Howto:
Prepare your Sample Sheet for Sequence Analysis

1. Sample Sheet Download

Go to http://www.evolution.unibas.ch/salzburger/protocols.htm and download the file sample_sheet_sequencing.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	SequencingAnalysis					

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 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

Below the header, the sample sheet contains the following table:

5	Well	Sample Name	Comment	Priority	Results Group 1	Instrument Protocol 1	Analysis Protocol 1
6	A01	sample_1		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
7	B01	sample_2		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
8	C01	sample_3		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
9	D01	sample_4		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
10	E01	sample_5		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
11	F01	sample_6		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
12	G01	sample_7		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
13	H01	sample_8		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
14	A02	sample_9		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
15	B02	sample_10		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
16	C02	sample_11		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
17	D02	sample_12		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
18	E02	sample_13		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
19	F02	sample_14		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
20	G02	sample_15		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2
21	H02	sample_16		100	SalzburgerLab_Sequences	Shortrun_Bd3_1	3130POP7_BDTv3-KB-Denovo_v5.2

1

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.

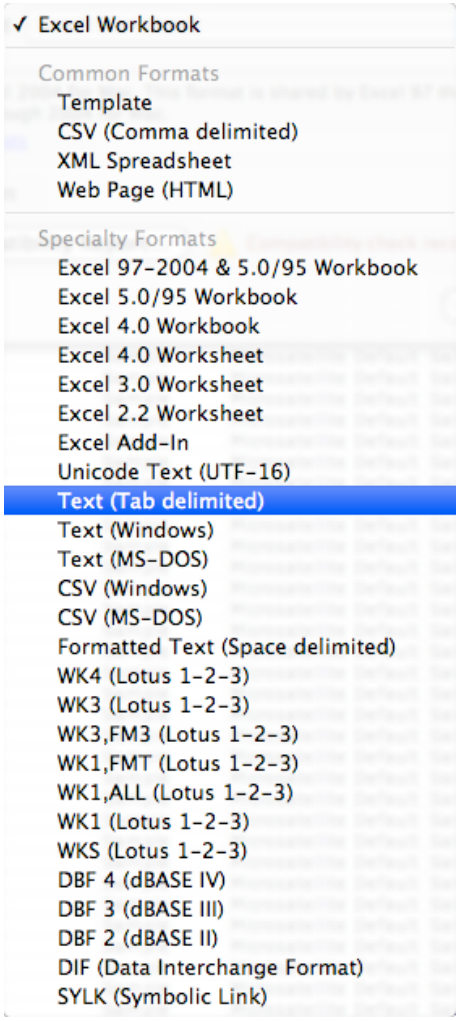
5 Enter either SchaererLab_Sequences, EbertLab_Sequences, KoellikerLab_Sequences, SalzburgerLab_Sequences, Botanical_Sequences, Tropical_Sequences, or NLU_Sequences .

6 Choose one of the following:
- Shortrun_Bd3_1 if you used a standard purification and fragment lengths are < 450 bp.
- Standardrun_Bd3_1 if you used a standard purification and fragment lengths are between 450 bp and 900 bp.
- XShortrun_Bdx3_1 if you used the X-Terminater purification kit and fragment lengths are < 450 bp
- XStandardrun_Bdx3_1 if you used the X-Terminater purification kit and fragment lengths are between 450 bp and 900 bp.

7 Don't change Analysis Protocol settings.

4. Export the Sample Sheet

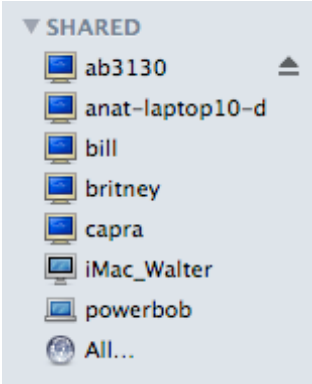
Save the Sample Sheet as a tab delimited text file with file extension .txt. Please choose a meaningful file name rather than “samplesheet.txt”.



