

Howto: Prepare your Sample Sheet for Microsatellite Analysis

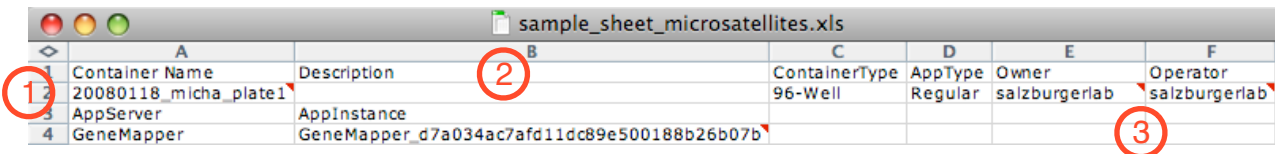
1. Sample Sheet Download

Go to <http://www.evolution.unibas.ch/salzburger/protocols.htm> and download the file sample_sheet_microsatellites.xls .
 Open this file in MS Excel.

2. Editing the Sample Sheet Header

! Always use underscores (_) instead of blanks or dashes !

In Excel, the file header will look like the following:



	A	B	C	D	E	F
1	Container Name	Description	ContainerType	AppType	Owner	Operator
2	20080118_micha_plate1		96-Well	Regular	salzburgerlab	salzburgerlab
3	AppServer	AppInstance				
4	GeneMapper	GeneMapper_d7a034ac7afd11dc89e500188b26b07b				

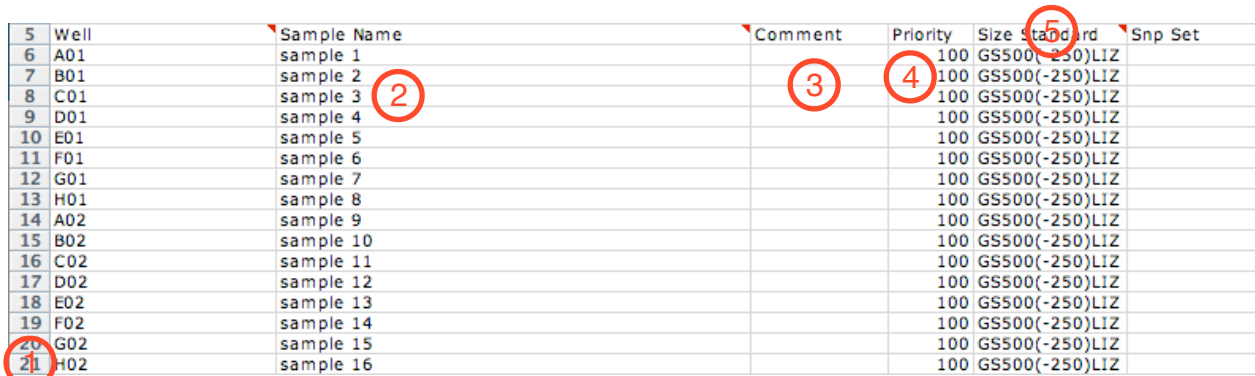
① Cell A2 is the plate name. Please replace the content of the cell with the name of your plate, according to the following format:
 date_yourname_yourplateID, where yourname should not be longer than 8 letters.
 The date in turn should have the format YYYYMMDD.

② Cell B4 must not be changed.

③ In cells E2 and F2, please choose one of the following options, depending on which group you're in: schaererlab, ebertlab, koellikerlab, salzburgerlab, botanicalinstitute, tropicalinstitute, nluinstitute .

3. Editing the Sample Sheet Columns

The first six columns will look like this:



	Well	Sample Name	Comment	Priority	Size Standard	Snp Set
5	A01	sample 1		100	GS500(-250)LIZ	
6	B01	sample 2		100	GS500(-250)LIZ	
7	C01	sample 3		100	GS500(-250)LIZ	
8	D01	sample 4		100	GS500(-250)LIZ	
9	E01	sample 5		100	GS500(-250)LIZ	
10	F01	sample 6		100	GS500(-250)LIZ	
11	G01	sample 7		100	GS500(-250)LIZ	
12	H01	sample 8		100	GS500(-250)LIZ	
13	A02	sample 9		100	GS500(-250)LIZ	
14	B02	sample 10		100	GS500(-250)LIZ	
15	C02	sample 11		100	GS500(-250)LIZ	
16	D02	sample 12		100	GS500(-250)LIZ	
17	E02	sample 13		100	GS500(-250)LIZ	
18	F02	sample 14		100	GS500(-250)LIZ	
19	G02	sample 15		100	GS500(-250)LIZ	
20	H02	sample 16		100	GS500(-250)LIZ	

