

LabChip – PerkinElmer

GXII Touch HT & 24 Protein Characterization Systems

INTRODUCTION

The Lumetics LINK™ software platform scans network locations for new measurement data files, copies data directly to a centralized database, and provides a powerful user interface for rapid multi-measurement multi-technique data aggregation, visualization, analysis, and reporting. LINK employs a client/server-based architecture where the LINK server hardware is provided by the end user and resides on the end user's network. The LINK client is a portable web-based application that may be placed on any computer with network connectivity to the LINK server. For successful import, the LINK webserver requires read access to the folders where user data resides.

LabChip electrophoresis provides exact sizing and quantitation for RNA, DNA, and protein analysis. The process is based on traditional gel electrophoresis principles that have been transferred to a chip format.

DETAILS

LINK requires the WellTable.csv data file. The PeakTable.csv, SizeTable.csv, and RawTable.csv are all optional data files. Files must be exported from the LabChip software, using export Single Table (not AIA). Optionally, PDF import as series attachment. PDF import as series attachment and Peak Table CSV import as series attachment, which append CSV series attachments to Word/PDF reports.

The following raw curve data may be imported, in addition to all available instrument/analysis settings and parameters calculated by the instrument software:

- Fluorescence vs. Migration Time
- Fluorescence vs. Size

New Feature: Line Chart X-Axis LINKdb field Markers

- Ability to plot LINKdb field as markers with custom labels to the Line Chart series. This feature will allow the user to select a LINKdb field with numeric data. The value of the LINKdb field corresponds to the x-axis value and will be drawn at this x-axis position just above the data for the line series the LINKdb field marker pertains to.
- If Migration Time (s) - Center is present in the peak table, LINK will dynamically calculate each peak of individual measurements by taking peak name in the nomenclature of Peak Name – Migration Time – Center, where peak name is the value of peak location within the type column of the peak table. These peak locations may be overlaid on the electropherogram as markers.
- This feature is only valid for single series value – for any series with more than one measurement averaged together, markers will not be displayed.
- This is configurable through the Line Chart Options menu and navigate to “Markers”. Within this field numeric LINKdb fields can be selected.

Feature: Line Chart LINKdb Fill Regions

- Ability to define fill regions on the chart, specifically a new LINKdb field is dynamically created and calculated upon import called “% Peak Integration Migration Time Ranges”, under the following regulations:
 - The curve data includes a % Purity number
 - The curve data includes Migration Time – Start
 - The curve data includes Migration Time – End
- When using a LINKdb field containing region coordinate(s), the area will only be filled if the number of measurements represented by each series is 1. Otherwise, no shading can be applied.



Import Method options can be defined and calculated each measurement during import if it is first created/defined and then requested within an Import Method. More information and instructions can be found in the Users Manual located in the software help menu (section 4.21). LabChip allows for optional custom calculation of LMWS and HMWS %Purities based on a specific size range (in kDa). The calculation will create the following LINKdb fields:

- Low molecular weight species (LMWS) % Purity < the start value of the range
- High molecular weight species (HMWS) % Purity ≥ the end value of the range
- % Purity for the peak(s) found within this range (start ≤ x < end)

If no import is used, by default LINK will calculate the LMWS and HMWS % Purity values around the maximum peak found in the PeakTable CSV file for the measurement.

LMWS / HMWS % Purity Size Range

Optionally specify a size range (in kDa) around to calculate the following three parameters stored as LINKdb fields:

- Low molecular weight species (LMWS) % Purity < the start value of the range
- High molecular weight species (HMWS) % Purity ≥ the end value of the range
- % Purity for the peak(s) found within this range (start ≤ x < end)

Start Size: End Size:

If these fields are left blank, LINK will instead calculate the LMWS and HMWS % Purity values around the maximum peak found in the PeakTable CSV file for the measurement.

Note:

