# Agilent Fragment Analyzer Automated CE System

# **Standard Operating Protocol**

## I. Overview of Fragment Analyzer Automated CE System

• Maximum sample capacity: 191 samples and 1 ladder

	DNF474 kit	DNF930 kit
Detection range	1 – 6,000 bp	75 – 20,000 bp
Sizing range	50 – 5,000 pg/µl	0.5 ng/µL – 50 ng/µL
Time for run	~1 hour 20 mins for 96 samples, run 12 samples in parallel	~1 hour for 96 samples, run 12 samples in parallel

# **II.** Reagents Preparation

Materials needed:

• High Sensitivity NGS Fragment Analysis Kit (DNF474) / dsDNA Reagent Kit (DNF930)

(Appendix: "Preparation guide for reagents")

- Semi-skirted 96-well PCR plates
  - BioRad #HSS-9601 SSIBio # 3450-00 4titude Framestar #4ti-0900, -0950, -0770/C Eppendorf #951020303 Greiner Bio-One #652280 Neptune #3742.X MidSci #AVRT1 Scientific Specialty #3450-00 VWR #83007-374

Procedures:

1. Warm up all reagent to room temperature before use.

Storage Temperature		DNF474 kit	
-20°C	<b>DNA Ladders</b>	<b>Diluent Markers</b>	Intercalating Dye
4 °C	Blank Solutions	0.25x TE Rinse Buffers	Separation Gels

Storage Temperature		DNF930 kit	
-20°C	<b>DNA Ladders</b>	<b>Internal Markers</b>	Intercalating Dye
4 °C	<b>Dilution Buffer 1X TE</b>		Separation Gels

**1x Inlet Buffer Solution** (4°C) and **1x Capillary Conditioning** (4°C). (Appendix: "Preparation guide for 1x IB and 1x CC loading")

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 Prepare the Sample plate and Rinse (DNF474)/ Marker (DNF930) plate according to manufacturer's quick guides (Appendix).
 \*DNA Ladders should be prepared for at least one well per run.
 \*Fill all empty wells in the rows of run with Blank Solutions (DNF474)/ 1X TE (DNF930).
 \*Check the plate with CPOS staff before loading samples.

### **III.** Instrument Preparation

- A. Materials needed:
- Gel/Dye mix
- Sample plate(s)
- Marker (DNF930) / Rinse (DNF 474) plate
- 1x Inlet Buffer Solution
- 1x Capillary Conditioning Solution

### **B. Reagent Preparation:**

#### 1. Gel/Dye mix

• Prepare the **Gel/Dye mix** by adding Intercalating Dye to Separation Gel (ratio of 1:10000) in a 50 mL tube according to the table below. Mark the date on the tube. Mix by inverting the tube. *Do not vortex*.

Number of run (row)	Volume of Separation Gel	Volume of Intercalating Dye
1	10 ml	1.0 µl
2	14 ml	1.4 µl
3	18 ml	1.8 µl
4	22 ml	2.2 µl
5	26 ml	2.6 µl
6	30 ml	3.0 µl
7	34 ml	3.4 µl
8	38 ml	3.8 µl

NOTE: 1) This volume includes 6 ml for priming. The remaining gel after run can used for up to 2 weeks after preparation

- Remove the tube of MilliQ in Gel fluid line (1 or 2), clean the fluid line with Kimwipe only. Prime (Main Menu>Utilities>Prime> Gel 1 or 2) twice with air to remove remaining fluid in the line. Inserting Gel fluid line into the Gel/Dye mix. Turn the tube instead of cap to close the tube. Ensure the fluid line is positioned at the bottom of the conical tube and stand properly in the slot.
- Update the solution levels in the Fragment Analyzer instrument control software. Main Menu> Utilities> Solution Levels.

### 2. 1x Capillary Conditioning Solution

• Prepare the **1x Capillary Conditioning Solution** by diluting 5x Capillary Conditioning Solution with MilliQ in a 50 mL tube according to volume in the table below. Mark the date on the tube. Mix by inverting the tube.