1 Of course, this table actually has 96 rows for the 96 well positions of your plate, of which only the first 16 are shown here. If your plate includes less than 96 samples, you should first of all remove the contents of all the rows of this table that are not needed for your runs, except of the contents of the first column. However, note that the AB3130 sequencer has 16 capillaries, which means that per run, 16 samples are processed. Therefore, the number of samples on your plate should always be a multiple of 16.

Furthermore, it is important to note that samples of your plate need to be entered in a vertical order (A1, B1, C1,..., H1, A2, A3...) instead of the more intuitive horizontal order (A1, A2, A3...)

2 The second column is the most important in this table. Please replace the content of these cells with the names of the samples on your plate. This way, you'll easily identify samples among the results. If you have less than 96 samples, leave cells empty, according to empty wells on your plate.

3 Comments are optional.

4 The default setting for priority is 100 and can remain unchanged.

5 Replace the content of this column with the name of the size standard you're using. Please pick a name from the following list:

- None
- GS120LIZ
- GS350
- GS400HD
- GS500
- GS500(-250)
- GS500(-250)LIZ
- GS500LIZ
- GS500LIZ139+
- GS500LIZ75+(-250)
- GS500LIZ75+(-250,-340)

Note that the software is case-sensitive and no blanks must be inserted.

User-Defined	User-Defined	Panel	Study	Sample Type	Analysis Method	Results Group	Instrument Protocol 1
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default
		None		Sample	Microsatellite Default	SalzburgerLab_Microsatellites	Fragment_G5_default

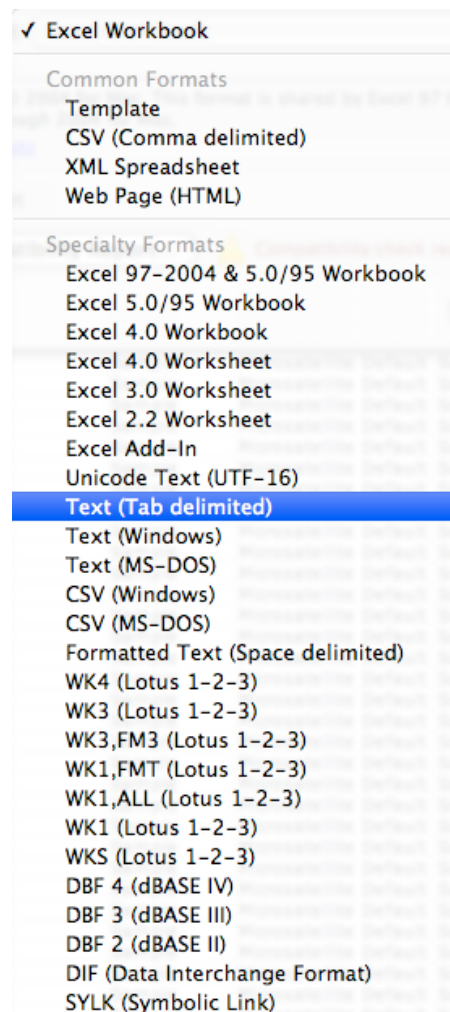
The next columns can be ignored, but the last few columns again need some editing:

6 Unless you predefined your own Panels, do not edit this column.

- 7 Options for this column include Sample, Positive Control, Allelic Ladder and Negative Control. However even if your run includes positive or negative controls, you're safe with the default setting (Sample).
- 8 Unless you have defined your own Analysis Method, don't edit this column.
- 9 Unless you're part of the Salzburger group, replace the contents of this column with either SchaeererLab_Microsatellites, EbertLab_Microsatellites or KoellikerLab_Microsatellites, Botanical_Microsatellites, Tropical_Microsatellites, NLU_Microsatellites.
- 10 For microsatellite analysis, keep the Instrument Protocol Fragment_G5_default.