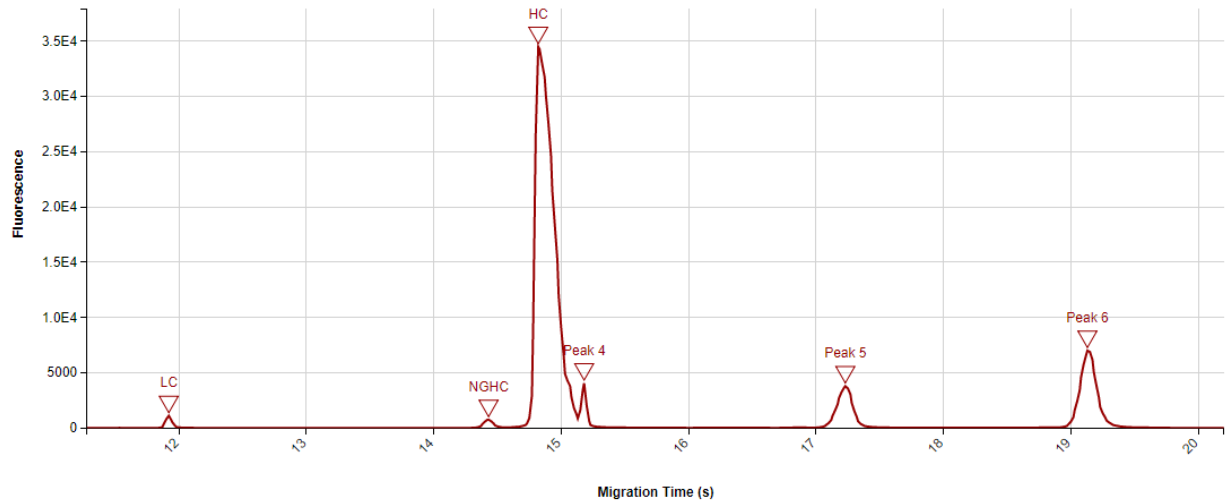
- LabChip provides measurements for particle size, migration time, and fluoresce. It also measures all aspects of each peak (ie. purity, baseline, concentration, area, FWHM, height, peak index, peak number, signal noise, etc). Slope and other raw data calculations can be made, as well as metadata importation.
- LINK currently does not import in all %Purity values from the _PeakTable.csv. I.e. %Purity values for some peak names (the "Type" column in the CSV file) like xXsys or MP will not be imported as they have more than one value for the same sample name. The %Purity values read or calculated upon import are:
 - **Sum - % Purity** (calculated by LINK as the sum of all % Purity values for a given sample name)
 - **mAb - % Purity** (read directly - only one peak name with this name per sample)
 - **Max Peak - % Purity** (read directly - only one peak name with this name per sample)
 - **LC - % Purity** (read directly - only one peak name with this name per sample)
 - **HC - % Purity** (read directly - only one peak name with this name per sample)
 - **LC + HC - % Purity** (calculated by LINK as the sum of the LC and HC peaks)
 - **LMWS - % Purity** (calculated by LINK as the sum of the purities "to the left" of the main peak (i.e. smaller retention times))
 - **HMWS - % Purity** (calculated by LINK as the sum of the purities "to the right" of the main peak (i.e. larger retention times))
- LINK imports all Migration Time values if there is a valid peak name (or "Type") for the migration time. If there is one value found, it is stored as that value. If there is more than one value (e.g. multiple "MP" peaks for a given sample), LINK will store the results as a string in a pseudo-array format: "["18.61667", "22.773344", "23.9569", ...]". This format of the "pseudo-array" is used as the format for the markers, which provides the ability to plot more than one marker value for a single LINKdb field.

EXAMPLES

Included below are dashboards from LabChip measurement files:

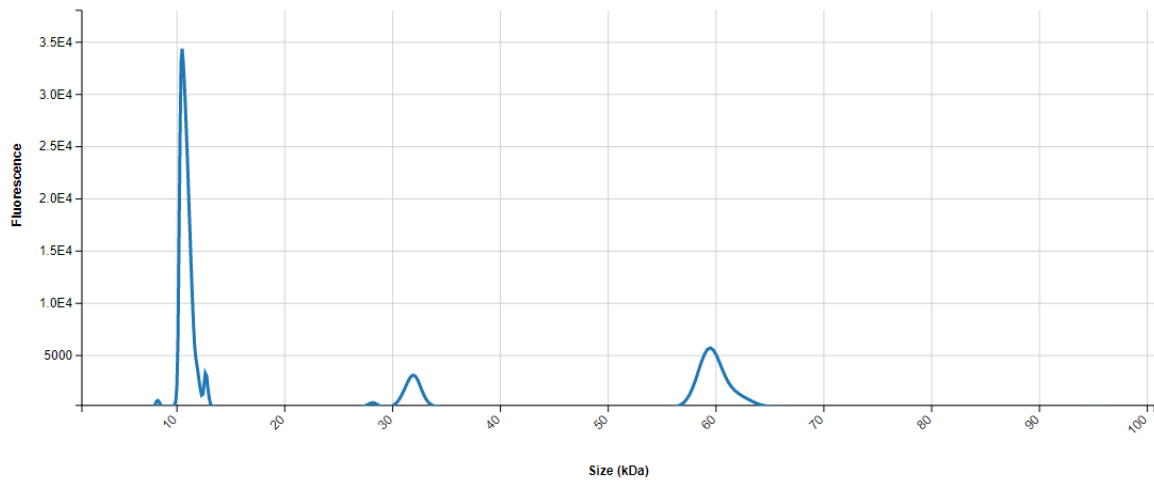
1. Line Chart plotting raw data curves for Fluorescence vs. Migration Time with LINKdb Field Markers