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Number of run	Volume of 1x Capillary	Volume of 5x Capillary	MilliQ needed
(row)	<b>Conditioning Solution</b>	<b>Conditioning Solution</b>	
		needed	
1	14 ml	2.8 ml	11.2 ml
2	18 ml	3.6 ml	14.4 ml
3	22 ml	4.4 ml	17.6 ml
4	26 ml	5.2 ml	20.8 ml
5	30 ml	6.0 ml	24.0 ml
6	34 ml	6.8 ml	27.2 ml
7	38 ml	7.6 ml	30.4 ml
8	42 ml	8.4 ml	33.6 ml

NOTE: 1) This volume includes 4 ml for an additional conditioning step that MUST BE performed after every use of the instrument. 2) The remaining volume after run can be used for up to 2 weeks after preparation and 1 month if stored at  $+4^{\circ}C$ 

- Insert Conditioning Solution fluid line into the Conditioning Solution. Turn the tube instead of cap to close the tube. Ensure the fluid line is positioned at the bottom of the conical tube and stand properly in the slot.
- Update the solution levels in the Fragment Analyzer instrument control software. Main Menu> Utilities> Solution Levels.

### 3. 1x Inlet Buffer

- Mix and use Inlet Buffer at Room Temperature only.
- 2.6 ml of 5x Inlet Buffer and 10.4 ml of MilliQ water to prepare 13 ml of 1x Inlet Buffer.
- Mix by gently inverting the tube.
- Discard any liquid in row A in the 96-well Deep Well Plate in the Buffer drawer (B). Reuse the plate and added 1ml of 1x Inlet Buffer prior to your run.

### 4. 0.25X Rinse Buffer (DNF474)

- Discard any liquid in the 96 well PCR Plate in the Buffer drawer (M). Reuse the plate and add 100  $\mu$ l of **0.25X Rinse Buffer** to the indicated current using row.
- Spin the plate shortly to remove air bubbles.

### 5. Sample Plate (DNF474)

- Use 96-well PCR plates in approved list in P.2 only for loading sample. Plates not in the list will **DAMAGE THE CAPILLARIES**. Check your plate with CPOS staff before loading samples.
- Add 22  $\mu$ l of the **Diluent Marker** to each well to be analyzed.
- Add 2 µl of Ladder in one of the well that containing 22 µl Diluent Marker.
- Add 2 µl of samples in other wells that containing 22 µl **Diluent Marker**. Mix the solution by swirling with the pipette tip while pipetting up/down.
- You may change the ratio of the sample / ladder to **Diluent Marker** if necessary. Update the dilution factor in the software for proper analysis.
- Fill any unused wells within the row with 24  $\mu$ l/well of Blank Solution.
- Remove the bubbles by spinning the plate shortly.
- Load the Sample plate in sample drawer 1 or 2 and perform the separation immediately. Otherwise store the plate at +4 °C until use.

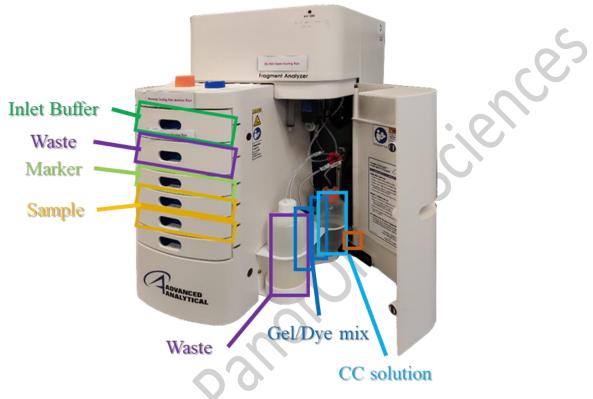
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### C. Procedure:

- 1. Sign on the Log Book before start.
- 2. Turn on the **Fragment Analyzer's Power Switch** and computer.
- 3. Login to computer user account with the password in the lower left corner.
- 4. Open Fragment Analyzer Instrument control Software. User ID: User

### Password: 1234

Acknowledge the maintenance reminder. Maintenance is performed by CPOS Staff.



- 5. Check the Waste Bottle and the Waste plate at the Waste Tray (W) and empty if needed.
- 6. Remove any solution from Buffer Tray (B).
- 7. Load 1 mL 1x Inlet Buffer Solution per well.
- 8. Load 1x Capillary Conditioning Solution.
- 9. Take out the Gel fluid line 1 or 2 from the storage MilliQ tube
- 10. **Prime** with the tube with air. ("Utilities" -> "Prime" -> check "Gel 1" or "Gel 2" -> "OK").

