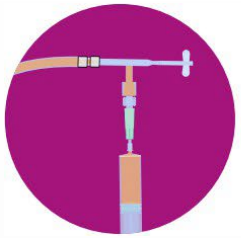

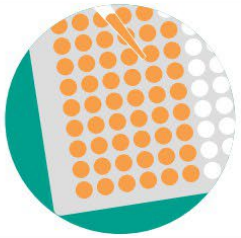
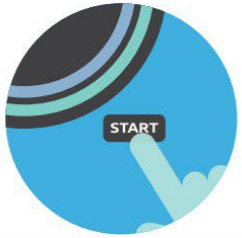

PATsmart™ REBEL® System

Guide to Pivot Tables

RFE + SMA Data Processing

26 Nov 2025

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REBEL Output File Types – What you'll find in your Batch folder

User-Focused

1. Comma-Separated Values (.csv) files are created to store PATsmart™ REBEL® System data output
   a) The entire batch file always ends in "Results.csv" – Go-to file for processing and analysis as it contains ALL data
   b) Each replicate within a batch has a dedicated .csv file – May also be used to process data
   c) The batch file with the same name but without "Results" is the batch record sheet – Contains batch sequence info but cannot be used to analyze results
   d) If SIMCA® CSV Reports is turned ON (System Settings > Storage/Export), then a file ending in "…SIMCA.csv" will be generated – Intended for import into Satorius SIMCA for further processing

2. Report files (.pdf) are also generated for each replicate – Contains analyte concentration, percent standard error, and electropherogram (please refer to the "PDF Electropherogram Reading Guide" to better understand and interpret the graph
   a) Quantitative Calibrations and Performance Qualifications also produce report files
   b) Offer quick, summarized, color-coded results for when comprehensive data processing isn't required

REBEL Output File Types (cont.)

Support-Focused

1. Telemetry (.tel) files are for Repligen support to analyze and diagnose customer issues and REBEL instrument readings
   a) If "TEL Data Files" is turned ON (System Settings > Storage/Export), then these files will be automatically created – ensure it is ON as to not encounter any issues in the future
   b) Should be sent ONLY to Repligen support, when necessary
   c) Batch and QC .tel files may be uploaded here – only upload at the request of your Repligen support representative and be sure to include their name in the description: https://repligen.com/supportupload/?product=REBEL

2. Assay (.json) files are also generated with each batch run and are required to be able to read the .tel files
   a) Please email these files to your Repligen support representative whenever you upload any .tel files to the link above
   b) Are not used for any data processing or viewing and cannot be opened by themselves

Range Finding Experiment (RFE)

A Range Finding Experiment (RFE) is used to establish which dilution factors (DF) might be best to utilize for preparation and analysis of lab-specific samples

The convenient Range Finding Tool (RFT) can be found under System Settings

> Tools to run an RFE batch on fresh media (including supplements if necessary)

Refer to “REBEL V1.2 Dilution Range Finding Tool.pdf” for more guidance

With the modified worksheets you’re about to create from the “Results.csv” file, along with the Range Finding – Dilution Report PDF & CSV files, will help determine optimal DF(s) needed for sample analysis

Depending on the analytes of interest, one or a few DFs may be chosen for prepping samples to afford the most accurate and robust results

- For example, the minimum DF (10x) is usually required to quantify the micronutrients (βAla, B1, B6-OH, B6-Oxo, GABA, NAM, and Sarcosine) since they’re conventionally lower in concentration than the AAs in numerous media types across many applications – “Recommended” DF would be 10x
- However, 10x is often too low of a dilution for other analytes with higher concentrations, necessitating use of another DF to allow monitoring of these analytes in the same sample

Range Finding Experiment (RFE) - Examples

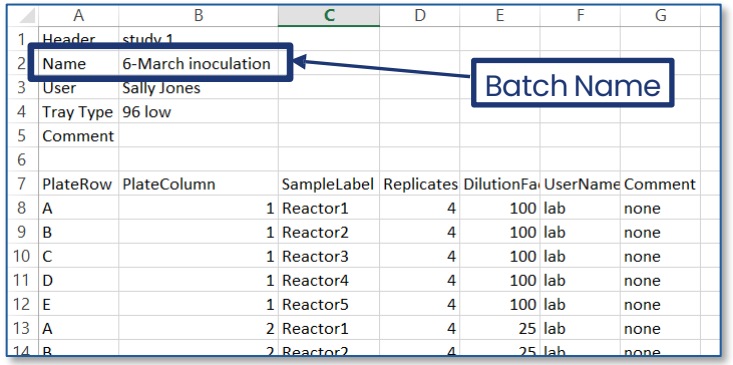
Depending on the analytes of interest, one or several DFs may be chosen from the RFE for preparing each sample to generate the most accurate and precise results for all target analytes:

- Example 1: Trent's T-Cell Lab is interested in only 10 of the analytes monitored by the REBEL and all 10 are observed within optimal range at a single DF of 25x. They will only need to prepare samples at DF = 25x for each time point.
- Example 2: Catie's CHO Lab is interested in 15 of the analytes monitored by the REBEL. Of these 15 analytes, 10 are observed within optimal range at DF = 100x, and 5 are observed within optimal range at DF = 10x. They will want to prepare each sample at both DF = 100x and 10x, in separate vials, to quantify all 15 targets.
- Example 3: Milla's Media Development Lab is interested in all analytes monitored by the REBEL because they create formulations for as-needed applications. They will frequently use the RFT whenever they have a new formulation to analyze and may need to use several DFs for each new sample tested. In one case, they find that they should prepare each sample at DF = 10x to monitor the micronutrients, DF = 100x to monitor analytes at intermediate concentrations, and DF = 500x to monitor higher concentrated analytes like AQ, Asp, and Glu. Therefore, they'll prepare each sample at three DFs (10x, 100x, and 500x), in separate vials, to quantify their numerous targets.

The Results File

- **Filename format is:**
  - [date/time stamp]-[REBEL serial number]-[batch name]-Results.csv
    - *Ex. 20200322T121701-SN0129-6-March inoculation-Results.csv*
  - 'batch name' is designated by the Name field in batch runsheet .csv file

Batch Runsheet .csv File



	A	B	C	D	E	F	G
1	Header	study 1					
2	Name	6-March inoculation					
3	User	Sally Jones					
4	Tray Type	96 low					
5	Comment						
6							
7	PlateRow	PlateColumn	SampleLabel	Replicates	DilutionFa	UserName	Comment
8	A	1	Reactor1	4	100	lab	none
9	B	1	Reactor2	4	100	lab	none
10	C	1	Reactor3	4	100	lab	none
11	D	1	Reactor4	4	100	lab	none
12	E	1	Reactor5	4	100	lab	none
13	A	2	Reactor1	4	25	lab	none
14	B	2	Reactor2	4	25	lab	none

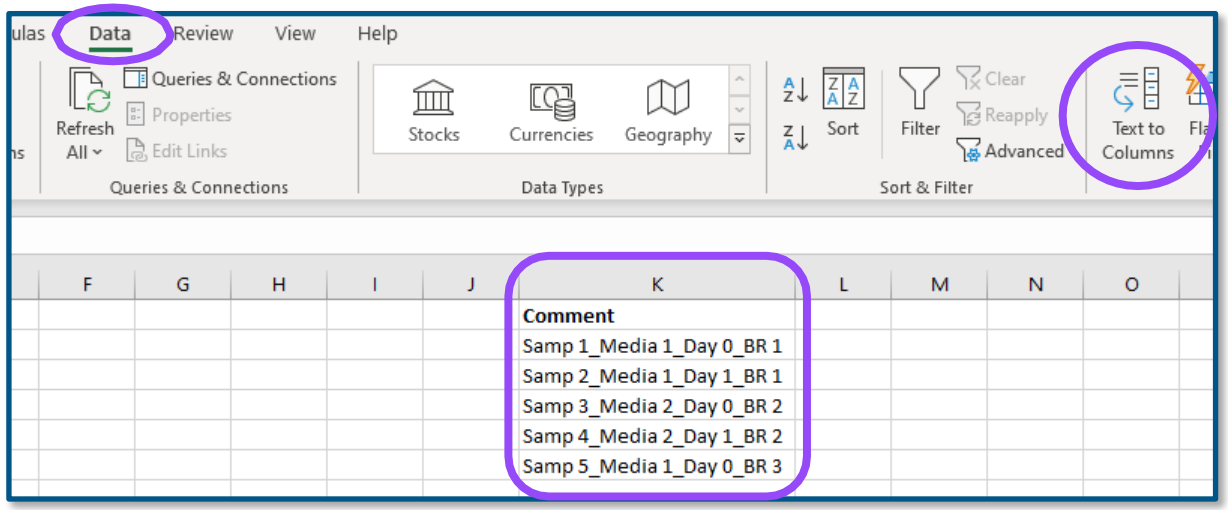
Results .csv File

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	**Sample Label**	**User**	**Time Started**	**Dilution Factor**	**Batch Label**	**REBEL S/N**	**REBEL Chip S/N**	**Comment**	**Replicate Number**	**Analyte Full Name**	**Abbreviation**	**Concentration**	**Standard Error**
2	Reactor1	lab	14:05 2020.03.22	100	6-March inoculation	129	RC000537	none	1	Pyridoxine	B6-OH	0.14	0.09
3	Reactor1	lab	14:05 2020.03.22	100	6-March inoculation	129	RC000537	none	1	DL-Isoleucine	Ile	0.18	0.07
4	Reactor1	lab	14:05 2020.03.22	100	6-March inoculation	129	RC000537	none	1	γ-Aminobutyric acid	GABA	0.31	0.12
5	Reactor1	lab	14:05 2020.03.22	100	6-March inoculation	129	RC000537	none	1	DL-Proline	Pro	0.60	0.24
6	Reactor1	lab	14:05 2020.03.22	100	6-March inoculation	129	RC000537	none	1	DL-Leucine	Leu	3.47	0.21
7	Reactor1	lab	14:05 2020.03.22	100	6-March inoculation	129	RC000537	none	1	DL-Glutamic acid	Glu	3.86	0.34
8	Reactor1	lab	14:05 2020.03.22	100	6-March inoculation	129	RC000537	none	1	Choline	Choline	3.94	0.29
9	Reactor1	lab	14:05 2020.03.22	100	6-March inoculation	129	RC000537	none	1	DL-Cystine	Cystine	10.89	1.18

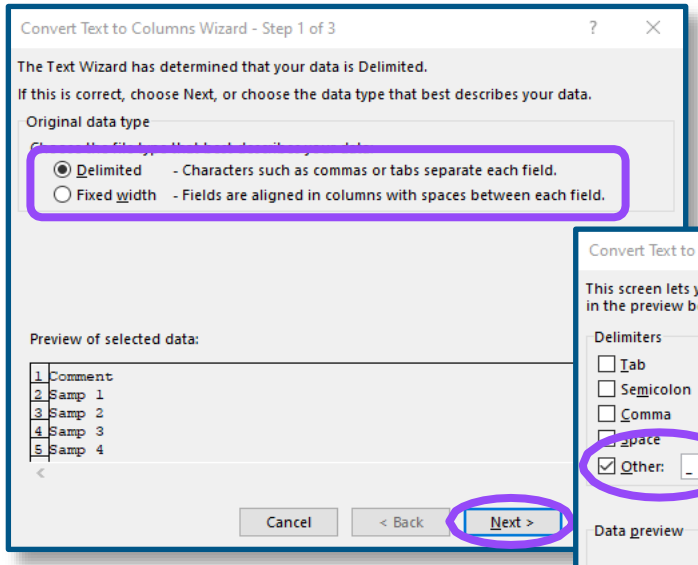
The –Results.csv file includes data from all replicates in a layout suitable for creating **Pivot Tables** and **Pivot Charts** in Excel

First thing, after opening the Results.CSV file is to **Save As .XLSX** so any changes made throughout processing may be saved

Delimiting a Single Column of Data Labels into Several Columns

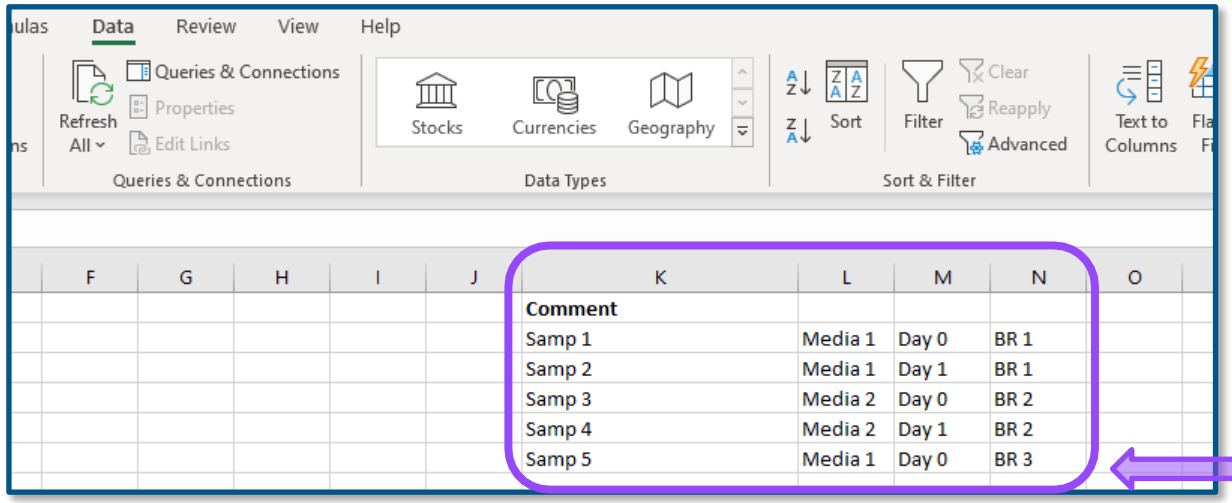


1) Select single column with data labels
2) Data > Text to Columns
3) Ensure "Delimited" is selected > Next

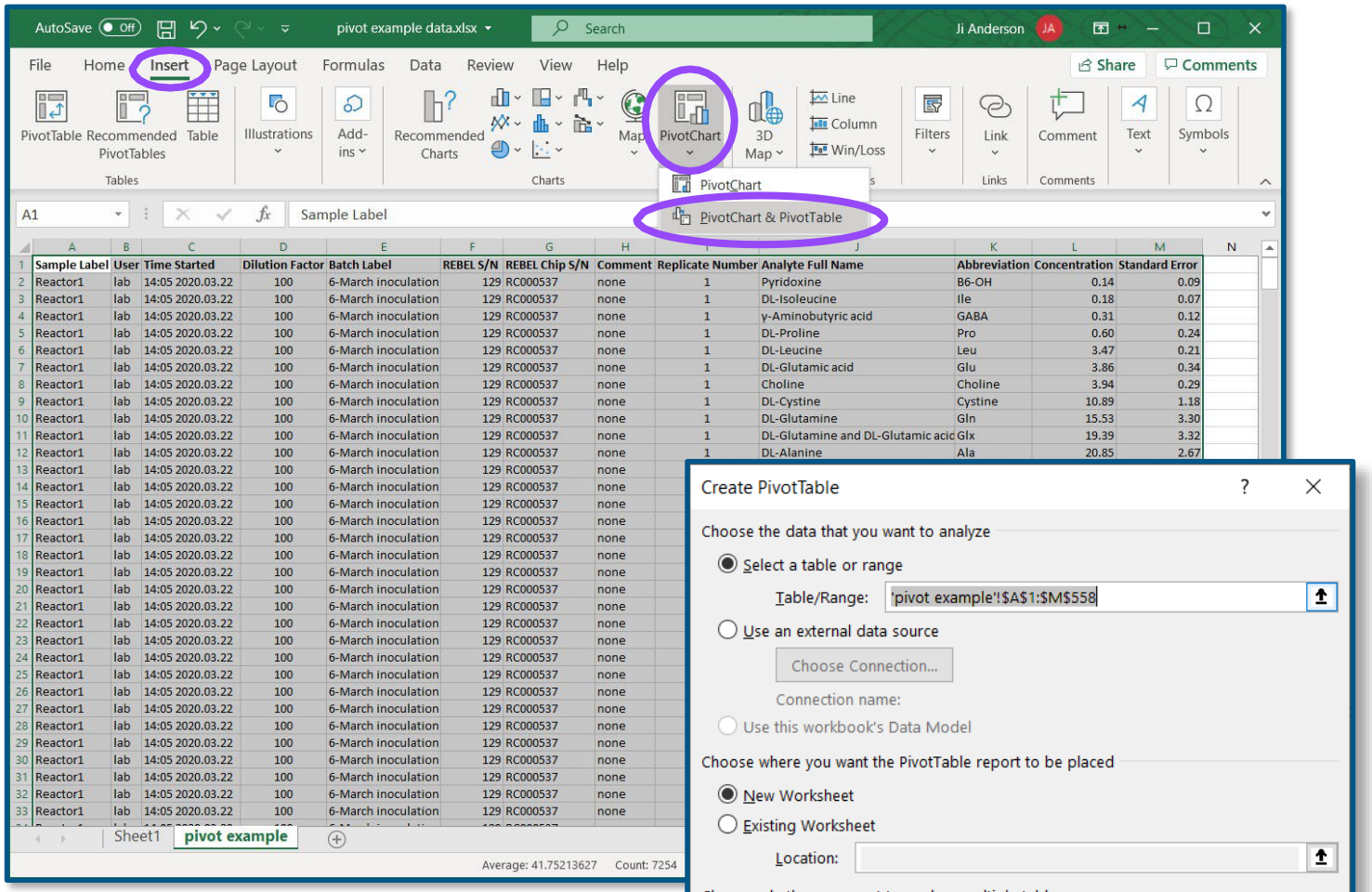


4) Select Delimiter
Example: Underscore
"_"

