

## Fragment Analyzer SS NGS, HS NGS & RNA Analysis Kits

### INSTRUMENT

**Manufacturer:** Advanced Analytical Technologies  
**Distributor:** Kem-En-Tec Nordic ([info@kem-en-tec.dk](mailto:info@kem-en-tec.dk))  
**Technical support:** Klaus T. Nielsen ([kn@kem-en-tec.com](mailto:kn@kem-en-tec.com))

**Owner:** University of Tampere / LAS  
**Location:** ARVO E215  
**Responsible person(s):** Hanna Selin, tel. 050 1901 260, email: hanna.selin@uta.fi  
 (Heini Kallio, tel. 040 558 4354, email: heini.kallio@uta.fi)

**RESERVATIONS** (*billing according to reservations*) in AGENDO:

<https://next.cirklo.org/biomeditech/>

### ANALYSIS KITS:

- Standard Sensitivity **NGS** Fragment Analysis Kit, #DNF-473  
 -Sizing range: 1 – 6000 bp  
 -Input concentration range: 5 – 100 ng/μl
- High Sensitivity **NGS** Fragment Analysis Kit, #DNF-474  
 -Sizing range: 1 – 6000 bp  
 -Input concentration range: 50 – 5000 pg/μl
- Standard Sensitivity **RNA** Analysis Kit (15nt), #DNF-471  
 -For total RNA Analysis  
 -Input concentration range: 5 – 500 ng/μl
- *Genomic DNA 50 Kb Analysis Kit, #DNF-467 (SEPARATE PROTOCOL)*  
 -Sizing range: 75 – 50 000 bp  
 -Input concentration range: 25 – 250 ng/μl
- *CRISPR Discovery Gel Kit, #DNF-970 (SEPARATE PROTOCOL)*  
 -Sizing range: 1 – 6000 bp  
 -Input concentration range: 0,005 – 2 ng/μl

### REAGENTS:

Stored at +4 °C E218 cold room	Stored at -20°C E217 freezer room	Stored at -80 °C Telstar Igloo -80C freezer, shelf A	Stored at RT E215
Separation Gels	Intercalating Dye ( <i>same for all Fragment Analyzer Analysis Kits</i> )	RNA Ladder (2 μl aliquotes)	5x Capillary Conditioning Solution
1x & 5x Inlet Buffer			Milli-Q Water
Blank Solutions	Diluent Markers		Gel/Dye Mixture (at FA)
0.25x & 0.6x TE Rinse Buffers	SS & HS NGS Ladders (12 μl aliquots → 5 runs)		Capillary Storage Solution
1x dilution of Capillary Conditioning Solution			

- Reagents are stored in room E215 (RT), E217 freezer room or E218 cold room. Opened reagents and dilutions (*1x Capillary Cond. & 1x Inlet buffer*) are marked with opening date and/or "X".
- RNA Ladder is stored in Telstar Igloo -80 °C freezer at shelf A in front of the lab E215
- Please open a new reagent tube or bottle in order of the expiration dates and mark the opening date and/or "X" to the tubes
- Take the reagents to warm up to room temperature (RT) for 30 minutes prior to use except the **RNA Diluent Marker and RNA Ladder** which should be thawed **on ice**
- All reagents are harmless and can be discarded by pouring down the sink

**OTHER SUPPLIES** (*stored at the shelf or drawer under the instrument table or above the sink*):

- Capillary Storage Solution (*AATI #GP-440-0100-100/Kem-En-Tech*)
- Specified 96 Well Semi-Skirted PCR Plate (list of approved plates at Appendix A) for samples (drawers 1-3) and Rinse buffer (drawer M)
- 96-well DeepWell 1 mL Plate (*Fisherbrand #12-566-120/Kem-En-Tech*) (drawer W)
- BD Falcon 50 ml centrifuge tubes (*BD #352070, #734-0448/VWR*)
- Pipettes (Biohit mLine and 12-channel Thermo ClipTip)
- Electronic dispenser (Biohit) and dispenser tips (0.5/1.0/2.5 ml)
- Serum pipettes (*for discarding 1x Inlet Buffer from the 96 DeepWell 1 mL Plate in row A*) and serological 10 ml pipettes
- Microplate seals (*#4ti-0510/Biotop*)