5. Submit your Sample Sheet (Mac Version)

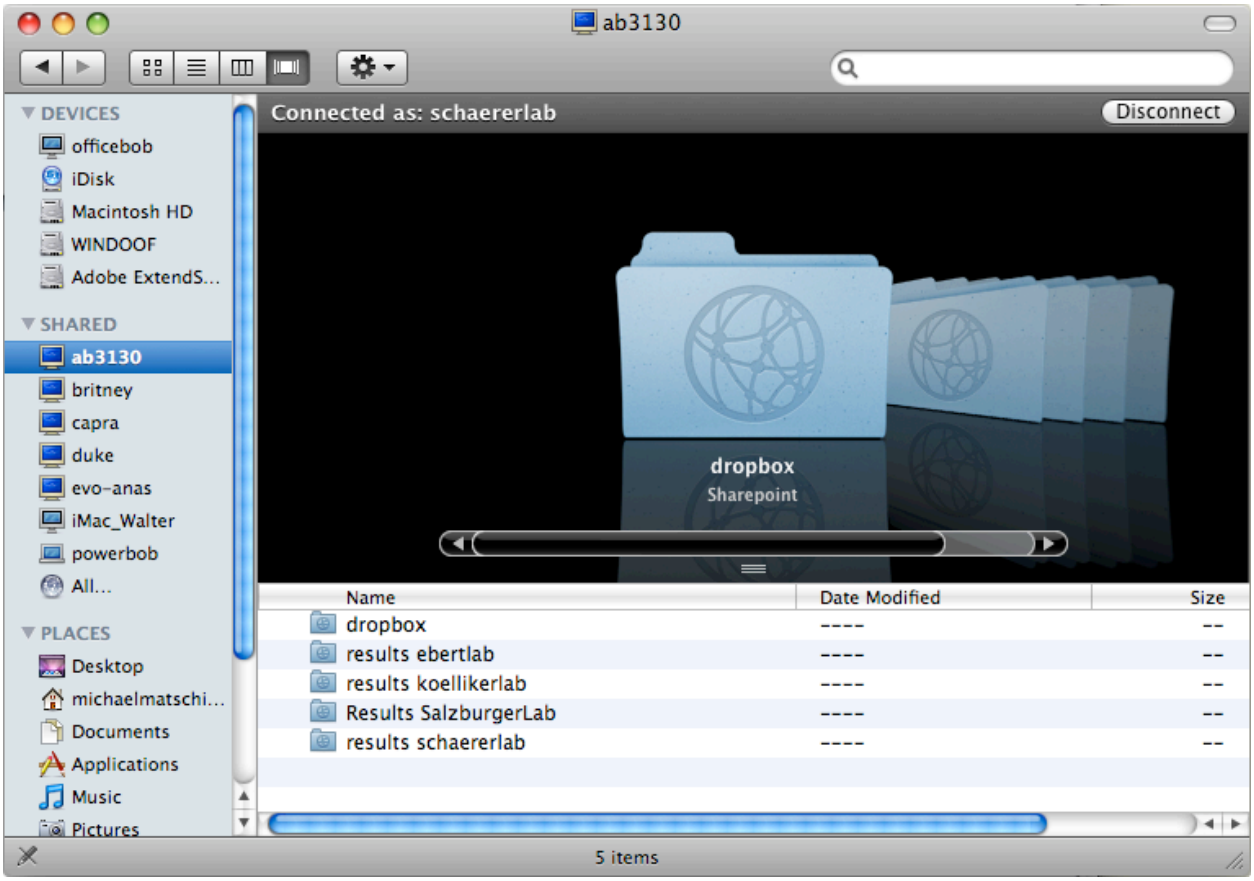
If you're on a Mac, please proceed the following:

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 schaererlab, ebertlab, koellikerlab or salzburgerlab and the password that you have been given. If you do not yet have a password, please contact somebody from the Salzburger group. You should see something similar to the following picture:



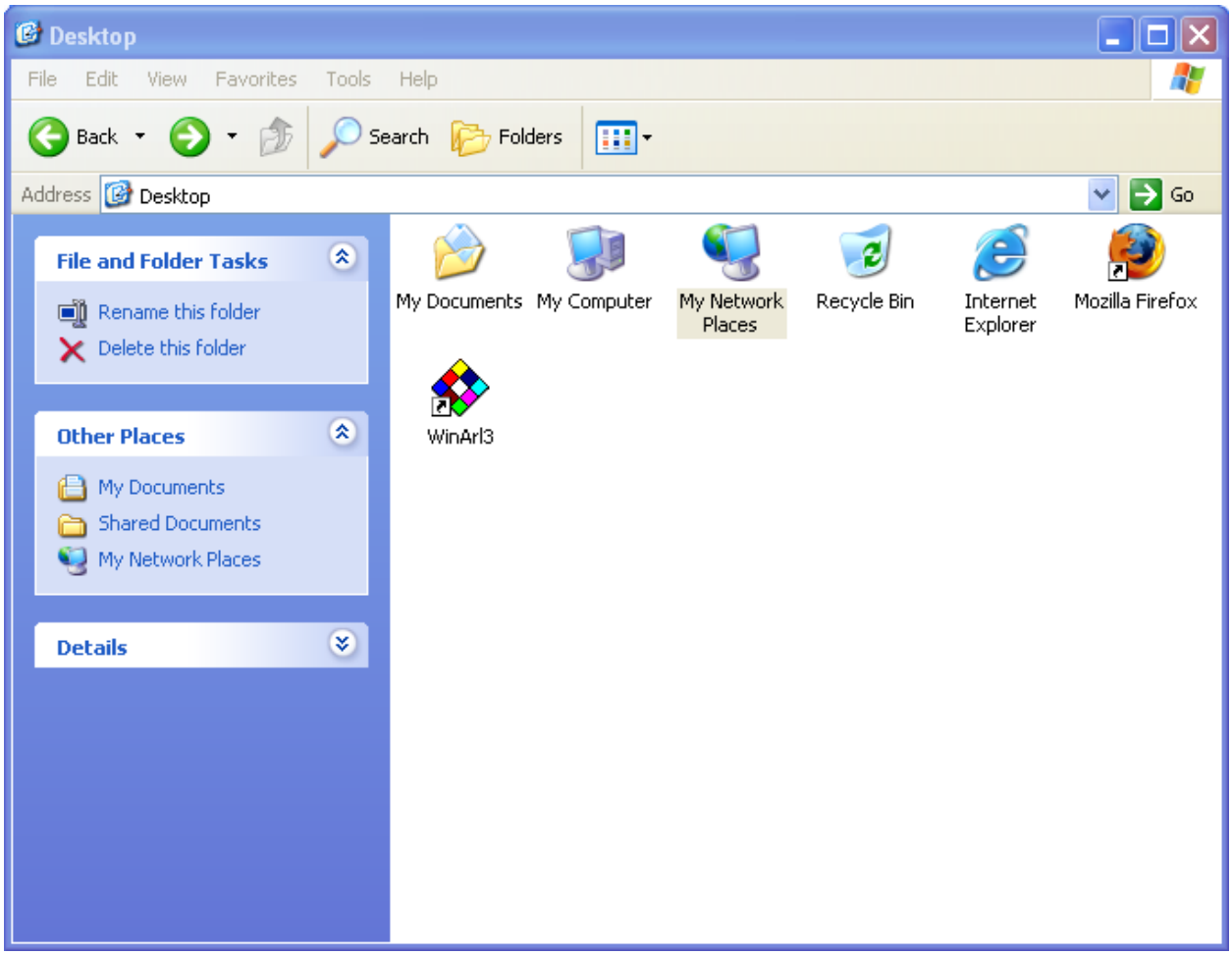
You have access only to the folder called dropbox as well as one of the results folders, depending on your group.

Copy your sample sheet into the folder named dropbox.