5) Finish



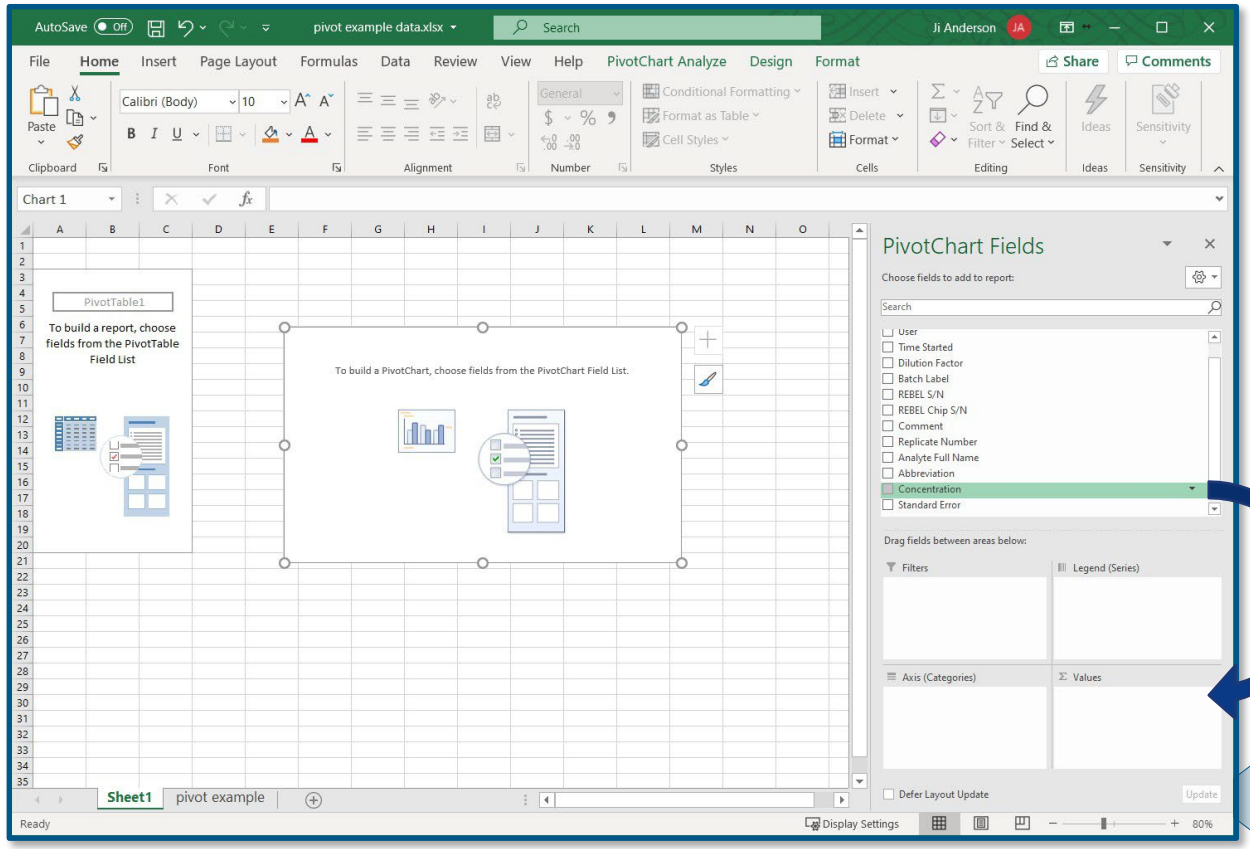
Generating a Pivot Table/Chart



Generate a pivot table and pivot chart by

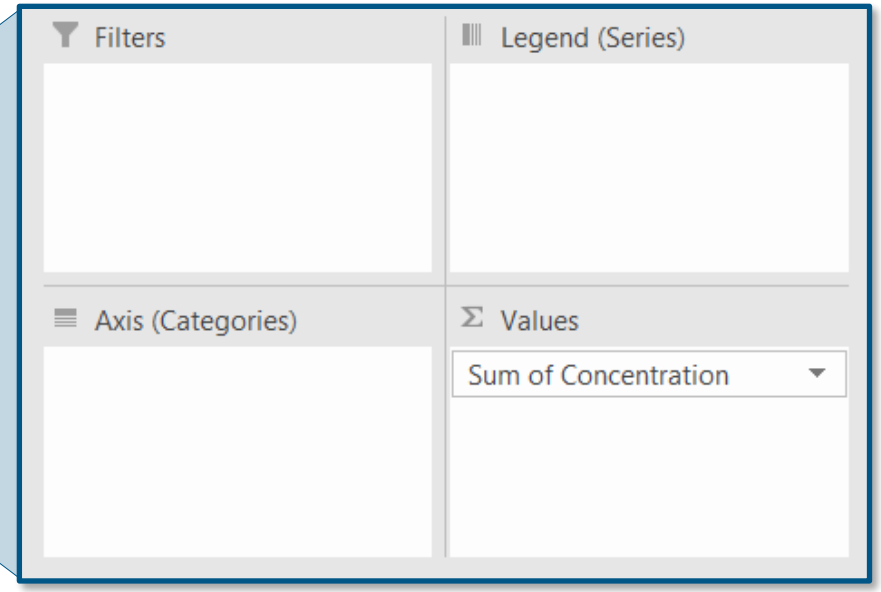
- Selecting the entire dataset
  Click anywhere in the dataset and hit “Ctrl+A”
- Then select
  Insert > PivotChart > PivotChart & PivotTable
- Click OK when prompted

Construct the Pivot Table / Chart

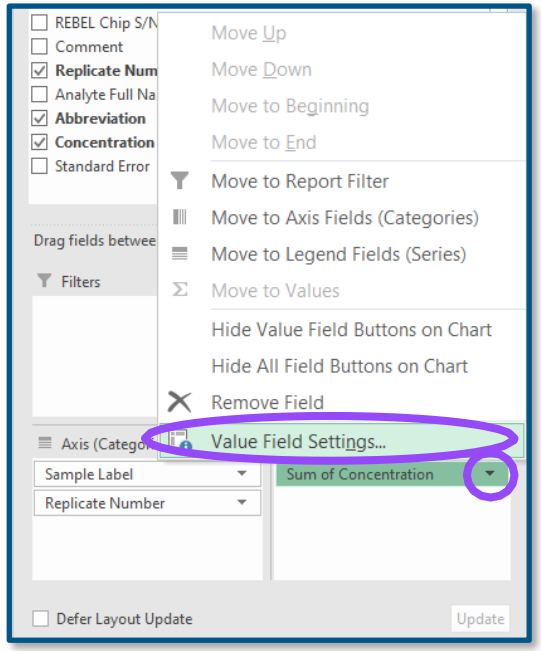


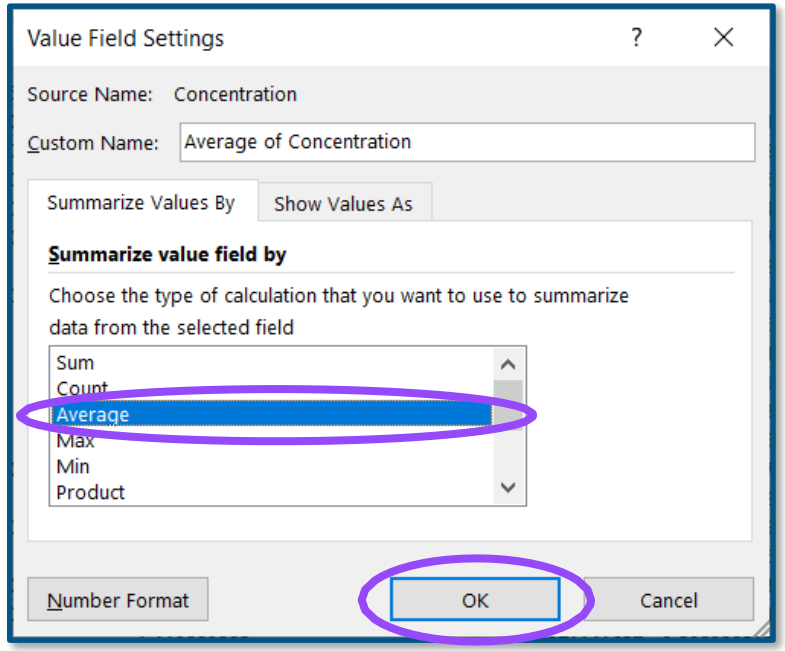
Large datasets can be quickly organized and visualized by rearranging the fields

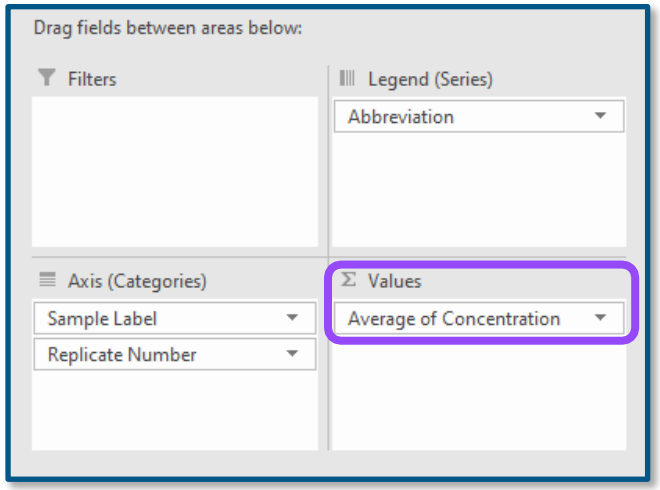
- Construct the pivot table and chart by dragging data fields into appropriate ‘areas’
- Results (in mM) are in the ‘Concentration’ field, which should be placed in the ‘Values’ area



Display Concentration Averages







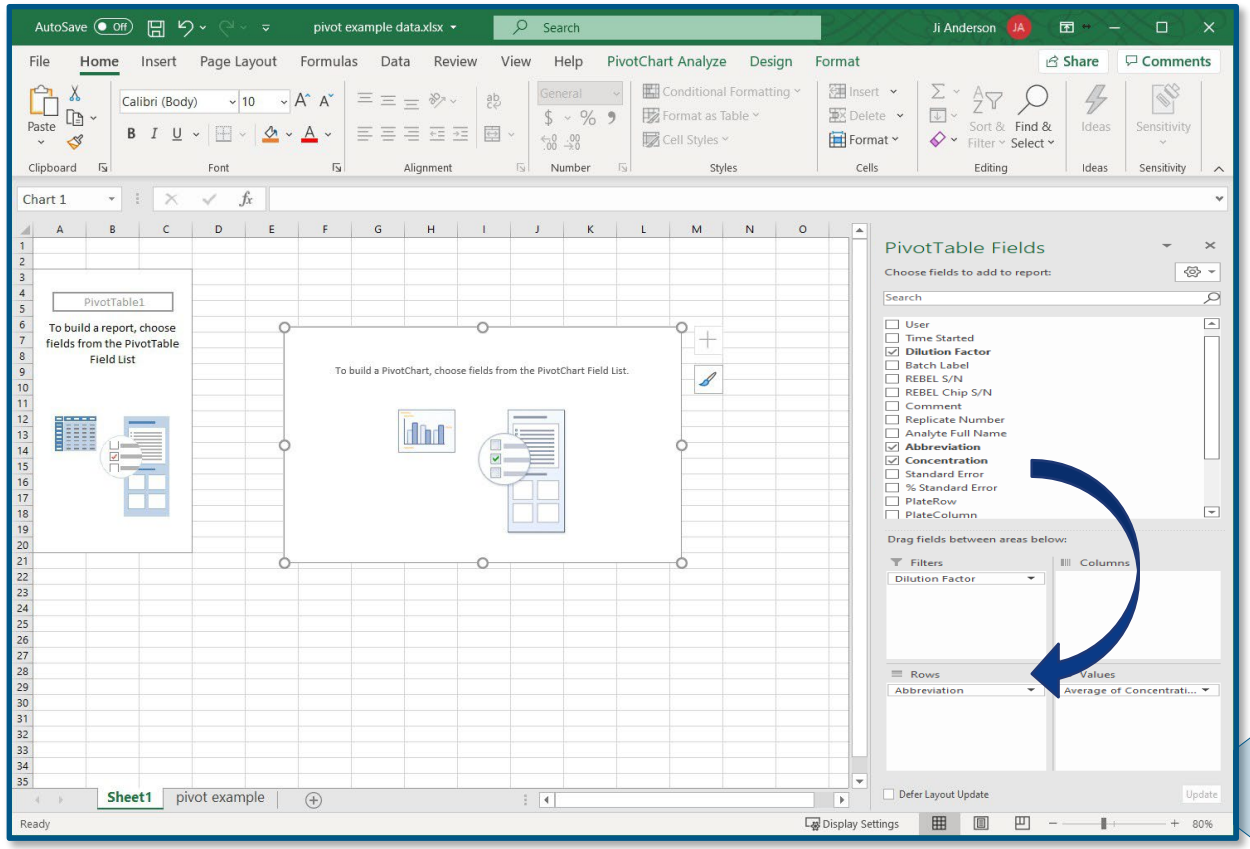
Pivot tables will default to display the Value Field as a Sum

To change the Value Field to display Average:

- Click the dropdown arrow next to Sum of Concentration > Value Field Settings
- Select Average > OK

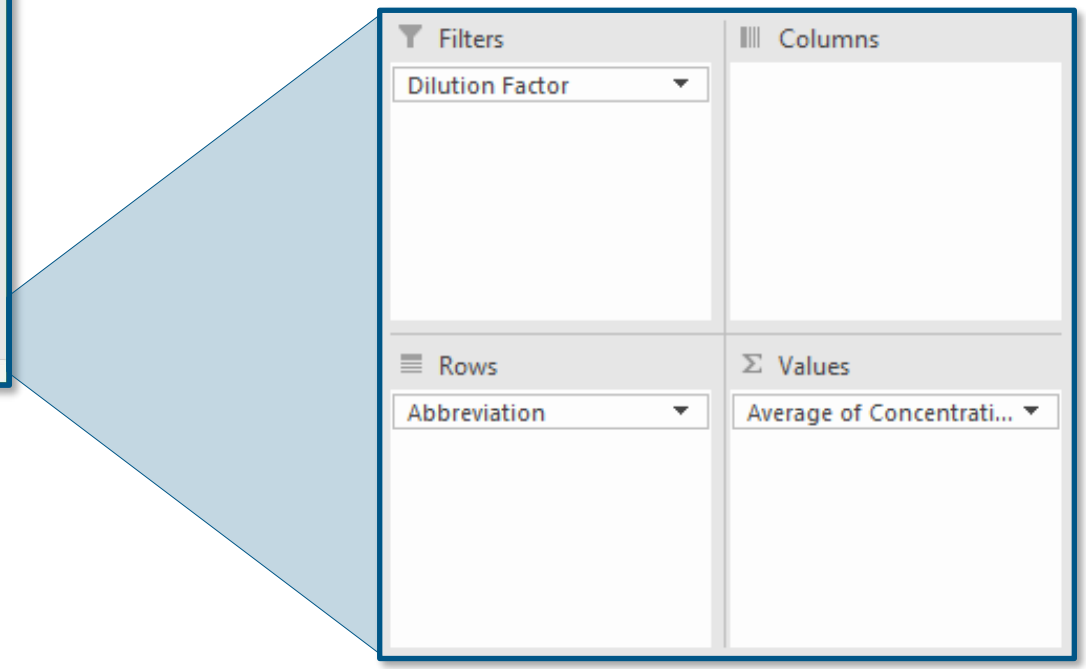
The Value Field should now display the Average of Concentration