Fluid Selected	Cycles	1		
Conditioning	Fill Rate	300	*	uL/s
Gel2	Empty Rate	300	(Å)	uL/s

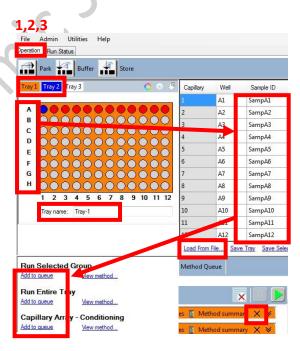
- 11. Clean the outside surface of the tube with Kimwipe.
- 12. Put the Gel/Dye mix solution to the Gel line.
- 13. Update the solution levels to the software ("Utilities" -> "Solution levels").

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	Check Solution Volume	es		×
	Check the fluid volumes be waste is empty and that the full. Record the solution volume	e gel and conditionir		
		Volume (mL)	Solution name	
	Gel 1	30.0 🚔	474 gel	
	Gel 2	30.0 🚖	ddH2O	
	Conditioning Solution	50.0 🜩		
	Waste	0.0 🜩		
		Ok	Cancel	l és

- 14. Load Marker (DNF930) / Rinse (DNF 474) plate into Marker tray (M).
- 15. Load Sample plate(s) into put into Sample Tray I (and II). \*REMOVE any PLATE SEAL before loading the plate into tray. !!!The seal would DAMAGE THE CAPILLARIES!!! \*Load all plate into tray with A1 IN INNER LEFT CORNER.

# IV. Software Settings

- 1. In Operation tab, the Tray (1 or 2) that loaded with sample plates.
- Select the sample row that loaded with sample. Sample name can be input in "Sample ID" column or import from .csv or .txt file. Enter Tray name with prefix of "Supervisor Name\_User Name" and followed by the experiment name
- For analyzing single row of samples, click "Add to queue" under "Run Selected Group".
   For analyzing more than 1 row of samples, click "Add to queue" under "Run Entire Tray".
   Remove extra queue with "X" next to "Method summary".
- 4. In Separation Setup window, Select or input:
- Method: Name of Analysis Kit Used DNF-474-33 – HS NGS Fragment 1-6000bp methods/ DNF-930-33 – DNA 75-20000bp methods
- In "Edit", select the row of marker or rinse buffer loaded
- Gel: Position of the gel loaded (Gel 1 or Gel 2)
- Tray Name: Same as name in Step 2.
- Folder Prefix: Enter in form of "Supervisor Name\_User Name"
- Any Notes: Enter if necessary
- OK: to add the method to queue.
- 5. Select other row or plates in the Tray window and repeat steps 3-4



Method:	DNF-474-33 - HS NGS Fragment 1-6000bp.mthds
Gel:	
Tray name:	Tray-1
Folder Prefix:	
	Copy results
Copy path:	
Notes:	

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- Click "Add to queue" under "Capillary Array Conditioning" and select "Default conditioning" to remove gel in the capillaries after your experiment.
- 7. Verify all method in queue and trays (Inlet buffer, Rinse buffer/Marker, Sample tray I or II, Gel I or II, Conditioning Solution) are loaded with
- appropriate container/plate with sufficient reagents.
- 8. Click start to initiate the run.
- Separation status can be observed in "Run Status" tap. Queue of Separation can be modified or added in the Operation tap. Separation method should be always followed by "Default conditioning".

	onditioning Method		
Method:	Default Conditioning.mthdc		✓ <u>Vie</u>
	ſ	OK	Cancel

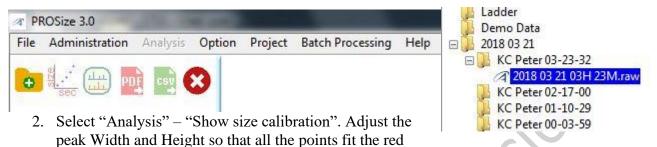
**DO NOT Open Top Compartment or Drawer B and W.** The high voltage would be stopped when any of these drawers is opened.