**QUICK CHECK LIST** (for more instructions, see the specific sections)

1. Take the reagents to RT or on ice (RNA Diluent Marker and RNA ladder) at least 30 minutes prior to performing the run

From the cold room:

- 1x (or 5x) Inlet Buffer
- TE Rinse Buffer (*0.6x for SS NGS / 0.25x for HS NGS & RNA*)
- Separation Gel (in case of new gel/dye mixture is required)
- Blank solution if required (*BF-2000 for SS NGS / BF25 for HS NGS & RNA*)
- 1x Capillary Conditioning Solution

From the freezer room:

- Aliquoted SS NGS or HS NGS Ladder
- RNA / SS NGS / HS NGS Diluent Marker
- Intercalating dye (in case of new gel/dye mixture is required)
- Aliquoted RNA Ladder is stored at -80 °C and should be thawed and kept on ice

2. Turn on the computer and the instrument
3. Turn on the **Fragment Analyzer Software** (User ID: "Administrator", no password).
4. Check the **Waste Bottle** and the **Waste plate** at the Waste drawer (W) and empty if needed. Update the solution level to the software (*Utilities – Solution levels*).
5. If necessary, insert (or add) the **Gel/Dye mix** solution to the desired Gel fluid line (1 or 2) and update the solution level to the software (*Utilities – Solution levels*).
6. Check the level of **Capillary Conditioning Solution** and add or replace if necessary and update the solution level to the software (*Utilities – Solution levels*).
7. Replace the **1x Inlet Buffer** in the 96-well Midi plate at row A in the Buffer drawer (B) (once a day). Press "Park" – replace the buffer – place the plate back – press "Buffer"
8. Place the **0.6X** (*SS NGS Kit*) or **0.25X** (*HS NGS Kit and RNA Kit*) **Rinse buffer** into drawer M.
9. Prepare the sample plate and load into one of the three sample trays. If you place a plastic seal on the plate in order to spin the plate, **remember to remove the seal before running the plate to avoid capillary damage!**
  - Quick start guides are in the folder "Quick Start Guides" at the desktop.

**NOTE! WHEN USING THE INSTRUMENT FOR THE FIRST TIME, CONTACT THE PERSON(S) RESPONSIBLE FOR INTRODUCTION!**

## PROTOCOL

### 1. GEL/DYE MIX PREPARATION

- A gel/dye mix is valid for up to 2 weeks after preparation (*it has been noticed empirically that RNA gel/dye mixture is also valid for 2 weeks even though the manual states that it has to be prepared for every run*).

**NOTE!** For both NGS kits the Separation Gel is the same!

- If necessary, prepare a fresh mixture:
  - Bring the **Separation Gel** and **Intercalating Dye** (*same for all kits*) to RT prior to mixing.
  - Add an appropriate volume of Intercalating Dye to Separation Gel in a 50 mL tube according to the table below.
    - NOTE!** *When switching applications between RNA/NGS/gDNA kits at the certain Gel fluid line 1 or 2 you need to do 5 mL more of the mix due to priming – see the example for 12 samples at the table and the step 7.*

# of samples	Volume of Intercalating Dye	Volume of Separation Gel
12	1,0 µl (1,5 µl for priming)	10 mL (15 mL for priming)
24	1,5 µl	15 mL
36	2,0 µl	20 mL
48	2,5 µl	25 mL
60	3,0 µl	30 mL
72	3,5 µl	35 mL
84	4,0 µl	40 mL
96	4,5 µl	45 ml

- Mix by gently inverting the tube – do not vortex!
- Mark the date on the tube.
  - NOTE!** If there is still less than 2 weeks old mixture left at the instrument, a fresh gel/dye mixture can be mixed with the old one to achieve the required total amount of the mixture (*e.g. if there's still 5 mL of the mixture left, add 0,5 µl of Intercalating Dye and 5 mL Separation Gel to obtain required 10 mL for 12 samples*). Do not change the date
- Place the gel/dye mixture onto the instrument and insert into the desired **Gel fluid line** (1 or 2). Ensure the fluid line is positioned at the bottom of the conical tube.
- Update the solution levels in the Fragment Analyzer instrument control software. From the **Main Menu**, select **Utilities – Solution Levels**. A menu will be displayed to enter in the updated fluid levels
- PRIMING:** When switching applications between RNA/NGS/gDNA/CRISPR kits on the certain Gel fluid line 1 or 2, prime the fluid line after loading fresh gel/dye mix. From the **Main Menu** select **Utilities – Prime** – select the desired fluid line 1 or 2.
- Leave the gel/dye mixture in the instrument after the run.