Range Finding Experiment – Adding Data to Table

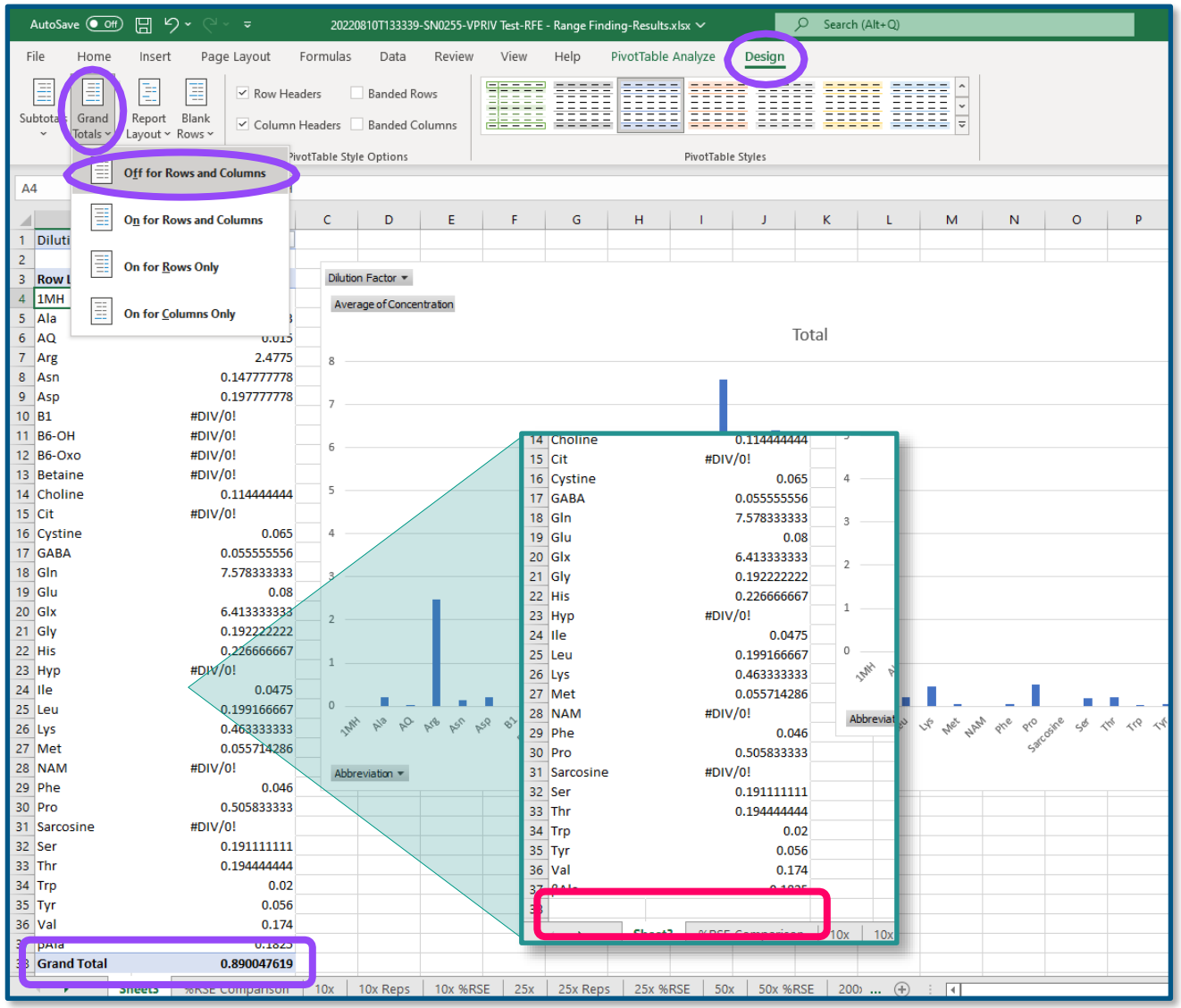


Add ‘Dilution Factor’ and ‘Abbreviation’

- ‘Dilution Factor’ should be placed in the ‘Filters’ area
- ‘Abbreviation’ should be placed in the ‘Rows’ area – Note: ‘Rows’ is labeled ‘Axis’ if you click on the chart rather than the table



Range Finding Experiment – Removing Grand Totals



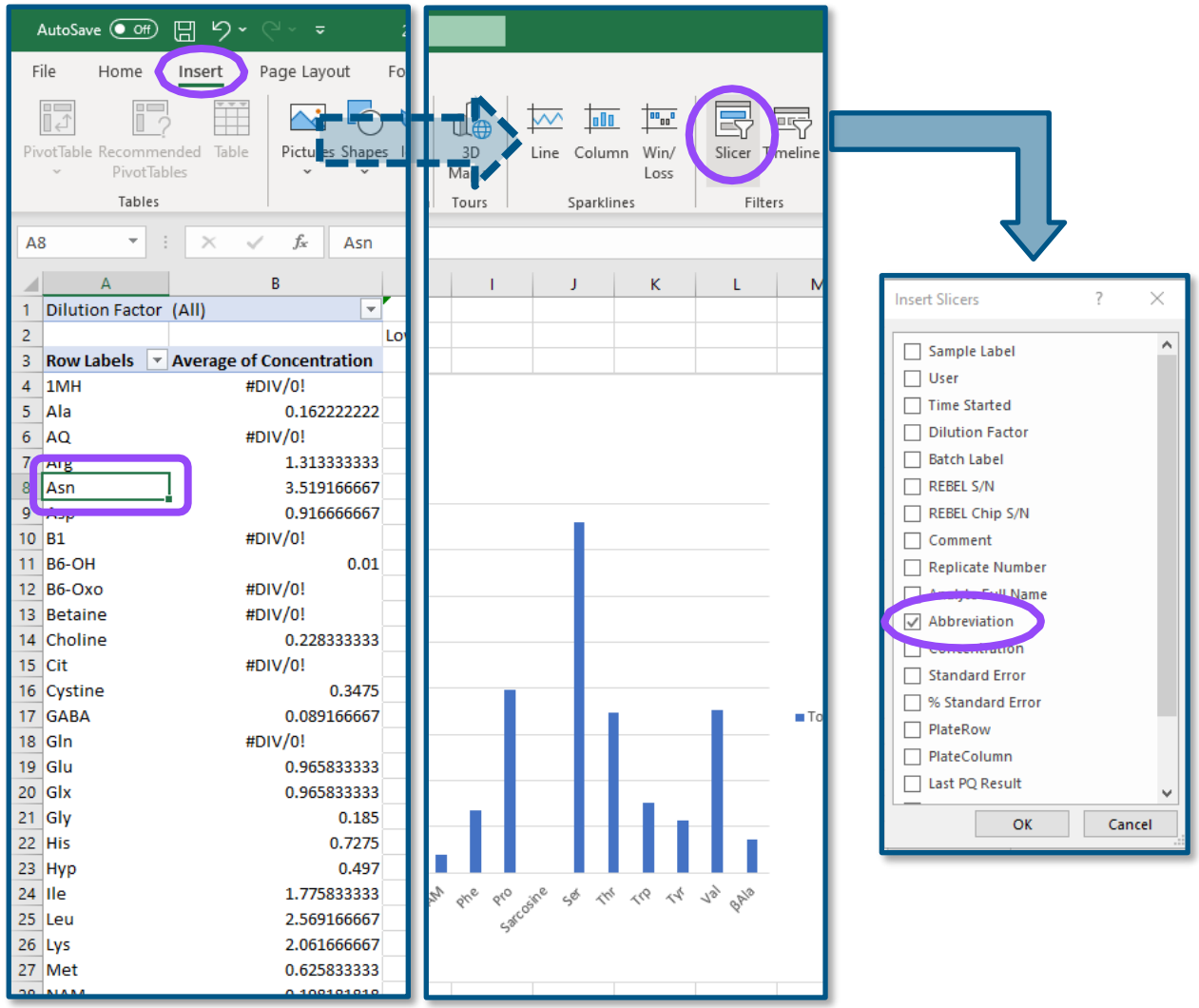
Remove ‘Grand Totals’ row as it is unnecessary to this analysis

Select any cell in table

Design > Grand Totals (dropdown) > Off for Rows and Columns

Grand totals should be removed from table for ease of use since they’re unnecessary for this analysis

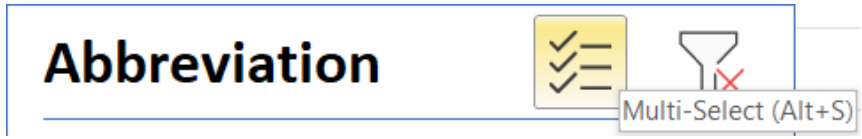
Range Finding Experiment – Removing Undetected Analytes



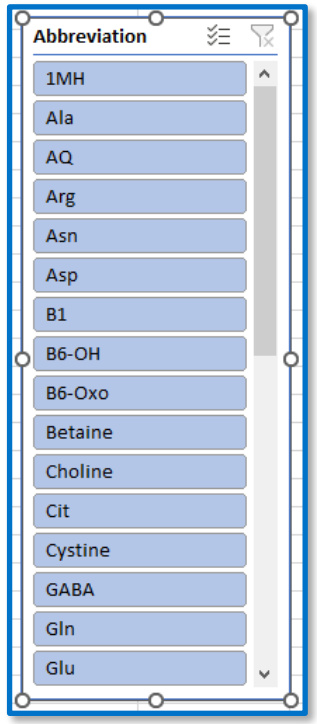
Now you have a list of all analytes showing an Average Concentration for all Dilutions Factors

Remove any analyte with a Concentration of '#DIV/0!' – analytes have no reported value

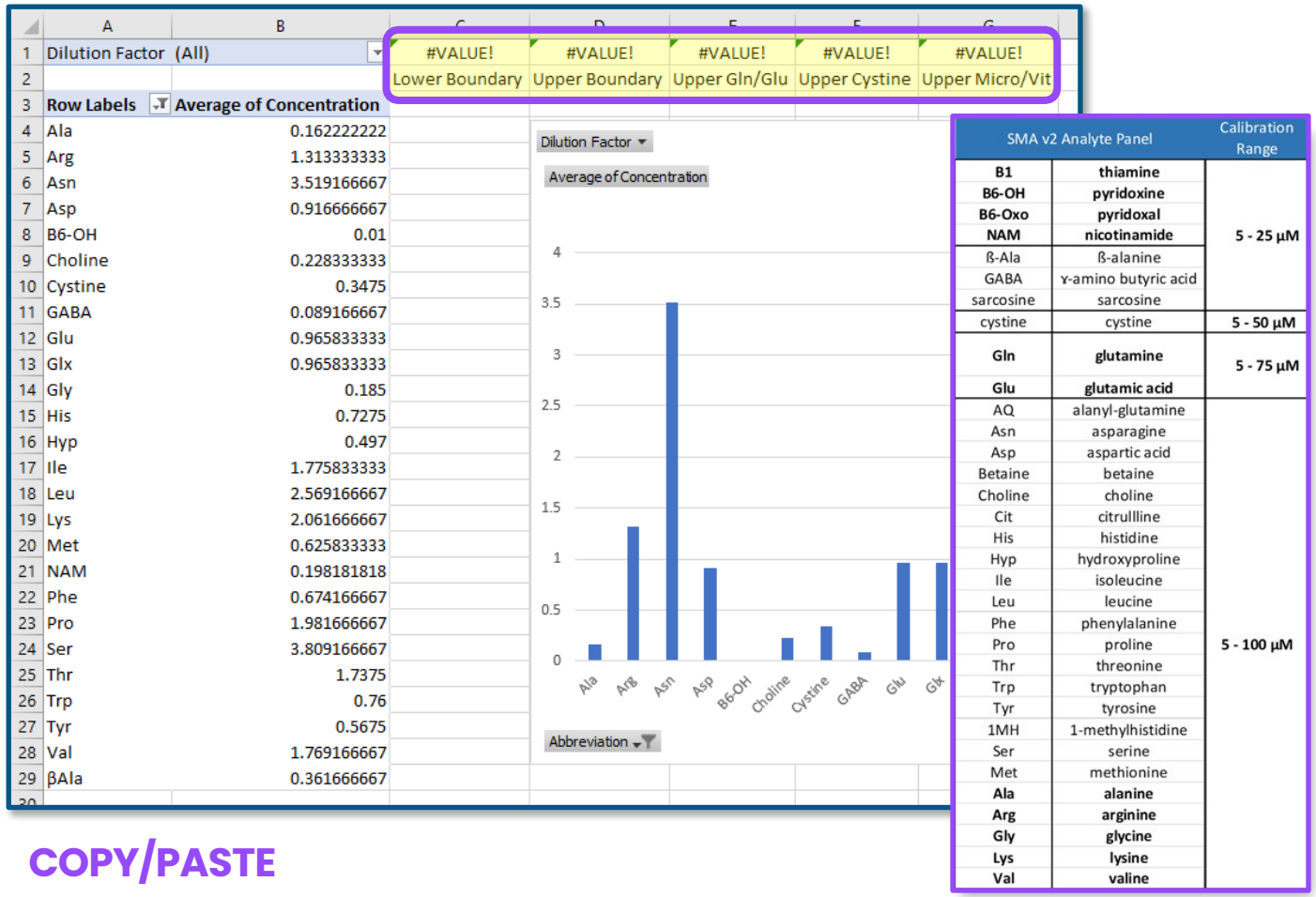
- Select any cell in the table
  Insert > Slicer
- Select "Abbreviation", click OK
- Click "Multi-Select" when the window on the right appears:



This will insert a Slicer window (right) to allow you to select or deselect analytes from your list



Range Finding Experiment – Establishing Dynamic Range Boundaries



Dilution Factor	(All)	#VALUE!	#VALUE!	#VALUE!	#VALUE!	#VALUE!
		Lower Boundary	Upper Boundary	Upper Gln/Glu	Upper Cystine	Upper Micro/Vit
Row Labels	Average of Concentration					
Ala	0.162222222					
Arg	1.313333333					
Asn	3.519166667					
Asp	0.916666667					
B6-OH	0.01					
Choline	0.228333333					
Cystine	0.3475					
GABA	0.089166667					
Glu	0.965833333					
Glx	0.965833333					
Gly	0.185					
His	0.7275					
Hyp	0.497					
Ile	1.775833333					
Leu	2.569166667					
Lys	2.061666667					
Met	0.625833333					
NAM	0.198181818					
Phe	0.674166667					
Pro	1.981666667					
Ser	3.809166667					
Thr	1.7375					
Trp	0.76					
Tyr	0.5675					
Val	1.769166667					
βAla	0.361666667					

SMA v2 Analyte Panel		Calibration Range
B1	**thiamine**	
B6-OH	**pyridoxine**	
B6-Oxo	**pyridoxal**	
NAM	**nicotinamide**	**5 - 25 µM**
ß-Ala	ß-alanine	
GABA	γ-amino butyric acid	
sarcosine	sarcosine	
cystine	cystine	**5 - 50 µM**
Gln	**glutamine**	**5 - 75 µM**
Glu	**glutamic acid**	
AQ	alanyl-glutamine	
Asn	asparagine	
Asp	aspartic acid	
Betaine	betaine	
Choline	choline	
Cit	citrullline	
His	histidine	
Hyp	hydroxyproline	
Ile	isoleucine	
Leu	leucine	
Phe	phenylalanine	
Pro	proline	**5 - 100 µM**
Thr	threonine	
Trp	tryptophan	
Tyr	tyrosine	
1MH	1-methylhistidine	
Ser	serine	
Met	methionine	
Ala	**alanine**	
Arg	**arginine**	
Gly	**glycine**	
Lys	**lysine**	
Val	**valine**	

Delete the copy/pasted list of analytes

Ensure "(All)" is selected for the DF filter

Copy and paste the table below to cell C1 in your worksheet

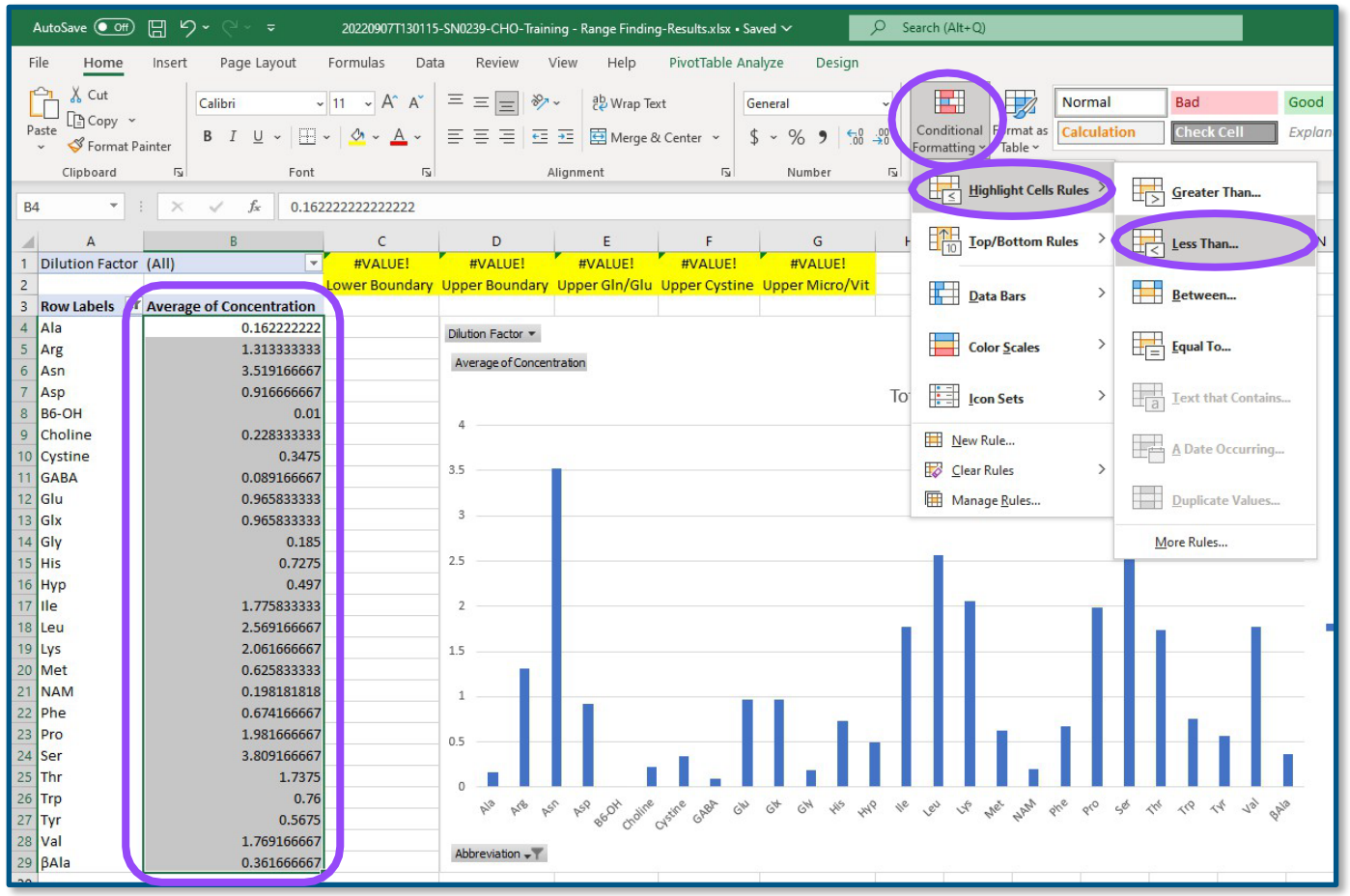
- Equations convert units from µM (dynamic range of REBEL) to mM (true concentration of analytes) and accounts for DF (cell B1)
- Lower bound for all analytes is 5 µM
- Upper bound is 25, 50, 75, or 100 µM depending on the analyte
- You'll receive an error (#VALUE!) since we have not selected an individual DF yet, this is expected

