

# Core Facility Genomics

News Flash – December 2023

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## HPC Genomics project

The HPC Genomics project, spearheaded by the Genome Analysis department, offers AUMC colleagues the valuable opportunity to leverage our High-Performance Computing (HPC) cluster. HPC, short for High-Performance Computing, empowers users on our cluster to execute resource-intensive software and handle large datasets.

To facilitate collaboration and knowledge sharing, we host monthly HPC user meetings every third Thursday of the month. During these sessions, users can pose questions, engage in discussions on specific topics, or request assistance with software installations. For comprehensive guidance, we've developed a wiki accessible to everyone. This resource walks users through the essential steps of utilizing the cluster; you can explore it at <https://hg-aumc.gitlab.io/genome-analysis/hpc-wiki/>.

Our dedicated team, comprised of Daoud, Rick, Adri, and Reinier, collectively manages a team forum. This platform serves as a hub for supporting members of the HPC Genomics community, ensuring that they receive the assistance they need.

For more information about the HPC cluster you can watch our latest (19<sup>th</sup>) CFG User Meeting on our [website](#).

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## 20th Core Facility Genomics (CFG) user webinar

The topic of the next webinar on the **12<sup>th</sup> of December** is:

***“Nanopore”***

Program:

- 1) Desiree de Bruin (MSc Forensic Science), Dept. of Human Genetics, Genome Diagnostic laboratory, Epigenetics of disease.  
Title: “Nanopore Sequencing: Towards an All-In-One Forensic DNA Analysis Technology”
- 2) Dr Norbert Moldovan, Dept. of Pathology, Cancer Center Amsterdam.  
Title: “Ouro-seq: Full-length circular RNA characterization in liquid biopsies and self-collected samples of ovarian cancer patients”

Norbert Moldovan is a postdoc computational biologist affiliated with the Department of Pathology, Cancer Center Amsterdam. His research has centered around the innovative utilization of cell-free DNA fragmentomic features for cancer detection. He developed bioinformatic tools for long- and short-read genomic and transcriptomic data analysis. Norbert recently secured the ZonMw Off Road grant, to explore the usability of the Nanopore sequencing technology for full-length circular RNA characterization in liquid biopsies and self-collected samples.

Find the [link](#) to this meeting and records of our previous meetings at [the CFG website](#). If you want to be on our CFG User meeting list to be invited for our future meetings, please email the [CFG](#).

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## CFG costs

The Core Facility Genomics (CFG) has run a European tender for sequencing in 2020. Three sequencing partners were contracted as the outcome of this tender (GenomeScan B.V., Radboud and UMC Utrecht). Part of this tender agreement is a yearly request for bids for the regular (weekly) sequencing from all 3 partners. From January 2024 this will change to the NovaSeq Xplus at the UMC Utrecht.

Last week the information has been send out. Did you missed it or do you have questions? [Please let us know](#).

## Plasmidsaurus

The CFG is hosting a dropbox at location AMC for Plasmidsaurus samples. All details of using Plasmidsaurus go to <https://www.plasmidsaurus.com>. If you want to use the CFG Dropbox at location AMC, please [contact the CFG](#) or check [the document](#) in K2 iProva. Orders are Shipped Every Tuesday at 12 Noon Sharp!

This free service runs entirely on volunteers. Hence, when dropping off an order, a voluntary tasty donation for coffee/tea time is highly appreciated.

## 4200 TapeStation System

Since October, the TapeStation 2200 on location VUmc has been replaced by the TapeStation 4200. That makes that at the CFG there are two 4200 TapeStation Systems available and at both location large numbers of samples can be measured by the CFG. The **VUMC system** is located at the CFG in the Medical Faculty building. The **AMC system** is located at G2-105-3 in the AMC.



The advantage of the 4200 TapeStation System compared to the 2200 TapeStation System is that there is less loss of tape lanes and that more samples can be measured in a run. The 4200 TapeStation System makes it possible to quickly determine the QC of the DNA/RNA from 1-96 samples with wide range of ScreenTape applications, including assays for genomic and cell-free DNA.

Interested? We love to show you the system and help you on your way. Please contact us at [cfg@amsterdamumc.nl](mailto:cfg@amsterdamumc.nl).

## Update documents

The CFG updated a few CFG sample user submission procedures.

At first the [NGS Sequencing submission form](#). In this form the Analysis part is optimized. In the newest version you need to make a choice to either 'No analysis, get fastq files', or choose an analysis and pipeline appropriate for the data.

Also the submission forms automatically will be send to [cfg@amsterdamumc.nl](mailto:cfg@amsterdamumc.nl) when using the 'Save & E-mail submission form' button. From now on all NGS CFG Sequencing communication will be done via [cfg@amsterdamumc.nl](mailto:cfg@amsterdamumc.nl). The month December will be considered a transition month were all CFG users will be informed.

Because of the changes mentioned above, the related documents are updated too:

[NGS Sequencing submission procedure](#)

[CFG: Gebruik NGS Sequencing submission form](#)

The second major update is for the [DNA/RNA sample user submission procedure](#). This was needed to combine the different isolations the CFG does on both locations. And to make a clear sample submission form that needs to be used for submission of projects: [CFG: DNA- and RNA-isolation, sample submission form](#).

Another update we would like to point out is the [Nanopore submission form](#). The option to choose for the PromethION is added. PromethION technology allows you to sequence (direct and long read) whole genomes cost efficiently.

Please note that *adaptive sampling* (targeted sequencing) is now available with both PromethION and MinION technology. The new type of flowcells (double pore, R10), in combination with PromethION's output (MinION ~ 50 Gb vs. PromethION ~ 290 Gb) increases sequence accuracy tremendously as well. R10 flowcells are available for both MinION and PromethION applications.

For **all** users it is necessary that they use the most up-to-date version of the documents. They can be found in [K2 iProva](#) for internal users and at the [CFG website](#) for external users.

20th

Core Facility Genomics (CFG)

user webinar

12th of December 16:00-17:00

"Nanopore"

To join: [Teams link](#)

For more info:

[cfg@amsterdamumc.nl](mailto:cfg@amsterdamumc.nl)