



Free e-seminars

Next-Generation Sequencing

Join our e-seminars to learn how you can optimize your Next Generation Sequencing (NGS) workflow with Agilent offering. You will have the opportunity to listen and speak with our experts.

1. **Advances in Target Enrichment Methods: Update on the Agilent SureSelect Target Enrichment Portfolio as Presented at AGBT**

Date and time: **Thursday, March 4th, 2010 – 5 pm** CET (Paris time)
Speaker: Emily LEPROUST - Director Applications and Chemistry R&D
Registration: <https://agilenteseminar-emea.webex.com/agilenteseminar-emea/onstage/g.php?t=a&d=842767631>

Whether you want to hear the latest news about the SureSelect Target Enrichment System, or whether you're new to the field of target enrichment, this eSeminar is a unique opportunity for you to interact live with Agilent R&D. After a brief introduction to the Agilent SureSelect Target Enrichment platform, we will give an overview of existing products, with a focus on human exon capture, discuss latest advances and give you an outlook into future developments.

2. **Next Generation Sequencing: Improved Library Quantification with Agilent Technologies**

Date and time: **Thursday March 11th, 2010 – 11 am** CET (Paris time)
Speaker: David HOWELLS, Field Application Engineer
Registration: <https://agilenteseminar-emea.webex.com/agilenteseminar-emea/onstage/g.php?t=a&d=841545004>

Next-generation DNA sequencing workflows require an accurate quantification of the DNA molecules to be sequenced for optimal performance of the instrument. Here, we demonstrate the use of qPCR for quantification of DNA libraries used in next-generation sequencing. We find that the quantification data generated with the Bioanalyzer and qPCR are comparable for high quality library preparations. We also show that qPCR quantification may allow improvements to current NGS workflows, including reducing the amount of library DNA required, increasing the accuracy in quantifying amplifiable DNA, and avoiding amplification bias by reducing or eliminating the need to amplify DNA before sequencing.

3. **Implementing quality control in the next-generation sequencing workflow with the Agilent 2100 Bioanalyzer**

Date and time: **Thursday March 18th, 2010 – 11 am** CET (Paris time)
Speaker: Ruediger SALOWSKY, Product Manager Bioanalyzer - RNA/DNA Solutions
Registration: <https://agilenteseminar-emea.webex.com/agilenteseminar-emea/onstage/g.php?t=a&d=847185868>

The next-generation sequencing (NGS) workflow requires the implementation of quality control procedures to increase workflow efficiency. It is imperative that the quality of the RNA or DNA starting material as well as DNA libraries are evaluated from the start. Difficulties can often arise when only fragmented or low concentrated starting material is available. Furthermore, most NGS sample preparation protocols require PCR amplification to generate DNA libraries prior to sequencing. PCR artifacts may contribute to sequencing bias, ultimately affecting results.

Here we discuss how the Agilent 2100 Bioanalyzer helps to fulfill NGS sample prep QC criteria by ensuring the quality of RNA and DNA starting material and genomic libraries.

Each e-seminar will last about 1 hour. Prior registration is required to attend.
For more information, you can also contact your Agilent Sales Representative:
<http://www.agilent.com/chem/contactus>