4. Export the Sample Sheet

Save the Sample Sheet as a tab delimited text file with file extension .txt. Please choose a meaningful file name rather than "samplesheet.txt".

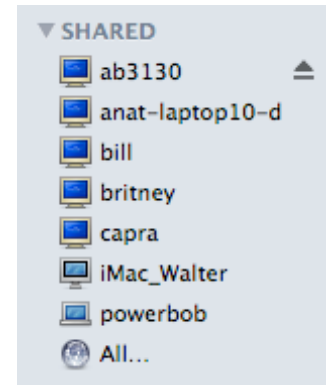


5. Submit your Sample Sheet (Mac Version)

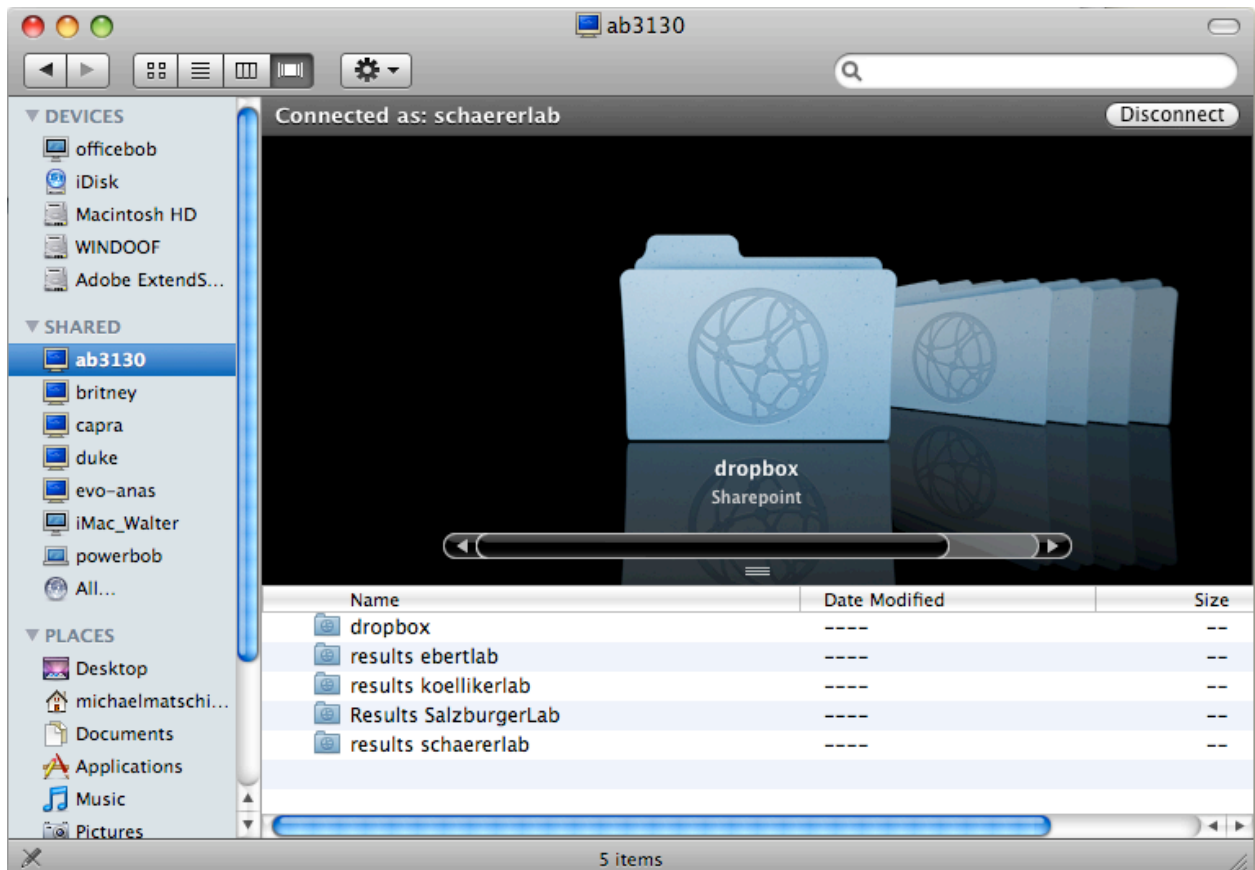
If you're on a Mac, please proceed the following:

Activate the Finder and connect to the computer ab3130 by clicking on its symbol in the category "Shared"

Alternatively, you can use Go > Connect to Server... from the Finder menu, then find ab3130 by clicking "Browse".