## 2. CAPILLARY CONDITIONING (CC) SOLUTION PREPARATION

- Capillary Conditioning Solution is the same for all kits.
- Place the 1x CC Solution onto the instrument in the Conditioning Solution location in a 50 mL Falcon tube (*a typical 12-capillary experiment cycle consumes less than 4 mL but the instrument requires at least 10 mL in the tube*).
- Update the solution levels in the Fragment Analyzer instrument control software. From the **Main Menu**, select **Utilities – Solution Levels**. A menu will be displayed to enter in the updated fluid levels.
- 1x CC Solution should be added to the system as use demands or if it hasn't been changed within 2 weeks.
  - NOTE! If there is less than 2 weeks old 1x CC Solution left at the instrument, new 1x CC Solution can be mixed into the same tube to achieve the required total amount (*e.g. if there's still 5 mL of the 1x CC solution left, add 5 mL of new 1x CC solution to obtain required 10 mL for 12 samples*). Do not change the date on the tube
- If necessary, prepare the **1x** Capillary Conditioning Solution to a 250 mL glass bottle by adding 50 mL of the **5x** Capillary Conditioning Solution to 200 mL of Milli-Q water. Mix by gently inverting the bottle. Mark the date and your initials. 1x CC Solution can be used up to **2 weeks** after preparation when stored in the instrument or **3 months** when stored at +4 °C. Store most of the 1x buffer at +4 °C and leave an appropriate aliquot in the instrument.

## 3. INLET BUFFER PREPARATION

- Inlet Buffer is the same for all kits. Bring the 1x or 5x Inlet Buffer to RT prior mixing and use.
- 1x Inlet Buffer in the 96-well Deep Well Plate in the Buffer drawer (B) **has to be replaced daily** (in case you are the first user of the day):
  1. From the **Main Menu** press "**Park**"-icon to bring the plate to the tray B.
  2. Remove the old buffer from the **row A** by pipetting it to the sink with a serum pipette. Add exactly 1 ml of 1x Inlet Buffer to every well at row A in the 96 DeepWell Plate. Do not overfill!
    - **Note!** *The Storage Solution is at the same plate at row H and is replaced only once in a month, so empty only the row A!*
  3. Place the plate back to the tray B and press "**Buffer**".
- If necessary, prepare the **1x Inlet Buffer** to a 250 mL glass bottle by adding 50 mL of the **5x Inlet Buffer** to 200 mL of Milli-Q water. Mix by gently inverting the bottle. Bring the 5x Inlet Buffer to RT prior diluting. Mark the date and your initials. 1x buffer can be used up to **3 months** after preparation when stored at +4 °C.
- **Replace the 96-well Deep Well Plate and Capillary Storage solution monthly.** When taking a new Deep Well Plate, pipette exactly 1.1 ml of Capillary Storage Solution to the wells at **row H**. Mark the date to the plate. Row H is used for the store location and the array moves to this position at the end of the experimental sequence.

#### 4. INSTRUMENT PREPARATION (waste containers and rinse buffer plate)

- Check the fluid level of the waste bottle and waste tray (drawer W) and empty as needed. Update the waste bottle solution level to the software.
- Prepare a new 96-well plate filled with **100 µl/well** of **0.6x TE Rinse Buffer** with **SS NGS Kit** or **0.25x TE Rinse Buffer** with **HS NGS Kit** using the electronic dispenser pipette at **row A** daily. Use **200 µl/well** of **0.25x TE Rinse Buffer** with **SS RNA Kit**. If necessary, spin the plate shortly to reduce air bubbles.
- Use only specified semi-skirted 96-well PCR plates (Appendix A) in the instrument. Using wrong kind of plates may lead to capillary damage!
- Place the prepared **Rinse Buffer plate** into drawer “M”. Ensure the plate is loaded with well A1 towards the back left on the tray.