SEPARATION, Method: 'DNF-474-33 - HS NGS Fragment 1-6000bp.mthds', Tray: Samp. tray 1, 8, Gel: 1 🖉 View/Edit Notes 📱 Method summary 🗙 S	7, 8		
SEPARATION, Method: 'DNF-474-33 - HS NGS Fragment 1-6000bp.mthds', Tray: Samp. tray 1, B, Gel: 1 💋 View/Edit Notes 🚊 Method summary 🗙 S	Method Queue		× 🗉
	SEPARATION, Method: 'DNF-474-33 - HS NGS Fragment 1-6000	bp.mthds', Tray: Samp. tray 1, A, Gel: 1	🦯 View/Edit Notes 📱 Method summary 🗙 😽
CONDITIONING, Method: 'Default Conditioning (View/Edit Notes ) Method summary (View/Edit Notes ) Method summar	SEPARATION, Method: 'DNF-474-33 - HS NGS Fragment 1-6000	bp.mthds', Tray: Samp. tray 1, B, Gel: 1	🦯 View/Edit Notes 📱 Method summary 🗙 🕅
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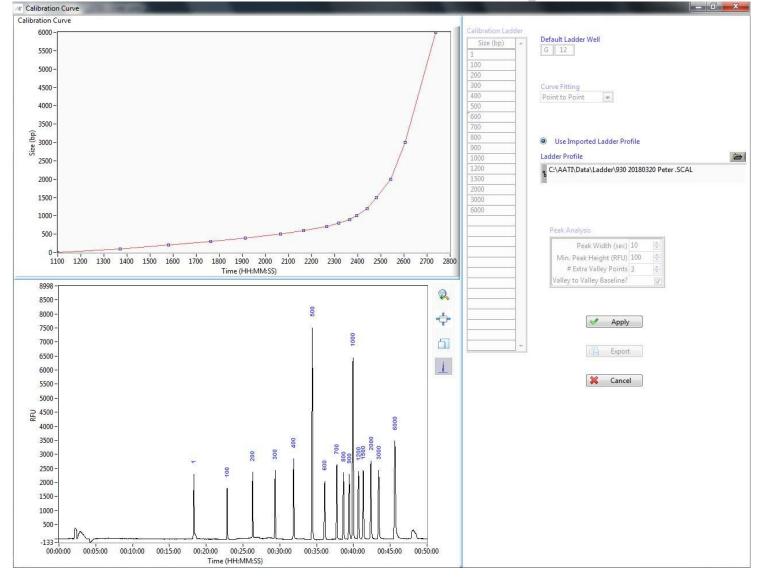
## V. Data Analysis

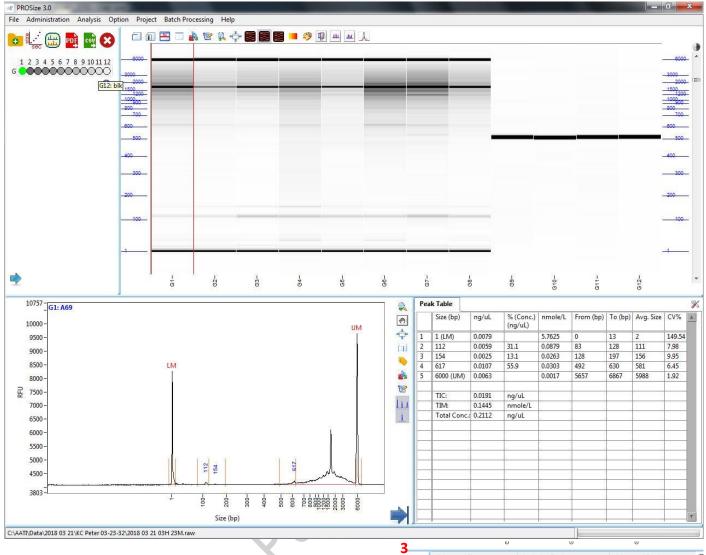
You can install *PROSize 3.0* on your own computer to analyze the data.

1. Open your run by clicking "File" – "Open File". Select the correct file and click "Open". The data is saved in ":C\AATI\Data\" by default according to date.



line. Right click on the peak to add or remove single peak. If the ladder is not ok, you can import ladder from a previous successful run.





Change the dilution factor if your dilution is not 12 (2 μl sample + 22 μl Diluent). It can be changed by clicking on × icon on the upper right corner of a peak table. Select "Quantification", change the dilution factor and press "Apply to selected" or "Apply to all".