Note: Boundaries for different sets of analytes can be found in Calibration Range table provided by FAS during training (left)

COPY/PASTE

=5*B1/1000	=100*B1/1000	=75*B1/1000	=50*B1/1000	=25*B1/1000
Lower Boundary	Upper Boundary	Upper Gln/Glu	Upper Cystine	Upper B1/B6-OH/B6-Oxo/NAM/βAla/GABA/Sarcosine

Range Finding Experiment – Conditional Formatting, Lower Boundary



Set up Conditional Formatting for visual cues as to which analytes are out of range

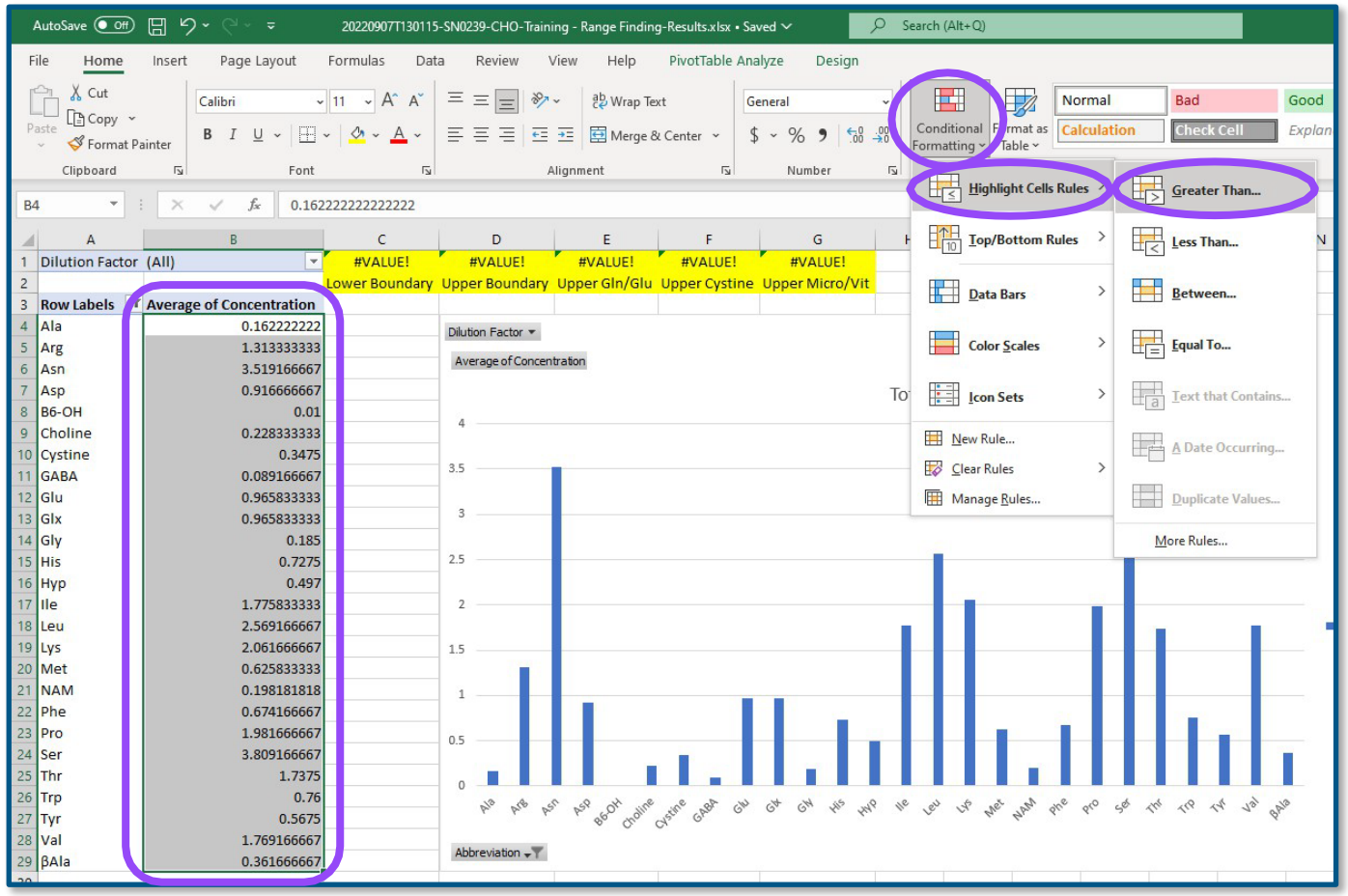
- Select all the Concentration cells for every analyte since all analytes have the same lower bound
- Apply CF so any value LESS THAN

  Lower Boundary will highlight

  Conditional Formatting > Highlight Cells Rules > Less Than… > Click on cell C2 to input > OK
- C2 should be where your equation for Lower Boundary is set, if not please select appropriate cell for CF, above

Note: Which color you choose doesn't matter, default is red

Range Finding Experiment – Conditional Formatting, Upper Boundaries



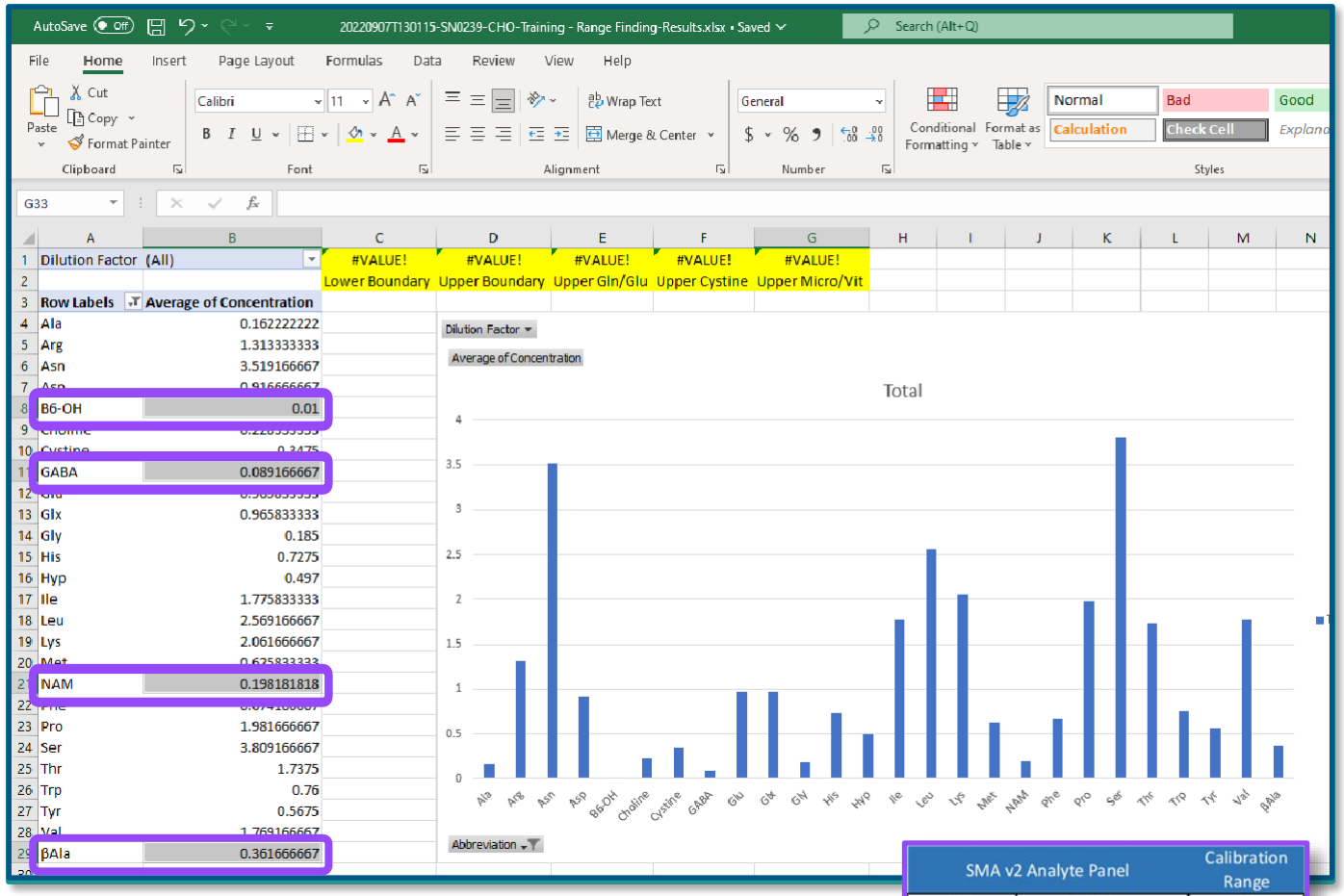
Set up further Conditional Formatting

- Select all the Concentration cells for every analyte again since most analytes have the same upper bound
- Apply CF so any value GREATER THAN Upper Boundary will highlight

  Conditional Formatting > Highlight Cells Rules > Greater Than… > Click on cell D2 to input > OK
- D2 should be where your equation for Upper Boundary is set, if not please select appropriate cell for CF, above

Note: Which color you choose doesn't matter, default is red but a different color than you used for Lower is suggested

Range Finding Experiment – Conditional Formatting, Upper Boundaries



SMA v2 Analyte Panel		Calibration Range
B1	thiamine	5 - 25 µM
B6-OH	pyridoxine	
B6-Oxo	pyridoxal	
NAM	nicotinamide	
ß-Ala	ß-alanine	
GABA	γ-amino butyric acid	
sarcosine	sarcosine	

Example: B6-OH, GABA, NAM, and βAla are the analytes of the seven in this Micronutrient/Vitamin list remaining

Set up CF for Cystine, Gln/Glu, and the Micronutrient/Vitamins

- Select Concentration cells for Gln, Glu, and Glx, if any remain in the list

  Apply CF so any value GREATER THAN cell E1 will highlight

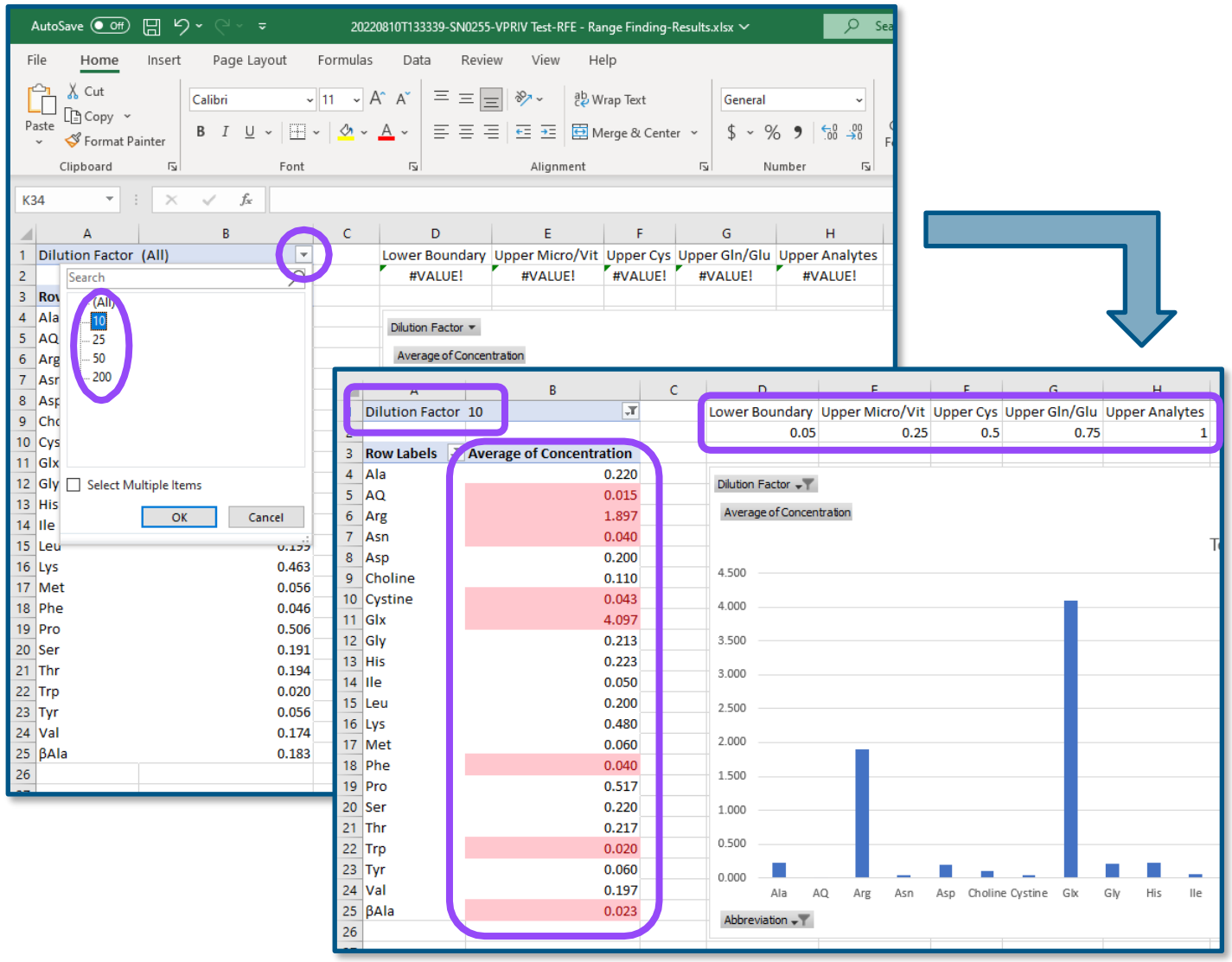
- Select Concentration cell for Cystine, if it remains in the list

  Apply CF so any value GREATER THAN cell F1 will highlight

- Select Concentration cells for any of the SEVEN analytes remaining in the Micronutrient/Vitamins list (see example, left)

  Apply CF so any value GREATER THAN cell G1 will highlight

Range Finding Experiment – Quick Check



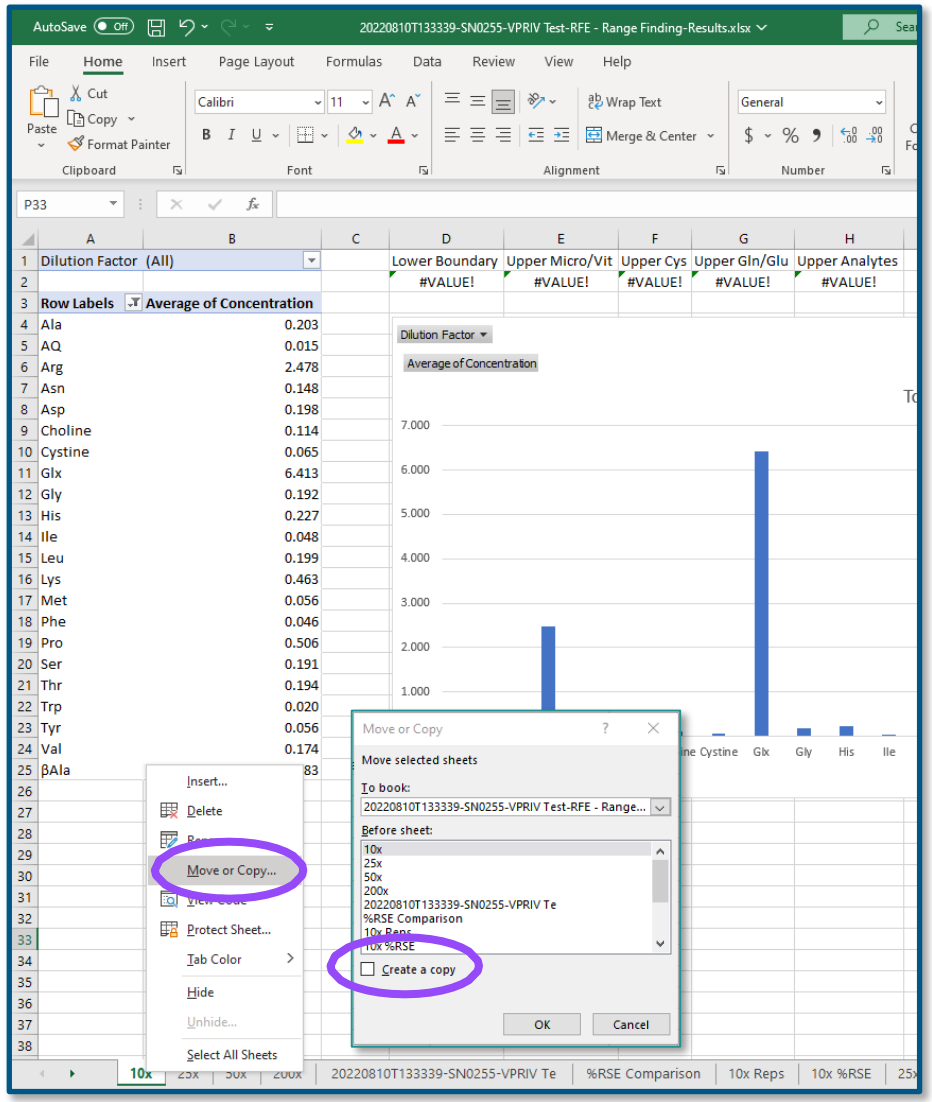
Check to ensure everything was set up properly so far:

1. Choose a DF from the dropdown menu in B1
2. Boundary values should change to real values
3. Some cells you set CF for will highlight if out of range (both above or below)

Example: 10x DF was selected along with red highlight/text for CF

All concentrations out of this calculated range (above and below bounds) are highlighted in red

Range Finding Experiment – Copy Sheet for all DFs



Note: It's important to establish bounds and CF before making copies so you don't have to set them for each sheet

Make a copy of this worksheet for each DF run in the RFE

Right Click sheet name > Move or Copy…

> Check 'Create a copy' > Select

placement of sheet > OK

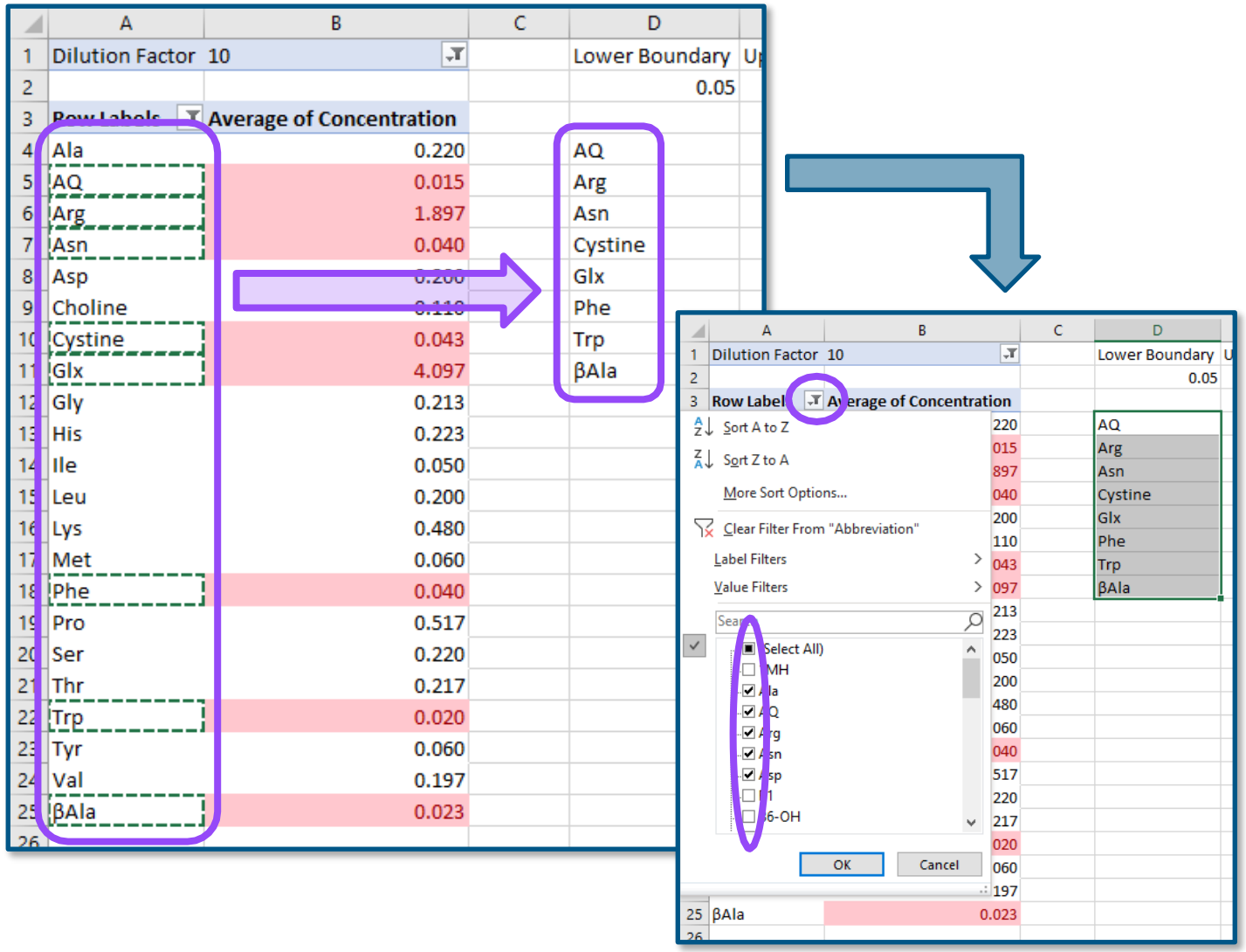
Label sheets for each DF and select appropriate DF from dropdown in B1

Example: 10x, 25x, 50x, and 200x DFs were run for entire RFE

Make 3 copies of worksheet

Label first '10x', second '25x', third '50x', and last '200x'

Range Finding Experiment – % Relative Standard Error



Start with one DF (e.g., '10x')

Make another copy of this worksheet and label '10x %RSE'

Right Click sheet name > Move or Copy…

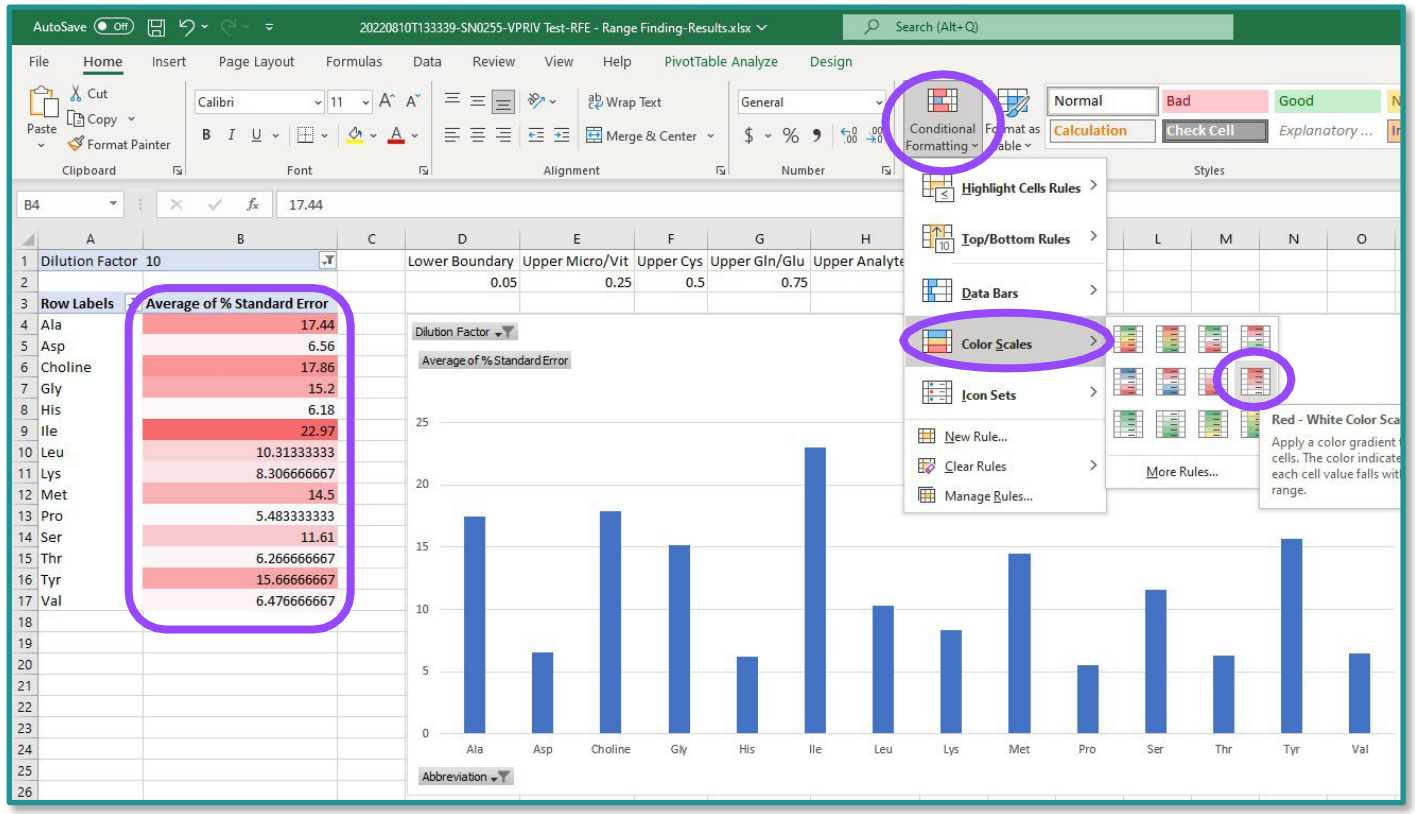
> Check 'Create a copy' > Select placement of sheet > OK

Remove color-highlighted analytes

- Highlight all cells of those analyte names using Ctrl and paste the list elsewhere in the sheet
- Use 'Row Labels' dropdown menu in table
- De-select all necessary analytes

This will leave a list of analytes that fall within the calibration range for that specific Dilution Factor

Range Finding Experiment – % Relative Standard Error (cont.)



Depending on the color scale selected, the column of %SE will display color highlights based on relative error within the specified range of analytes

Delete the copy/pasted list of analytes

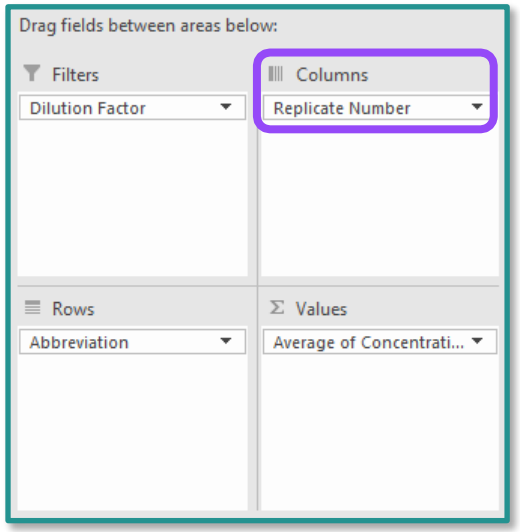
Swap ‘Concentration’ for ‘% Standard Error’ in the ‘Values’ area, and display Average instead of Count (see slide 11 for instructions)

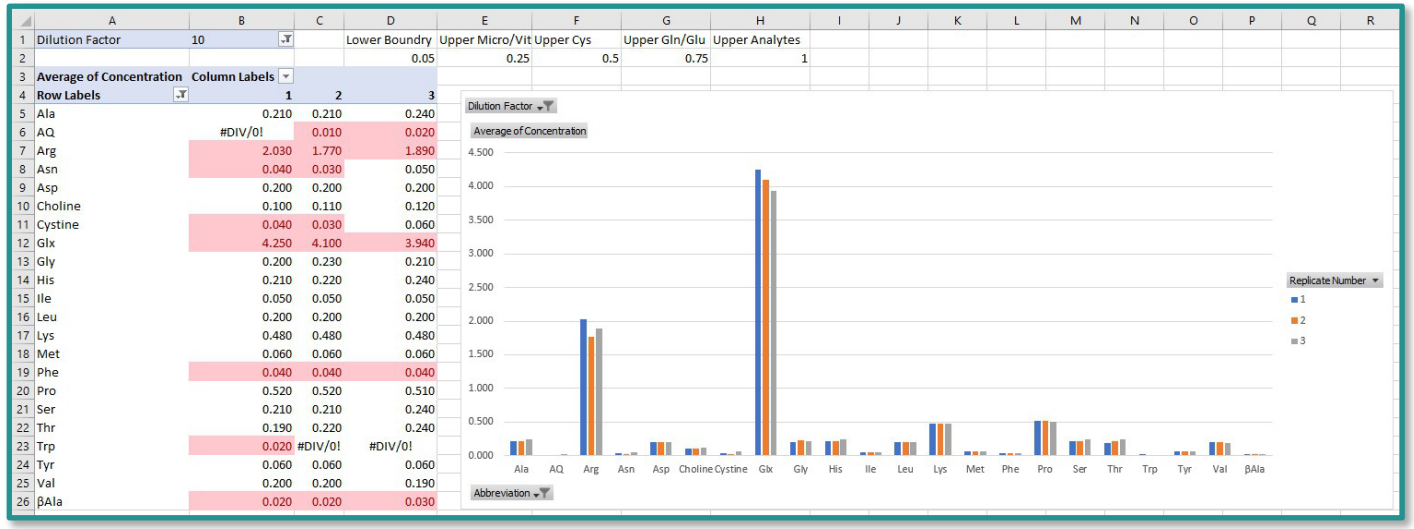
Set up Conditional Formatting for visual comparison of relative error for that DF

- Select all the %SE cells for every analyte
- Apply CF with Color Scale displaying higher %RSE in darker colors

  Conditional Formatting > Color Scales
- Which color you choose doesn’t matter, Red - White suggested

Range Finding Experiment – Replicate Analysis





Dilution Factor	10		Lower Boundry	Upper Micro/Vit	Upper Cys	Upper Gln/Glu	Upper Analytes
			0.05	0.25	0.5	0.75	1
Average of Concentration	Column Labels						
Row Labels	1	2	3				
Ala	0.210	0.210	0.240				
AQ	#DIV/0!	0.010	0.020				
Arg	2.030	1.770	1.890				
Asn	0.040	0.030	0.050				
Asp	0.200	0.200	0.200				
Choline	0.100	0.110	0.120				
Cystine	0.040	0.030	0.060				
Glx	4.250	4.100	3.940				
Gly	0.200	0.230	0.210				
His	0.210	0.220	0.240				
Ile	0.050	0.050	0.050				
Leu	0.200	0.200	0.200				
Lys	0.480	0.480	0.480				
Met	0.060	0.060	0.060				
Phe	0.040	0.040	0.040				
Pro	0.520	0.520	0.510				
Ser	0.210	0.210	0.240				
Thr	0.190	0.220	0.240				
Trp	0.020	#DIV/0!	#DIV/0!				
Tyr	0.060	0.060	0.060				
Val	0.200	0.200	0.190				
βAla	0.020	0.020	0.030				

Make a 3rd copy of the same DF worksheet (e.g., '10x') and label '10x Replicates'

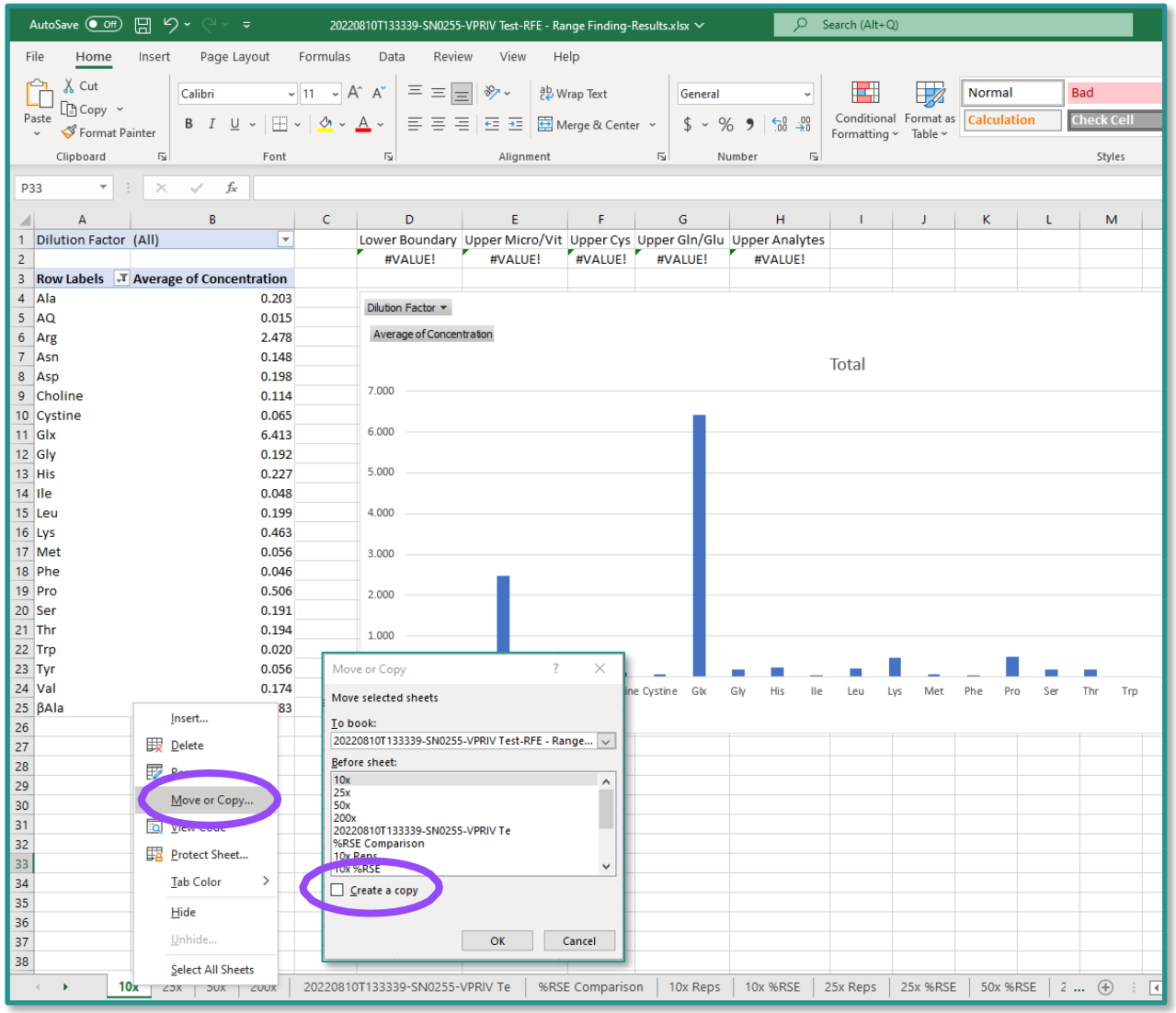
Right Click sheet name > Move or Copy… > Check 'Create a copy' > Select placement of sheet > OK

Add 'Replicate Number' to 'Columns' area

Use this view of the pivot table/chart to compare replicates for why certain %RSE are observed

- Are the concentrations for a particular analyte close to the lower/upper boundary?
- How much does the concentration vary from replicate to replicate?
- Is the avg concentration an accurate representation of the replicate data set?