Fluorescence vs. Migration Time

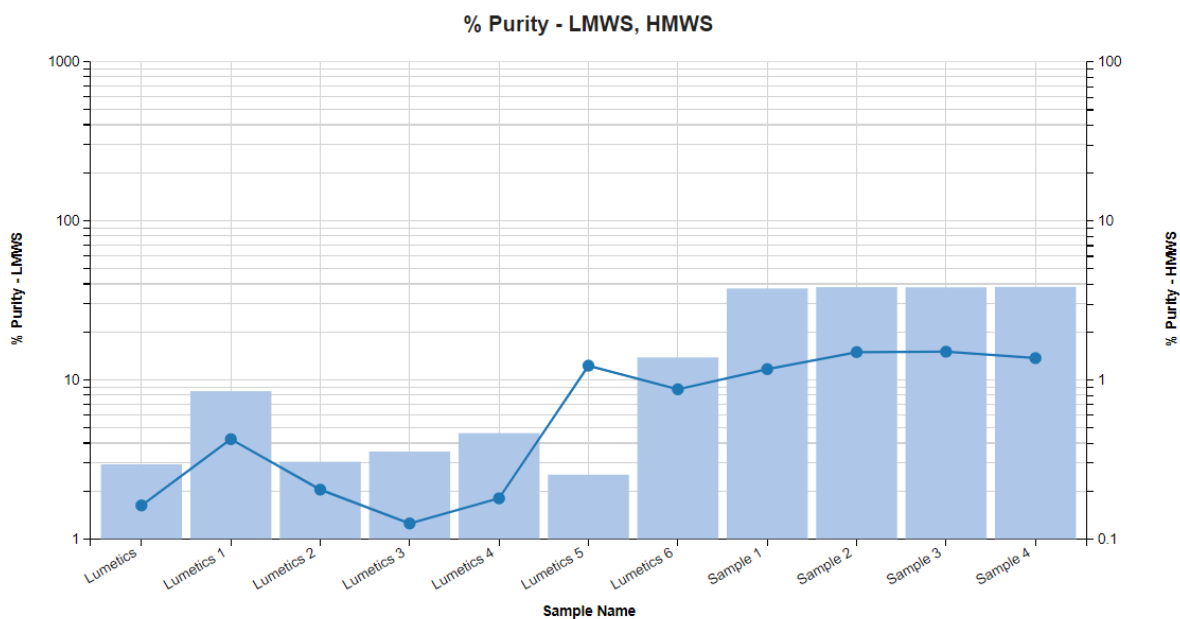


2. Line Chart plotting raw data curves for Fluorescence vs. Size

Fluorescence vs. Size



3. Column Chart plotting raw data curves for %Purity LMWS & HMWS vs. Sample Name



3. Tabular Summary examples:

Measurement Summary Table – Instrument Settings

LINK Record ID #	Sample Name	Barcode	Analysis Date	Chip ID	Well Number - AVG	Well Label	Date_Time
1	Sample A	1001	2017-03-15 11:51:10	P464P-0563N-01	1	C03	2017\03\15 11:51:10
2	Sample B	1001	2017-03-15 11:51:10	P464P-0563N-01	2	C04	2017\03\15 11:51:10
3	Sample C	1001	2017-03-15 11:51:10	P464P-0563N-01	3	C05	2017\03\15 11:51:10
4	Sample D	1001	2017-03-15 11:51:10	P464P-0563N-01	4	C06	2017\03\15 11:51:10
5	Sample E	1001	2017-03-15 11:51:10	P464P-0563N-01	5	C07	2017\03\15 11:51:10
6	Sample F	1001	2017-03-15 11:51:10	P464P-0563N-01	6	C08	2017\03\15 11:51:10
7	Sample G	1001	2017-03-15 11:51:10	P464P-0563N-01	7	C09	2017\03\15 11:51:10
8	Sample H	1001	2017-03-15 11:51:10	P464P-0563N-01	8	C10	2017\03\15 11:51:10
9	Sample I	1001	2017-03-15 11:51:10	P464P-0563N-01	9	C11	2017\03\15 11:51:10

Measurement Summary Table – Measurement Results

LINK Record ID #	Sample Name	HC - % Purity - AVG	HMWS - % Purity - AVG	LC - % Purity - AVG	LC + HC - % Purity - AVG	LMWS - % Purity - AVG	Max Peak - % Purity - AVG	Fluorescence (Size (kDa) >=1) - AVG	Fluorescence (Migration Time (s) >=1) - AVG
1	Sample A	61.37	1.17	36.18	97.55	37.46	61.37	464401.77	467751.80
2	Sample B	60.33	1.50	36.65	96.98	38.18	60.33	491583.95	494571.65
3	Sample C	60.44	1.51	36.45	96.89	38.06	60.44	482851.85	486532.29
4	Sample D	60.32	1.37	36.96	97.28	38.31	60.32	467751.31	471435.35
5	Sample E	60.67	1.33	36.76	97.43	38.00	60.67	482087.88	485100.90
6	Sample F	60.43	1.82	36.24	96.67	37.75	60.43	470440.97	473855.45
7	Sample G	60.47	1.90	36.63	97.10	37.63	60.47	473632.79	477033.41
8	Sample H	60.78	1.67	36.05	96.83	37.54	60.78	485023.62	488356.66
9	Sample I	61.47	1.35	35.98	97.45	37.18	61.47	477926.26	481360.49

DASHBOARD DOWNLOADS

Included below is a link to downloadable dashboards for LabChip measurement files:

<http://lumetics.com/dashboards/LabChip/LabChip.zip>

CONTACT LUMETICS

For direct assistance, please contact Lumetics LINK™ Support:

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