Click "Connect As..." to log on to ab3130 using the username schaeererlab, ebertlab, koellikerlab or salzburgerlab and the password that has been given to you. If you do not yet have a password, please contact somebody from the Salzburger group. You should see something similar to the following picture:



You have access only to the folder called dropbox as well as one of the results folders, depending on your

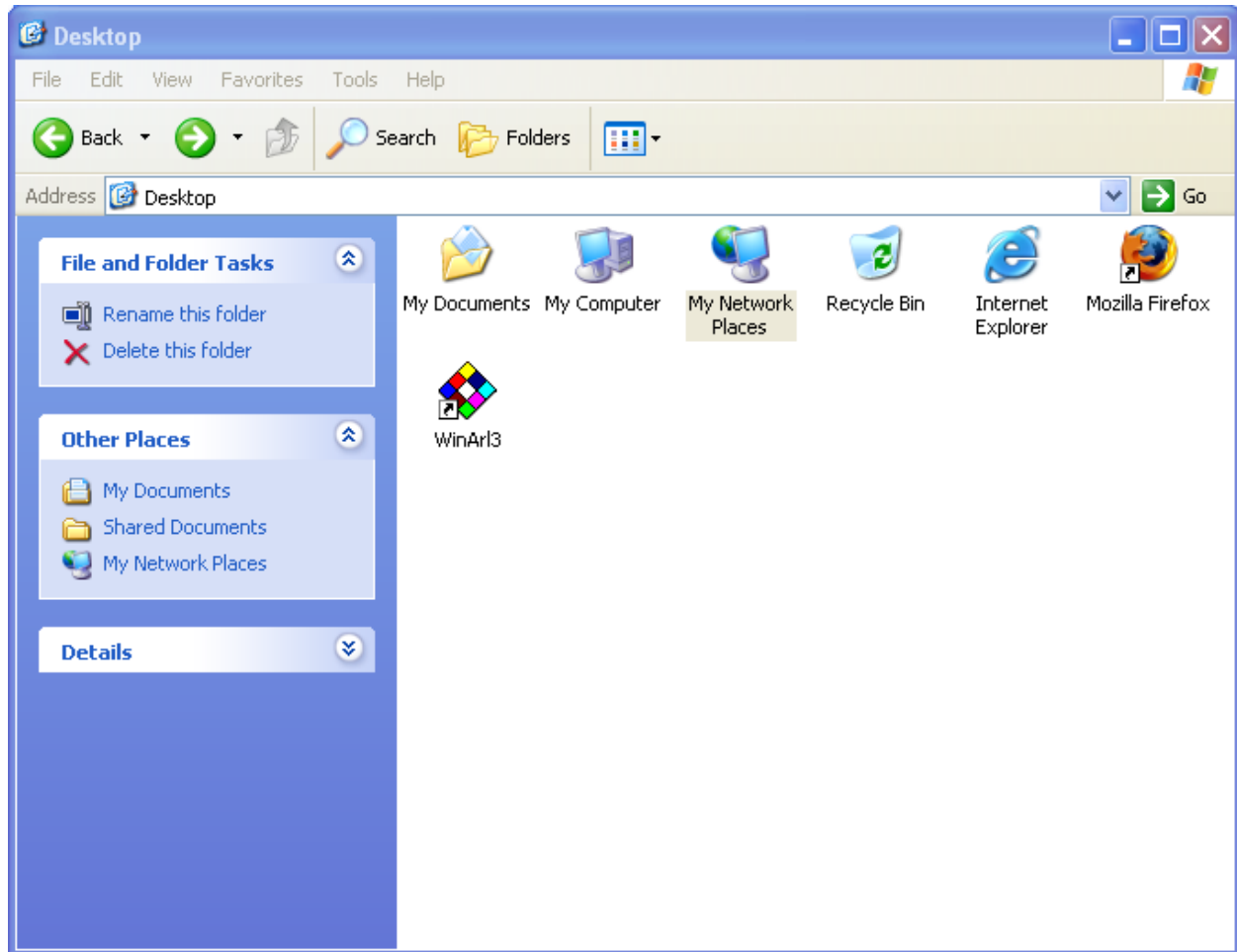
group.