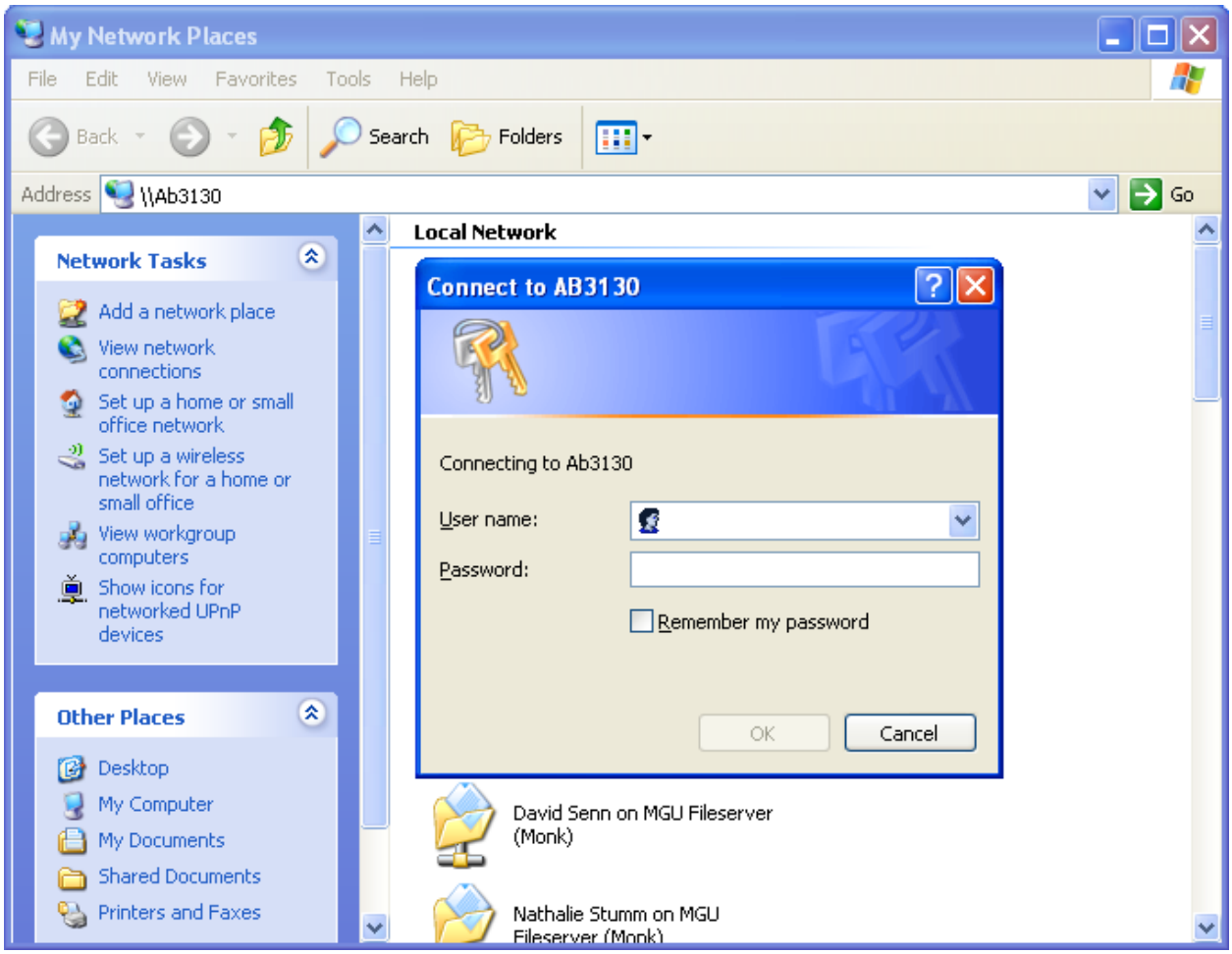
6. Submit your Sample Sheet (Windows Version)

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

On the desktop, click on My Network Places.