Range Finding Experiment – %RSE and Replicate Analysis for all DFs



Repeat the steps from slides 17 – 19 for each of the DFs ran in the RFE

This will create both %RSE and Replicate Analysis worksheets for each DF

Right Click sheet name > Move or Copy…

> Check ‘Create a copy’ > Select

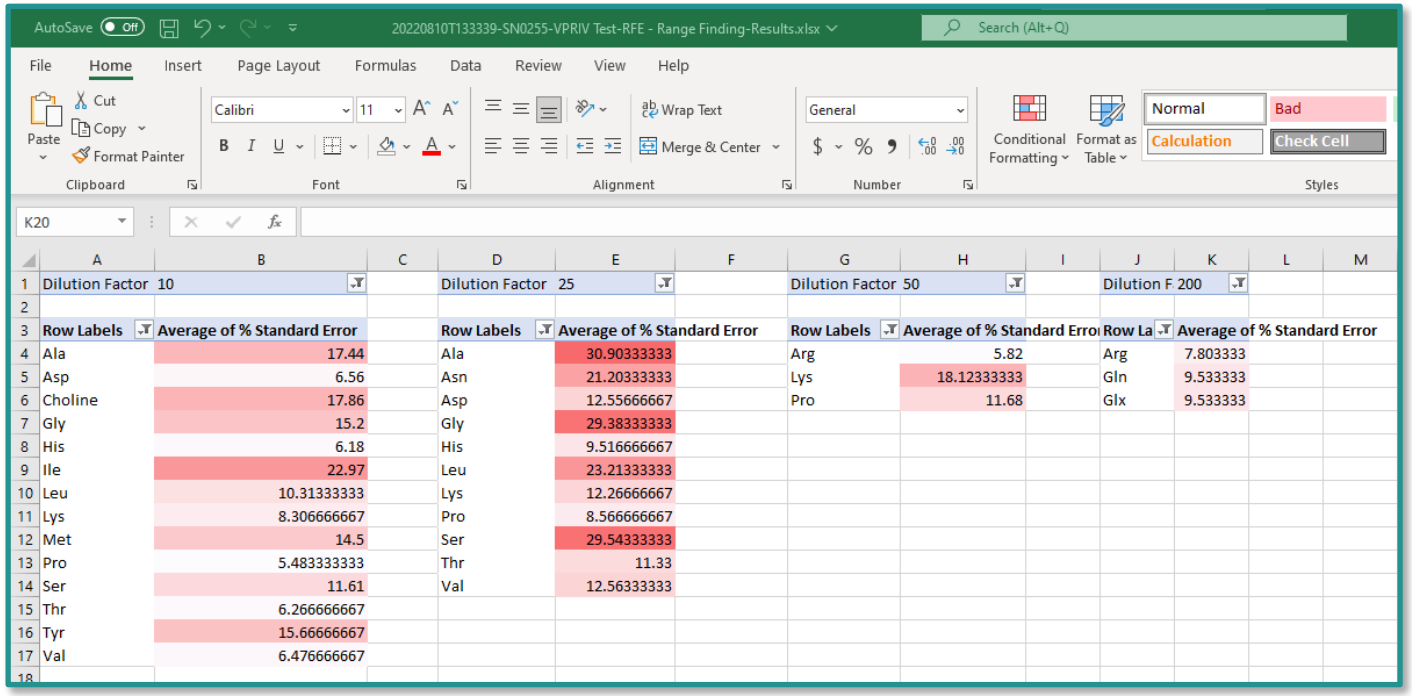
placement of sheet > OK

Example: 10x, 25x, 50x, and 200x DFs were run for entire RFE

Should currently have the following sheets: 10x, 10x %RSE, 10x Reps, 25x, 25x %RSE, 25x Reps, 50x, 50x %RSE, 50x

Reps, 200x, 200x %RSE, 200x Reps

Range Finding Experiment – % Relative Standard Error Comparison



Dilution Factor	10		Dilution Factor	25		Dilution Factor	50		Dilution F	200	
Row Labels	Average of % Standard Error		Row Labels	Average of % Standard Error		Row Labels	Average of % Standard Erro		Row La	Average of % Standard Error	
Ala	17.44		Ala	30.90333333		Arg	5.82		Arg	7.803333	
Asp	6.56		Asn	21.20333333		Lys	18.12333333		Gln	9.533333	
Choline	17.86		Asp	12.55666667		Pro	11.68		Glx	9.533333	
Gly	15.2		Gly	29.38333333							
His	6.18		His	9.516666667							
Ile	22.97		Leu	23.21333333							
Leu	10.31333333		Lys	12.26666667							
Lys	8.306666667		Pro	8.566666667							
Met	14.5		Ser	29.54333333							
Pro	5.483333333		Thr	11.33							
Ser	11.61		Val	12.56333333							
Thr	6.266666667										
Tyr	15.66666667										
Val	6.476666667										

Depending on the color scale selected, the columns of %SE will display color highlights based on relative error of all DFs in the worksheet

Use this to compare analytes observed in multiple DFs to determine which DF affords the lowest %RSE for that analyte

Make a 2nd copy of one of the %RSE worksheets (e.g., '10x %RSE') and label this one '%RSE Comparison'

Right Click sheet name > Move or Copy…

> Check 'Create a copy' > Select placement of sheet > OK

Delete the boundaries and then copy and paste the %RSE tables from each DF into this sheet so that they are side by side

Highlight the %SE columns in all the tables at once and reset the Conditional Formatting ➔ Color Scale (see slide 18) so that the color gradient is relative to all tables in the worksheet

Spent Media Analysis

While the RFE is useful for determining optimal dilutions at which to prepare your samples, typical use of the REBEL for sample analysis is for Spent Media Analysis (SMA)

Each lab, and even experiments within a single lab, may involve interest in different types of analyses of the resulting sample data, examples include:

- Time course study
- Before/after feedings analysis
- Bioreactor comparison
- Commercial or in-house media lot-to-lot comparison

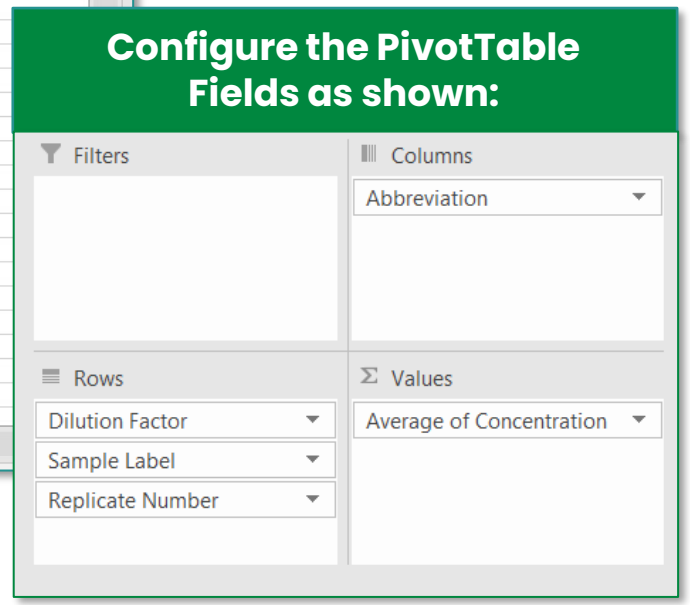
How you visualize the data to best interpret results is experiment-dependent, more examples of other ways to view data follow but are not the only way to conduct data processing

View A – Results for All Analytes from All Runs

Average of Concentration	Column Labels																										
Row Labels	Ala	Arg	Asn	B6-OH	B6-Oxo	Choline	Cit	Cystine	GABA	Gln	Glu	Glx	His	Hyp	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val	βAla
25	**7.26**	**4.88**	**8.55**	**0.01**	**0.06**	**0.14**		**0.50**	**0.04**			**5.70**	**1.63**	**0.04**	**5.60**	**0.98**	**4.63**	**10.33**	**3.18**	**1.86**	**1.09**	**1.19**	**0.36**	**1.23**	**10.71**	**0.23**
Reactor1	**0.94**	**5.68**	**9.06**	**0.01**		**0.19**		**1.08**	**0.04**			**6.82**	**2.05**	**0.04**	**3.86**	**1.49**	**5.76**	**10.76**	**2.30**	**1.19**		**1.95**		**1.75**	**13.85**	
1	0.98	5.75	9.20			0.19		1.06	0.04			6.69	2.02		2.91	1.73	5.93	11.18	2.87	2.80		1.91		1.69	14.72	
2	0.87	5.53	8.98			0.24		1.15	0.04			6.78	2.04	0.04	4.80	1.53	5.57	10.43	0.35	0.53		1.88		1.76	12.39	
3	0.96	5.75	8.99	0.01		0.15		1.02	0.03			7.00	2.10			1.19	5.77	10.66	3.66	0.25		2.06		1.80	14.45	
Reactor2	**8.03**	**5.24**	**9.01**		**0.06**	**0.05**		**0.69**	**0.03**			**6.09**	**1.86**		**5.37**	**1.26**	**5.17**	**10.66**	**0.85**	**0.80**	**2.84**	**1.47**	**0.29**	**1.48**	**11.40**	**0.05**
1	8.24	5.09	8.84		0.06			0.67	0.03			6.08	1.73		5.25	1.35	4.96	10.63	0.69	0.95	3.19	1.41	0.34	1.40	11.53	0.06
2	8.26	5.33	9.22			0.03		0.77	0.03			6.27	1.94		5.37	1.17	5.35	10.80	1.08	0.83	3.00	1.52	0.30	1.53	11.68	
3	7.60	5.31	8.97		0.06	0.08		0.64	0.02			5.90	1.92		5.51	1.26	5.20	10.54	0.79	0.62	2.33	1.49	0.23	1.52	10.98	0.04
Reactor3	**9.56**	**4.80**	**8.58**		**0.07**			**0.51**	**0.03**			**5.69**	**1.52**		**6.13**	**0.93**	**4.55**	**10.35**	**3.71**	**2.47**	**1.09**	**1.04**	**0.38**	**1.17**	**10.82**	**0.05**
1	10.18	5.13	8.89		0.07			0.57	0.02			6.29	1.60		6.12	1.03	4.77	10.75	4.06	3.02	1.33	1.05	0.42	1.15	12.18	0.05
2	8.94	4.80	8.62		0.08			0.55	0.04			5.57	1.51		6.69	0.93	4.58	10.26	4.76	2.79	1.07	1.03	0.38	1.16	10.86	0.05
3		4.48	8.24		0.06			0.42	0.03			5.20	1.46		5.59	0.82	4.30	10.04	2.32	1.61	0.88	1.04	0.33	1.18	9.42	0.06
Reactor4	**9.00**	**4.31**	**8.03**		**0.06**			**0.15**	**0.05**			**5.10**	**1.30**		**6.24**	**0.62**	**3.80**	**9.84**	**4.51**	**2.39**	**0.29**	**0.76**	**0.38**	**0.87**	**8.97**	**0.34**
1	10.72	4.38	8.07		0.06			0.18				5.48	1.29			0.70	3.85	9.87	4.47	2.60	0.41	0.76	0.42	0.87	9.51	0.38
2	8.78	4.41	8.25					0.17				5.12	1.34		6.77	0.61	3.91	10.02	4.80	2.47	0.25	0.80	0.37	0.87	9.23	0.35
3	7.49	4.15	7.76		0.06			0.11	0.05			4.70	1.26		5.71	0.54	3.65	9.63	4.26	2.11	0.21	0.73	0.34	0.88	8.17	0.31
Reactor5	**9.54**	**4.36**	**8.07**		**0.05**			**0.08**	**0.08**			**4.83**	**1.40**		**6.02**	**0.59**	**3.88**	**10.02**	**4.52**	**2.42**	**0.13**	**0.71**	**0.39**	**0.87**	**8.52**	**0.41**
1	9.92	4.47	8.31		0.07			0.09				5.26	1.36		5.53	0.67	3.98	10.27	4.23	2.61	0.11	0.69	0.39	0.83	8.43	0.41
2	9.14	4.30	7.76					0.09				4.50	1.38		6.05	0.52	3.69	9.64	4.71	2.22	0.11	0.67	0.38	0.84	8.33	0.34
3	9.57	4.30	8.16		0.03			0.07	0.08			4.74	1.46		6.49	0.57	3.97	10.14	4.61	2.43	0.16	0.76	0.38	0.93	8.80	0.48
100	**50.66**	**38.58**	**68.77**	**0.08**	**0.68**	**1.58**	**0.12**	**4.51**	**0.32**	**7.10**	**13.27**	**19.78**	**24.04**	**0.84**	**2.71**	**2.75**	**38.84**	**80.55**	**19.52**	**0.47**	**3.66**	**21.48**	**0.59**	**22.46**		**2.24**
Reactor1	**17.82**	**44.36**	**91.16**	**0.12**	**0.20**	**3.44**		**9.66**	**0.33**	**12.96**	**4.93**	**13.41**	**29.35**		**1.68**	**1.73**	**49.13**	**92.03**	**30.72**	**0.53**		**35.38**		**29.86**		
1	20.85	43.41	92.16	0.14		3.94		10.89	0.31	15.53	3.86	19.39	30.23		0.18	3.47	48.10	99.31	24.68	0.60		40.35		26.49		
2	16.66	47.43	97.57	0.13	0.13	3.26		9.68	0.35			4.46	29.66		3.37	1.32	53.07	95.70	26.06	0.51		33.93		29.38		
3	15.96	42.24	83.76	0.08	0.27	3.11		8.42	0.34	10.40	6.00	16.39	28.15		1.47	0.39	46.23	81.08	41.41	0.48		31.85		33.71		
Reactor2	**63.31**	**39.61**	**70.59**	**0.07**	**0.47**	**0.86**		**5.59**	**0.25**	**8.94**	**18.84**	**27.78**	**25.20**		**2.95**	**1.59**	**39.87**	**76.70**	**15.18**	**0.42**		**25.60**		**29.98**		**0.37**
1	74.36	40.98	72.29	0.09	0.58	1.35		6.42	0.27	6.21	6.15	12.36	26.46			2.84	39.47	75.74	15.70	0.39		28.16		32.27		0.34
2	59.00	39.74	74.64	0.07	0.26	0.51		5.34	0.20	9.89	8.45	18.34	24.87			0.66	41.02	78.57	16.34	0.38		23.65		27.80		0.42
3	56.57	38.11	64.83	0.06	0.57	0.73		5.01	0.28	10.73	41.91	52.64	24.27		2.95	1.28	39.14	75.79	13.49	0.49		24.98		29.88		0.35
Reactor3	**66.02**	**37.69**	**68.91**		**0.83**	**0.43**		**4.11**	**0.28**	**1.97**		**20.54**	**22.13**	**1.11**	**3.65**	**1.78**	**37.44**	**80.00**	**14.49**	**0.38**		**18.26**	**0.59**	**19.30**		**0.67**
1	70.60	37.11	72.87		0.85	0.28		4.52	0.29			17.55	22.14		5.23	3.22	37.13	78.95	15.40			17.98		20.24		0.89
2		35.10	64.03		0.91	0.64		4.00	0.29	1.97			21.08		2.18	0.34	34.92	73.68	16.86	0.36		17.25		19.82		0.48
3	61.43	40.86	69.84		0.75	0.39		3.80	0.26			23.54	23.19	1.11	3.56		40.28	87.37	11.21	0.40		19.55	0.59	17.86		0.62
Reactor4	**35.84**	**56.23**	**0.04**	**0.84**		**0.12**	**1.99**	**0.37**	**3.24**		**13.32**	**22.20**	**0.82**		**3.96**	**34.62**	**78.05**	**12.16**	**0.35**	**5.96**	**15.03**		**17.72**		**3.58**