Copy your sample sheet into the folder named dropbox.

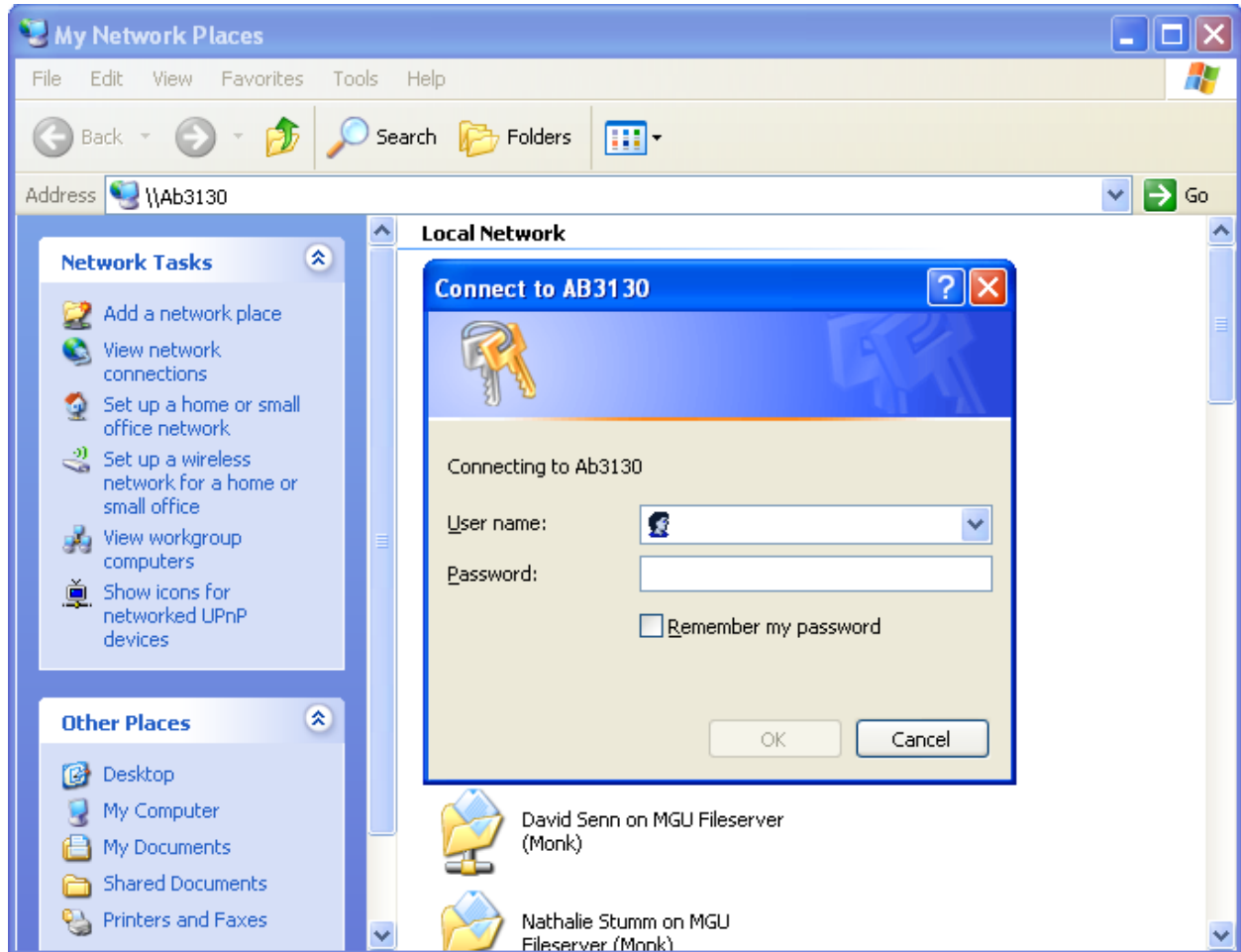
6. Submit your Sample Sheet (Windows Version)

If you're on Windows, you can submit your sample sheet the following:

On the desktop, click on My Network Places.

