953	135380...	8140000	5397600	0	0	1	0	0	1
14	0.60601	1.0407	0.7331				0	57.426	663490...	420780...	242710...	7	4	10	7	4	10
15	NaN	NaN	NaN				0	4.5381	3446500	1936500	1510000	0	0	1	0	0	1
16	0.0810...	3.3769	1.283				0	191.38	464670...	254420...	210260...	20	25	18	20	25	18
17	NaN	NaN	NaN				0.0094...	0.94881	7212000	2895100	4316900	0	0	1	0	0	1
18	NaN	NaN	0.59947				0	4.8189	124850...	7841100	4643800	0	0	1	0	0	1
19	NaN	NaN	NaN				0	3.4842	513390...	425040...	8834400	0	2	0	0	2	0
20	1.0224	0.46729	0.67218				0	84.494	446610...	320330...	126280...	3	6	10	3	6	10
21	NaN	NaN	NaN				0.0014...	1.7605	1550900	1295900	254970	0	1	0	0	1	0
22	NaN	NaN	0.0379...				0	54.024	5748300	5706900	41385	0	0	4	0	0	4
23	NaN	NaN	0.88542				0	2.965	6351000	3160500	3190500	0	0	1	0	0	1
24	NaN	NaN	0.90245				0	5.0359	193560...	134310...	5924700	0	1	1	0	1	1
25	NaN	2.0667	NaN				0	4.787	266540...	102710...	163830...	1	3	2	0	2	1
26	NaN	NaN	0.61849				0	5.9197	104520...	6450000	4002100	0	0	1	0	0	1
27	NaN	NaN	1.4144				0	3.3244	103470...	4940000	5407100	0	0	2	0	0	2
28	0.96779	0.39904	NaN				0	3.0785	100530...	850920...	154400...	2	2	0	2	2	0
29	0.97586	0.90167	0.81699				0	202.54	213370...	132590...	807790...	13	26	28	13	26	28
30	NaN	NaN	NaN				0	2.6081	5259800	3040000	2219800	0	0	1	0	0	1
31	0.84727	0.60973	0.36602				0	20.291	100360...	713550...	290030...	4	4	3	4	4	3
32	NaN	NaN	2.8061				0.0014...	1.6726	117460...	386590...	787980...	1	1	2	1	1	2

1607 items

Version 1.5.1.6

First steps

1507 entries remain from initially 1628.

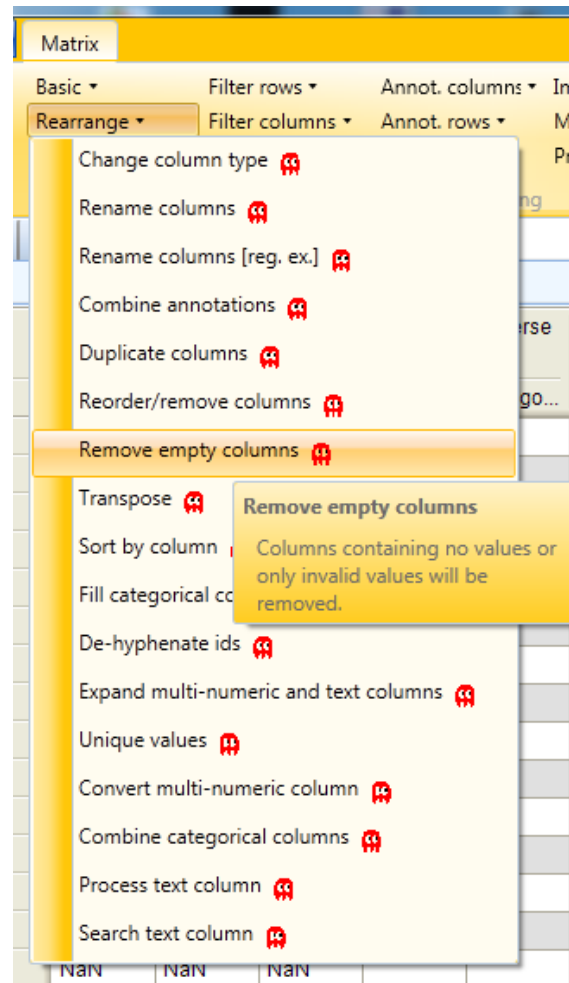
The screenshot shows the Perseus software interface. The main window displays a data matrix with 1507 items. The matrix has columns for various data types, including Expression, Q-value, Score, Intensity, Peptides, and Razor + unique peptides. The sidebar on the right shows a workflow diagram with steps like 'Generic matrix u...', 'matrix1', 'Filter rows based...', 'matrix2', 'Filter rows based...', 'matrix3', 'Filter rows based...', and 'matrix4'. Below the workflow, a summary of the data is provided:

- Creator: Annette
- 02/18/2015 18:02:58
- Origin: D:\SLAC Workshop 2015\combined\txt\proteinGroups.txt
- File: proteinGroups.txt
- Quality: (small values are good.)
- Rows (1507)
- Expression columns (3)
- Categorical columns (3)
- String columns (4)
- Numerical columns (17)
- Multi-numerical columns (8)
- Categorical rows (0)
- Numerical rows (0)

The bottom status bar indicates '1507 items' and 'Version 1.5.1.6'.

First steps

Since all three categorical columns are empty now, we can remove them to clean up the table.



First steps

After removal of empty columns, the data can be processed further...