#### 5. SAMPLE PLATE PREPARATION

- Allow the **NGS Diluent Marker (DM)** Solution to warm up to RT prior to use or thaw the **RNA Diluent Marker (DM)** Solution on ice.
- Allow the **HS NGS** or **SS NGS Ladder** (from the kit to be used) to warm up to RT prior to use.
- **RNA Ladder** is in 3 µl aliquots in -80 °C. Spin the tube after thawing to ensure liquid is at the bottom of the tube. **Both RNA samples and RNA Ladder have to be heat-denatured at 70 °C for 2 min, cooled immediately to +4 °C and kept on ice before use.**
- Use only specified semi-skirted 96-well PCR plates (Appendix A) in the instrument. Using wrong kind of plates may lead to capillary damage!
- Check the total input sample concentration from the User Guide of the kit to be used.
- Run the samples immediately once prepared or cover the plate with a cover film, store the plate at +4 °C and run ASAP. Alternatively, to prevent evaporation, place a mineral oil overlay on each sample (50 µl/well).
  1. Pipette **22 µl of the DM Solution** to each well in a row that is to contain **sample** or **Ladder** with an electronic dispenser pipette.
  2. Fill any unused wells within the row with **24 µl/well of Blank Solution** (*BF-2000 for SS NGS / BF25 for HS NGS & RNA*).
  3. Pipette **2 µl of Ladder** into the well 12 containing 22 µl DM Solution in every row to be analyzed.
  4. Pipette **2 µl of each sample** into the wells 1-11 containing 22 µl DM Solution. (*You can also use only 1 µl of each sample + 23 µl DM Solution if your samples are precious, just remember to change the dilution factor when starting to process the data after the analysis. However, this is not recommended for RNA assay.*)

5. **Mix well** by either swirling the pipette tip while pipetting up/down or using the 12-channel pipette set to 20 µl for mixing.
6. Check that there are no air bubbles trapped in the bottom of the wells. If necessary, remove the bubbles by either centrifuging the plate shortly in a mini plate spinner, tapping it against the table or using a clean pipette tip.
7. Place the Sample plate in one of the three sample trays (drawers 1, 2 and 3). Load (or create) the experimental method.

## 6. PERFORMING AN EXPERIMENT

1. To set up an experiment, from the Main Menu of the Fragment Analyzer instrument control software, select the **Operation** tab.
2. Select the sample tray location (1, 2 or 3) by left clicking the **Sample Tray #** dropdown or by clicking the appropriate **sample plate tab** and choosing the appropriate location.
3. Left click a well of the desired sample plate row. Enter the sample name if desired into the respective **Sample ID** cell by left clicking the cell and typing the name or import the sample information from .txt or .csv file by selecting the **Load from File...** -option.
4. Under the **Run Selected Group** field press **Add to queue**. The **Separation Setup** pop-up form will appear to the screen:
  - From the **Method** dropdown menu select the right method:
    - *DNF-473-33 – SS NGS Fragment 1-6000bp.mthds*
    - *DNF-474-33 – HS NGS Fragment 1-6000bp.mthds*
    - *DNF-471-33 – SS Total RNA 15nt.mthds*
  - Select the **Gel** line (1 or 2)
  - The **Tray Name** can be entered if it's necessary to identify the sample plate.
  - The **Folder Prefix** can be entered to amend the folder name for the results
  - The results can be copied to another directory location by checking the **Copy Results** box and selecting the desired **Copy Path**
  - Any **Notes** can be entered regarding the experiment
5. Once all information has been entered, press **OK** to add the method to queue. After a row (or tray) has been added to the queue, the method(s) will be listed on the main screen under the **Method Queue**. Repeat the steps 4-5 for any remaining sample rows. Additional experiments can be programmed and added to the Method Queue at any time while the instrument is running.
6. Once the experiment has been loaded onto the queue, the method can be viewed or edited by pressing the **Method Summary** field.
7. Prior to starting the experiment, verify all trays (buffer/storage, rinse, waste, sample, etc.) have been loaded into their respective drawer locations!
8. Press the **Play** icon to start. To clear the run queue of all loaded runs, press the **Clear** icon.