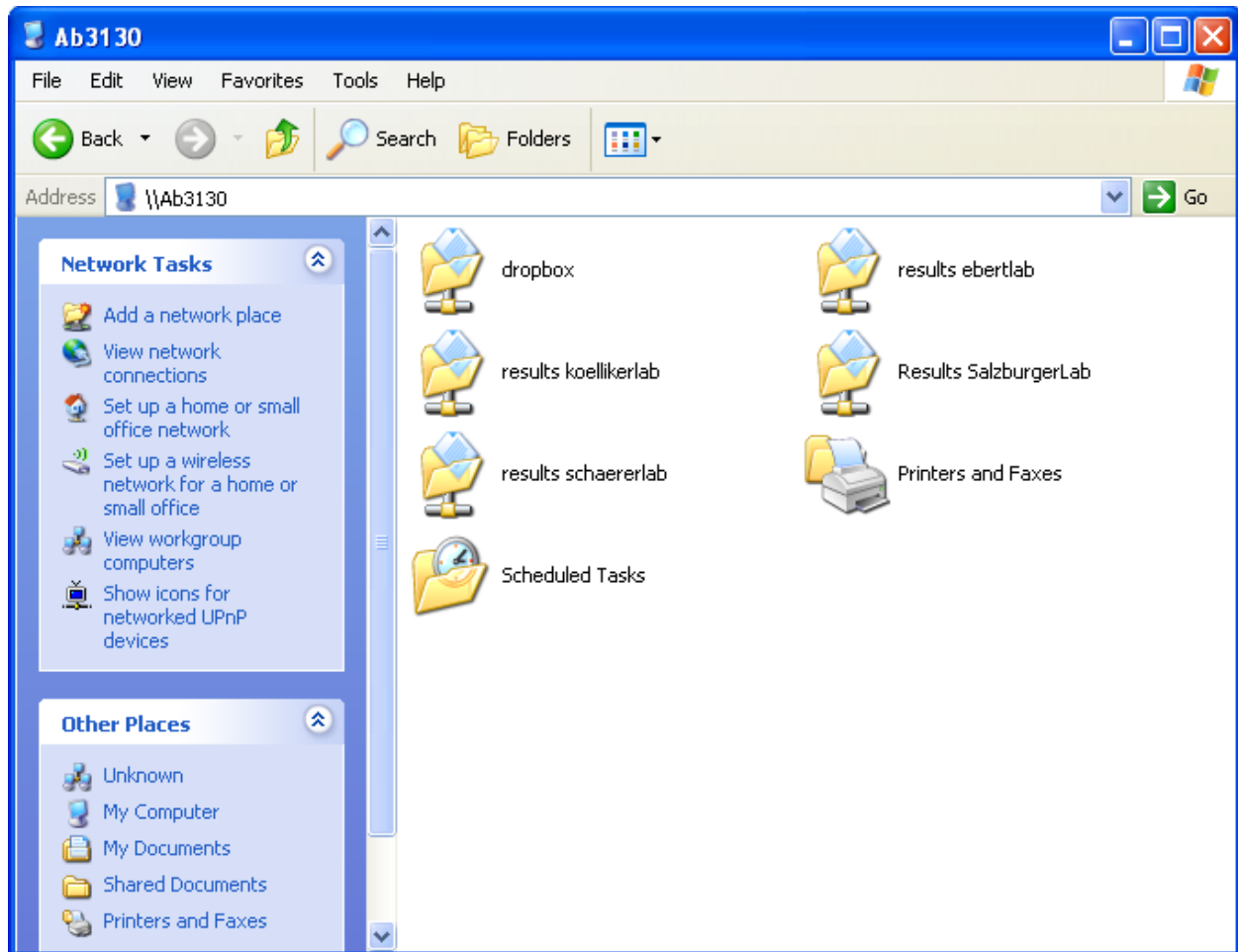


In the Network Places folder, type “\\Ab3130” in the address bar, and you’ll receive an authentication prompt:



Connect to ab3130 using one of the user names schaeererlab, ebertlab, koellikerlab and type in your password.

Once you're connected, you'll see the following folder (minus the Printers and Faxes and the Scheduled Tasks):



Copy and paste your sample sheet into the folder called dropbox.