2	Advanced Flag	Inclusion	Region	Advanced Settings	I
	Peak Analysis	Marker Analysis	Quantification	Smear Analysis	Flag
- -	_			1	
ī.		e Lower Marker		inal Conc. (ng/uL)	
	() Use	e Upper Marker	C	.5	
6	0	Ladder	D	ilution Factor	
	0	Ludder	1	2 ≑	
	<u>p</u>				
	Apply	to All		Apply to Selected	
	0			0	

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4. Select "Marker Analysis", change the Marker Information and press "Apply to selected" or "Apply to all". If the software hasn't placed the lower (LM) and upper marker(UM) correctly for a certain sample, right-click on the correct peak and choose "Set as lower marker" or "Set as upper marker".

Advanced Flag	Inclusion	n Region	Advanced Settings	
Peak Analysis	Marker Analysis	Quantification	Smear Analysis	Flag
Marker Peak	Analysis	Marker Informa	tion	_
Valley to Va	Width (sec) 5 ley Baseline? /alley Points 3	First Peak	> 2000 🔹 RFU	
Use Both Ma		Upper Marker Last Peak	> 500 🗣 RFU	

- 5. Change other parameters including the baseline ("Peak Analysis" - "Manual Baseline Setpoints" -"Start (min)" and "End (min)"; 12-48 for DNF474; 12-28 for DNF930), peak analysis and smear analysis.
- 6. Data can be exported in .csv 🗳 and .pdf 🖳 for The data is given in three different concentration TIC = total integrated concentration in ng/ $\mu$ L, total integrated molarity in nmole/L and total concentration in  $ng/\mu L$ . Be aware that based on application, you may want to use for example 7 rather than the total concentration.

	2 (*)	Advanced Flag		Inclusion Region			Advanced Settings	E
		Peak Analysis	Marker Analysis		Quantification		Smear Analysis	Flag
rmat.	÷		Start Size (bp	) End S	ize (bp)	Disp	ay Smear Range	
ns:	11		20	1500			$\bigcirc$	
TIM =			0	0				
$\Pi \mathbf{v} \mathbf{I} \equiv$			0	0				
	2		0	0				
			0	0				
your	TT V		0	0				
ΪC	1		0	0				
IC I			0	0		$\checkmark$		

7. Exit the program. Your changes are saved automatically. In case you want to return to the original raw data without any changes made by you, go to the corresponding folder to delete .ANAI and .PKS files.

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LM

Accept Change

Set As Lower Marker

Set As Upper Marker

Move Peak Start/End Points

Copy Image to Clipboard

Export Data to Clipboard

Marker Analysis

Peak Width (sec) 5

Min. Peak Height (RFU) 500

# Extra Valley Points 3

Filter Binomial

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Valley to Valley Baseline?

Filter Selec

# of Points 3

Export Data to Excel

Cancel

Add Peak

Split Peak

Merge Peaks

Delete Peak

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Advanced Setting

Smear Analysis

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Flag

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Inclusion Regio

Size (bp)

Quantification

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Analysis Regio

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Annual Baseline Setpoints

Start (min) End (min)

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10400

10200

10000

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Set Display Starting Time (min)

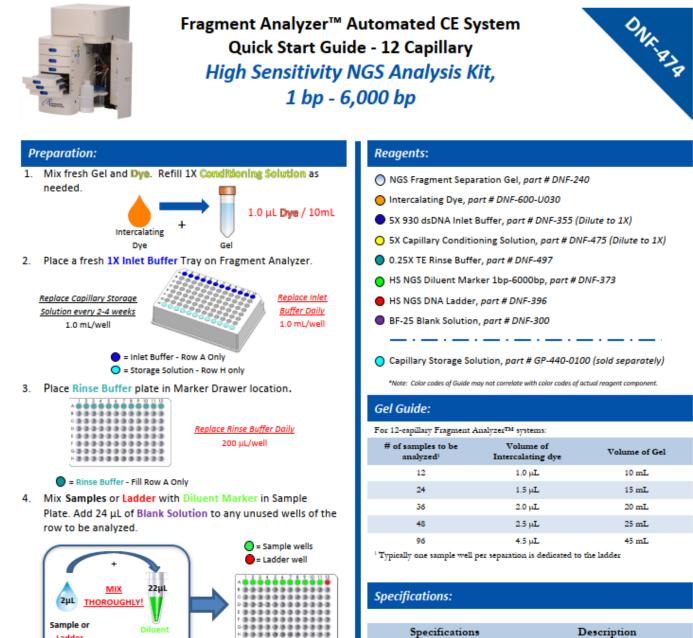
Advanced Flag

Peak Analysis

Peak Analysis

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12-Cap Unit - One Row Ladder Well 12