The screenshot displays the Perseus software interface. The top menu bar includes options like Matrix, Basic, Rearrange, Normalization, Quality, Tests, Annot. columns, Annot. rows, Imputation, Modifications, Proteomic ruler, Clustering, Visualization, Clustering/PCA, Misc., Basic, Multi-proc., and Export. Below the menu is a toolbar with icons for various functions. The main window is divided into two panes. The left pane, titled 'Data', shows a table with 1507 items. The table has columns for Type, A, B, C, Q-value, Score, Intensity, Peptides A, Peptides B, Peptides C, Razor + unique peptides, and Unique peptides A, B, C. The right pane, titled 'matrix5', shows a workflow diagram with steps: Generic matrix u..., matrix1, Filter rows based..., matrix2, Filter rows based..., matrix3, Filter rows based..., matrix4, Remove empty c..., matrix5 (highlighted), Transform, matrix6, Rename columns, and matrix7. A sidebar on the right provides metadata for matrix5: Creator: Annette, 02/18/2015 18:02:58, Origin: D:\SILAC Workshop 2015\combined\txt\proteinGroups.txt, File: proteinGroups.txt, Quality: (small values are good.), Rows (1507), Expression columns (3), Categorical columns (0), String columns (4), Numerical columns (17), Multi-numerical columns (8), Categorical rows (0), Numerical rows (0).

Type	A	B	C	Q-value	Score	Intensity	Peptides A	Peptides B	Peptides C	Razor + unique peptides	Unique peptides A	Unique peptides B	Unique peptides C	
1	NaN	NaN	0.80343	0	4.0745	188920...	9885200	9006800	0	0	3	0	0	3
2	NaN	NaN	0.64703	0.0034...	1.4653	183450...	124320...	5912800	0	1	2	0	1	2
3	NaN	0.50649	0.81553	0	6.6682	931260...	667470...	263780...	1	5	3	1	5	3
4	NaN	NaN	1.1326	0	14.438	968950...	496020...	472930...	0	1	7	0	1	7
5	NaN	NaN	NaN	0.0014...	1.9054	960480	832250	128230	0	1	0	0	1	0
6	NaN	NaN	NaN	0.0078...	1.1743	1918800	1124800	793970	1	0	0	1	0	0
7	NaN	NaN	NaN	0	5.6441	1161600	1156300	5326.8	0	0	2	0	2	0
8	NaN	NaN	NaN	0.0095...	0.99659	254400	254400	0	0	3	0	0	1	0
9	NaN	NaN	NaN	0.0077...	1.1381	128280	128280	0	0	2	0	0	1	0
10	NaN	0.33634	0.5571	0	4.9443	374210...	305720...	6849100	0	2	2	0	2	2
11	NaN	NaN	0.14989	0	26.421	296510...	251130...	4537400	0	2	4	0	2	0
12	NaN	NaN	NaN	0	21.108	8887900	5066000	3821900	0	1	2	0	0	1
13	NaN	NaN	0.75698	0	3.1953	135380...	8140000	5397600	0	0	1	0	0	1
14	0.60601	1.0407	0.7331	0	57.426	663490...	420780...	242710...	7	4	10	7	4	10
15	NaN	NaN	NaN	0	4.5381	3446500	1936500	1510000	0	0	1	0	0	1
16	0.0810...	3.3769	1.283	0	191.38	464670...	254420...	210260...	20	25	18	20	25	18
17	NaN	NaN	NaN	0.0094...	0.94881	7212000	2895100	4316900	0	0	1	0	0	1
18	NaN	NaN	0.59947	0	4.8189	124850...	7841100	4643800	0	0	1	0	0	1
19	NaN	NaN	NaN	0	3.4842	513390...	425040...	8834400	0	2	0	0	2	0
20	1.0224	0.46729	0.67218	0	84.494	446610...	320330...	126280...	3	6	10	3	6	10
21	NaN	NaN	NaN	0.0014...	1.7605	1550900	1295900	254970	0	1	0	0	1	0
22	NaN	NaN	0.0379...	0	54.024	5748300	5706900	41385	0	0	4	0	4	0
23	NaN	NaN	0.88542	0	2.965	6351000	3160500	3190500	0	0	1	0	0	1
24	NaN	NaN	0.90245	0	5.0359	193560...	134310...	5924700	0	1	1	0	1	1
25	NaN	2.0667	NaN	0	4.787	266540...	102710...	163830...	1	3	2	0	2	1
26	NaN	NaN	0.61849	0	5.9197	104520...	6450000	4002100	0	0	1	0	0	1
27	NaN	NaN	1.4144	0	3.3244	103470...	4940000	5407100	0	0	2	0	0	2
28	0.96779	0.39904	NaN	0	3.0785	100530...	850920...	154400...	2	2	0	2	0	2
29	0.97586	0.90167	0.81699	0	202.54	213370...	132590...	807790...	13	26	28	13	26	28
30	NaN	NaN	NaN	0	2.6081	5259800	3040000	2219800	0	0	1	0	0	1
31	0.84727	0.60973	0.36602	0	20.291	100360...	713550...	290030...	4	4	3	4	4	3
32	NaN	NaN	2.8061	0.0014...	1.6726	117460...	386590...	787980...	1	1	2	1	2	1

1507 items

Version 1.5.1.6

More...

- Additional Perseus tutorials at our webpage
 - Analysis of SILAC data
 - Analysis of label-free quantification data (under construction)
 - Analysis of large-scale phosphoproteomics data (under construction)
- Official Perseus documentation
 - http://141.61.102.17/perseus_doku/
- Video tutorials from MaxQuant Summer Schools
 - <http://www.youtube.com/channel/UCKYzYTm1cnmc0CFAMhxDO8w>