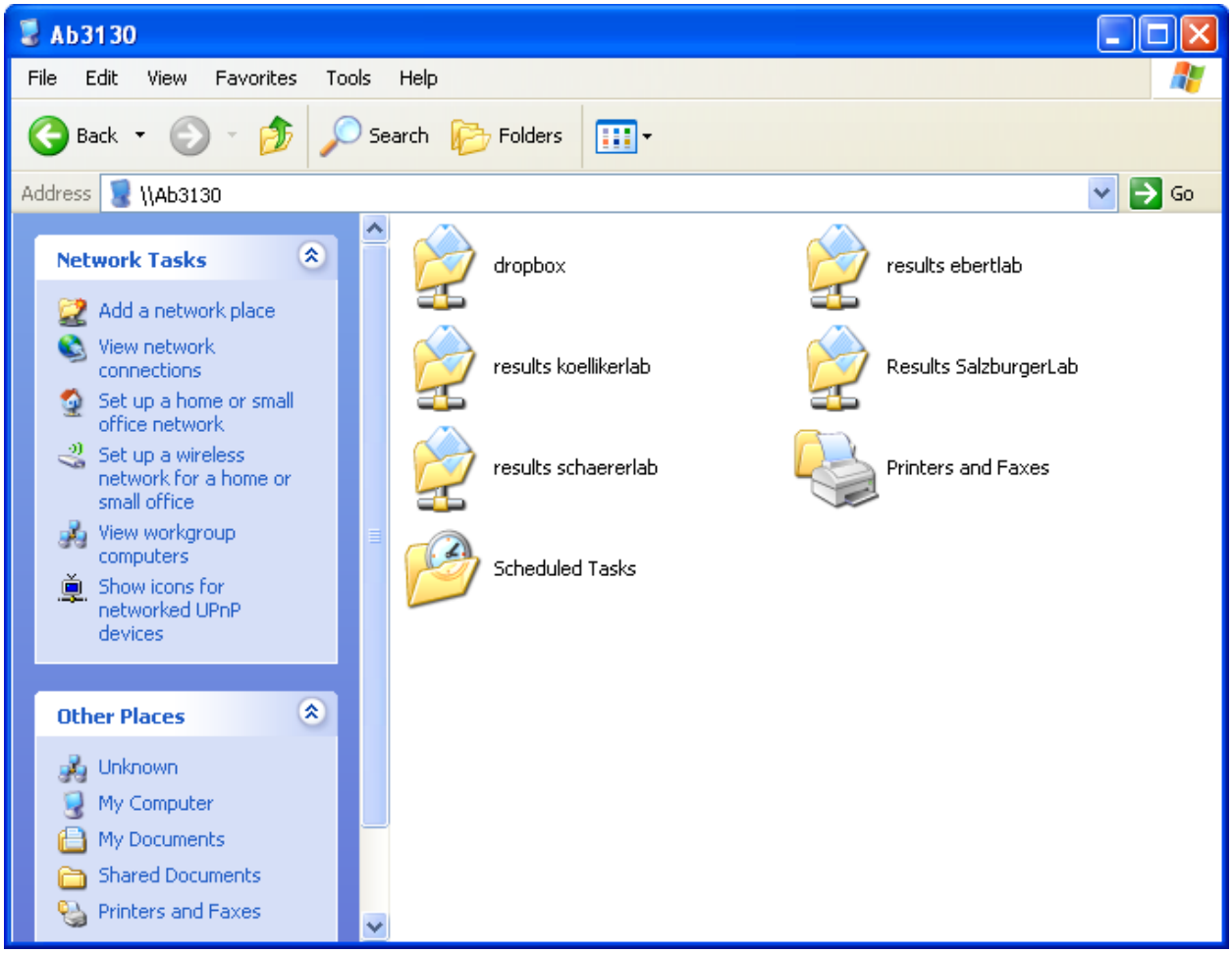


In the Network Places folder, type “\\Ab3130” in the address bar, and you’ll receive an authentication prompt:



Connect to ab3130 using one of the user names schaererlab, 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.