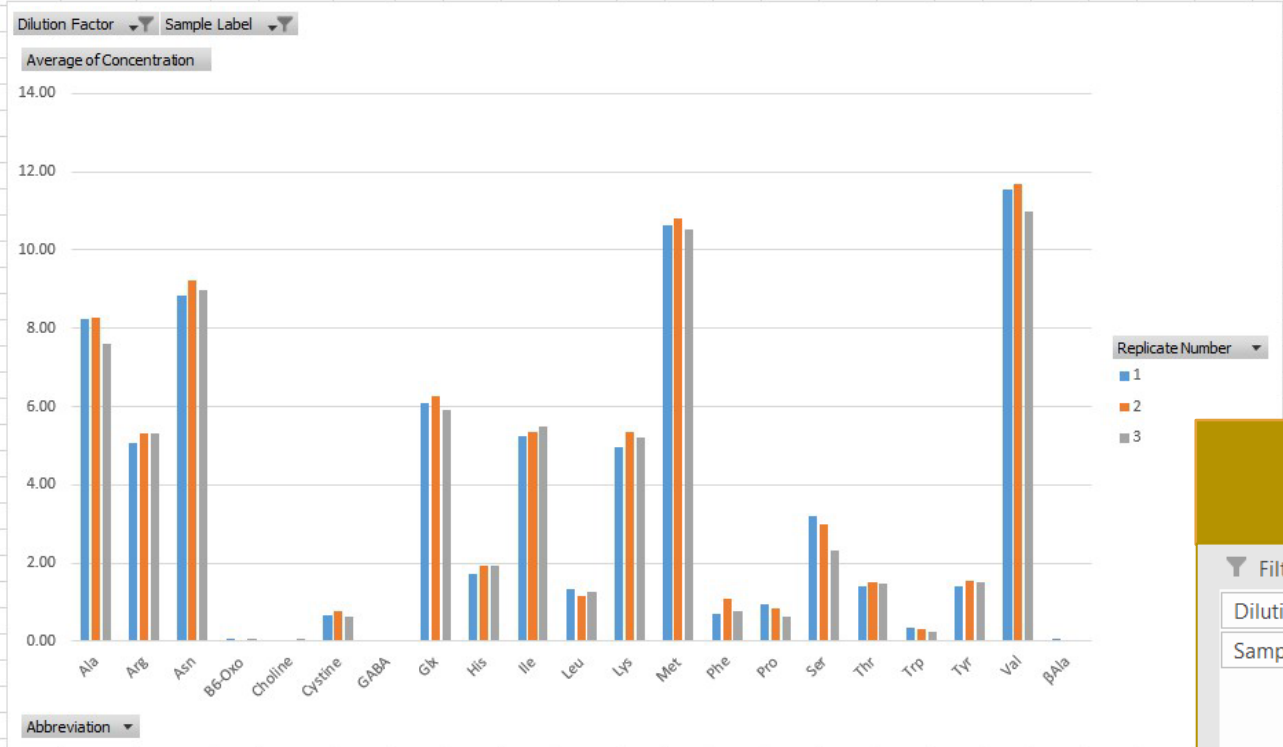
Sheet1 | pivot example

Configure the PivotTable Fields as shown:

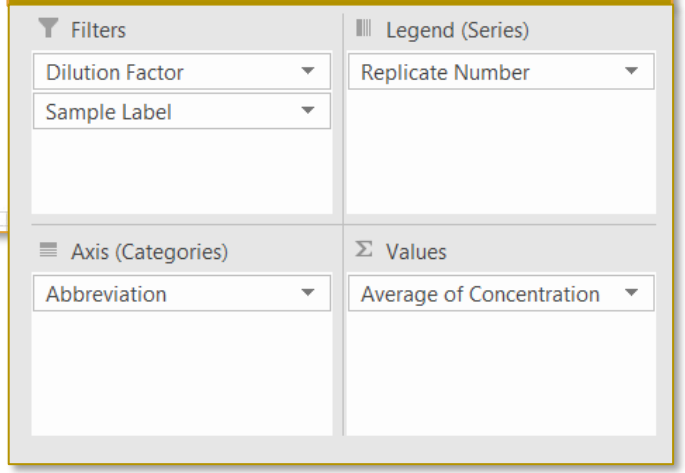


View B – All Analytes in a Single Sample

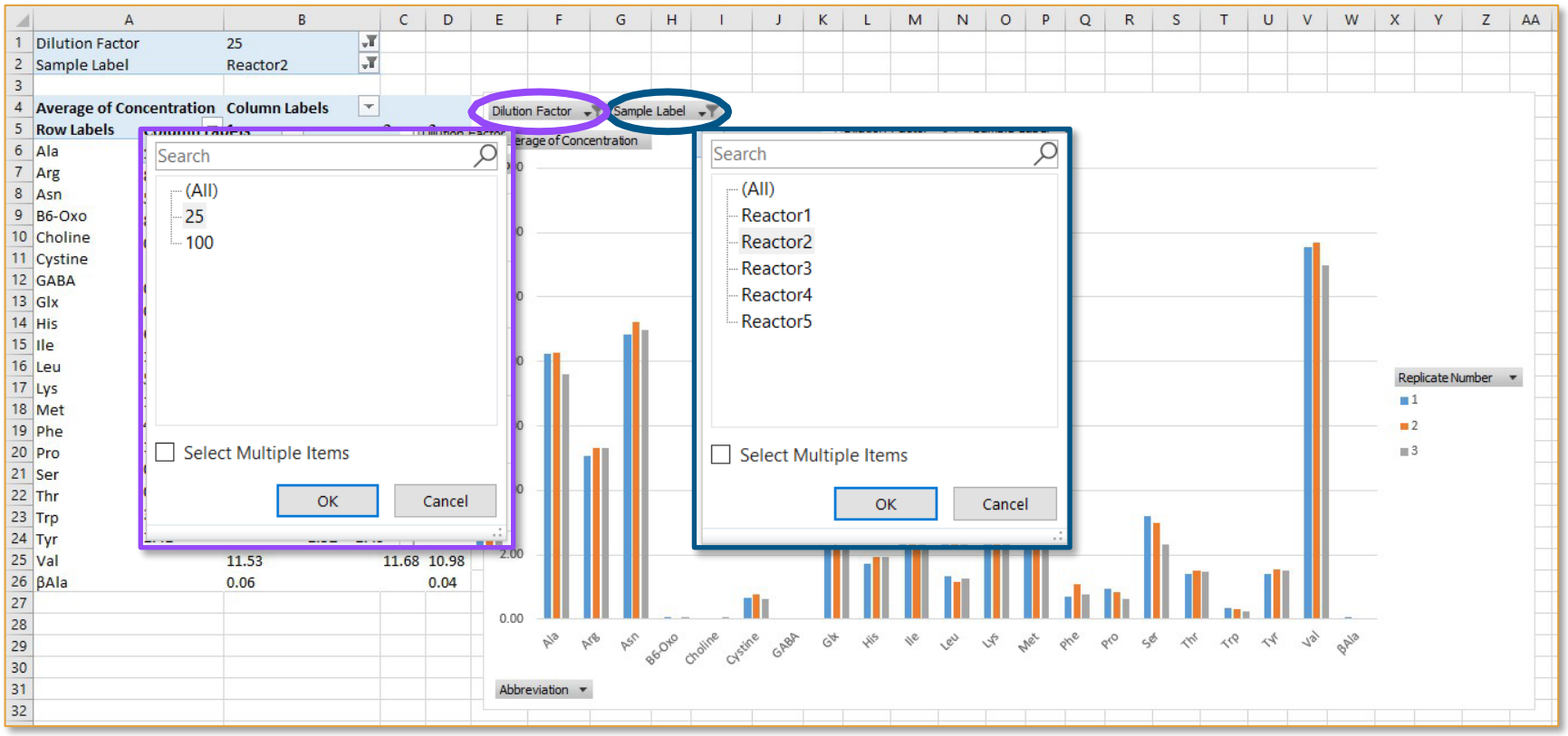
	A	B	C	D
1	Dilution Factor	25		
2	Sample Label	Reactor2		
3				
4	**Average of Concentration**	**Column Labels**		
5	**Row Labels**	**1**	**2**	**3**
6	Ala	8.24	8.26	7.60
7	Arg	5.09	5.33	5.31
8	Asn	8.84	9.22	8.97
9	B6-Oxo	0.06		0.06
10	Choline		0.03	0.08
11	Cystine	0.67	0.77	0.64
12	GABA	0.03	0.03	0.02
13	Glx	6.08	6.27	5.90
14	His	1.73	1.94	1.92
15	Ile	5.25	5.37	5.51
16	Leu	1.35	1.17	1.26
17	Lys	4.96	5.35	5.20
18	Met	10.63	10.80	10.54
19	Phe	0.69	1.08	0.79
20	Pro	0.95	0.83	0.62
21	Ser	3.19	3.00	2.33
22	Thr	1.41	1.52	1.49
23	Trp	0.34	0.30	0.23
24	Tyr	1.40	1.53	1.52
25	Val	11.53	11.68	10.98
26	βAla	0.06		0.04



Configure the PivotTable Fields as shown:



View B – All Analytes in a Single Sample (cont.)

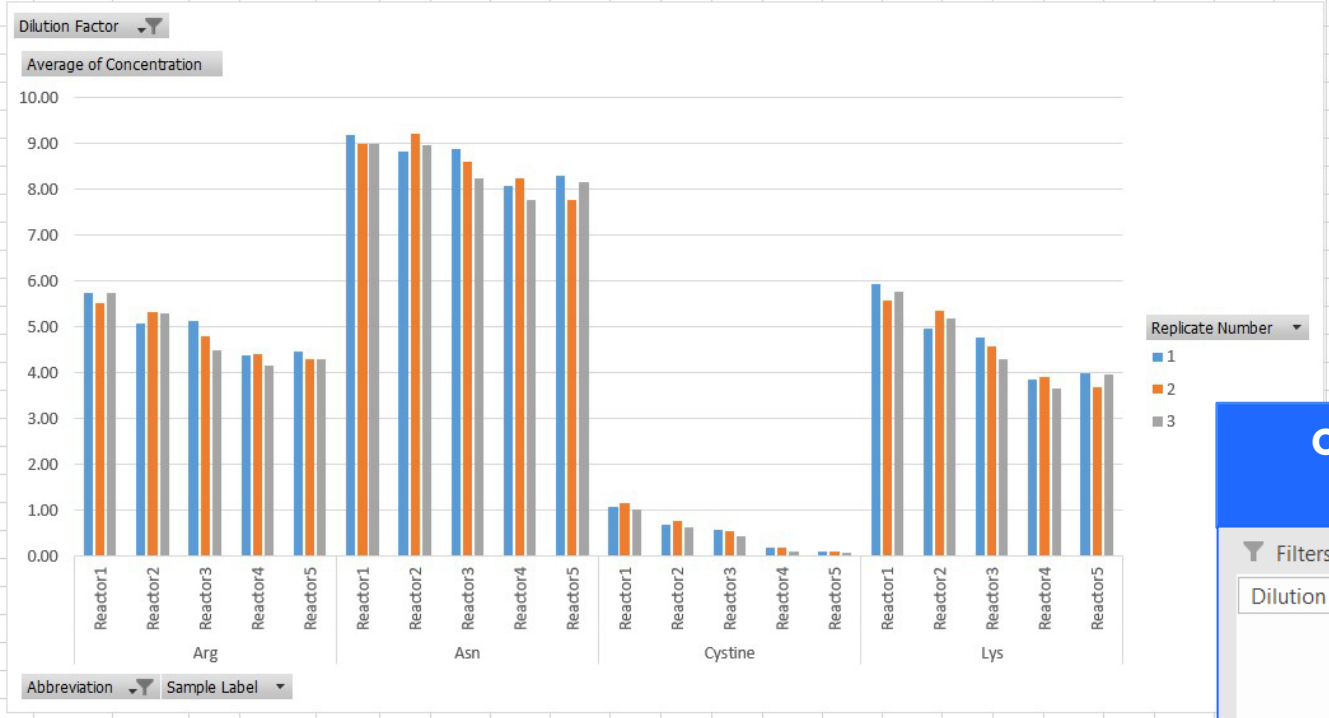


- Select Dilution Factor from the dropdown on the chart
- Select Sample Label from the dropdown on the chart

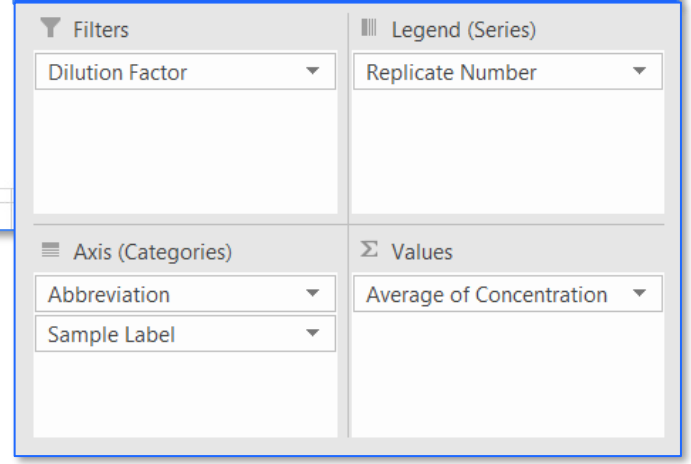
If you Select Multiple Items, the table and chart will display an average value of the data from all selected dilution factors/samples

View C – Display One or More Analytes Over All Samples

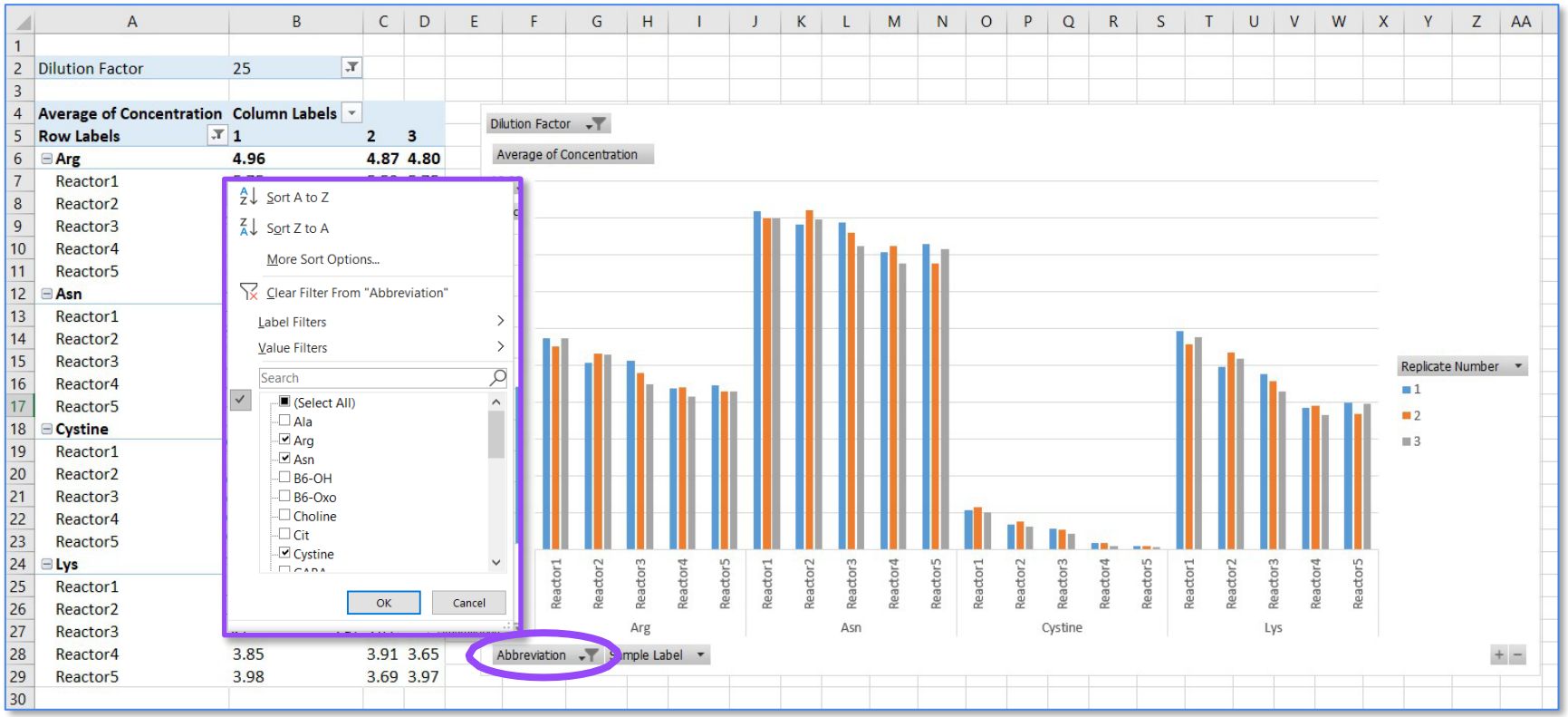
	A	B	C	D
1				
2	Dilution Factor	25		
3				
4	**Average of Concentration**	**Column Labels**		
5	**Row Labels**	**1**	**2**	**3**
6	**Arg**	**4.96**	**4.87**	**4.80**
7	Reactor1	5.75	5.53	5.75
8	Reactor2	5.09	5.33	5.31
9	Reactor3	5.13	4.80	4.48
10	Reactor4	4.38	4.41	4.15
11	Reactor5	4.47	4.30	4.30
12	**Asn**	**8.66**	**8.57**	**8.42**
13	Reactor1	9.20	8.98	8.99
14	Reactor2	8.84	9.22	8.97
15	Reactor3	8.89	8.62	8.24
16	Reactor4	8.07	8.25	7.76
17	Reactor5	8.31	7.76	8.16
18	**Cystine**	**0.51**	**0.55**	**0.45**
19	Reactor1	1.06	1.15	1.02
20	Reactor2	0.67	0.77	0.64
21	Reactor3	0.57	0.55	0.42
22	Reactor4	0.18	0.17	0.11
23	Reactor5	0.09	0.09	0.07
24	**Lys**	**4.70**	**4.62**	**4.58**
25	Reactor1	5.93	5.57	5.77
26	Reactor2	4.96	5.35	5.20
27	Reactor3	4.77	4.58	4.30
28	Reactor4	3.85	3.91	3.65
29	Reactor5	3.98	3.69	3.97
30				



Configure the PivotTable Fields as shown:



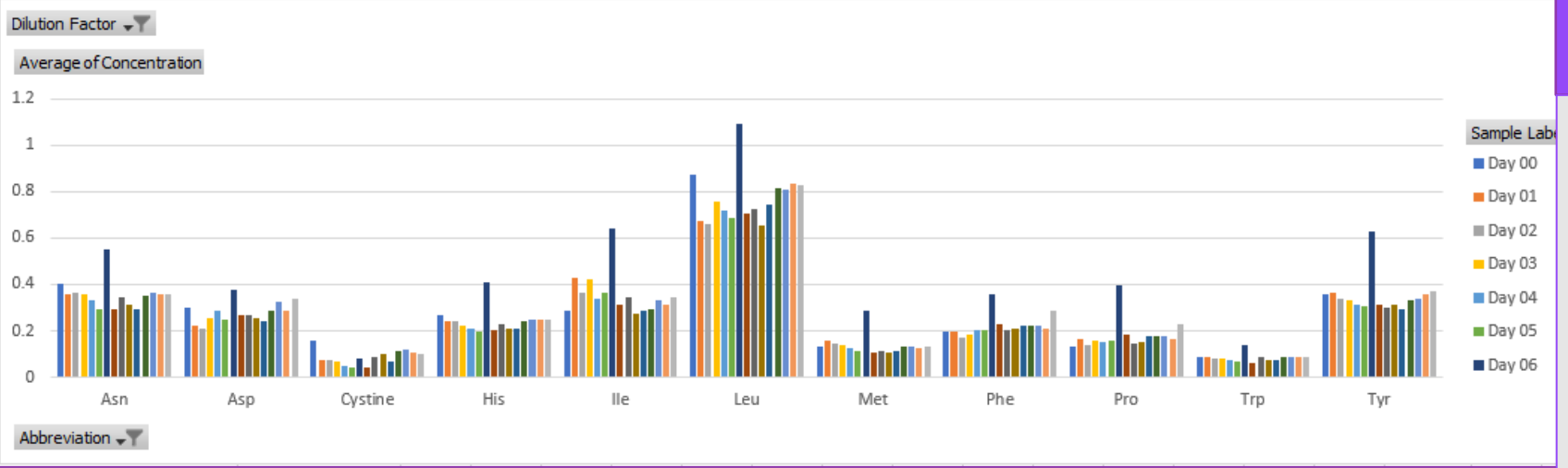
View C – Display One or More Analytes Over All Samples (cont.)



