Determination of dsDNA in purified solutions

UV-spectrophotometric direct measurement at 260 nm

Introduction

The quantification of DNA in solutions is an important application in bioanalytics. In purified DNA solutions, for example, their assay can be relatively easily and swiftly determined by spectrophotometric measurement of the optical density (absorption) at the 260 nm wavelength.

At this wavelength, DNA – both, single-stranded (ssDNA) as well as double-stranded (dsDNA) - and RNA exhibit their absorption maximum. Depending on the DNA concentration, the absorption/optical density increases linearly in an absorption spectrum from 0.1-1.5 Abs. Following the Beer-Lambert law, specific factors can be used to draw conclusions regarding the concentration of ssDNA, dsDNA, and RNA in the sample. These factors are calculated from the respective specific absorption coefficients.

At an OD_{260} value of 1 and an optical path length of 10 mm, the following factors are calculated:

- ssDNA 33 µg/mL
- dsDNA 50 µg/mL
- ssRNA 40 µg/mL

DNA purity

In many cases, DNA solutions are contaminated with proteins or organic compounds that have been used to purify the DNA.

One advantage of the spectrophotometric method is that in addition to quantifying the DNA content it also allows statements about the purity of the DNA.

Proteins, for example, absorb light at a wavelength of 280 nm. If the solution contains proteins, the optical density at the 280 nm wavelength rises. The ratio of the absorption values of 260 nm to 280 nm can be used to estimate the purity of the solution. In pure DNA solutions, the reference value for the OD260/OD280 ratio is 1.8, for pure RNA solutions the reference value is 2.0.



When the measured value is lower, it can be assumed that proteins are present in the solution.

Besides the OD_{260}/OD_{280} ratio, the c ratio is also frequently calculated. At the 230 nm wavelength, organic compounds absorb such as carbohydrates, guanidine and phenol, which is frequently used as an extraction agent. Their absorption at 230 nm produces a reduction in the OD_{260}/OD_{230} ratio. As with the OD_{260}/OD_{280} ratio, a reference value of 1.8 applies for DNA solutions and one of 2.0 for RNA solutions^[1].

Experimental

This Application Note describes the quantification of dsDNA in samples. The analysis is quick and easy. The method is preprogrammed on the corresponding Spectroquant[®] Prove 300 and Spectroquant[®] Prove 600 photometers with firmware version 1.5 or above.

Separate application notes are available for ssDNA and RNA.

Method

The optical density OD (absorption) is measured at 230, 260 and 280 nm. The dsDNA concentration is calculated on basis of the OD_{260} value. The ratios OD_{260}/OD_{280} and OD_{260}/OD_{230} allow statements about the purity of the DNA-solution.



Measuring range

• 5-37500 µg/mL dsDNA (method no. 2512)

Sample material

• Purified dsDNA solutions

Reagents, Instruments and Materials:

Instruments

For the dsDNA measurement one of the following Spectroquant $\ensuremath{^{\textcircled{\$}}}$ photometers is necessary:

Cat. No.	Product	
1.730 2 8	Spectroquant [®] UV/VIS Spectrophotometer Prove 600 plus	
1.73027	Spectroquant [®] UV/VIS Spectrophotometer Prove 300 plus	
Also first generation Prove instruments are compatible and		

Also first generation Prove instruments are compatible and preprogrammed with this method.

Software for data maintenance

The Spectroquant[®] Prove Connect to LIMS software package provides an easy way to transfer your data into a preexisting LIMS system. This software can be purchased under:

Cat. No.	Product
Y11086	Prove Connect to LIMS

Materials

Cat. No.	Product	
100784	Rectangular quartz cell 10 mm	
Z600288	500288 Semi-micro rectangular quartz cell 10 mm*	

*Due to the optical characteristics of the Prove Spectrophotometers the use of 10 mm micro cells is not possible. Plus, due to the automatic cell detection of the Prove instruments it is important to use semi-micro cells with complete side walls.

Analytical approach

Sample preparation

- Homogenize samples by swirling carefully
- Dilute the sample, if necessary. For dsDNA concentrations > 50 µg/mL a dilution is necessary. The following table gives suggestions how to dilute the sample depending on the estimated dsDNA concentration. Please note that the minimum sample volume is 0.6 mL for the 10 mm semi-micro cell or 1.5 mL for the 10 mm cell. The maximal possible sample dilution factor is 500 (dilution 1+499). It is recommended to dilute with the buffer used as sample solvent. The optimal buffer has a pH value of 7.5–8.5 and a low salt content, e.g. TE-buffer. The usage of buffers ensures a higher reproducibility in comparison to water due to a stable pH value, while a low salt content ensures fewer interferences during measurement.^[1, 2]

Estimated dsDNA concentration [µg/mL]	Dilution	Exemplary dilution procedure
5-50	-	Use the sample undiluted
50 -1000	1+19	Pipette 0.250 mL sample into test
		tube and add 4.75 mL solvent.
1000-5000	1+99	Pipette 0.050 mL sample into test
		tube and add 4.95 mL solvent.
5000-37500	1+499	Pipette 0.010 mL sample into test
		tube and add 4.99 mL solvent.