## 7. AFTER COMPLETION OF THE EXPERIMENT(S)

- After completion of the last queued experiment, the instrument stage will automatically move to the Store location.
- **Throw away both the Sample plate and the Rinse Buffer plate** (from drawer M) and **empty and rinse the waste tray** (from drawer W). Update the waste solution level in the Fragment Analyzer instrument control software. From the *Main Menu*, select *Utilities – Solution Levels*. A menu will be displayed to enter in the updated fluid levels.
- **Turn off the instrument and the computer.**

## 8. PROCESSING EXPERIMENTAL DATA

The data is viewed and processed using PROSize 2.0 software. You can use PROSize on Fragment Analyzer's computer or on your own computer. If you want to install the PROSize program on your own computer, ask Heini Kallio ([heini.kallio@uta.fi](mailto:heini.kallio@uta.fi)) to give you the PROSize installer.

1. Open your run by clicking File – Open File. Select the correct file and click 'Open'.
2. **Look at the ladder first.** In principle, as long as the ladder looks good, the results are reliable (refer to the user guides to see the representative ladder results). If the ladder is not ok, you can import ladder from a previous successful run. Select Analysis – Show size calibration. Choose 'Export' and save the ladder to your folder. Then open the run where the ladder was not optimal. Select Analysis – Show size calibration. Select 'Use imported ladder profile' and choose the saved ladder from your folder.
3. **Remember to change the dilution factor if your dilution is not 12** (2 µl sample + 22 µl Diluent Marker Solution). It can be changed by clicking a tool icon on the upper right corner of a peak table that says 'Set individual parameters'. Select 'Quantification', change the dilution factor and press 'Apply to selected' or 'Apply to all'.
4. **If the software hasn't placed the lower and upper marker correctly for a certain sample, you can manually correct this** (for example, some small contaminants may cause the software to interpret the contaminant as a lower marker). Select the individual sample that has the incorrect peak(s) called as markers and right-click on top of the correct peak(s). Choose 'Set as lower marker' or 'Set as upper marker'.
5. **The data is given in three different concentrations:** TIC = total integrated concentration in ng/µL, TIM = total integrated molarity in nmole/L and total concentration in ng/µL. Be aware that based on your application, you may want to use for example TIC rather than the total concentration.
6. **If you want to analyze peaks with certain sizes, go to 'Set individual parameters' and select 'Smear analysis'.** Determine the start and end size and press 'Apply to selected' or 'Apply to all'.
7. **Exit the program by selecting File – Exit. There is no need to save your changes. The changes are automatically saved when you exit the program.** In case you want to return to the original raw data without any changes made by you, go to drive C – AATI – Data and delete .ANAI and .PKS files from



your run's folder. This will delete your changes and you can start analyzing the raw data from the beginning.

8. **In case of technical problems, contact Klaus T. Nielsen ([kn@kem-en-tec.com](mailto:kn@kem-en-tec.com))**. It is advisable to zip your results and send them to Klaus; Select Help – Zip opened data file.

## Appendix A

### List of approved Sample/Marker PCR Plates (semi-skirted)

#### Approved Vendor/Part Number; Description

- VWR # 83007-374; VWR® 96-Well PCR Plates, Half-Skirted Plates, Natural
- VWR # 89049-178; VWR® 96-Well Thermal Cycling Plate
- Eppendorf # 951020303 (various colors); Eppendorf\* 96-Well twin.tec\* PCR Plates, Semiskirted
- MidSci Pryme # AVRT1; Pryme PCR Ergonomic Plates, 96x0.2ml, Semi-Skirted, Natural
- BioRad Hard-Shell # HSS-9601; Hard-Shell® Full-Height 96-Well Semi-Skirted PCR Plates
- Greiner Bio-One # 652280; 96W PCR Microplate, Polypropylene, Half-Skirt, Natural, No Lid
- 4titude Framestar # 4ti-0900, -0950, -0770/C; FrameStar® 96 semi-skirted
- Scientific Specialty # 3450-00; 96-Well "Semi Skirt" UltraFlux® PCR Plate
- Neptune # 3742.X; Semi-Skirted 96-Well PCR Plates