Specifications	Description
DNA Sizing Range	100 bp - 6,000 bp
Separation Resolution	100 bp - 2000 bp <u>&lt;</u> 5%; 2000 bp - 6000 bp <u>≤</u> 10%
DNA Sizing Accuracy	<u>+</u> 5% or better
DNA Sizing Precision <sup>1</sup>	2% CV
DNA Fragment Concentration Range <sup>1</sup>	$5~pg/\mu L$ to 500 $pg/\mu L$ input DNA
DNA Smear Concentration Range <sup>1</sup>	50 pg/µL to 5,000 pg/µL input DNA
DNA Quantification Accuracy <sup>4</sup>	<u>+</u> 25%
DNA Quantification Precision <sup>1</sup>	15% CV
Maximum DNA Concentration	500 pg/µL per fragment; 5 ng/µL total

1: Using DNA Fragment standards and DNA smears prepared in 1X TE buffer



Software:

Ladder

1. Select Tray and Row to run for 12-Cap.

Marker

- 2. Enter Sample ID and Tray ID (optional).
- 3. Select "Add to Queue", select the DNF-474-(22, 33 or 55) HS NGS Fragment 1-6000bp method from the Dropdown menu.
- 4. Enter Tray Name, Folder Prefix, and Notes (optional), Select OK to add Method to the Queue.
- Select > to Start the Separation.

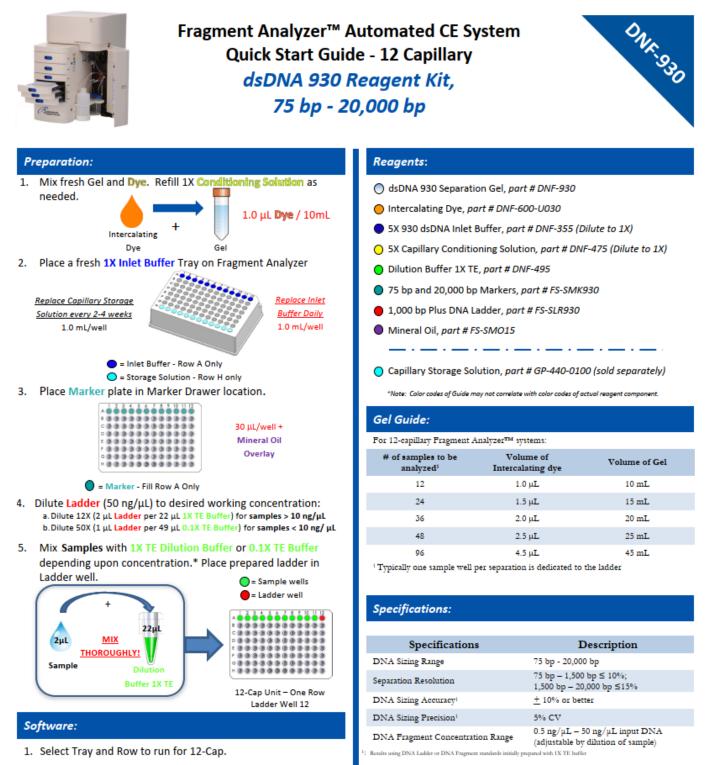
\*Please refer to the Kit User Manual for additional details.

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- 2. Enter Sample ID and Tray ID (optional).
- Select "Add to Queue", select the DNF-930-(22, 33 or 55)
  DNA 75-20,000bp method from the Dropdown menu.
- 4. Enter Tray Name, Folder Prefix, and Notes (optional), Select **OK** to add Method to the Queue.
- 5. Select ⊳ to Start the Separation.

\*Please refer to the Kit User Manual for additional details.

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