Note

Depending on the DNA concentration, the absorption/ optical density increases linearly in an absorption range from 0.1-1.5 Abs at 260 nm. The instrument checks automatically if the measured absorbance of the sample is in this range. If the absorbance is higher than 1.5 Abs a message appears "Condition not met – higher dilution necessary". If the absorbance is below 0.1 Abs, no result will be displayed, the instrument shows "---" instead of a result.

Preparing the measurement solutions

Blank for zero adjustment

- Blank for zero adjustment
- For zero adjustment use the sample solvent (e.g. used buffer).

Measurement sample

• For the measurement sample use the prepared sample solution.

Measurement

- Open the method list (<Methods>) and select method No. 2512 "dsDNA".
- For each measurement series, a zero adjustment is required. It is recommended to use the same cell for zero adjustment and for sample measurement. The zeroing procedure for the measurement series is automatically prompted by the instrument. For zero adjustment fill the 10-mm rectangular quartz cell with the solvent used for dilution. After prompting, place the filled rectangular quartz cell in the cell compartment, the zero adjustment is executed automatically. Confirm the implementation of zero adjustment with **"OK"**. The zero adjustment is valid for the entire measurement series.
- The sample dilution must be entered. An input mask pops up. Enter the dilution in the form 1+x and tap <OK> to confirm.
- Fill the measurement sample into the same or a matched 10-mm rectangular quartz cell and insert the cell into the cell compartment. The measurement starts automatically.
- Tap **<OK>** to confirm.
- Read off the results from the display.

Results

The following results are given by the instrument:

- dsDNA concentration in µg/mL
- OD260/OD280 ratio
- OD260/OD230 ratio
- Optical densities (absorptions) at 230, 260 and 280 nm

Data transfer Prove spectrophotometers

After measurement transfer the values measured on the Prove spectrophotometer using Prove Connect to LIMS.

Adjustments

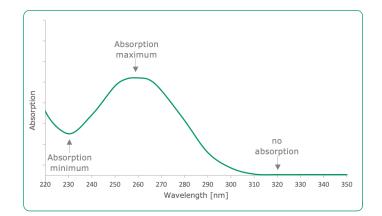
The preprogrammed dsDNA factor of 50 may differ under given circumstances from the actual factor. This is because the factor is dependent on the content of the nucleic bases and correspondingly may differ from one DNA sample to the next. For the case that the exact dsDNA factor is known and the objective is to enhance the accuracy of the measurement, it is possible to adapt the dsDNA factor in the method: Select method 2512, close the input mask by pressing "X". Press "Settings" and select "Factors" from the list.

Tap on the entry field "dsDNA Factor", enter the corrected dsDNA factor, and confirm with "OK".

Interferences

As described above proteins or organic substances can interfere with the measurement. By measuring the OD_{260}/OD_{280} and OD_{260}/OD_{230} ratios it can be checked whether any such substances are present in the sample. In case of doubt run a spectrum from 230–320 nm. Pure DNA solutions should have an absorption maximum at 260 nm and an absorption minimum at ca. 230 nm. Moreover, the spectrum should show no absorption at 320 nm.

Another substance that interferes the analysis is RNA, which absorption spectrum is like that of DNA.



Conclusion

The measurement of the optical density at 260 nm is a fast and easy way to quantify the dsDNA content of your sample. By measuring the OD260/OD280 and OD260/OD230 ratios it can be checked if the sample is contaminated with proteins and other organic compounds.

The method is preprogrammed in the Spectroquant[®] Prove 300 and 600, so there is no need for a manual calculation of the results. The results can be read of directly from the instrument display.

For more information visit, SigmaAldrich.com/photometry

References

- R. E. Farell, RNA Methodologies: Laboratory Guide for Isolation and Characterization, 5. Edition, Elsevier, 2017.
- Oxford Gene Technology, Understanding and measuring variations in DNA sample quality, 08/2011.

To place an order or receive technical assistance

 In Europe, please call Customer Service:

 France:
 0825
 045
 645
 S

 Germany:
 069
 86798021
 S
 Italy:
 848
 845
 645
 U

z. Spain: 901 516 645 Option 1 Switzerland: 0848 645 645 United Kingdom: 0870 900 4645

For other countries across Europe, please call: +44 (0) 115 943 0840 Or visit: **MerckMillipore.com/offices** For Technical Service visit: **MerckMillipore.com/techservice**

MerckMillipore.com

© 2021 Merck KGaA, Darmstadt, Germany and/or its affiliates. All Rights Reserved. Merck, Milli-Q, Millipore, Supelco, Sigma-Aldrich, SAFC, Bioreliance, ProSep, Fractogel, Eshmuno, Chromabolt and the vibrant M are trademarks of Merck KGaA, Darmstadt, Germany or its affiliates. All other trademarks are the property of their respective owners. Detailed information on trademarks is available via publicly accessible resources. Merck KGaA Frankfurter Strasse 250 64293 Darmstadt, Germany



MK_AN8074EN Ver. 1.0 36287 01/2024