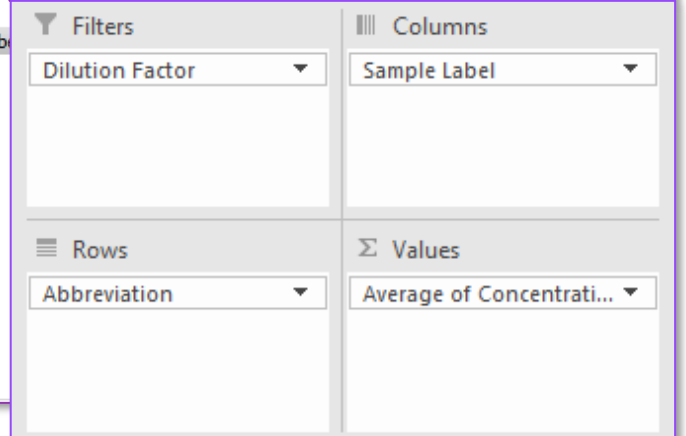
Select specific analytes from the Abbreviations dropdown at the bottom of the chart

View D – Time Course – All Analytes + Bar Chart

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	Dilution Factor	10		Lower Bound		Upper Bound													
2				0.05		1													
3	Average of Concentration	Column Labels																	
4	Row Labels	Day 00	Day 01	Day 02	Day 03	Day 04	Day 05	Day 06	Day 07	Day 08	Day 09	Day 10	Day 11	Day 12	Day 13	Day 14			
5	Asn	0.405	0.355	0.365	0.36	0.33	0.295	0.55	0.295	0.345	0.31	0.295	0.35	0.365	0.36	0.355			
6	Asp	0.3	0.22	0.21	0.255	0.29	0.25	0.375	0.265	0.27	0.255	0.245	0.285	0.325	0.29	0.34			
7	Cystine	0.16	0.075	0.075	0.07	0.05	0.045	0.08	0.045	0.09	0.1	0.07	0.115	0.12	0.11	0.1			
8	His	0.27	0.245	0.24	0.22	0.21	0.2	0.41	0.205	0.23	0.21	0.21	0.24	0.25	0.25	0.25			
9	Ile	0.285	0.43	0.365	0.42	0.34	0.365	0.64	0.315	0.345	0.275	0.285	0.295	0.335	0.31	0.345			
10	Leu	0.875	0.67	0.66	0.755	0.715	0.685	1.09	0.705	0.725	0.655	0.745	0.815	0.81	0.835	0.825			
11	Met	0.135	0.16	0.145	0.14	0.125	0.115	0.285	0.11	0.115	0.105	0.115	0.13	0.13	0.125	0.13			
12	Phe	0.2	0.2	0.17	0.185	0.205	0.205	0.36	0.23	0.205	0.21	0.22	0.22	0.225	0.21	0.285			
13	Pro	0.13	0.165	0.14	0.16	0.155	0.16	0.395	0.185	0.145	0.15	0.18	0.175	0.175	0.165	0.23			
14	Trp	0.09	0.09	0.08	0.08	0.075	0.07	0.14	0.065	0.085	0.075	0.075	0.09	0.09	0.09	0.085			
15	Tyr	0.355	0.365	0.34	0.335	0.31	0.305	0.625	0.31	0.3	0.31	0.295	0.335	0.34	0.355	0.37			

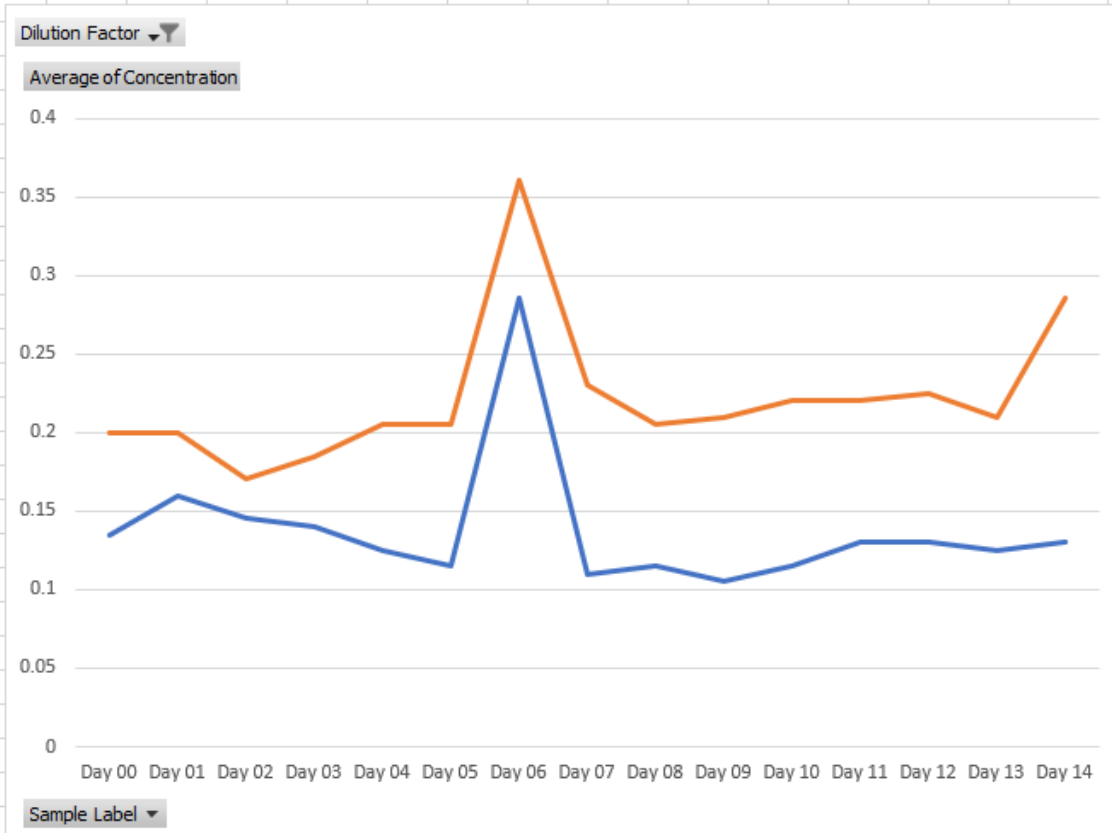


Configure the PivotTable Fields as shown:

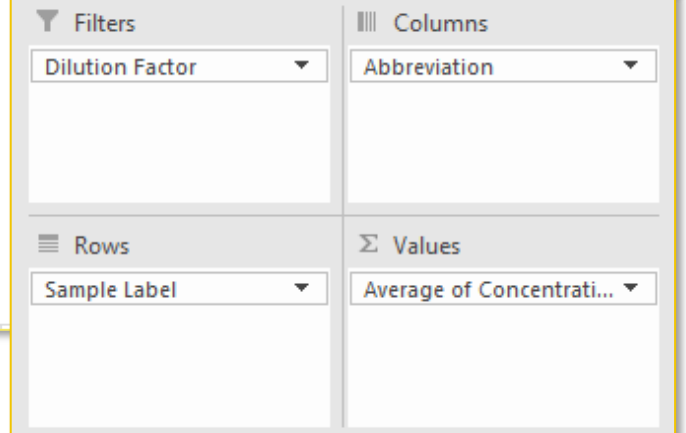


View E – Time Course – Select Analytes + Line Graph

	A	B	C	D	E	F	G
1	Dilution Factor	10		Lower Bound		Upper Bound	
2				0.05		1	
3	Average of Concentration	Column Labels					
4	Row Labels	Met	Phe				
5	Day 00	0.135	0.2				
6	Day 01	0.16	0.2				
7	Day 02	0.145	0.17				
8	Day 03	0.14	0.185				
9	Day 04	0.125	0.205				
10	Day 05	0.115	0.205				
11	Day 06	0.285	0.36				
12	Day 07	0.11	0.23				
13	Day 08	0.115	0.205				
14	Day 09	0.105	0.21				
15	Day 10	0.115	0.22				
16	Day 11	0.13	0.22				
17	Day 12	0.13	0.225				
18	Day 13	0.125	0.21				
19	Day 14	0.13	0.285				

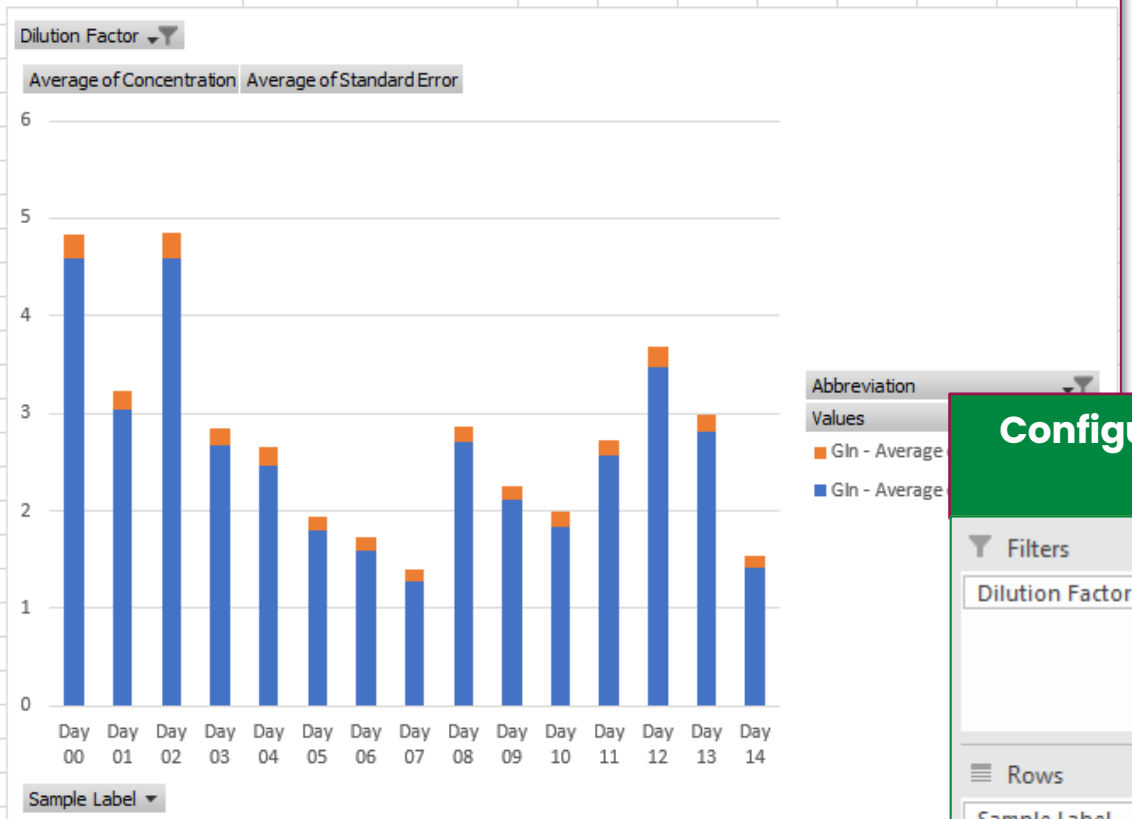


Configure the PivotTable Fields as shown:

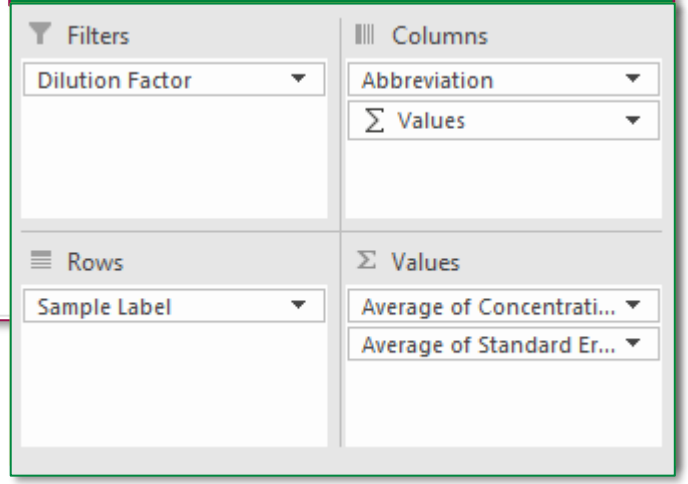


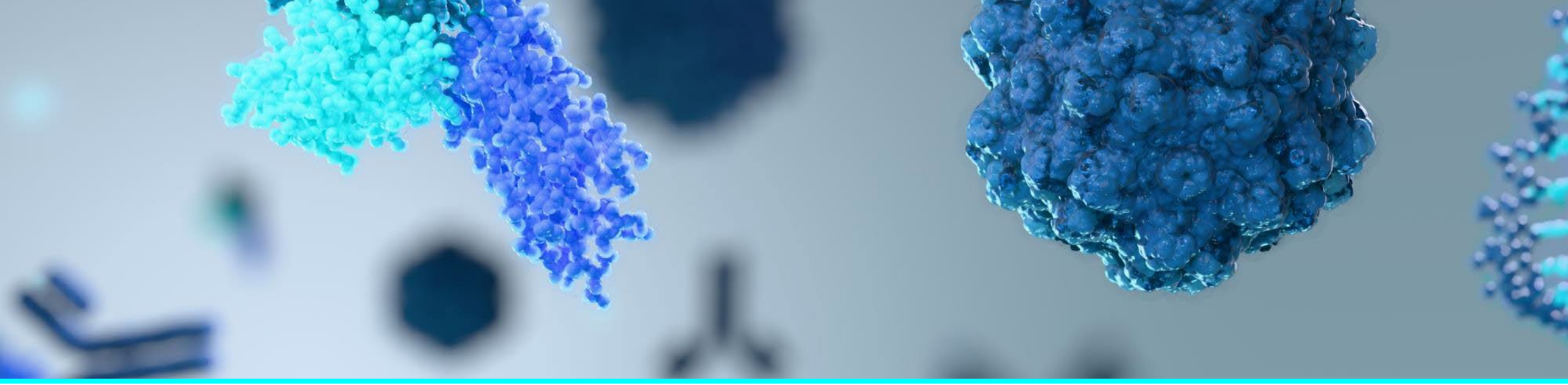
View F – Time Course – Single Analytes + Bar Chart with %SE

	A	B	C	D	E	F	G
1	Dilution Factor	100		Lower Bound		Upper Bound	
2				0.05		1	
3		Column Labels					
4		Gln					
5	Row Labels	Average of Concentration	Average of Standard Error				
6	Day 00	4.58	0.26				
7	Day 01	3.045	0.185				
8	Day 02	4.595	0.255				
9	Day 03	2.665	0.18				
10	Day 04	2.465	0.18				
11	Day 05	1.8	0.14				
12	Day 06	1.595	0.135				
13	Day 07	1.27	0.125				
14	Day 08	2.7	0.16				
15	Day 09	2.105	0.145				
16	Day 10	1.84	0.145				
17	Day 11	2.57	0.155				
18	Day 12	3.475	0.205				
19	Day 13	2.815	0.175				
20	Day 14	1.41	0.12				



Configure the PivotTable Fields as shown:





Thank you

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